Development of Models to Assess Effects of Water-Level Fluctuations on Reproductive Success of Common Loons

Project Completion Report to the International Joint Commission
USGS Project Number 11EMNB0000004
IJC Project 1042100753

Steve Gutreuter[1,3], Steve Windels[2] and Ryan Maki[2]

[1]U.S. Geological Survey
Upper Midwest Environmental Sciences Center
2630 Fanta Reed Road
La Crosse, Wisconsin 54603

[2]U.S. National Park Service
Voyageurs National Park
360 Highway 11 East
International Falls, Minnesota 56649

[3]Present address: Roswell, Georgia
sgutreuter@gmail.com

December 10, 2013

U.S. Department of the Interior
U.S. Geological Survey

Contents

Executive Summary

Effects of Water-Level Fluctuations on Reproductive Success

Appendices

Appendix A. Estimators of Water-Level Extremes

Appendix B. Hierarchical Bayesian Models

Appendix C. Rule Curve Evaluation

Executive Summary

1.1 Problem Description

The objectives of this project were to develop and test statistical models to quantify any effects of water-level fluctuation on reproductive success of common loons (*Gavia immer*; Fig. 1.1) in Minnesota lakes, and then use the best-performing model to quantify any observable effects of the 2000 Rule Curves on loons of Rainy Lake and the Namakan Reservoir complex. Reproductive success was defined as the number of chicks per nesting pair that survived through fledging (the onset of flight).

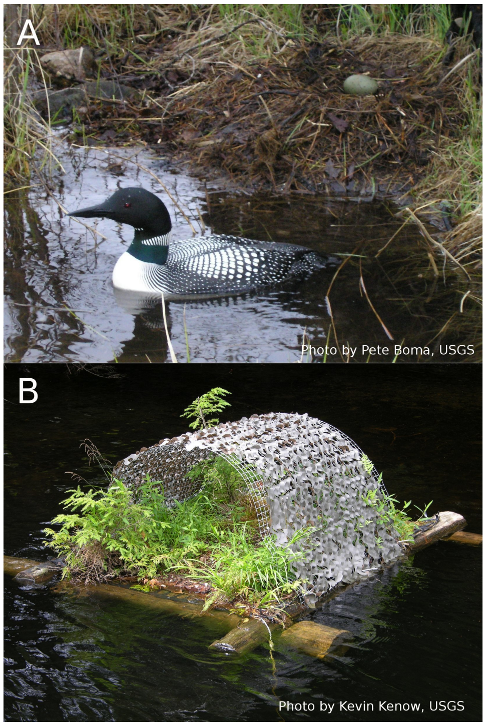

Photo by Pete Boma, USGS

Photo by Kevin Kenow, USGS

Figure 1.1. A. Adult loon with a single egg in a nest. Nests are placed along shorelines, and may be vulnerable to flooding. B. Nesting raft with canopy to conceal eggs and chicks from predators.

The water-levels in Rainy Lake and the Namakan Reservoir complex (Namakan, Kabetogama, Crane, Sand Point and Little Vermilion Lakes) are regulated by a hydropower dam between International Falls, MN and Fort Francis, ON, and a secondary pair of dams at Kettle and Squirrel Falls which separate Rainy Lake from the Namakan Reservoir complex. From 1970 through 1999, dam operations (1970 Rule Curves; Fig. 1.2) reduced the amplitude of water-level fluctuations in Rainy Lake and increased the amplitude in the Namakan Reservoir complex relative to natural conditions. The 2000 Rule Curves primarily reduced the amplitude in the Namakan Reservoir complex.

The common loon is the Provincial Bird of Ontario and the State Bird of Minnesota. Loons are highly territorial and actively compete for both nesting and feeding sites (Paruk, 1999). Loons typically nest along shorelines of lakes and rivers, preferentially near drop-offs and on sheltered sides of islands or floating bogs (McIntyre and Barr, 1997). Because common

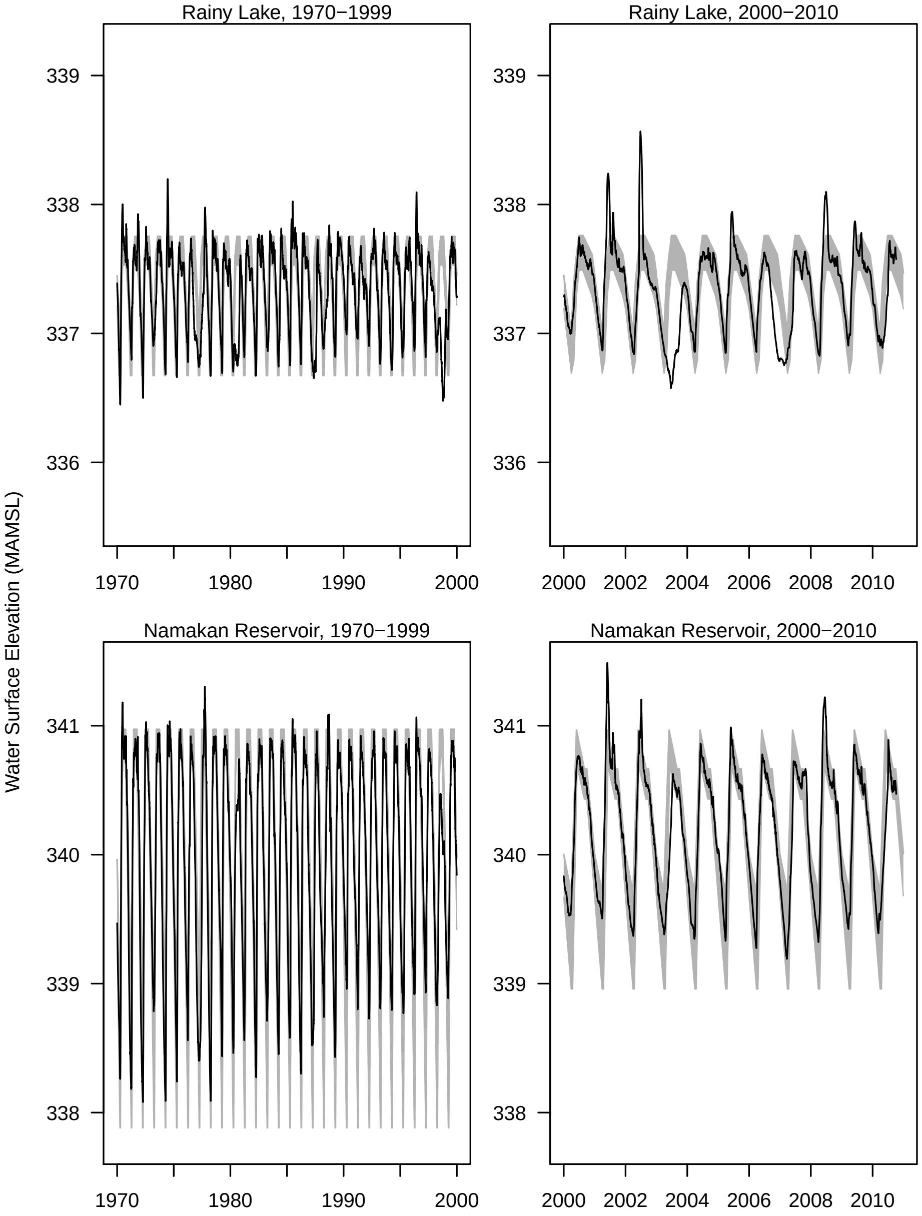

Figure 1.2. Observed surface elevations (black lines) and the 1970 and 2000 Rule Curves (gray bands) for Rainy Lake and the Namakan Reservoir.

loons nest close to the water, nests are vulnerable to water-level fluctuations. Breeding pairs will attempt to elevate nests during water-level rises, but large and rapid rises may flood nests causing mortality in eggs. As a consequence, water-level fluctuations may be a major source of variation in reproductive success (Belant and Anderson, 1991), and artificial floating nests have been used to help ameliorate effects of water-level fluctuations (Fair and Poirier, 1992; Piper et al., 2002; DeSorbo et al., 2007). However, increased levels of territorial aggression among breeding males have also been observed from competition for artificial nesting platforms (Mager et al., 2008), and net benefits remain somewhat uncertain.

Predation may also be a significant source of mortality among eggs and chicks (Belant and Anderson, 1991; McIntyre and Barr, 1997; Evers, 2007). Potential predators include large fishes and especially *Esox* spp., mammals and predatory birds. Bald eagles (*Haliaeetus leucocephalus*) are considered to be a major predator on chicks (Paruk, 1999), and may even prey on nesting adults (Vlietstra and Paruk, 1997). Predation by bald eagles may introduce a temporal trend in reproductive-success data because their abundance has been increasing steadily since the 1960's (`http://www.fws.gov/midwest/eagle/population/chtofprs.html`). Unfortunately, regional data from other potential predators were lacking.

1.2 Approach

1.2.1 Data

Data from lakes having a surface area of at least 405 ha (1,000 acres) were obtained from the Minnesota LoonWatcher Survey (LWS; `http://www.dnr.state.mn.us/eco/nongame/projects/loon_survey.html`), the Minnesota Loon Monitoring Program (MLMP; `http://www.dnr.state.mn.us/eco/nongame/projects/mlmp_state.html`), and from research conducted by Voyageurs National Park (VOYA) from 1979–2009. The LWS and MLMP surveys were conducted by citizen-volunteers who sent observations to the Minnesota Department of Natural Resources. The LWS volunteers made observations during "late summer" and MLMP volunteers made observations during the first half of July. Some volunteers surveyed entire lakes, but most surveys were conducted on unspecified portions of lakes. The LWS recorded counts of breeding pairs, chicks and total adults. Not all adults breed, so that breeding pairs were some fraction of the total adults observed. Because surveys were made during mid- to late summer after some chicks have fledged (begun flying), we assume that chick counts from all surveys provided a consistent measure of reproductive success. That assumption depends upon minimal mortality after chicks reach six weeks of age, which may be reasonable (Evers, 2007). The MLMP recorded counts of total adults and chicks, but not counts of breeding pairs. The VOYA surveys made detailed recordings of chicks, pairs and adults within established loon territories on Rainy, Namakan, Kabetogama and Sand Point Lakes, and were conducted by trained experts. A total of 871 lake-years of observations were used in this study.

Water-level recordings were obtained from within the nesting season from each lake. Daily water-level recordings were available from a few large lakes, but otherwise as few as three values were available. Two covariates were computed from the water-level series from each lake. The maximum of the daily rate of water-level increases measures the pace of water-level rises. Large fast increases in water level may overwhelm loons ability to elevate nests. The maximum rise during the nesting season measures the peak net increase in water level. Large and persistent water-level rises may flood nests and thwart re-nesting attempts by loons.

Based on the literature, the nesting season was defined as a 60-day long window within each lake. For model fitting, data were used only from lakes from which there were at least three years of data for which there were at least six recordings of water level within the 60-day nesting season. We also evaluated models based on 45-day nesting seasons.

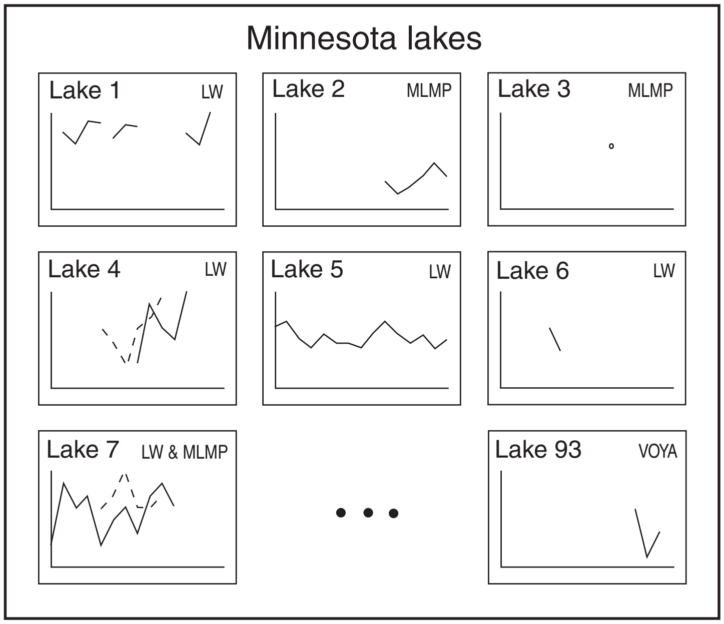

Figure 1.3. Hierarchical structure of Minnesota loon data. Lake numbers and graphs are fictitious and presented only to illustrate characteristics of each loon survey program. The horizontal axes represent time and the vertical axes represent an arbitrary measure of loon abundance.

The data have a natural hierarchical structure (Fig. 1.3). At the top level, all data were obtained from Minnesota lakes, and provide information about the loon population breeding on Minnesota lakes. At the second level, multiple lakes were surveyed by each program. Some lake surveys were occasionally interrupted, perhaps when different volunteers left or joined either the LWS or MLMP (Fig. 1.3, Lake 1). Typically, individual lakes were surveyed during relatively few years (Fig. 1.3, Lakes 2, 3, 6 and 93), but annual recordings were available from a few lakes (Lake 5). Sometimes multiple volunteers within a program sampled the same lake, and their observations may have overlapped in time (Lake 4). In a few cases, LWS and MLMP surveys were completed on the same lake (Fig. 1.3, Lake 7). Data from any one lake provided relatively little information on any effect of water-level fluctuation on loon reproductive success. However, borrowing of strength across the entire ensemble of lakes enabled more precise prediction of the effect of water-level fluctuations on the reproductive success of common loons.

1.2.2 Models

The empirical models developed in this study predict likely effects of water-level fluctuations on the reproductive success of common loons on Minnesota lakes, measured as the number of chicks per nesting pair during mid- to late summer. That measure of reproductive success was influenced directly by factors specific to the nesting lakes, including water-level regime, predation on chicks and other lake-specific factors. In contrast, the abundance of the larger regional loon population was also influenced by adult mortality rates (Grear et al., 2009) and other factors which operated during migration and on the wintering grounds. The models developed in this study do not address the population dynamics of loons or trends in abundance.

Einstein's admonition that "everything should be made as simple as possible, but not simpler" provided guiding philosophy for model development. Unfortunately, the structure of the data and the goal of the modeling required substantial complexity (Fig. 1.4). Model adequacy was assessed from predictions of validation data that were not used to fit the models. Therefore the data were split into two sets. The model fitting set was used in model development, and a smaller validation set was withheld and used to assess the ability of the model to make new predictions. Relevant input data included counts of adult loons, breeding pairs, and chicks, measures of water-level fluctuation, and an index of eagle (predator) abundance. Only breeding pairs produce chicks, and counts of breeding pairs were not available from the MLMP. Therefore an imputation submodel (Fig. 1.4) was needed to predict pair counts from the MLMP. Pair counts were also made with error because identification of pair bonds is likely less certain than simple identification of common loons. Therefore the imputation submodel also provided the means to estimate the pair counts that would be expected in the absence of measurement error. The reproductive-success submodel (Fig. 1.4) has the expected pair counts, water-level fluctuations and eagle counts as input predictor variables to estimate chick counts. The bottom-level model parameters for the effects of expected pair counts and water levels are specific to each lake. However, a top-level generalizes the effect of water-level fluctuations across all lakes.

Hierarchical Bayesian model formulations, which respect the structure of the data, were used to "borrow strength" from the entire set of lakes to identify the effect of water-level fluctuation on reproductive success. Bayesian

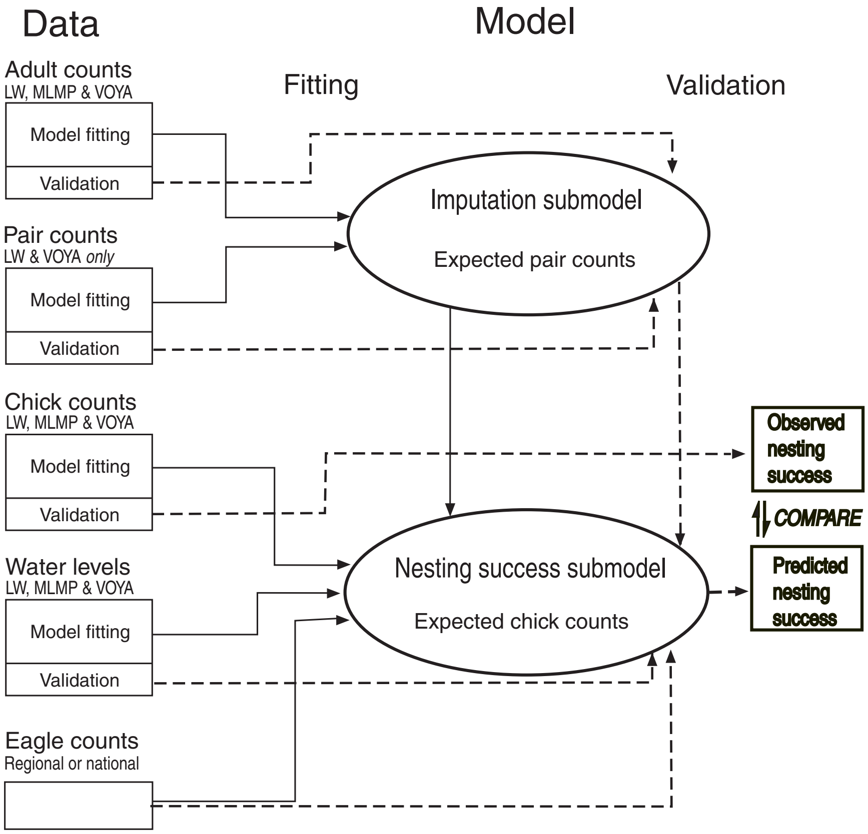

Figure 1.4. General structure of model design for assessment of effects of water-level fluctuation on reproductive success of common loons. Reproductive success was defined as the number of chicks per pair that survived their first summer of life.

methods (Ellison, 2004; Gelman et al., 2004; Carlin and Louis, 2009) were selected for this study because they: (a) produce intuitive, easily understood inferences based on probability or odds; (b) accommodate the hierarchical structure of the data; (c) enable inclusion of measurement/estimation error in the predictor covariates; and (d) enable modeling or imputation of missing data in a way that fairly represents the resulting uncertainty. Bayesian inferences are based on the posterior probability distributions of model parameters. Posterior distributions are proportional to the product of the likelihood function, which contains all of the relevant information in the observed data, and the prior probability distributions of the model parameters. Prior distributions quantify beliefs about the parameters that existed before observing the data. This study universally incorporated vague prior distributions, which contain little information about the parameters. Furthermore where sample sizes are large, as in this study, the likelihood (data) dominates the inference and even strongly informative priors have little influence on the posterior distribution. Therefore the inferences of this study benefit from the capabilities of Bayesian methods but are still dominated by the likelihood in the spirit of frequentist methods.

Nine model variations were evaluated (Table 1.1). All models assumed that chick and pair counts followed Poisson distributions within lakes, but included lake-specific latent random effects which resulted in potentially over-dispersed Poisson distributions across lakes. Either lognormal or log-t distributions were assumed for the lake-specific random effects, which were estimated from the data.

Table 1.1. Summary characteristics of hierarchical Bayesian models for evaluation of effects of water-level fluctuations on loon reproductive success. Duration is the assumed length of the nesting season (days) and Lake-effect is the assumed distribution for the lake-specific latent random effects.

Model	Duration	Water-level covariate	Lake-effect
1	60	Max. daily rise rate	lognormal
2	60	Max. daily rise rate	log-t
3	60	Max. rise	lognormal
4	60	Max. rise	log-t
5	60	Both	lognormal
6	60	Quadratic max. rise	lognormal
7	45	Quadratic max. rise	log-t
8	45	Same as Model 5	lognormal
9	45	Max. rise	log-t

1.3 Findings

All models predicted reduced reproductive success from increased daily rates of water-level rise or net water-level rises during the loon nesting season. The best models predicted all major features of the data, and also yielded plausible predictions of observations that had not been used in model fitting. Model 6 (Table 1.1) performed best in the Minnesota data based on the Deviance Information Criterion and based on out-of-sample validations. Reproductive success is maximized where water-levels are constant during the nesting season, and decline both during substantial water-level decreases and increases (Fig. 1.5).

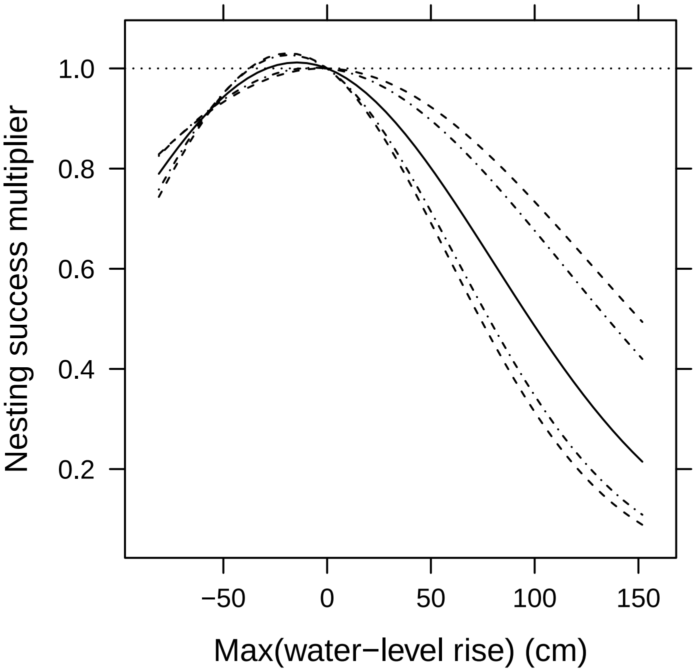

Figure 1.5. Multiplicative effect of water-level covariates on baseline reproductive success of common loons. The solid line is the posterior mean predicted effect and the pairs of dotted-dashed and dashed lines enclose regions having posterior probability of 0.90 and 0.95, respectively. regions, respectively.

The water-level regimes of the 1970 and 2000 Rule Curves on Rainy Lake and the Namakan Reservoir were used as input to Models 6. Estimates of the effects of the Rule Curves were based on posterior predictions from the counts of adult loons and pairs made during 2005, which were replicated over the 30-year history of water levels under the 1970 Rule Curves and over the 11-year history of water levels under the 2000 Rule Curves. The bald eagle index was held fixed at the mean value for the period of record in order to isolate and identify any effect of water-level fluctuation. Because chick counts were not included in the replicated data, those data do not inform the model fit. Thus, the model yielded conditional out-of-sample posterior retrodictions of reproductive success from 1970–1999 and from 2000-2009 given a constant adult population fixed at the 2005 observations and eagle abundance fixed at the mean. The resulting predictions are likely biased for true nesting success within each time period, but yield comparable and valid predictions of changes in nesting success that are attributable to 2000 Rule Curves.

Table 1.2. Posterior predictions of differences in mean chicks per pair between the 2000 and 1970 Rule Curves based on Model 6 and the maxima of water-level rises over the 60-d nesting seasons in Rainy Lake and the Namakan Reservoir (Namakan, Kabetogama and Sand Point Lakes). Adult loon counts and bald eagle abundance was held fixed in these comparisons in order to isolate the effect of water-level fluctuation. Given the data and model, credible sets contain the true mean differences with probability 0.95.

	Chicks per pair			Chicks	
Lake	Percent change	Mean difference	Credible set	Mean difference	Credible set
Rainy	-6.2	-0.09	-0.05–0.01	-1.3	-4.5–1.8
Namakan	45.3	0.16	0.09–0.24	4.2	1.3–7.7
Kabetogama	45.4	0.12	0.07–0.17	4.0	1.2–7.1
Sand Point	45.4	0.08	0.04–0.12	0.5	-0.3–1.5

By hypothesis, the reduced amplitude of the 2000 Rule Curve on the Namakan Reservoir (Namakan, Kabetogama and Sand Point Lakes) should reduce the maxima of water-level rises during the nesting season and result in improved loon reproductive success. Model 6—based on the maxima of water-level rises during the presumptive 60-day nesting season—predicts increases of approximately 45% in the reproductive success of common loons, as measured by chicks per pair, under the 2000 Rule Curve on the lakes of the Namakan Reservoir (Table 1.2). The data and model support the hypothesis that the 2000 Rule Curve for the Namakan Reservoir has aided increased reproductive success of common loons. As expected based on water levels (Fig. 1.2), the Pr = 0.95 credible set for change in nesting success on Rainy Lake includes zero (Table 1.2).

The data and models of this study provide information about effects of water-level fluctuations, bald eagle predation and/or regional trend and Minnesota climatic regime on the reproductive success of common loons on the breeding lakes. Therefore these models do not provide information on any ultimate effects of those factors on the regional abundance of loons, which is also influenced by factors that operate during migration and on the wintering grounds. Regional population growth rates may be highly sensitive to adult mortality rates, for which evidence of density-dependence is equivocal based on models of New Hampshire populations (Grear et al., 2009).

Therefore information is currently lacking to predict the consequences of variable reproductive success on abundance of loons in Minnesota and western Ontario. For example, if adult mortality rates are independent of adult population density, then the average annual additions of approximately eight chicks per year (Table 1.2) would eventually add more breeding pairs on the Namakan Reservoir. In turn those new breeding pairs would produce additional chicks, creating a trend of increasing population size via the same mechanism by which the compounding of interest (new chicks) increases the principle (loon population size) over time. Given that loons first breed at age 4–7 years (McIntyre and Barr, 1997), the time-frame for observation of unequivocal population increase may be decades. However if adult mortality rates increase strongly with adult densities or if regional nesting territories are fully occupied, then no increase in population size may be realized. Ongoing monitoring would be required to resolve that unanswered question. Regardless, it is clear that the rate of reproductive success of common loons has improved under the 2000 Rule Curve on the Namakan Reservoir.

Effects of Water-Level Fluctuations on Reproductive Success of Common Loons

2.1 Introduction

2.1.1 Problem Description

The objectives of this project were to develop and test statistical models to quantify any effects of water-level fluctuation on reproductive success of common loons (*Gavia immer*) in Minnesota lakes, and to use the best-performing model to quantify any observable effects of the 2000 Rule Curves on loons of Rainy Lake and the Namakan Reservoir complex. Reproductive success was defined as the number of chicks per nesting pair that survived through their first summer.

The water-levels in Rainy Lake and the Namakan Reservoir complex (Namakan, Kabetogama, Crane, Sand Point and Little Vermilion lakes) are regulated by a primary hydropower dam between International Falls, MN and Fort Francis, ON, and a pair of secondary dams at Kettle and Squirrel Falls which separate Rainy Lake from the Namakan Reservoir complex (Fig. 2.1). The primary dam became operational in 1909 and the secondary dams became operational in 1914. Lac La Croix, an unregulated and nearly pristine lake above Namakan Lake, presented a natural hydrograph for comparison. Overall, dam operations have tended to reduce the amplitude of annual water-level fluctuations in Rainy Lake, while increasing the amplitude in the Namakan Reservoir complex (Fig. 2.2), although water-level patterns varied considerably through the early 1950's. Dam operations have also created highly regular and unnatural annual cycles that differ markedly from the more variable natural hydrograph from Lac La Croix. Near-decadal cycles are apparent in the hydrograph from Lac La Croix, wherein sequences of low- and high-water years alternate, and include periods of low intra-annual variability (Fig. 2.2).

Dam operations have followed water-level Rule Curves prescribed by the International Joint Commission. Dam operators strive to maintain water levels within the date-specific Rule Curve bounds, and have been remarkably successful (Fig. 2.3). The 1970 Rule Curves maintained a narrow range of intra-annual variation on Rainy Lake while creating a nearly 3-m range of intra-annual fluctuation on the Namakan Reservoir. The 2000 Rule Curves were designed to reduce intra-annual water-level fluctuations on the Namakan Reservoir, and have reduced the intra-annual range by approximately 1 m with negligible effect on water levels in Rainy Lake.

2.1.2 Biology of the Common Loon

The common loon is the Provincial Bird of Ontario and the State Bird of Minnesota. Loons are migratory waterfowl which breed in the northern-tier States and throughout much of Canada. Arrival on nesting and summer-feeding lakes is largely determined by the timing of ice-out, and nesting may commence 4–6 weeks afterward (Evers, 2007). Typically two eggs are laid during the first nesting attempt; one-egg nests are common and three-egg nests are rare (McIntyre and Barr, 1997). The incubation period for two-egg nests averages 28 days. Nesting failures are not uncommon, and mated pairs may re-attempt nesting (McIntyre and Barr, 1997). Nests may be reconstructed quickly and replacement eggs may be laid within 8–19 days of initial nest loss. Incubation of replacement eggs may rarely extend into July (McIntyre, 1988). Therefore the nesting season for common loons is protracted and variable.

Loons typically nest close to water along shorelines of lakes and rivers, preferentially near drop-offs and on sheltered sides of islands or floating bogs (McIntyre and Barr, 1997). Because common loons nest along shorelines,

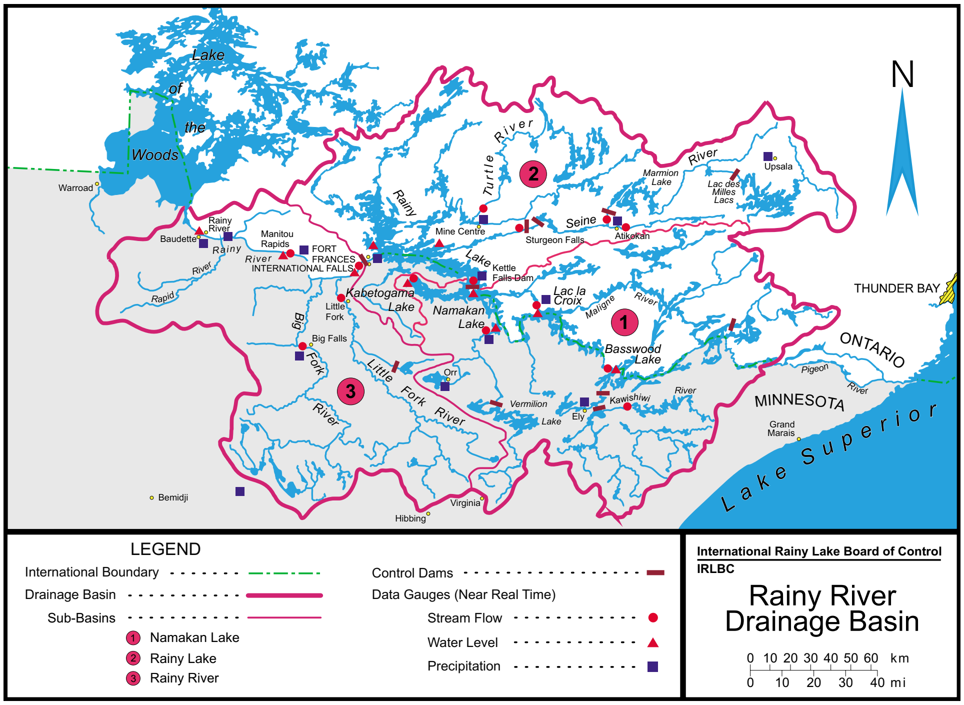

Figure 2.1. Rainy River Basin, northern Minnesota and southwestern Ontario.

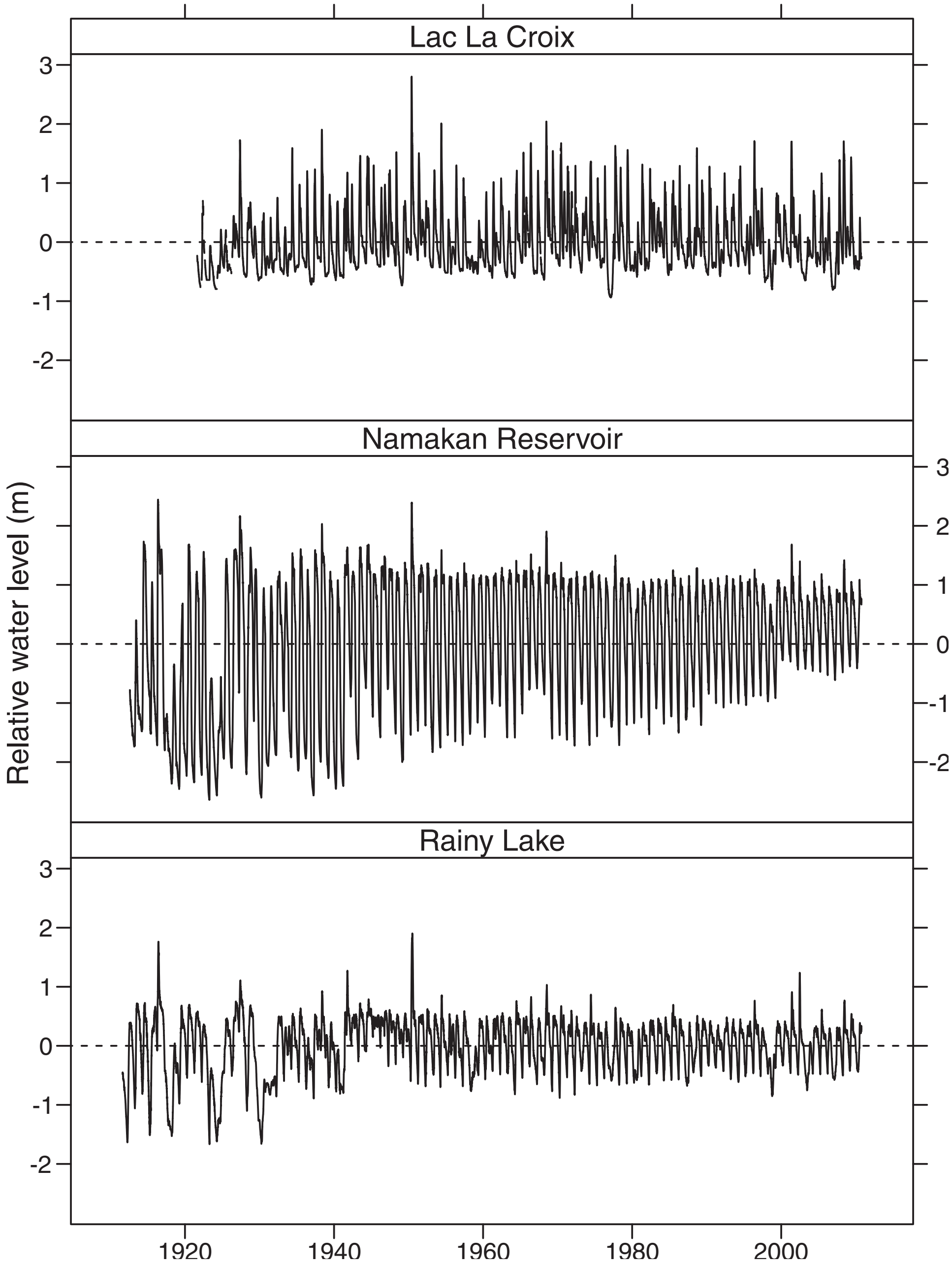

Figure 2.2. Historic hydrographs for Lac La Croix, the Namakan Reservoir and Rainy Lake, Minnesota and Ontario. Water levels are centered at zero (historic mean water-surface elevations above mean sea level were subtracted from the observed daily elevations for each lake) for comparison. Data source: Lake of the Woods Control Board.

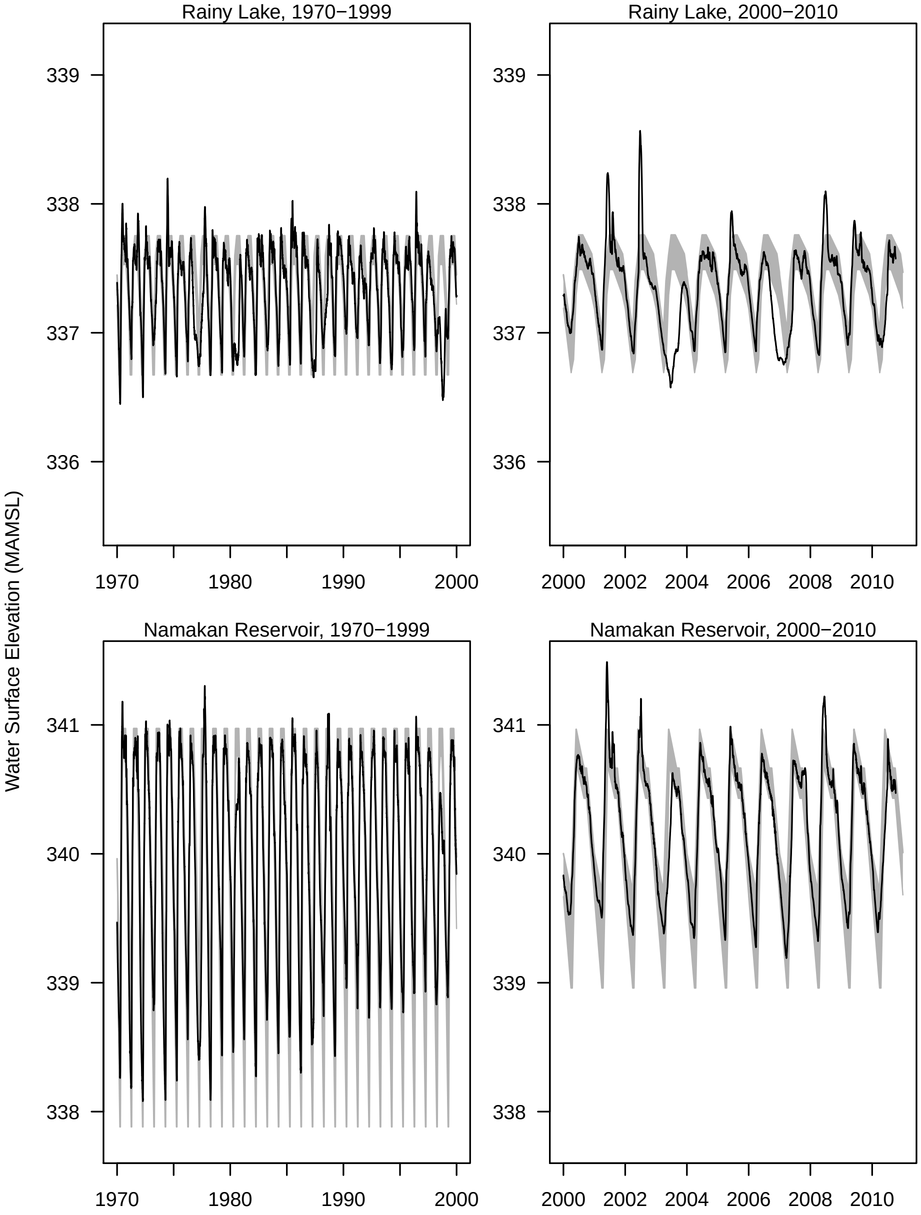

Figure 2.3. Observed surface elevations (black lines) and the 1970 and 2000 Rule Curves (gray bands) for Rainy Lake and the Namakan Reservoir.

nests are vulnerable to water-level fluctuations(Barr, 1986). Nesting pairs may attempt to elevate nests during water-level rises (Barr, 1986), but large and rapid rises may flood nests causing mortality in eggs. As a consequence, water-level fluctuations may be a major source of variation in reproductive success (Belant and Anderson, 1991).

Reproductive success seems generally lower on reservoirs than on natural lakes (Fair, 1979). Frequency of loon reproductive success was lower in the Namakan Reservoir complex (larger water-level fluctuation) than on Rainy Lake (lower water-level fluctuation) or on inland lakes of Voyageurs National Park, and approximately 60% of nesting failures on Rainy and Namakan Lakes during 1983–1986 were attributed to flooding (Reiser, 1988). DeSorbo et al. (2007) analyzed data from New England lakes and estimated a 21% reduction in successful nesting attempts in lakes that had fluctuating water levels. Their data did not quantify water-level fluctuations, nor did they distinguish increases from decreases.

Artificial floating nests have been used to help ameliorate effects of water-level fluctuations (Fair and Poirier, 1992; DeSorbo et al., 2007). Piper et al. (2002) documented improved nesting success on platforms, but attributed the effect to protection from mammalian predators rather than reduced flooding. However, increased levels of territorial aggression among breeding males have also been observed from competition for nesting platforms (Mager et al., 2008), and net benefits remain somewhat uncertain.

Loons are highly territorial and actively compete for nesting, chick-rearing and feeding sites (Paruk, 1999). Territorial combat between adult loons may be lethal (McIntyre and Barr, 1997), and adult loons may also intrude into pair territories and kill chicks (Kenow et al., 2003). Not all adult loons attempt nesting or defend territories. Nesting adults (loons that are at least 4–6 years old) may comprise 54–77% of the total number of returning loons, which also include non-breeding sub-adults, older loons that have been displaced from established territories and non-breeding territory defenders (Evers, 2007).

Predation may also be a significant source of mortality among eggs and chicks (Belant and Anderson, 1991; McIntyre and Barr, 1997). Potential predators include large fishes and especially *Esox* spp., mammals and predatory birds. Bald eagles (*Haliaeetus leucocephalus*) may be a significant predator on eggs and chicks (Paruk, 1999), and may even prey on nesting adults (Vlietstra and Paruk, 1997). Predation by bald eagle may introduce a temporal trend in nesting-success data because their abundance has been increasing steadily since the 1960's (`http://www.fws.gov/midwest/eagle/population/chtofprs.html`).

2.2 Methods

2.2.1 Data

Loon Counts

Data consisting of counts of common loons on Minnesota lakes were obtained from two monitoring programs implemented by citizen volunteers, and a comprehensive monitoring effort on Rainy Lake and three lakes of the Namakan Reservoir complex (Namakan, Kabetogama and Sand Point, 1979–2009; Windels et al., In prep) within Voyageurs National Park (VOYA). The voluntary monitoring programs were managed by the Minnesota Department of Natural Resources, which provided data used in this study.

The Minnesota Loon Monitoring Program (MLMP: `http://www.dnr.state.mn.us/eco/nongame/projects/mlmp_state.html`)), coordinated by the Minnesota Department of Natural Resources, has been in operation since 1994. Volunteers visit each of more than 600 lakes distributed among six "index areas" during the first half of July. The volunteers count the numbers of adult loons and juveniles (young-of-the-year birds, henceforth called chicks), and record ancillary information. Some counts were made from the shoreline, especially on small lakes, and others were made from boats. Volunteers are encouraged to use binoculars, and are provided with written instructions for observation, bird identification and recording. The Minnesota LoonWatcher Survey (LWS: `http://www.dnr.state.mn.us/eco/nongame/projects/loon_survey.html`) is also coordinated by the Minnesota Department of Natural Resources, and has been in operation since 1979. LoonWatcher volunteers report observations from lakes "at the end of the season", and count the numbers of nesting pairs, adults and chicks. Only MLMP and LWS observations from lakes of at least 405 ha (1,000 acres) were used in the present study.

Prediction of Nesting Seasons from Ice-out Dates

Data on historical ice-out dates on Minnesota lakes were obtained from the Minnesota State Climatology Office, St. Paul. The historical ice-out records included observations from many, but not all, of the combinations of lake and year from which loon counts were available. Actual lake×year observations of ice-out dates were used when possible. Otherwise, yearly mean ice-out dates were computed from within each of five temperature zones based on 30-year average May temperatures, and applied to lakes within those zones (Fig. 2.4). Ice-out dates were converted to day-of-the-year (1 = January 1).

Recordings of dates of first nesting attempts by common loons were made from the large lakes of VOYA, 2004–2006, but were not available from the MLMP or LWS. Therefore the VOYA data were used to estimate the dates of first nesting attempts from the other combinations of lake and year based on 5th-percentile predictions from quantile regression of first-nesting date on day-of-the year. The resulting formula for estimation of day-of-the-year of

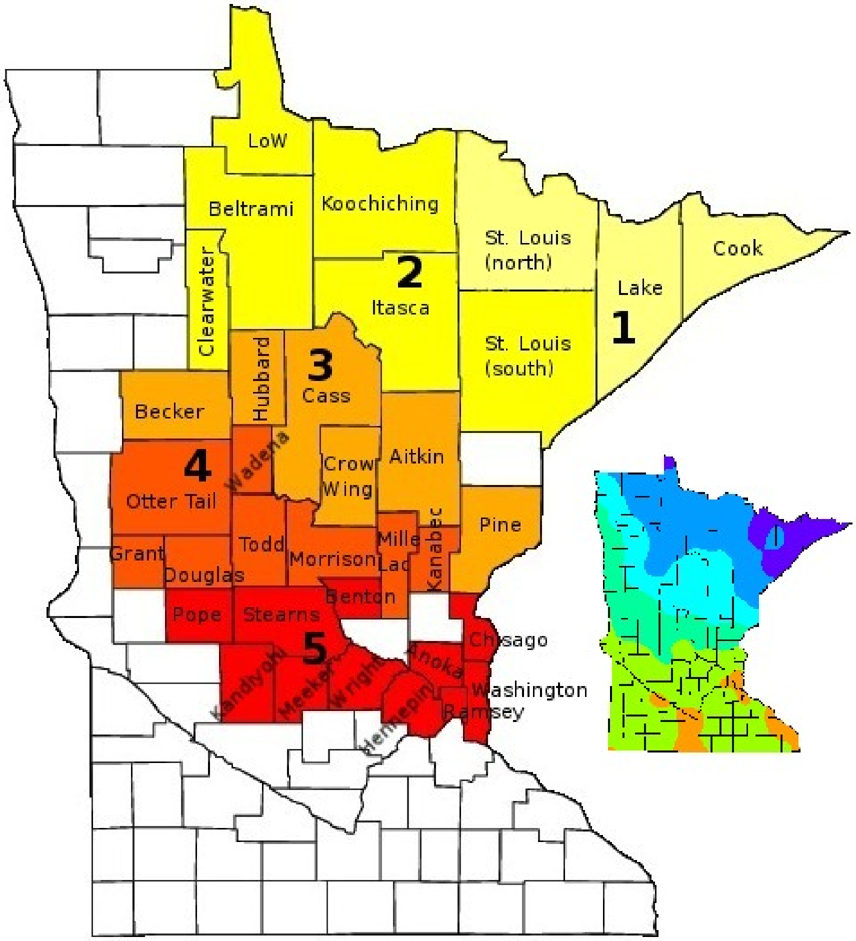

Figure 2.4. Minnesota counties from which loon-count data were available, shaded by assignments to April temperature categories 1–5. St. Louis county was split to better conform to temperature patterns (inset; `http://www.climate.umn.edu/doc/historical/temp_norm_adj.htm`).

first nesting is given by $\mathsf{doy\_nest} = 70.37 + 0.56\mathsf{doy\_io}$, where $\mathsf{doy\_io}$ denotes the day-of-the-year of ice out. Nesting seasons were defined as the 60-day intervals beginning with either the observed day of first nesting (VOYA) or with $\mathsf{doy\_nest}$ (LWS and MLMP). A similarly defined 45-day nesting season was also considered to evaluate sensitivity to variation in the duration of the assumed nesting season.

Water Levels

Water-level recordings were obtained from the LWS, MLMP or from gages operated by the U.S. Geological Survey or dam operators. Water-surface elevations were typically recorded at somewhat regularly spaced temporal intervals (e.g., weekly, daily, etc.), and the numbers of water-level recordings varied among lakes and years. Therefore the quality of water-level data varied among lakes. Data were retained only from those lakes from which there were at least six water level recordings within the loon nesting seasons during each of at least three years. The requirement for six observations per nesting season insured some minimal ability to estimate the maxima of changes in water level, and the requirement for at least three years of data provided ability to estimate lake-specific latent random effects. Those selection criteria resulted in 939 lake-years of data (Table 2.1). The actual number of water-level readings varied from six to 60 (daily recordings).

Table 2.1. Loon sample survey counts from Minnesota lakes of at least 405 ha.

Survey program	Lakes	Lake-years
LoonWatcher Survey (LWS)	77	631
Minnesota Loon Monitoring Program (MLMP)	22	228
Voyageurs National Park (VOYA)	4	80

The principal hypothesis was that loon reproductive success is influenced, in part, by rises in water levels during the nesting season that are sufficient to flood nests. Therefore the magnitudes of rises are of primary interest. Two aspects of water-level rises are plausibly important. First, the maximum of daily rates of water-level rises is a measure of the magnitude and speed of rises. Fast rises may overwhelm loons' ability to relocate or elevate nests. Second, large increases in water levels over longer periods of time might also reduce nesting success. For example, even slow but large rises could force successive re-nesting attempts, delaying or even preventing successful hatching. Therefore two water-level covariates were examined: $\mathsf{max.dwdt}$, the maximum of the daily rates of water-level increase ($\mathrm{cm}\cdot\mathrm{d}^{-1}$) and $\mathsf{max.dw}$, the maximum rise (cm) during the nesting season.

Both $\mathsf{max.dwdt}$ and $\mathsf{max.dw}$ were estimated from the water-level series from each combination of lake and year. The precision of those estimates varies greatly because the water-level series included 6–60 water-level readings. Although water level varies continuously with time, the observed maxima from daily data likely provide reasonable (essentially error-free) esti-

Table 2.2. Estimators of finite-population maxima $\hat{X}_{N:N,j}$ and extreme ranges (differences between estimated maxima and minima) $\hat{D}_{N,j}$. The naive estimators $\hat{X}_{N:N,1}$ and $\hat{D}_{N,1}$ are based entirely on observed extremes, whereas $\hat{X}_{N:N,2}$ and $\hat{D}_{N,2}$ are based on extensions of the solution of the "German tank problem" (Ruggles and Brodie, 1947) to continuous random variables. The remaining estimators add multiples of the finite-population standard error to the observed extremes. $\bar{\delta}_x$ is the average of the first differences of the x_j and s is the sample standard deviation. See text for other notation.

Population maximum	Extreme range
$\hat{X}_{N:N,1} = x_{n:n}$	$\hat{D}_{N,1} = x_{n:n} - x_{1:n}$
$\hat{X}_{N:N,2} = x_{n:n} + \bar{\delta}_x \sqrt{\frac{N-n}{N}}$	$\hat{D}_{N,2} = \hat{X}_{N:N,2} - \left(x_{1:n} - \bar{\delta}_x \sqrt{\frac{N-n}{N}} \right)$
$\hat{X}_{N:N,3} = x_{n:n} + \frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}}$	$\hat{D}_{N,3} = \hat{X}_{N:N,3} - \left(x_{1:n} - \frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}} \right)$
$\hat{X}_{N:N,4} = x_{n:n} + 1.5 \frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}}$	$\hat{W}_{N,4} = \hat{X}_{N:N,3} - \left(x_{1:n} - 1.5 \frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}} \right)$

mates of the maxima. However that is not the case where few readings are available, from which the *observed* maxima from the water-level series underestimate the true maxima. That bias is inversely related to the number of observations in the series. For example, it is clearly evident that a series consisting of only six observations is highly unlikely to manifest the true maximum daily rate of rise during 60-d nesting season, nor can the observed maximum be greater than the true maximum. Therefore plausible point estimates and standard errors for `max.dwdt` and `max.dw` are needed.

Assume a finite statistical population of N daily water levels, denoted $X_i, i = 1, \ldots, N$, and define $X_{1:N} \le \cdots \le X_{N:N}$ as the ordered set of water levels. The assumption of finite populations of water-level readings holds approximately because the best water-level recordings from Minnesota lakes are made daily, and variation within days is likely to be small relative to variation among days. The maximal order statistic (largest value) for the finite population is $X_{N:N}$, the minimal order statistic (smallest value) is $X_{1:1}$, and the range is denoted by $D_N = X_{N:N} - X_{1:N}$. Of those actual daily water levels, only some $n \le N$ are observed (measured). Those observations are denoted $x_j, j = 1, \ldots, n$, and their ordered values are denoted $x_{1:n} \le \cdots \le x_{n:n}$. Therefore $X_{N:N}$ and D_N must be estimated from the observed x_j. The limiting distribution of $x_{n:n}$ does not generally exist (David and Nagaraja, 2003). Balakrishnan et al. (2003) derived bounds on expectations of *sample* order statistics $x_{1:n} \le \cdots \le x_{n:n}$ from finite populations, but those bounds do not inform bounds on the $X_{1:N} \le \cdots \le X_{N:N}$. The "German tank problem" (Ruggles and Brodie, 1947) provides an estimate of the total number of items (observed and unobserved) based on a sample of (observed) sequential identifiers (serial numbers). In contrast, estimates of finite-population extremes based on a sample of real-valued observations x_j were needed for `max.dwdt` and `max.dw`. Given the apparent lack of a solution based on distribution theory, four ad hoc estimators of $X_{N:N}$ and D_N were considered (Table 2.2). The performances of those estimators of finite-population extremes and range were compared using Monte Carlo simula-

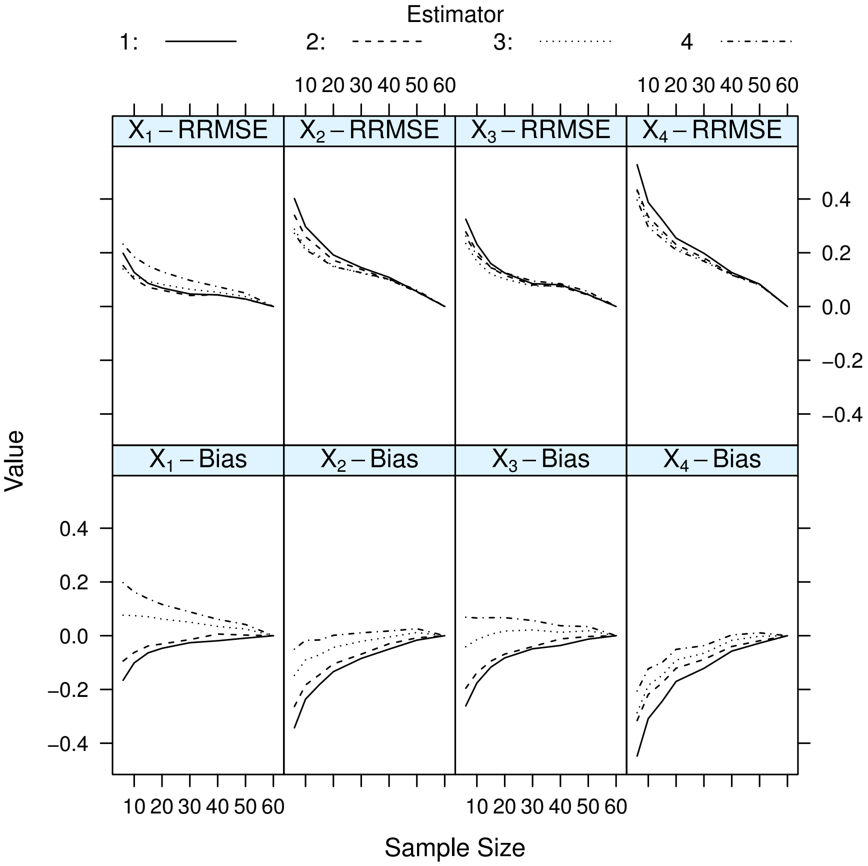

Figure 2.5. Relative root mean-squared error (RRMSE, top row) and relative bias (Bias, bottom row) of the four ad-hoc estimators of the unknown population maximum generated from four distributions X_i, $i = 2, \ldots, 4$. See text for explanation.

tion of four hydrographs (Appendix A). The theoretical hydrographs varied from close similarity to natural hydrographs to a highly variable white-noise process which assumes that daily water levels are serially independent. The white-noise process represents an extreme but implausible challenge because actual water levels on any day must be functions of water levels on the previous day. Both bias and relative root mean-squared error (overall prediction error) were compared. The naive estimator $\hat{X}_{N:N,1} = x_{n:n}$ underestimated the true maxima from all distributions (Fig. 2.5), as expected. All estimators performed poorly in the white-noise process. $\hat{X}_{N:N,3}$ was least biased in distribution 1, which mimicked natural hydrographs, and was competitive in high-variance autoregressive and moving average processes (distributions 2 and 3). Therefore max.dwdt was estimated using $\hat{X}_{N:N,3}$. The corresponding estimators of finite-population range, $\hat{D}_{N,j}$ performed similarly in Monte Carlo simulations, and $\hat{D}_{N,3}$ was selected as the estimator of max.dw.

For each combination of lake and year, finite-population estimates of max.dwdt and max.dw were made from the observed water-level series. Standard errors of the estimates were obtained using the finite-population bootstrap (McCarthy and Snowden, 1985). Estimates were made for both 60- and 45-day presumptive nesting seasons. Estimates of max.dwdt were never much less than zero, whereas both large rises (positive values) and drops (negative values) in max.dw were obtained (Fig. 2.6).

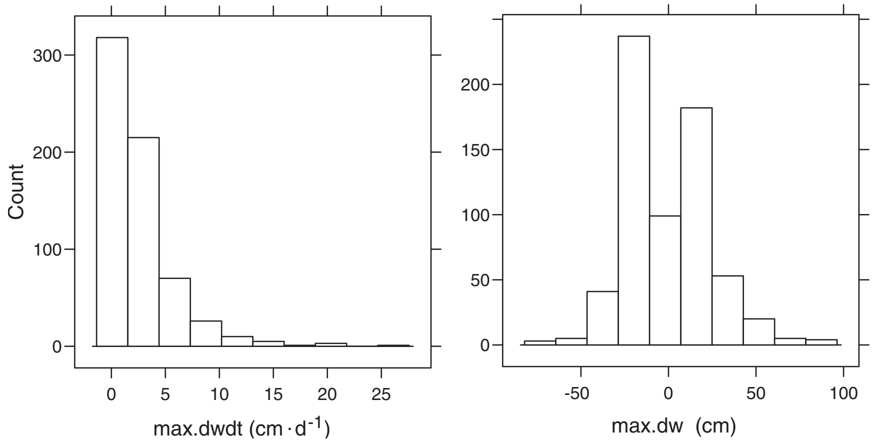

Figure 2.6. Marginal distributions of estimates of the maximum daily rate of water-level rise max.dwdt and maximum rise max.dw over 60-day presumptive nesting seasons in Minnesota loon-nesting lakes.

Ancillary Predictors

The reproductive success of common loons is influenced by more variables than water levels. Some eggs and chicks are lost to predators. Consistent regional data were available from one important predator, the bald eagle. The Wisconsin Bald Eagle and Osprey Survey (`http://dnr.wi.gov/land/`

`wildlife/harvest/harvest.htm`) has counted bald eagle nesting territories statewide since 1979 (Fig. 2.7). The trend from the Wisconsin survey is consistent with less complete counts (`http://www.fws.gov/midwest/eagle/population/index.html`) from the lower 48 States (1981–2000 and 2006), Minnesota (1990–2001 and 2005) and VOYA (1973–present). Therefore the Wisconsin data were used to construct regional index of bald eagle abundance. The regional bald eagle index was computed by standardizing (dividing the differences between counts and the mean count by the standard deviation) the Wisconsin territory counts. The bald eagle index is clearly confounded with any nearly linear temporal trend. Therefore the bald eagle index is also a surrogate for any temporal effects, and does not isolate unique effects of bald eagle predation. Regardless, the potential trend induced by this predator or any confounded factor that affects loon reproductive success should not be ignored.

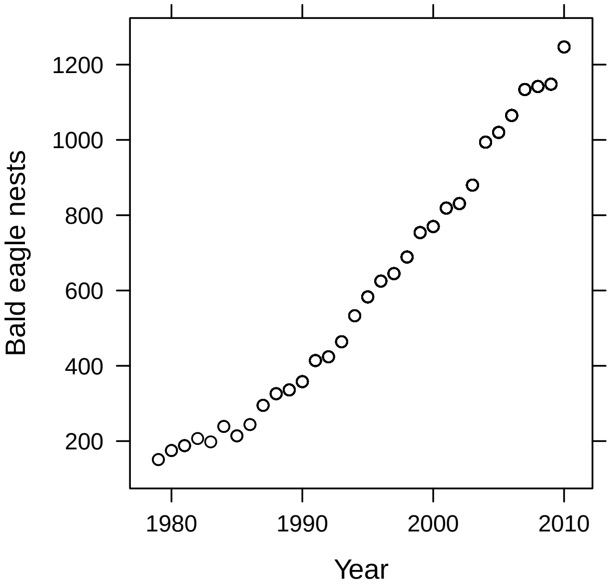

Figure 2.7. Numbers of occupied bald eagle territories tabulated by the Wisconsin Bald Eagle and Osprey Surveys, 1979-2010.

The southern limit of loon breeding range passes through southern Minnesota. Therefore a latitudinal or climatic effect on loon reproductive success is a plausible hypothesis. That hypothesis was examined using the day of year of ice out `doy_io`, which varied by more than 60 days in the Minnesota loon data (Fig. 2.8).

Numerous lake-specific factors might also affect loon reproductive success, including the abundance of fish prey, housing development along shorelines, mammalian predators and numbers of islands. All such factors were latent for lack of data, but were accommodated as aggregated lake-specific

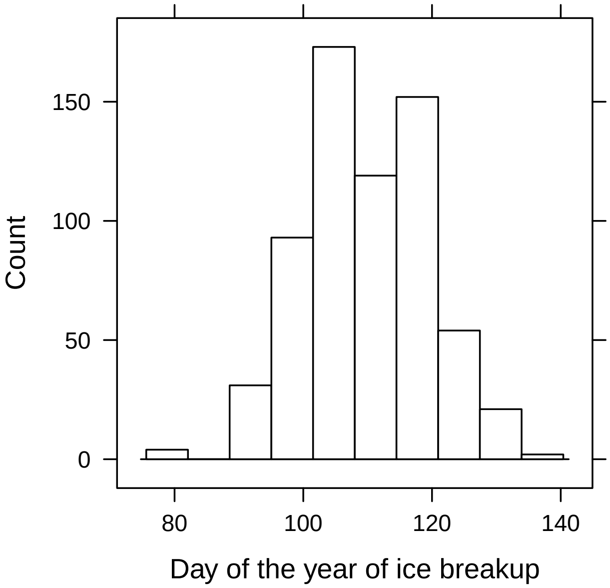

Figure 2.8. Distribution of the days of the year of spring ice breakup for combinations of lakes and years represented in the Minnesota loon data.

random effects which could be estimated from the hierarchical structure of the data.

2.2.2 Statistical Models of Reproductive Success

Bayesian modeling methods (Ellison, 2004; Gelman et al., 2004; Carlin and Louis, 2009) were selected for this study because they: (a) produce intuitive, easily understood inferences based on probability or odds; (b) accommodate the hierarchical structure of the data; (c) enable inclusion of measurement/estimation error in the predictor covariates; and (d) enable modeling or imputation of missing data in a way that fairly represents the resulting uncertainty. Bayesian inferences are based on the posterior distributions of model parameters. Posterior distributions are proportional to the product of the likelihood function, which contains all of the relevant information in the observed data, and the prior distributions of the model parameters. Prior distributions quantify beliefs about the parameters that existed before observing the data. This study universally incorporated vague prior distributions, which contain little information about the parameters. Furthermore where sample sizes are large, as in this study, the likelihood (data) dominates the inference and even strongly informative priors have little influence on the posterior distribution. Therefore the inferences of this study benefit from the capabilities of Bayesian methods but are still dominated by the likelihood in the spirit of frequentist methods.

Pair Counts

Only nesting pairs produce chicks, but counts of nesting loon pairs were not made by the MLMP. Further, pair counts depend on correct identification of pair bonds between female and male loons, and therefore may entail more counting error than simple counts of chicks or adults. Expected pair counts and counting-error variances were estimated from the complete data. Let X_{ij} denote pair counts and let W_{ij} denote counts of adults from lake i during year j. Loon counts can never be negative. The Poisson distribution is the simplest model for such data, but the variance is constrained to equal the mean in that distribution. The possibility of overdispersion (extra-Poisson variation) was included in the submodel for estimation of pair counts is given by

$$\begin{aligned} X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\ \lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_i \\ \epsilon_i &\sim \text{Normal}\left(0, \tau_X\right) \\ \tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\ \left(\theta_1, \theta_2\right) &\sim \text{Normal}\left(\mathbf{0}, \mathbf{\Omega}_\theta\right) \\ \mathbf{\Omega}_\theta &\sim \text{Wishart}\left(\rho_\theta \mathbf{R}_\theta, \rho_\theta\right), \end{aligned} \tag{2.1}$$

where $\lambda_{X,ij}$ is the conditional Poisson mean pair count, θ_1 and θ_2 are “regression” parameters for the linear and quadratic effect of adult counts W_{ij}, and ϵ_i is a normally distributed latent lake-specific random effect, which is the presumptive source of any extra-Poisson variation. The precision τ_X is the reciprocal of the variance of ϵ_i. A Gamma distribution is assumed for τ_X, and is equivalent to a vague (low information content) but proper Inverse Gamma prior distribution for the variance of ϵ_i. Any correlation between θ_1 and θ_2 is accommodated through the bivariate normal prior distribution having mean vector $\mathbf{0}$ and precision matrix $\mathbf{\Omega}_\theta$. That precision matrix is given the most vague but proper Wishart hyperprior distribution by choosing the dimension of θ for ρ_θ and where $\mathbf{R}_\theta$ is a scaling matrix of the order of the covariance matrix $\mathbf{\Sigma}_\theta = \mathbf{\Omega}_\theta^{-1}$ (Carlin and Louis, 2009). This model provided an excellent fit to the complete data from the LWS and VOYA surveys (Fig. 2.9). Further, random draws from the posterior predictive distribution (Gelman et al., 2004), which provide a measure of predictive performance on new data, look like the observed data indicating that all of the distributional assumptions of the pair-count submodel are approximately correct (Fig. 2.10).

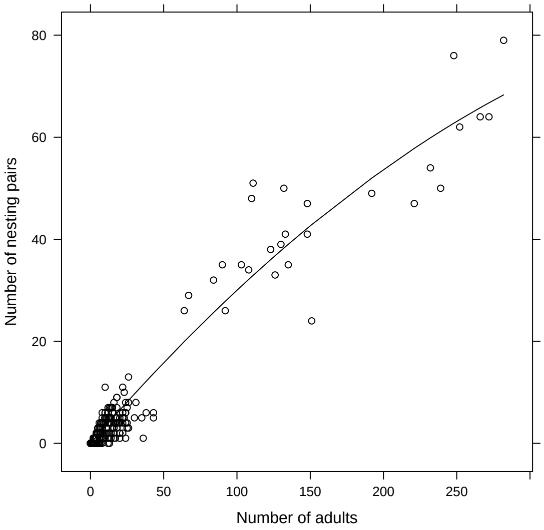

Figure 2.9. Fitted quadratic regression of common loon pair counts on adult counts from Minnesota lakes.

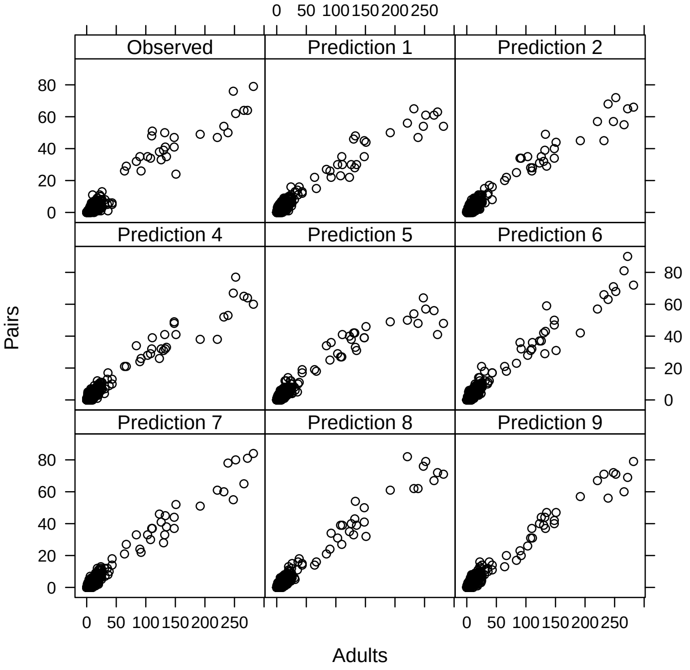

Figure 2.10. Observed pair and adult counts from LWS and VOYA surveys, and eight independent random samples from the posterior predictive distribution.

Hierarchical Models of Reproductive Success

The models of loon chick counts Y_{ij} are variations on the general form given by

$$\begin{array}{rcl} Y_{ij} & \sim & \mathrm{Poisson}\left(\lambda_{Y,ij}\right) \\ \lambda_{Y,ij} & = & \lambda_{X,ij}\exp\left(\beta_{1,i} + \beta_z \mathbf{z}_{ij}\right) \\ \beta_{1,i} & \sim & f\left(\beta_1, \tau_{\beta_1}\right) \\ \tau_{\beta_1} & \sim & \mathrm{Gamma}\left(3, 1\right) \\ \left(\beta_1, \beta_z\right) & \sim & \mathrm{N}\left(\mathbf{0}, \mathbf{\Omega}_\beta\right) \\ \mathbf{\Omega}_\beta & \sim & \mathrm{Wishart}\left(\rho_\beta \mathbf{R}_\beta, \rho_\beta\right), \end{array} \qquad (2.2)$$

where $\mathbf{z}_{ij}$ is a vector of predictor covariates (water-level variable, bald eagle index and day-of-the-year of ice breakup), the $\beta_{1,i}$ are lake-specific random-effects parameters, β_z is a parameter vector associated with $\mathbf{z}_{ij}$. Note that the expected values of pair counts $\lambda_{X,ij}$ (Eq. 2.1) appear as offsets (or "exposures"; simple multipliers), so that the exponential function $\lambda_{Y,ij}$ is a dimensionless model of the numbers of chicks per pair. Predictive strength is borrowed across lakes by assuming that the $\beta_{1,i}$ share a common mean β_1 and precision τ_{β_1} in the prior distribution $f\left(\beta_1, \tau_{\beta_1}\right)$. The Gamma$(3, 1)$ distribution provides a reasonably vague hyperprior specification for the precision τ_{β_1} in the prior for β_1. Two choices for $f\left(\cdot\right)$ were evaluated. The choice of a normal distribution results in a lognormal-Poisson mixture for Y and a heavy-tailed Student's t distribution having 3 degrees of freedom provides a log$t$-Poisson model for Y that is more robust to the presence of lakes having extreme reproductive success. Any correlation among $\beta = \left(\beta_1, \beta_z\right)$ is accommodated through the multivariate normal prior distribution having mean vector $\mathbf{0}$ and precision matrix $\mathbf{\Omega}_\beta$. Again, $\mathbf{\Omega}_\beta$ is given the most vague hyperprior that is still proper by choosing the dimension of β for ρ_β and where $\mathbf{R}_\beta$ is a scaling matrix of the order of the covariance matrix $\mathbf{\Sigma}_\beta = \mathbf{\Omega}_\beta^{-1}$.

Implementation

A total of nine model variations were evaluated using combinations of the two alternatives for $f\left(\cdot\right)$ (Eq. 2.2), 60- and 45-day presumptive nesting seasons, and alternative forms for water-level covariates (Table 2.3). The models based on 45-day nesting season were used to examine sensitivity to the assumption of nesting-season length on any effect of `max.dw`, which is plausibly a function of nesting-season length. Models 8 and 9 are the 45-day analogs of models 5 and 4, respectively, and model 7 is a near-analog of model 6. The effect of climate/latitude `doy_io` was omitted from Models 5–8 because model fitting failed when included in preliminary analyses.

Some samples were withheld from model fitting to evaluate out-of-sample predictive performance (Table 2.4). There was some overlap between the LoonWatcher and MLMP surveys; data were withheld from the MLMP

Table 2.3. Model variations on Eqs. (2.1–2.2) for the evaluation of effects of nesting-season water-level fluctuations on the reproductive success of common loons on Minnesota lakes. The water-level covariates were estimated over the duration of the presumptive nesting season. The bald eagle abundance index was included as a covariate in all models, but the day of the year of ice breakup was excluded from Models 5–8.

Model	Water-level covariate(s)	Lake-effect distribution $f(\cdot)$	Nesting season (d)	Water-level parameter(s)
1	Max. of daily rises: $z_1 = \mathsf{max.dwdt}$	lognormal	60	β_2
2	Max. of daily rises: $z_1 = \mathsf{max.dwdt}$	log-t	60	β_2
3	Max. rise: $z_1 = \mathsf{max.dw}$	lognormal	60	β_2
4	Max. rise: $z_1 = \mathsf{max.dw}$	log-t	60	β_2
5	Both: $z_1 = \mathsf{max.dwdt}$, $z_4 = \mathsf{max.dw}$	lognormal	60	β_2, β_5
6	Quadratic: $z_1 = \mathsf{max.dw}$, $z_4 = \mathsf{max.dw}^2$	lognormal	60	β_2, β_5
7	Quadratic: $z_1 = \mathsf{max.dw}$, $z_4 = \mathsf{max.dw}^2$	log-t	45	β_2, β_5
8	Both: $z_1 = \mathsf{max.dwdt}$, $z_4 = \mathsf{max.dw}$	lognormal	45	β_2, β_5
9	Max. rise: $z_1 = \mathsf{max.dw}$	log-t	45	β_2

surveys where overlap occurred. Finally, a premium was placed on predictive performance on large lakes. The LoonWatcher surveys spanned many years on both Leech (44,280 ha) and Vermilion Lakes (4,047 ha), so we withheld a subset of those samples.

This analysis used R version 2.15.1 (R Development Core Team, 2011). Bayesian Markov Chain Monte Carlo (MCMC) sampling was implemented using the R package BRugs version 0.7-7 (Thomas et al., 2006) running under Ubuntu Gnu Linux 10.04. Three independent Markov chains, each consisting of 5,000 post-convergence samples, were generated for each model. Convergence was always attained within an initial 6,000 iterations, as measured by Brooks-Gelman-Rubin diagnostics (Brooks and Gelman, 1997). All code and model fitting is documented in Appendix B.

Model comparisons were based on the Deviance Information Criterion (DIC; Spiegelhalter et al. (2002)), which is essentially an extension of the Akaike Information Criterion (AIC; Akaike 1973) to hierarchical Bayesian models. DIC was computed for Eqs. 2.1, 2.2 and the total. Models having smaller values of DIC are preferred, but DIC differences smaller than 5–10 between models may not be of practical importance (Carlin and Louis, 2009).

Predictive performance was evaluated by comparing the withheld chick counts (Table 2.4) with Pr = 0.95 Bayesian credible sets for the posterior predictive distributions. The posterior predictive distribution is the distribution of a future observable given the joint posterior distribution of the model parameters and the observed data (Gelman et al., 2004). Therefore the posterior predictive distribution for chick counts is the conditional distribution for the chick counts that were withheld from model fitting. This posterior-predictive check informs the accuracy of model predictions from

Table 2.4. List of samples withheld from model fitting and reserved for evaluation of out-of-sample predictive performance from the LoonWatcher Survey (LWS), Minnesota Loon Monitoring Program (MLMP) and Voyageur's National Park (VOYA).

Survey	Lake	County	Year(s) withheld	Samples
LoonWatcher	Leech	Cass	1993,1995,2004–05	4
LoonWatcher	Vermilion	St Louis	2005–10	6
MLMP	Farm Island	Aitkin	2001–02,2007–09	5
MLMP	Height of Land	Becker	2009	1
MLMP	Island	Becker	1996,1998–2009	14
MLMP	Otter Tail	Otter Tail	2004,2007	3
MLMP	Vermilion	St Louis	1995–2000	6
MLMP	White Earth	Becker	2003–09	6
VOYA	Kabetogama	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
VOYA	Namakan	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
VOYA	Rainy	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
VOYA	Sand Point	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
Totals				81

new observations.

Bayesian credible sets are intervals which, given the data, model and priors, contain the unknown parameter with the assigned probability, and therefore enjoy the natural interpretation which is lost to frequentist confidence intervals. For example given the data, model and priors, a Pr $= 0.95$ credible set for β_2 contains the true but unknown value of that parameter with 0.95 probability. In contrast, given the data and model, a 95% frequentist confidence interval yields a single realization of an interval which—if recalculated for each of a large number of identically distributed loon nesting histories and monitoring results—would produce a set of similar intervals among which 95% would contain the unknown parameter. However, the replication of nesting histories required by frequentist methods is impossible.

Model performance was also evaluated using Bayesian P-values (Carlin and Louis, 2009) for statistics other than the parameters of the models. Bayesian P-values smaller than 0.025 or larger than 0.975 indicate an inability of a model to fit the particular feature of the data. Bayesian P-values were computed for the largest chick count, the maximum number of chicks per nesting pair and the skewness of chick counts.

The parameters associated with the water-level covariates (Table 2.3) are of particular interest. Effects of the water-level covariates on loon reproductive success were quantified by computing the probability of an adverse effect (regardless of magnitude), denoted $\Pr(\beta_2 < 0)$, as the proportion of posterior realizations of $\beta_2 < 0$ in the Markov chains. However, any effect is also a function of water-level fluctuation and therefore the conditional mean and credible sets were computed for the multiplicative effect of the water-level covariate on the numbers of chicks per nesting pair given by $\exp(\beta_2 z_1)$.

Estimation of Effects of the 2000 Rule Curves on Rainy Lake and the Namakan Reservoir System

The best model (6) was used to estimate the effect of the 1970 and 2000 Rule Curves on the reproductive success of common loons on Rainy Lake and the Namakan Reservoir (Namakan, Kabetogama and Sand Point Lakes). Estimates of the effects of the Rule Curves were based on posterior predictions from the counts of adult loons and pairs made during 2005, which were replicated over the 30-year history of water levels under the 1970 Rule Curves and over the 11-year history of water levels under the 2000 Rule Curves. The bald eagle index was held fixed at the mean value for the period of record. Because chick counts were not included in the replicated data, those data do not inform the model fit. Thus, the model yielded conditional out-of-sample posterior "retrodictions" of reproductive success from 1970–1999 and from 2000-2010 given a constant adult population fixed at the 2005 observations and eagle abundance fixed at the mean. The resulting predictions are likely biased for true nesting success within each time period, but yield comparable and valid predictions of changes in nesting success that are attributable to 2000 Rule Curves.

For each model, 5,000 MCMC samples from the joint posterior distribution of chick counts and the numbers of chicks per pair were obtained from each of three independent Markov chains. Each MCMC sample produced retrodictions from 30 years under the 1970 Rule Curves and 11 years under the 2000 Rule Curves. The 1970 Rule Curves were treated as the baseline, and effects of the 2000 Rule Curves were quantified as differences from that baseline. The differences between the among-year means of predicted chick counts and chicks-per-pair were computed from each of the 15,000 combinations of MCMC samples and Markov chains from each lake. Then, for each lake, the means and $\Pr = 0.95$ Bayesian credible sets of differences between the 2000 and 1970 Rule Curves were computed.

Secondarily, out-of-sample posterior predictions under the 1970 and 2000 Rule Curves were compared with observed mean reproductive success rates during the intervals 1979–1999 and 2000–2009. Observations of reproductive success were incomplete during each interval, and therefore the observed means are error-prone estimates of the true but unknown means during the spans of the 1970 and 2000 Rule Curves. Further, the bald eagle abundance increased dramatically from 1979–2009 and therefore predictions based on constant eagle abundance are likely biased estimates of actual reproductive success during 1970–1999 and 2000–2009. However, comparisons between the out-of-sample posterior predictions from the 1970 and 2000 Rule Curves with observed nesting success provide a supplemental way to evaluate model performance.

Table 2.5. Deviance Information Criterion (DIC; smaller is better) and pD, the estimate of the number of effective model parameters, for chick counts. Models 1–6 for 60-day nesting seasons are not comparable to models 7–9 from 45-day nesting seasons. See Appendix B for DIC and pD for pair counts and the totals.

Model	Nesting season	Water-level covariate(s)	Lake-effect prior	pD	DIC	Rank
6	60	Quadratic: z_1 = max.dw, z_4 = max.dw^2	log-N	61.46	2,587	1
5	60	Both: z_1 = max.dwdt, z_4 = max.dw	log-N	63.6	2,592	2
4	60	Max. rise: z_1 = max.dw	log-t	62.70	2,593	3
2	60	Max. of daily rises: z_1 = max.dwdt	log-t	64.36	2,596	4
3	60	Max. rise: z_1 = max.dw	log-N	61.95	2,596	4
1	60	Max. of daily rises: z_1 = max.dwdt	log-N	63.24	2,597	5
7	45	Quadratic: z_1 = max.dw, z_4 = max.dw^2	log-t	64.22	2,526	1
8	45	Both: z_1 = max.dwdt, z_4 = max.dw	log-N	65.68	2,531	2
9	45	Max. rise: z_1 = max.dw	log-t	64.31	2,537	3

2.3 Results and Discussion

2.3.1 Model Comparison and Evaluation of Predictive Performance

The DIC differences between Model 6 and the alternatives models based on 60-day nesting season ranged from 10 to 5 (Table 2.5), which indicates a practical superiority of Model 6. The second-best model (5) incorporated both the maximum daily rate of water-level rise and the maximum rise in water-level over the 60-day nesting season as the water-level covariates. However, the Pr = 0.95 for the water-level covariate parameters of Model 5 both included zero (Appendix B). Model 4 was a close contender to Model 5 and, like Model 6, included `max.dw` as the water-level covariate. The choice of vague prior distribution for the latent lake-specific random effect $\beta_{1,i}$ (Models 1 versus 2 and 3 versus 4) had at most a modest effect on DIC. Overall, the models which included `max.dw` outperformed those which included `max.dwdt` as the water-level covariate. That is, reproductive success was better predicted by the maximum rise during the nesting season than by the maximum daily rate of rise. The DIC values from models based on 45-day nesting seasons are not comparable to those from the 60-day nesting seasons because the requirement for multiple water-level readings within the smaller time interval eliminated data from some lakes. Further consideration of the 45-day models is deferred.

All models based on 60-day nesting seasons had difficulty accommodating the skewness in chick counts (Table 2.6). The Bayesian P-values indicate that all models adequately predicted extreme chick counts and numbers of

Table 2.6. Bayesian P-values for the largest observed chick count, skewness of chick counts and largest observed chick:pair ratio. Values less than 0.025 or larger than 0.975 provide evidence of inability adequately predict those quantities.

Model	Maximum chick count	Skewness of chick counts	Maximum chicks per pair
1	0.85	0.98	0.94
2	0.81	0.98	0.53
3	0.80	0.97	0.91
4	0.82	0.98	0.55
5	0.83	0.97	0.54
6	0.82	0.98	0.96

fledged chicks per nesting pair. The flat-tailed Student-t prior on the $\beta_{1,i}$ better accommodated large observations of reproductive success (Models 1 versus 2 and 3 versus 4), as measured by numbers of fledged chicks per nesting pair. Therefore model choice was based entirely on DIC. Model 6 was clearly the best model; the other models were not considered further, and their results are relegated to Appendix B.

The best model (Model 6) generally predicted the withheld chick counts satisfactorily (Fig. 2.11). The prevailing containment of the withheld chick counts within the corresponding Pr = 0.95 credible sets from the posterior predictive distributions indicates that Model 6 produces reasonable predictions of new observations. The binned (Gelman and Hill, 2006) raw residuals (averages of differences between observed chick counts and posterior mean chick counts within consecutive groups of counts) were generally symmetrically distributed about zero when plotted against either posterior mean counts or the water-level covariates (Fig. 2.12), indicating that both models predict the central tendencies of the data.

2.3.2 Assessment of Effects of Water-Level Fluctuations on Reproductive Success of Common Loons

All models predicted decreasing loon reproductive success with increasing water levels during the presumptive 60-day nesting season. Based on Model 6, the posterior Pr = 0.95 credible set for the linear effect of the maximum increase in water-level rise β_2 had an upper bound of zero, and the Pr = 0.95 credible set for the quadratic effect β_4 excluded zero (Table 2.7). Model 6 predicted reduction of reproductive success to approximately 50% of baseline ($\mathsf{max.dw} = 0$) where the maximum rise during the 60-day nesting season reaches approximately 100 cm (Fig. 2.13). Substantial declines in water-levels during the nesting season were also detrimental to reproductive success. Model 6 predicted reductions in reproductive success of approximately 20% where water levels decrease by approximately 100 cm during the 60-day nesting season. That result supports the the hypothesis that falling water levels lead to nest stranding and increased risk of egg and chick losses to terrestrial predators (Fair and Poirier, 1992).

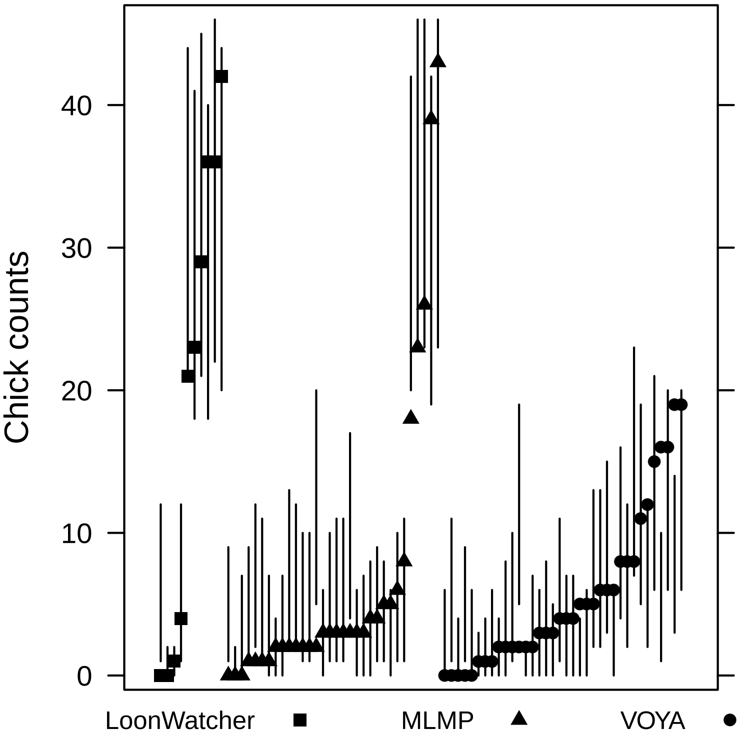

Figure 2.11. Out-of-sample posterior-predictive validation of Model 6. Solid symbols mark the chick counts that were withheld from model fitting and the vertical bars show corresponding Pr = 0.95 Bayesian credible sets from the posterior-predictive distribution of chick counts. Withheld chick counts are ordered by magnitude within the LWS, MLMP and VOYA survey programs for visual clarity.

Table 2.7. Summary of the joint posterior distribution of key parameters of Model 6. Standard deviation is denoted SD and Monte Carlo sampling error is denoted MC error.

Parameter	Mean	SD	MC error	Pr = 0.95 credible set
β_1	-0.3294	0.0717	2.2570E-03	(-0.4668, -0.1870)
β_2	-0.0016	0.0009	3.3240E-05	(-0.0034, 0.0000)
β_3	-0.0718	0.0248	6.0950E-04	(-0.1202, -0.0226)
β_4	-0.0056	0.0016	6.1490E-05	(-0.0090, -0.0024)

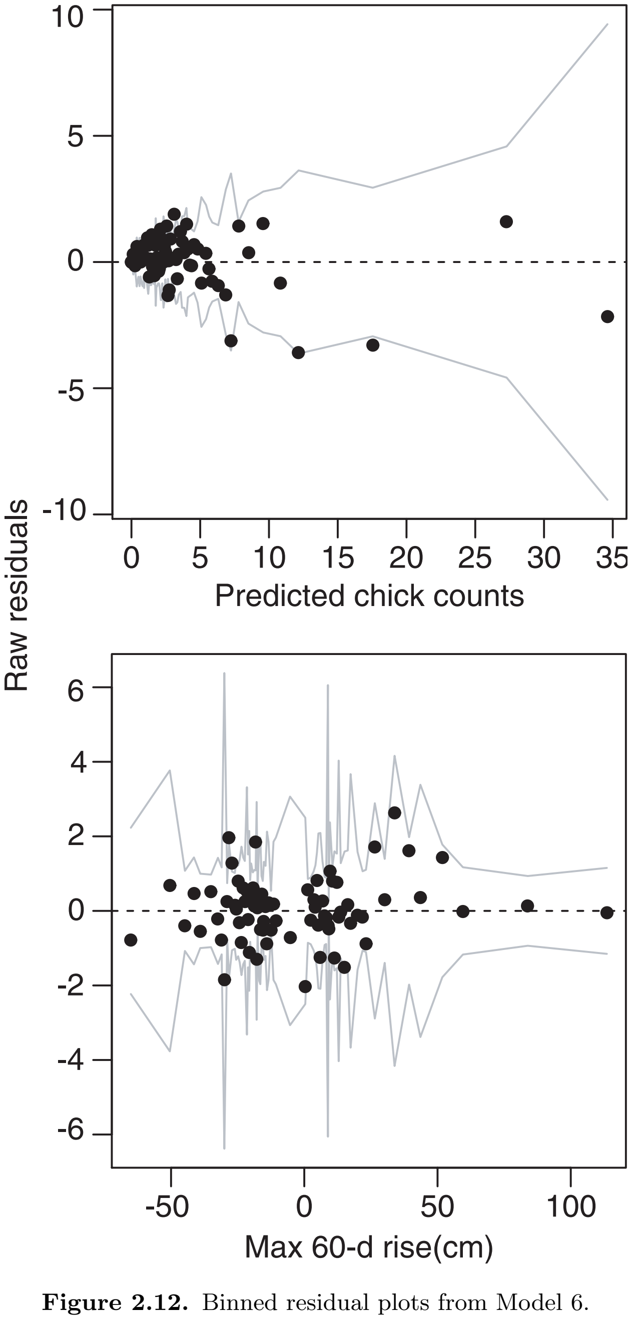

Figure 2.12. Binned residual plots from Model 6.

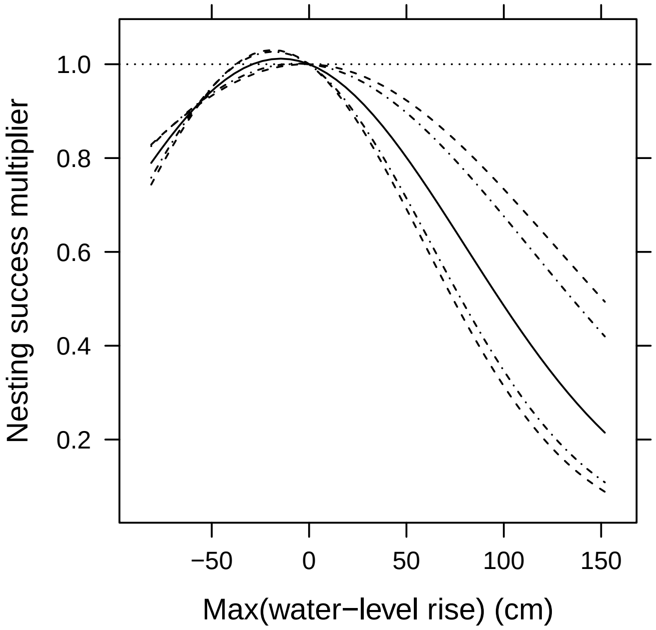

Figure 2.13. Multiplicative effect of water-level covariates on baseline reproductive success of common loons based on Model 6. The solid line is the posterior mean predicted effect and the pairs of dotted-dashed and dashed lines enclose Pr = 0.90 and Pr = 0.95 credible sets, respectively.

The regional bald eagle abundance index presented a consistent effect on common loon reproductive success in all nine models. The associated parameter β_3 (Eq. 2.2) had a posterior mean of approximately -0.07 in all models, and the Pr = 0.95 credible sets for that parameter always excluded non-negative values (Table 2.7). The bald eagle abundance index was completely confounded with a temporal trend (Fig. 2.7) and therefore the observed effect cannot be attributed uniquely to predation by bald eagles. Regardless of cause, the conditional effect was a reduction in loon reproductive success of approximately 23% from 1970 to 2010 across the set of survey lakes.

Perhaps surprisingly, the effect of latitude/climate had no detectable effect on reproductive success of common loons on the Minnesota lakes. The associated parameter β_4 (Eq. 2.2) had posterior distributions centered near zero from Models 1–4, and a very small effect in Model 9 (Appendix B). That is, reproductive success was not detectably lower from Minnesota lakes near the southern margin of the breeding range than from the northern lakes. Evidently the day-of-the-year of ice breakup has little effect on the reproductive success of common loons within the spatial extent of the Minnesota data.

The models based on 45-day nesting seasons were fitted to examine sensitivity to the assumption about duration of the nesting season. The rankings of models 7–9 were identical to their 60-day counterparts (Table 2.5), indicating that the superiority of Model 6 over Models 5 and 4 is not strongly contradicted under the assumption of a shorter nesting season. Loon life history supports the assumption of a 60-day nesting season, and the 45-day alternative also eliminates some data. Therefore inferences based on the 60-day models are based on more information and therefore should be preferred.

2.3.3 Evaluation of Effects of the 2000 Rule Curves for Rainy Lake and the Namakan Reservoir

Model 6 was used to quantify the effect of the 2000 Rule Curves on the reproductive success of common loons on Rainy, Namakan, Kabetogama and Sand Point Lakes (Appendix C). The 2000 Rule Curve on Rainy Lake is very similar to the 1970 Rule Curve (Fig. 2.3). The maxima of daily rates of water-level `max.dwdt` were largely unaffected by the 2000 Rule Curve (Table 2.8), and all values were near the low end of the range observed from Minnesota lakes (Fig. 2.13). In contrast, the large change in `max.dw` on the Namakan Reservoir (Table 2.8) more clearly reveals the difference between the 1970 and 2000 Rule Curves.

By hypothesis, the reduced amplitude of the 2000 Rule Curve on the Namakan Reservoir (Namakan, Kabetogama and Sand Point Lakes) should reduce `max.dw` and result in improved loon reproductive success. Model 6—based on the maxima of water-level rises during the presumptive 60-day nesting season—predicts a 45% increase in the reproductive success of common loons, as measured by chicks per pair, under the 2000 Rule

Table 2.8. Means of the estimated maxima of daily rates of water-level rise `max.dwdt` (cm $\cdot$ d^{-1}) and the maxima of rises `max.dw` (cm) during the presumptive 60-day loon nesting season under the 1970 and 2000 Rule Curves on Rainy Lake and the Namakan Reservoir.

	max.dwdt		max.dw	
Water body	1970	2000	1970	2000
Rainy Lake	4.0	6.8	36.8	37.1
Namakan Reservoir	5.9	6.6	102.1	49.0

Table 2.9. Posterior predictions of differences between mean chicks per pair under the 2000 and 1970 Rule Curves based on Model 6 and the maxima of water-level rises over the 60-d nesting seasons in Rainy Lake and the Namakan Reservoir (Namakan, Kabetogama and Sand Point Lakes). Adult loon counts and bald eagle abundance was held fixed in these comparisons to isolate the effect of water-level fluctuation. Given the data, model and priors, credible sets contain the true mean differences with probability 0.95.

	Chicks per pair			Chicks	
Lake	Percent change	Mean difference	Credible set	Mean difference	Credible set
Rainy	-6.2	-0.09	-0.05–0.01	-1.3	-4.5–1.8
Namakan	45.3	0.16	0.09–0.24	4.2	1.3–7.7
Kabetogama	45.4	0.12	0.07–0.17	4.0	1.2–7.1
Sand Point	45.4	0.08	0.04–0.12	0.5	-0.3–1.5

Table 2.10. Observed reproductive success, measured as the number of fledged chicks per mated pair, and posterior predictions under the 1970 and 2000 Rule Curves based on Model 6 and the maxima of water-level rises over the 60-d nesting seasons in Rainy Lake and the Namakan Reservoir (Namakan, Kabetogama and Sand Point Lakes). Adult loon counts and bald eagle abundance was held fixed in these comparisons in order to isolate the effect of water-level fluctuation. Given the data, model and priors, credible sets contain the true reproductive success with probability 0.95.

Lake	Rule curve	Observed	Predicted	Credible set
Rainy	1970	0.43	0.48	0.30–0.69
	2000	0.27	0.45	0.14–0.69
Namakan	1970	0.36	0.35	0.08–0.68
	2000	0.20	0.50	0.25–0.84
Kabetogama	1970	0.16	0.26	0.06–0.49
	2000	0.22	0.38	0.21–0.60
Sand Point	1970	0.26	0.17	0.04–0.33
	2000	0.34	0.25	0.13–0.40

Curve on the Namakan Reservoir (Table 2.9). Our results are consistent with that hypothesis. Observed loon reproductive success was generally in good agreement with model-based predictions, based on the assumptions of constant abundances of adult-loons and bald eagles, from the 1970 and 2000 Rule Curves. The lake-specific averages of observed reproductive success were within the Pr = 0.95 credible sets for the posterior predictions with the sole exception of Namakan Lake under the 2000 Rule Curve (Table 2.10). That is, the effect of the Rule Curves alone is sufficient to explain patterns in reproductive success of common loons from Rainy Lake and the Namakan Reservoir complex, with sole exception of Namakan Lake under the 2000 Rule Curve.

The reason for the discrepancy from Namakan Lake under the 2000 Rule Curve remains unknown. Observations were made only during 1979–1999 under the 1970 Rule Curve, and therefore it is possible that the observed mean overestimated nesting success during 1970–1999. Otherwise, an unknown lake-specific effect would seem to have reduced reproductive success on Namakan Lake under the 2000 Rule Curve relative to expectations based on the entire set of Minnesota lakes. Speculative possibilities include lake-specific effects of predators such as fishes and mammals, parasites and the prey base.

2.4 Summary and Conclusions

Data from two voluntary loon monitoring programs and from Voyageur's National Park were used to develop models of reproductive success of common loons on Minnesota lakes. All models predicted reduced reproductive success from increased daily rates of water-level rise or net water-level rises during the loon nesting season. The best models predicted all major features of the data, and also yielded plausible predictions of observations that had not been used in model fitting.

The water-level regimes of the 1970 and 2000 Rule Curves on Rainy Lake and the Namakan Reservoir were used as input to the best model of loon reproductive success. The leading model, which included the maxima of water-level rises during the presumptive 60-day nesting season, performed well over all of the data. The model predicted improvements in reproductive success of approximately 45% under the 2000 Rule Curve on three lakes of the Namakan Reservoir complex. Those model predictions were in general agreement with observations made from 2000-2009, with one exception. Observed reproductive success declined under the 2000 Rule Curve on Namakan Lake. The cause of that discrepancy remains unknown. Plausible hypotheses include overestimation of reproductive success over the time span of the 1970 Rule Curve and unknown local effects of predation, parasitism and food supply that were not measured by the data available to this study.

The data and models of this study provide information about effects of water-level fluctuations, bald eagle predation and/or regional trend and Minnesota climatic regime on the reproductive success of common loons on the breeding lakes. Therefore these models do not provide information on any effects of those factors on the regional population dynamics of loons, which are also influenced by factors that operate during migration and on the wintering grounds. Regional population growth rates may be highly sensitive to adult mortality rates, for which evidence of density-dependence is equivocal based on models of New Hampshire populations (Grear et al., 2009).

Therefore information is currently lacking to predict the consequences of variable reproductive success on abundance of loons in Minnesota and western Ontario. For example, if adult mortality rates are independent of adult population density, then the average annual additions of 8.7 chicks per year (Table 2.10) would eventually add more breeding pairs on the Namakan Reservoir. In turn those new breeding pairs would produce additional chicks, creating a trend of increasing population size via the same mechanism by which the compounding of interest (new chicks) increases the principle (loon population size) over time. Given that loons first breed at age 4–7 years (McIntyre and Barr, 1997), the time-frame for observation of unequivocal population increase may be decades. However if adult mortality rates increase strongly with adult densities or if regional nesting territories are fully occupied, then no increase in population size may be realized. Ongoing monitoring would be required to resolve that unanswered question. Regardless, it is clear that the rate of reproductive success of common loons has improved under the 2000 Rule Curve on the Namakan Reservoir.

2.5 Acknowledgments

Funding for this study was provided by the International Joint Commission through Contract Number 1042100753 to the U.S. Geological Survey (USGS). The Minnesota Department of Natural Resources provided data from the LoonWatcher Survey (LWS) and Minnesota Loon Monitoring Program (MLMP), and this project particularly benefited from the efforts of Sandy Fecht, Krista Larson and Pam Perry. Kevin Kenow (USGS) provided critical insights into the biology of common loons and recommendations for implementation. Geof Smith (NPS) managed data acquisition and Ben Schliffer (USGS) wrote code to extract and consolidate LWS and MLMP data from the numerous primary files. The numerous LWS and MLMP volunteers, and participants in the NPS loon surveys collected the data which made this project possible. Last, we are grateful to Douglas A. Wilcox, Kevin Kenow and an anonymous statistical reviewer who provided constructive critical comments which improved this product.

Bibliography

Akaike, H., 1973. Information theory and an extension of the maximum likelihood principle. In B. N. Petrov and F. Csaki, editors, *Second International Symposium on Information Theory*, pages 267–281. Akademiai Kiado, Budapest.

Balakrishnan, N., C. Charalabides, and N. Papadatos, 2003. Bounds on expectation of order statistics from a finite population. *Journal of Statistical Planning and Inference* **113**:569–588.

Barr, J., 1986. Population dynamics of the Common Loon (*Gavia immer*) associated with mercury-contaminated waters in northwestern Ontario. Technical report, Occasional Paper No. 56, Canadian Wildlife Service, Ottawa.

Belant, J. and R. Anderson, 1991. Common Loon, *Gavia immer*, productivity on a northern Wisconsin impoundment. *Canadian Field-Naturalist* **105**:29–33.

Brooks, S. P. and A. Gelman, 1997. General methods for monitoring convergence of iterative simulations. *Journal of Computational and Graphical Statistics* **7**:434–455.

Carlin, B. P. and T. A. Louis, 2009. Bayesian Methods for Data Analysis, 3rd ed. Chapman & Hall/CRC Press, Boca Raton.

David, H. A. and H. N. Nagaraja, 2003. Order Statistics, 3rd ed. Wiley-Interscience, Hoboken.

DeSorbo, C., K. Taylor, D. Kramar, J. Fair, J. J. Cooley, D. Evers, W. Hanson, H. Vogel, and J. Atwood, 2007. Reproductive advantages for common loons using rafts. *Journal of Wildlife Management* **71**:1206–1213. loons.

Ellison, A. M., 2004. Bayesian inference in ecology. *Ecology Letters* **7**:509–520.

Evers, D., 2007. Status assessment and conservation plan for the Common Loon (*Gavia immer*) in North America. Technical report, BRI Report 2007-20, U.S. Fish and Wildlife Service, Hadley, MA.

Fair, J., 1979. Water level fluctuations and Common Loon nest failure. In S. Sutcliffe, editor, *Proceedings of the North American Conference on Common Loon Research and Management*, pages 57–62. National Audubon Society, Washington, DC.

Fair, J. and B. Poirier, 1992. Managing for common loon on hydroelectric project reservoirs in northern New England. In L. Morse, S. Stockwell, and M. Pokras, editors, *The Loon and Its Ecosystem: Status, Management and Environmental Concerns*, page 221. U.S. Fish and Wildlife Service, Concord, NH.

Gelman, A., J. B. Carlin, H. S. Stern, and D. B. Rubin, 2004. Bayesian Data Analysis, 2nd ed. Chapman & Hall/CRC, Boca Raton.

Gelman, A. and J. Hill, 2006. Data Analysis Using Regression and Multilevel/Hierarchical Models. Cambridge University Press.

Grear, J., M. Meyer, J. Cooley, A. Kuhn, W. Piper, M. Mitro, H. Vogel, K. Taylor, K. Kenow, S. Craig, and D. Nacci, 2009. Population growth and demography of common loons in the northern United States. *Journal of Wildlife Management* **73**:1108–1115. loons.

Ince, D. C., L. Hatton, and J. Graham-Cumming, 2012. The case for open computer programs. *Nature* **482**:485–488.

Kenow, K., M. Meyer, F. Fournier, A. Elfessi, and S. Gutreuter, 2003. Effects of subcutaneous transmitter implants on behavior, growth, energetics, and survival of common loon chicks. *Journal of Field Ornithology* **74**:179–186.

Leisch, F., 2003. Sweave and beyond: computations on text documents. In K. Hornik, F. Leisch, and A. Zeileis, editors, *Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), Vienna*, pages 1–15. Technische Unitversität Wien, Vienna, Austria. http://www.ci.tuwien.ac.at/Conferences/DSC-2003/Proceedings/Leisch.pdf.

Mager, J. I., C. Walcott, and W. Piper, 2008. Nest platforms increase aggressive behavior in common loons. *Naturwissenschaften* **95**:141–147.

McCarthy, J. and C. Snowden, 1985. The bootstrap and finite population sampling. Technical report, Vital Health Statistics, Series 2, No. 95. The Department of Health and Human Services Publ. No. (PHS) 85-1369, Public Health Service, Washington.

McIntyre, J., 1988. The Common Loon: spirit of northern lakes. University of Minnesota Press, Minneapolis.

McIntyre, J. and J. Barr, 1997. Common loon (*Gavia immer*). In A. Poole and F. Gill, editors, *Birds of North America*, pages 1–31. The Academy of Natural Sciences, Philadelphia, PA, and The American Ornithologists' Union, Washington, DC.

Paruk, J., 1999. Territorial takeover in common loons (*Gavia immer*). *Wilson Bulletin* **111**:116–117.

Piper, W., M. Meyer, M. Klich, K. Tischler, and A. Dolsen, 2002. Floating platforms increase reproductive success of common loons. *Biological Conservation* **104**:199–203. loons.

R Development Core Team, 2011. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0.

Reiser, M., 1988. Effects of regulated lake levels on the reproductive success, distribution and abundance of the aquatic bird community in Voyageurs National Park, Minnesota. Technical report, Research/Resources Management Rport MWR-13, U.S. Department of the Interior, National Park Service, Omaha, NE.

Ruggles, R. and H. Brodie, 1947. An empirical approach to economic intelligence in World War II. *Journal of the American Statistical Association* **42**:72–91.

Spiegelhalter, D. J., N. Best, B. P. Carlin, and A. van der Linde, 2002. Bayesian measures of model complexity and fit (with discussion). *Journal of the Royal Statistical Society, Series B* **64**:583–639.

Thomas, A., B. O'Hara, U. Ligges, and S. Sturtz, 2006. Making BUGS open. *R News* **6**:12–17.

Vlietstra, L. and J. Paruk, 1997. Predation attempts on incubating common loons, *Gavia immer*, and the significance of shoreline nesting. *Canadian Field-Naturalist* **111**:656–657.

Windels, S., E. Beever, J. Paruk, A. Nelson, J. Fox, D. Evers, and C. MacNulty, In prep. Effects of 2000 rule curve on the reproductive success of the common loon *Gavia immer* in Voyageurs National Park. National Park Service, Voyageurs National Park, International Falls, MN.

Appendices

Appendix A
Comparative Evaluation of Estimators of Water-Level Fluctuation

This appendix is an image of the Reproducible Research Record for evaluation of the statistical properties of alternative estimators of water-level extremes. This reproducible research record (Ince et al., 2012) was implemented by the R noweb file `wl_est_simulation2.Rnw`. Execution of that file from R replicates the analysis and produces the LaTeX source file from which this appendix was generated. Thus, this appendix contains the printed record of the analysis.

Objective

The objective of this Monte Carlo simulation study is to explore the properties of ad hoc estimators of the maximum and range from hydrographs.

Implementation

This analysis used R version 2.14.0 (R Development Core Team, 2011). Computations were performed on `umesc-250.er.usgs.gov` running under Ubuntu Gnu/Linux 10.04LTS. This document was generated by the Sweave facility (Leisch, 2003) included with R.

Problem Description

Modeling of the effects of water-level fluctuations on the nesting success of common loons requires estimates of location and scale of extreme statistics. For example, loon nesting success is plausibly affected by the maximum daily rate of water-level increase and the maximum net increase in water level during the 60-day putative nesting season. Water-surface elevations are typically recorded at regularly spaced temporal intervals (e.g., weekly, daily, etc.). Therefore the quality of water-level data varies among lakes. From some lakes as few as six readings might be available and from others as many as 60 readings. Although water level varies continuously with time, the observed maxima from daily data likely provide reasonable (essentially error-free) estimates of the maxima. However that is not the case where few readings are available. We need plausible estimates of the maxima and ranges of functions of water-surface elevations and measures of uncertainty.

For some random variable X_i, $i = 1 \cdots n$ having distribution function $f(X|\theta)$, define $X_{1:n} \leq \cdots \leq X_{n:n}$ as the ordered set of variates. The maximal order statistic is denoted by $X_{n:n}$, the minimal order statistic is denoted by $X_{1:1}$ and the range is denoted by $W = X_{n:n} - X_{1:n}$. The limiting distribution of $X_{n:n}$ does not generally exist (David and Nagaraja, 2003). The assumption of finite populations of water-level readings holds approximately because the best water-level recordings from Minnesota lakes are made daily, and diel variation is likely to be insignificant. Therefore we make that assumption. Let x denote an observable sample from X. Balakrishnan et al. (2003) derived bounds on expectations of *sample* order statistics $x_{1:n} \leq \cdots \leq x_{n:n}$ from finite populations, but those bounds do not inform bounds on the $X_{1:n} \leq \cdots \leq X_{n:n}$. The famous "German tank problem" (Ruggles and Brodie, 1947) provides an estimate of the total number of items (observed and unobserved) based on a sample of (observed) sequential identifiers. In contrast, we need estimates of finite-population extremes based on a sample of real-valued observations. A search of the literature did not reveal a general solution supported by sampling theory.

Therefore we resort to evaluation of a set of ad hoc estimators. Let $X_N = \{X_i\}, i = 1, \cdots, N$ denote a set of water levels of length N, and let $x_n = \{x_i\}, i = 1, \cdots, n$ for $n \leq N$ denote a sample of observations from X_N. We seek estimates of the maximum and range of X_N based on information contained in x_n. Let $\{X_{1:N}, X_{N:N}\}$ and $\{x_{1:n}, x_{n:n}\}$ denote the extremes of X_N and x_n, respectively. Trivially $x_{1:n} = X_{1:N}$ and $x_{n:n} = X_{N:N}$ for $n = N$. We evaluate the following ad hoc estimators of $X_{N:N}$:

$$\hat{X}_{N:N,1} = x_{n:n} \tag{A-1}$$

$$\hat{X}_{N:N,2} = x_{n:n} + \bar{\delta}_x \sqrt{\frac{N-n}{N}} \tag{A-2}$$

$$\hat{X}_{N:N,3} = x_{n:n} + \frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}} \tag{A-3}$$

$$\hat{X}_{N:N,4} = x_{n:n} + 1.5\frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}} \tag{A-4}$$

where $\bar{\delta}_x$ is the average of first differences of $x_{i:n}$. Each of those estimators satisfies $\hat{X}_{N:N} = x_{n:n}$ for $n = N$. The naive estimate $\hat{X}_{N:N,1}$ may underestimate $X_{N:N}$ for $n < N$, and the bias is likely to be severe for small n. $\hat{X}_{N:N,2}$ adds the product of the sample mean of x and the finite-population correction factor to the observed maximum. $\hat{X}_{N:N,3}$ adds one standard error of the estimate of $\bar{X}$ to the observed maximum $x_{n:n}$. Last $\hat{X}_{N:N,4}$ adds 1.5 times the standard error of the estimate of $\bar{X}$ to the observed maximum

$x_{n:n}$. The population range is defined as $W_N = X_{N:N} - X_{1:N}$, and we seek estimates based on the following ad hoc estimators

$$
\begin{aligned}
\hat{W}_{N,1} &= x_{n:n} - x_{1:n} && \text{(A-5)}\\
\hat{W}_{N,2} &= \hat{X}_{N:N,2} - \left(x_{1:n} - \bar{\delta}_x \sqrt{\frac{N-n}{N}} \right) && \text{(A-6)}\\
\hat{W}_{N,3} &= \hat{X}_{N:N,3} - \left(x_{1:n} - \frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}} \right) && \text{(A-7)}\\
\hat{W}_{N,4} &= \hat{X}_{N:N,3} - \left(x_{1:n} - 1.5\frac{s}{\sqrt{n}} \sqrt{\frac{N-n}{N}} \right) && \text{(A-8)}
\end{aligned}
$$

where $\bar{\delta}$ is the average of the lag-1 differences in $x_{1:n}, \cdots, x_{n:n}$, similar to the corresponding estimates of $X_{N:N}$. Lacking general limiting distributions for $\hat{X}_{N:N,j}$ and $\hat{W}_{N,j}, j = 1, \cdots, 4$, we must resort to Monte Carlo simulation to compare the performances of the estimators.

We evaluate the performances of the estimators based on relative bias given by

$$\text{rBias} = \frac{\sum_{i=1}^{M} \left(\hat{\theta}_i - \theta \right)}{\theta M}$$

where the $\hat{\theta}_i$ are M estimates of some parameter θ, and based on relative root mean-squared error given by rRMSE $= \frac{\sqrt{MSE}}{\theta}$ where

$$\text{MSE} = \frac{\sum_{i=1}^{M} \left(\hat{\theta}_i - \theta \right)^2}{M}.$$

Distributions

Water-level data in lakes have characteristics that aid identification of plausible distributions. Water levels have lower and upper bounds in reservoirs and drainage lakes, and even practical annual limits may be assumed for most seepage lakes. The lower bounds in reservoirs and drainage lakes are fixed by the lower control point of dams and the elevation of the outlet, respectively. Upper bounds of reservoirs and drainage lakes are fixed by emergency spillways and alternate over-land flow paths. For those reasons, the distributions of both $X_{N:N}$ and W_N are likely to have compact support. However it is also useful to investigate properties of estimators from distributions that have long tails.

To evaluate properties of $\hat{X}_{N:N,j}, j = 1, \cdots, 4$ we selected four distributions that present a wide range of challenges to estimation of $X_{N:N}$. We drew $N = 60$ random values which were defined as populations from which samples of size n were drawn, at random, for the simulations. We drew X_1 as the sum of a deterministic increasing trend and an AR(4) process generated from $\mathrm{N}(0, 0.01)$ innovations and AR parameter $\theta = (0.6, 0.2, 0.1, 0.08)$.

The series X_1 mimics the natural trend of increasing water-levels during the spring nesting season, and may typify natural conditions. We drew X_2 as an AR(4) process similar to X_1 but scaled to zero mean and variance 0.16. We drew X_3 as an ARMA(4,4) process based on AR parameter θ and MA parameter $\phi = \theta$. Last, we drew $X_4 \sim \mathrm{N}(0,1)$ (white noise). The series X_4 almost certainly presents a much greater challenge to estimation of $X_{n:n}$ than natural hydrographs because of the implausible serial independence and large relative variation.

```
R> library(lattice)
R> ltheme <- canonical.theme(color = FALSE) ## in-built B&W theme
R> ltheme$strip.background$col <- "transparent" ## change strip bg
R> lattice.options(default.theme = ltheme) ## set as default
R> library(coda)
R> stdize <- function(x){(x - mean(x))/sd(x)}

R> set.seed(7351335)
R> N <- 60
R> days <- 1:N
R> # Simple mimic [Deterministic trend + AR(4), Var(X1) approx. = 0.05 ]
R> X1 <- arima.sim(list(order=c(4,0,0), ar=c(0.6,0.2,0.1,0.08)),
+                  n=N, rand.gen=rnorm)
R> X1 <- X1/12
R> X1 <- ((0:(N-1))/(N-1)) + X1
R> X1 <- stdize(X1)
R> # AR(4) N(0,0.01)
R> X2 <- arima.sim(list(order=c(4,0,0), ar=c(0.6,0.2,0.1,0.08)),
+                  n=N, rand.gen=rnorm, sd=0.1)
R> X2 <- (X2 - .006)/.396
R> X2 <- stdize(X2)
R> # ARMA(4,4) N(0,0.01)
R> X3 <- arima.sim(list(order=c(4,0,4), ar=c(0.6,0.2,0.1,0.08),
+                  ma=c(0.6,0.2,0.1,0.08)), n=N, rnorm, sd=0.1)
R> X3 <- (X3-0.039)/.757
R> X3 <- stdize(X3)
R> # White noise -- N(0,1)
R> X4 <- arima.sim(list(order=c(0,0,0)), n=N, n.start=1,
+                  rand.gen=rnorm)
R> X4 <- stdize(X4)
R> X <- cbind(X2,X3,X4)
R> X <- as.mcmc(X)
R> fig1 <- acfplot(X,aspect=1,ylim=c(-.2,1),xlab="Days", layout=c(3,1),
+                  col="black",
+          strip = strip.custom(bg="white", factor.levels =
+                  c(expression(X[2]),
+                    expression(X[3]),expression(X[4]))))
R> days_l <- rep(days,4)
```

```
R> X <- c(X1,X2,X3,X4)
R> var <- c(rep("X1",N),rep("X2",N),rep("X3",N),rep("X4",N))
R> df <- data.frame(days_l,X,var)
R> fig2 <- xyplot(X~days_l|var,data=df,layout=c(4,1), col="black",
+                 type="l",xlab="Days",ylab="X",
+                 strip = strip.custom(bg="white",
+                   factor.levels =
+                  c(expression(X[1]),expression(X[2]),
+                    expression(X[3]),expression(X[4]))))
R> rm(days, days_l, X, X1, X2, X3, X4)
```

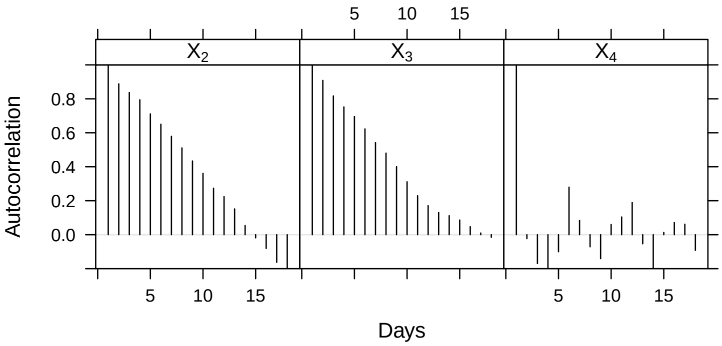

Figure A-1. Sample autocorrelation functions for X_i, $i = 2, \ldots, 4$.

Sample autocorrelation functions (ACFs) for X_2–X_4 are given in Fig. (A-1). The ACF of the stationary part of X_1 is identical to the ACF of X_2. Sample series representing 60-day segments of X_1–X_4 are given in Fig. (A-2).

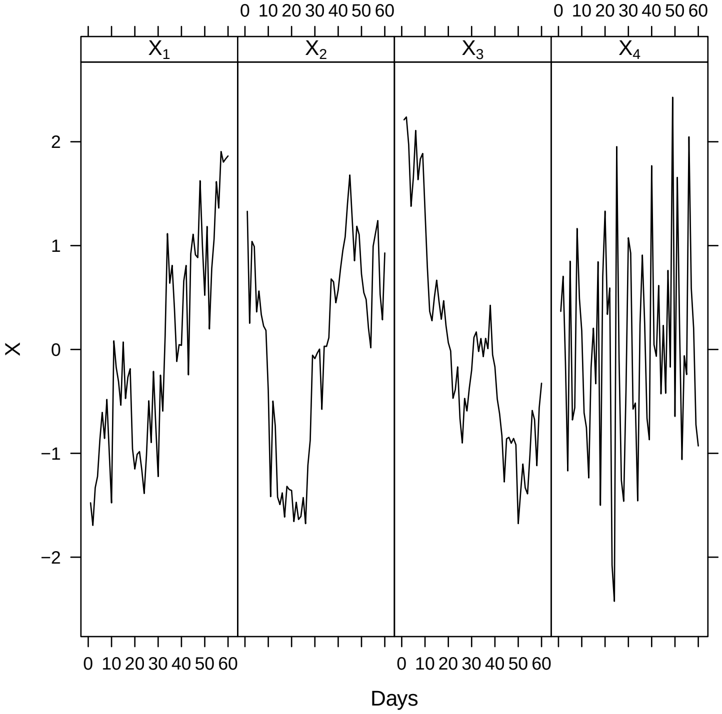

Figure A-2. Example 60-d segments of X_i, $i = 1, \ldots, 4$.

Monte Carlo Simulations

We simulate 500 populations of 60-day hydrographic records. Typically, water levels are recorded at regular time intervals. From each population we draw samples, without replacement, of size $n = 6, 10, 15, 20, 30, 40, 50, 60$. For samples of size $n \leq 30$ selection from the populations is systematic beginning with a random start. For samples of size 40 and 40, we make random draws without replacement. Samples of size 60 include the entire populations. We then compute the sample estimators, relative bias, and relative MSE.

```
R> # SET PARAMETERS FOR SIMULATION
R> n <- c(6, 10, 15, 20, 30, 40, 50, 60)  # Sample sizes
R> N <- 60                                # "Population" size
R> Nreps <- 500                           # No. reps in simulation
R> set.seed(7351337)                      # Fix RNG seed
R> theta <- c(0.6,0.2,0.1,0.08)           # AR & MA parameter choices
R> fpc <- sqrt((N-n)/(N))                 # Finite pop. correction
R> # INITIALIZE STORAGE ARRAYS
R> # Array indexing: h indexes Nreps replicate "populations"
R> #                 i (implicit) indexes 4 generating distributions
R> #                 j indexes length(n) sample sizes
R> #                 k indexes estimator
R> #                 l (implicit) indexes "population" size, N
R> # X[h,i]          "Population" h from distribution i
R> # maxX[h,i]       True max from X[h,i]
R> # obsMax[h,i,j]   Observed max in rep h, dist. i and sample-size j
R> # obsW[h,i,j]     Observed range in h,i,j
R> # estMax[h,i,j,k] Estimated max in h,i,j based on estimator k
R> # estW[h,i,j,k]   Estimated range in h,i,j based on estimator k
R> X <- array(0, dim=c(N,4))
R> maxX <- W <- array(0, dim=c(Nreps,4))
R> obsMax <- obsW <- obsMin <- array(0, dim=c(Nreps, 4, length(n)))
R> estMax <- estW <- array(0, dim=c(Nreps, 4, length(n), 4))
R> # SIMULATE AD HOC ESTIMATION
R> for (h in 1:Nreps){
+   # Generate h "populations" from the i=4 distributions
+   Xdum <- arima.sim(list(order=c(4,0,0), ar=theta), n=N,
+                     rand.gen=rnorm)
+   Xdum <- Xdum/12
+   X[,1] <- as.vector(((0:(N-1))/(N/3)) + Xdum)
+   X[,1] <- round(stdize(X[,1]), digits=5)
+   Xdum <- arima.sim(list(order=c(4,0,0), ar=theta), n=N,
+                     rand.gen=rnorm, sd=0.1)
+   X[,2] <- as.vector((Xdum - .006)/.396)
+   X[,2] <- round(stdize(X[,2]), digits=5)
```

```
+   Xdum <- arima.sim(list(order=c(4,0,4), ar=theta, ma=theta),
+                     n=N, rand.gen=rnorm, sd=0.1)
+   X[,3] <- as.vector((Xdum-0.039)/.757)
+   X[,3] <- round(stdize(X[,3]), digits=5)
+   X[,4] <- rnorm(N, mean=0, sd=1)
+   X[,4] <- round(stdize(X[,4]), digits=5)
+   # Find "population" max and range for rep. h and dist. i.
+   maxX[h,] <- apply(X, 2, max)
+   W[h,] <- maxX[h,] - apply(X, 2, min)
+   # Draw, from the "populations", temporally systematic samples
+   # beginning with random starts, and estimate max and range;
+   # j indexes sample size vector n.
+   st <- round(runif(length(n), rep(1,8), N/n))   # random starts
+   inc <- floor(N/n)                              # systematic increment
+   minc <- sdx <- array(0, dim=c(4,length(n)))
+   for (j in 1:length(n)){
+     if (n[j]<=30) {indx <- st[j] + (0:(n[j]-1))*inc[j]} else
+        {indx <- sort(sample(1:60,n[j],replace=FALSE))}
+     x <- X[indx,]                                # Draw the sample
+     minc[,j] <- abs(apply(apply(x,2,sort),2,mean))
+     sdx[,j] <- apply(x,2,sd)
+     obsMax[h,,j] <- apply(x, 2, max)
+     obsMin[h,,j] <- apply(x, 2, min)
+     obsW[h,,j] <- obsMax[h,,j] - obsMin[h,,j]
+     estMax[h,,j,1] <- obsMax[h,,j]
+     estMax[h,,j,2] <- obsMax[h,,j] + fpc[j]*minc[,j]
+     estMax[h,,j,3] <- obsMax[h,,j] + (sdx[,j]/sqrt(n[j]))*fpc[j]
+     estMax[h,,j,4] <- obsMax[h,,j] + 1.5*(sdx[,j]/sqrt(n[j]))*fpc[j]
+     estW[h,,j,1] <- obsMax[h,,j] - obsMin[h,,j]
+     estW[h,,j,2] <- estMax[h,,j,2] -
+       (obsMin[h,,j] - fpc[j]*minc[,j])
+     estW[h,,j,3] <- estMax[h,,j,3] -
+       (obsMin[h,,j] - (sdx[,j]/sqrt(n[j]))*fpc[j])
+     estW[h,,j,4] <- estMax[h,,j,4] -
+       (obsMin[h,,j] - 1.5*(sdx[,j]/sqrt(n[j]))*fpc[j])
+                            }
+                     }
R> rbias.Max <- array(0,dim=c(4,length(n),4))
R> rRMSE.Max <- array(0,dim=c(4,length(n),4))
R> rbias.W <- array(0,dim=c(4,length(n),4))
R> rRMSE.W <- array(0,dim=c(4,length(n),4))
R> for(i in 1:4){
+     for(j in 1:length(n)){
+         for(k in 1:4) {
+             rbias.Max[i,j,k] <-
+               mean((estMax[,i,j,k]-maxX[,i])/maxX[,i])
```

```
+             rRMSE.Max[i,j,k] <-
+               sqrt(mean(((estMax[,i,j,k]-maxX[,i])/maxX[,i])^2))
+             rbias.W[i,j,k] <- mean((estW[,i,j,k]-W[,i])/W[,i])
+             rRMSE.W[i,j,k] <-
+               sqrt(mean(((estW[,i,j,k]-W[,i])/W[,i])^2))
+         }
+     }
+ }
R> # Maximum Plot
R> lattice.options(default.theme = modifyList(standard.theme(color = FALSE),
+                   list(strip.background = list(col = "transparent"))))
R> data1 <- data.frame(rbias.Max)
R> Value <- c(data1[1,1:32],data1[2,1:32],data1[3,1:32],data1[4,1:32])
R> Value <- round(as.numeric(Value),digits=5)
R> DistStat <- c(rep("max(X1) Bias",32),rep("max(X2) Bias",32),
+               rep("max(X3) Bias",32),rep("max(X4) Bias",32))
R> Pop <- c(rep("X1",32),rep("X2",32),rep("X3",32),rep("X4",32))
R> Statistic <- rep("rBias",32)
R> Estmnd <- rep("Maximum",32)
R> Estimator <- c(rep(1,8),rep(2,8),rep(3,8),rep(4,8))
R> sampn <- rep(n[1:8],4)
R> df <- data.frame(Estmnd,Statistic,Pop,DistStat,Estimator,sampn,Value)
R> colnames(df) <- c("Estimand","Statistic","Distribution",
+                   "DistStat","Estimator","n","Value")
R> data2 <- data.frame(rRMSE.Max)
R> Value2 <- c(data2[1,1:32],data2[2,1:32],data2[3,1:32],data2[4,1:32])
R> Value2 <- round(as.numeric(Value2), digits=5)
R> DistStat2 <- c(rep("max(X1) RRMSE",32),rep("max(X2) RRMSE",32),
+                rep("max(X3) RRMSE",32),rep("max(X4) RMSE",32))
R> Statistic <- rep("rRMSE",32)
R> df2 <- data.frame(Estmnd,Statistic,Pop,DistStat2,Estimator,sampn,Value2)
R> colnames(df2) <- c("Estimand","Statistic","Distribution",
+                    "DistStat","Estimator","n","Value")
R> df <- rbind(df,df2)
R> write.table(df,file='wl_sim_max_results.txt',row.names=FALSE)
R> legend1 <- list(space="top",title="Estimator",cex.title=.9,
+                 text=c("1:","2:","3:","4"),type="l",lty=c(1,2,3,4),
+                 points=FALSE,lines=TRUE,columns=4,cex=0.9,
+                 col=rep("black",4))
R> #legend1 <- list(space="top",title="Estimator",cex.title=.9,type="l",
R> #                columns=4,cex=0.9,col="black",
R> #                lines=list(lty=c(1,2,3,4),points=FALSE,col=rep("black",4)))
R> maxPlot <- xyplot(Value~n|DistStat,df,groups=Estimator,layout=c(4,2),
+                   type="l",lty=c(1,2,3,4),auto.key=legend1,ylab="Value",
+                   col="black",xlab="Sample Size",strip =
+                   strip.custom(factor.levels =
```

```
+                 c(expression(X[1]-Bias),expression(X[2]-Bias),
+                   expression(X[3]-Bias),expression(X[4]-Bias),
+                   expression(X[1]-RRMSE),expression(X[2]-RRMSE),
+                   expression(X[3]-RRMSE),expression(X[4]-RRMSE))))
R> # Range Plot
R> data1 <- data.frame(rbias.W)
R> Value <- c(data1[1,1:32],data1[2,1:32],data1[3,1:32],data1[4,1:32])
R> Value <- round(as.numeric(Value), digits=5)
R> Estmnd <- rep("Range",32)
R> DistStat <- c(rep("range(X1) Bias",32),rep("range(X2) Bias",32),
+               rep("range(X3) Bias",32),rep("range(X4) Bias",32))
R> Pop <- c(rep("X1",32),rep("X2",32),rep("X3",32),rep("X4",32))
R> Statistic <- rep("rBias",32)
R> Estimator <- c(rep(1,8),rep(2,8),rep(3,8),rep(4,8))
R> df <- data.frame(Estmnd,Statistic,Pop,DistStat,Estimator,sampn,Value)
R> colnames(df) <- c("Estimand","Statistic","Distribution",
+                   "DistStat","Estimator","n","Value")
R> data2 <- data.frame(rRMSE.W)
R> Value2 <- c(data2[1,1:32],data2[2,1:32],data2[3,1:32],data2[4,1:32])
R> Value2 <- round(as.numeric(Value2), digits=5)
R> DistStat2 <- c(rep("range(X1) RMSE",32),rep("range(X2) RMSE",32),
+                rep("range(X3) RMSE",32),rep("range(X4) RMSE",32))
R> Statistic <- rep("rRMSE",32)
R> df2 <- data.frame(Estmnd,Statistic,Pop,DistStat2,Estimator,sampn,Value2)
R> colnames(df2) <- c("Estimand","Statistic","Distribution",
+                    "DistStat","Estimator","n","Value")
R> df <- rbind(df,df2)
R> write.table(df,file='wl_sim_range_results.txt',row.names=FALSE)
R> rangePlot <- xyplot(Value~n|DistStat,df,groups=Estimator,layout=c(4,2),
+                     type="l",lty=c(1,2,3,4),auto.key=legend1,ylab="Value",
+                     col="black",xlab="Sample Size",strip =
+                     strip.custom(factor.levels =
+                   c(expression(X[1]-Bias),expression(X[2]-Bias),
+                     expression(X[3]-Bias),expression(X[4]-Bias),
+                     expression(X[1]-RRMSE),expression(X[2]-RRMSE),
+                     expression(X[3]-RRMSE),expression(X[4]-RRMSE))))
```

Results

The performance of the four estimators of the population maximum is shown in Fig. A-3. The naive estimator (1) underperforms the ad hoc estimators in terms of relative RMSE and relative bias. The performance of the four estimators of the population range is shown in Fig. A-4. The naive estimator (1) underperforms the ad hoc estimators in terms of relative RMSE and relative bias.

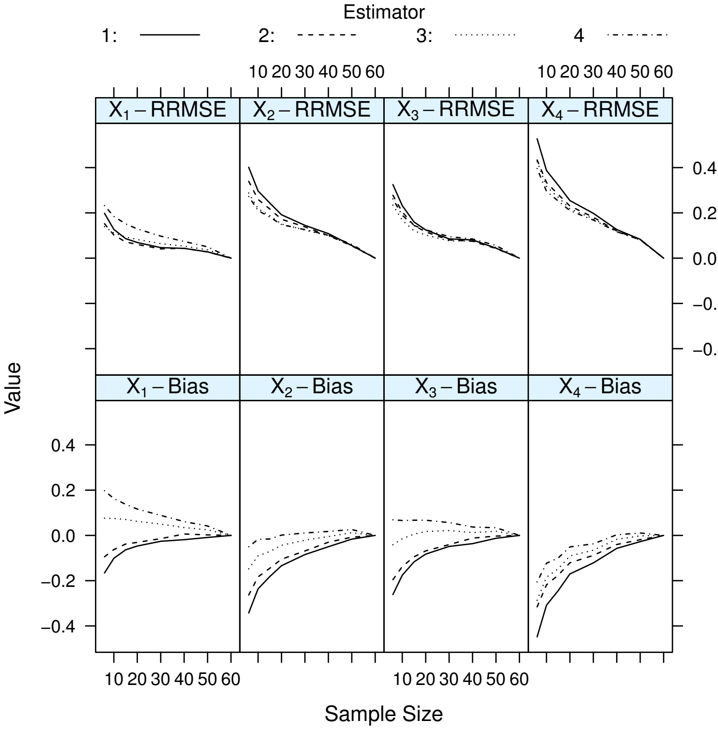

Figure A-3. Relative root mean-squared error (RRMSE) and relative bias (Bias) of four ad-hoc estimators of the unknown population maximum generated from four distributions X_i, $i = 2, \ldots, 4$. The distribution of X_1 is similar to natural hydrographs and the white-noise process that generate X_4 probably represents an extreme challenge to estimation of the population maximum. Samples were drawn from 500 independent replicates of each distribution.

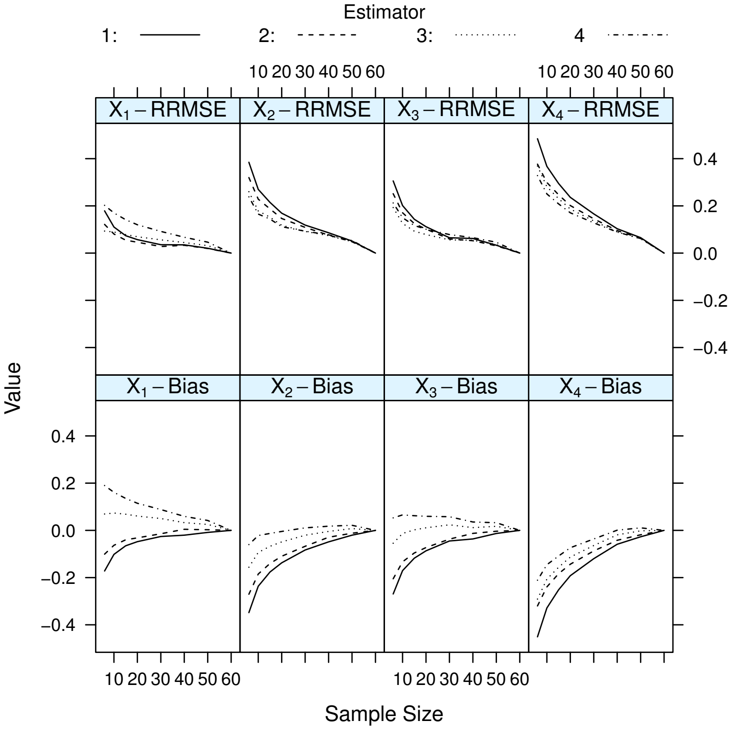

Figure A-4. Relative root mean-squared error (RRMSE) and relative bias (Bias) of four ad-hoc estimators of the unknown population range generated from four distributions X_i, $i = 2, \ldots, 4$. The distribution of X_1 is similar to natural hydrographs and the white-noise process that generate X_4 probably represents an extreme challenge to estimation of the population range. Samples were drawn from 500 independent replicates of each distribution.

Appendix B
Hierarchical Bayesian Models of Nesting Success of Common Loons

This appendix is an image of the Reproducible Research Record for evaluation of the statistical properties of alternative estimators of water-level extremes. This reproducible research record (Ince et al., 2012) was implemented by the R noweb file `loon-models.Rnw`. Execution of that file from R replicates the analysis and produces the LaTeX source file from which this appendix was generated. Thus, this appendix contains the printed record of the analysis.

Introduction

Objective

The objective of this analysis is to identify any effects of water-level rises on the nesting success of common loons *Gavia immer* on Minnesota lakes. Nesting success is quantified by counts of loon chicks during late summer (July–August). Data were provided by the Minnesota Department of Natural Resources from two loon-monitoring programs staffed by citizen volunteers. The LoonWatcher (LW) program records counts of adults, nesting pairs and chicks from undefined partial or complete circuits of lakes. The Minnesota Loon Monitoring Program (MLMP) records only counts of adults and chicks. Covariates include estimates of measures of water-level increases during the presumptive 60-day nesting season, as determined from the day of ice-out, a bald eagle regional abundance index obtained from the Wisconsin Department of Natural Resources, and the day-of-the year of ice-out.

Implementation

This analysis used R version 2.15.1 (R Development Core Team, 2011). Bayesian Markov Chain Monte Carlo sampling was implemented using the R package BRugs version 0.7-7 (Thomas et al., 2006). Computations were performed on `umesc-250.er.usgs.gov` running under Ubuntu Gnu Linux 10.04.

Data Description

The data are from the Minnesota Loon Monitoring Program (MLMP), the Minnesota Volunteer LoonWatcher Program (LWP) and from the National Park Service Voyageurs National Park (VOYA), and are documented in Metadata for Data File loon_comb.csv, S. Gutreuter, April 1, 2011. The LWP and MLMP data are collected by citizen volunteers. Data were obtained from 93 lakes of at least 405 hectares in surface area, and from variable numbers of years within those lakes. The loon data are described more thoroughly in *Metadata for Data File loon_comb.csv* (S. Gutreuter, 13 December 2011).

All sources contain counts of chicks and adults made in late summer, so that the variable chicks is a surrogate for the numbers of fledged loons. The LWP and VOYA data also contain counts of nesting pairs. Only nesting pairs produce chicks, so that pairs is the more appropriate offset variable for chicks.

Water-level data were obtained from various sources, including the LWP and MLMP. Water-level readings were available from variable and sporadic dates within lakes. Only water-level data from within 60-day windows beginning with the of nesting are relevant. The maximum of the daily rates of water-level rise (max_dwldt_60; $\mathrm{cm} \cdot \mathrm{d}^{-1}$) and the maximum amplitude of water-surface elevation (max_wldif_60; cm) were computed from within the 60-day windows (ret1 = 1). Details of estimation of water-level covariates are given in *Reproducible Research Record: Monte Carlo Simulation Study of Properties of Ad Hoc Estimators of Extremes of Water-Level Fluctuation* (S. Gutreuter and C. Spanbauer, 18 November 2011).

Data were retained for analysis from those lakes from which there were at least three years of loon counts and at least six water-level measurements within each 60-day putative nesting season.

Data extraction

Extract the loon-count and water-level data from `loon_comb.csv` and extract the Wisconsin bald eagle nest index from `EagelNestSurvey.csv`:

```
R> library(BRugs)
R> library(xtable)
R> library(moments)
R> library(latticeExtra)
R> library(arm)
R> setwd("/home/sgutreuter/projects/NRPP-Voya/R/loons")
R> old.par <- par
R> options(SweaveHooks = list(fig=function() par(mar=c(5.1,4.1,1.1,2.1))))
R> datdir <- paste((Sys.getenv("DATA")), "/projects/NRPP-Voya/Loons/", sep="")
R> bugsdir <- paste((Sys.getenv("HOME")),
+                    "/projects/NRPP-Voya/R/loons/BUGS/", sep="")
R> eagledata <- read.csv(paste(datdir, "EagleNestSurvey.csv", sep=""))
```

```
R> loondata <- read.csv(paste(datdir, "loon_comb.csv", sep=""))
R> loondata <- loondata[(!loondata$adults == 0 & loondata$ret1 == 1),]
R> ## Omit records having implausible chick and/or pair counts:
R> ## -------------------------------------------------------------------
R> ##   9 chicks and 1 pair were reported from Birch Lake (Todd Co.)
R> ##     during 2002.  That is impossible and the data are omitted.
R> loondata <- loondata[!(loondata$lkcode==770084 & loondata$year==2002),]
R> ##   14 chicks and 3 pairs were reported from Kabekona L. (Hubbard Co.)
R> ##     during 1997.  4.6 chicks/pair is implausible, and data omitted.
R> loondata <- loondata[!(loondata$lkcode==290075 & loondata$year==1997),]
R> ##   4 chicks from 1 pair was reported from Cross L. (Crow Wing Co.)
R> ##     during 1980.  That ratio has not been reported elsewhere, and
R> ##     the next highest ratio is 3:1, which is known to be possible, but
R> ##     rare.  The 1980 Cross Lake record is omitted.
R> loondata <- loondata[!(loondata$lkcode==180312 & loondata$year==1980),]
R> ## -------------------------------------------------------------------
R>
R> loondata <- merge(loondata, eagledata, by.x="year", by.y="year")
R> loondata <- loondata[order(loondata$source, loondata$lkcode, loondata$year),]
R> ## Hold out selected data from model fitting to enable out-of-sample
R> ## predictive evaluation by setting chicks <- NA.
R> chicks.temp <- rep(-9,nrow(loondata))
R> chicks.holdouts <- rep(-9,nrow(loondata))
R> loondata$chicks.all <- loondata$chicks
R> loondata$pairs.all <- loondata$pairs
R> for(i in 1:nrow(loondata)){
+         if(loondata$holdout[i]==1){
+                 chicks.holdouts[i] <- loondata$chicks[i]
+                 chicks.temp[i] <- NA}
+         else{ chicks.holdouts[i] <- NA
+              chicks.temp[i] <- loondata$chicks[i]}
+ }
R> loondata$chicks <- chicks.temp
R> loondata$chicks.holdouts <- chicks.holdouts
R> rm("chicks.temp")
R> year <- loondata$year
R> yr <- as.factor(year-1978)
R> lake <- as.factor(loondata$lake)
R> lkcode <- as.factor(loondata$lkcode)
R> lkno <- charmatch(lkcode, unique(lkcode))
R> adults <- loondata$adults
R> pairs <-  loondata$pairs
R> chicks <- loondata$chicks
R> ix <- (!is.na(loondata$pairs.all)) & loondata$pairs.all>0
R> cpp.obs <- loondata$chicks.all[ix]/loondata$pairs.all[ix]
R> max.cpp.obs <- max(cpp.obs,na.rm=TRUE)
```

```
R> eagleindx <- (loondata$eaglenests -
+              mean(loondata$eaglenests))/sd(loondata$eaglenests)
R> survey <- as.factor(loondata$source)
R> mean.doy.io <- round(mean(loondata$doy_io))
R> doy_io <-  loondata$doy_io - mean.doy.io
R> max.dwdt <- loondata$est_max_dwl_ddoy60
R> mean.max.dwdt <- mean(max.dwdt)
R> max.dwdt <- max.dwdt - mean.max.dwdt
R> v.max.dwdt <- loondata$v_est_max_dwl_ddoy60
R> v.max.dwdt[v.max.dwdt==0] <- 0.0001
R> tau.max.dwdt <- 1/v.max.dwdt
R> max.dw <- loondata$est_delta_wl60
R> mean.max.dw <- mean(max.dw)
R> max.dw <- max.dw - mean.max.dw
R> v.max.dw <- loondata$v_est_w_diffwl60
R> v.max.dw[v.max.dw==0] <- 0.0001
R> tau.max.dw <- 1/v.max.dw
R> N <- length(adults)
R> nlakes <- max(lkno)
R> if ( !file.exists(paste(bugsdir, "chains", sep="")))
+     dir.create(paste(bugsdir,"chains",sep=""))
R> if ( !file.exists(paste(bugsdir, "inputs", sep="")))
+     dir.create(paste(bugsdir,"inputs",sep=""))
R> if ( !file.exists(paste(bugsdir,"preds", sep="")))
+     dir.create(paste(bugsdir,"preds",sep=""))
R> predir <- paste(bugsdir,"preds/",sep="")
R> dicNode <- c("chicks","pairs","total")
R> dicMod <- data.frame(row.names=NULL)
R> dicMod2 <- data.frame(row.names=NULL)
R> plot1 <- histogram(loondata$est_max_dwl_ddoy60, type="count", col="white",
+                    xlab="max(daily water-level rise) (cm/day)")
R> plot2 <- histogram(loondata$est_delta_wl60, type="count", col="white",
+                    xlab="max(water-level increase) (cm)")
R> plot3 <- xyplot(loondata$eaglenests ~ year, type="p",
+                 col=c(rep("black",2)), lty=c(0,1),
+                 xlab="Year", ylab="Bald eagle nests")
R> plot4 <- histogram(loondata$doy_io, type="count", col="white",
+                    xlab="Day of the year of ice breakup")
```

Validation Samples

Some samples were withheld from model fitting to evaluate out-of-sample predictive performance (Table B-1). Data were withheld from the VOYA lakes from multiple years under operation of both the 1970 and 2000 Rule Curves. There was some overlap between the LoonWatcher and MLMP surveys; data were withheld from the MLMP surveys where overlap occurred.

Finally, we place some premium on predictive performance on large lakes. The LoonWatcher surveys spanned many years on both Leach and Vermilion Lakes, so we withheld a subset of those samples.

Table B-1. List of samples withheld from model fitting and reserved for evaluation of out-of-sample predictive performance

Survey	Lake	County	Year(s) withheld	Samples
LoonWatcher	Leech	Cass	1993,1995,2004–05	4
LoonWatcher	Vermilion	St Louis	2005–10	6
MLMP	Farm Island	Aitkin	2001–02,2007–09	5
MLMP	Height of Land	Becker	2009	1
MLMP	Island	Becker	1996,1998–2009	14
MLMP	Otter Tail	Otter Tail	2004,2007	3
MLMP	Vermilion	St Louis	1995–2000	6
MLMP	White Earth	Becker	2003–09	6
VOYA	Kabetogama	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
VOYA	Namakan	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
VOYA	Rainy	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
VOYA	Sand Point	St Louis	1983–1985, 1997, 2001, 2003, 2005, 2007, 2009	9
Totals				81

Model Description

Chicks are produced only by mated pairs, so that pair count is an obvious predictor of chick counts. Pair counts were recorded during LoonWatcher and NPS surveys, but not during MLMP surveys. Therefore pair counts from the MLMP surveys must be estimated from adult counts, and that is accomplished with an imputation-like model using data from all survey types. Counts of adult loons are assumed, of practical necessity, to have been measured without error. Adult counts require only identification of adult loons, which is an easy task. In addition, identification of mated pairs requires correct identification of associations between adults based only on survey sightings, which is affected by the spatial locations of males and females at particular points in time. Therefore it is plausible that pair counts are subject to greater error than are adult counts, and the models incorporate that estimation error.

Plausible models of nesting success predict the numbers of chicks per nesting pair as non-negative functions of alternative measures of water-level fluctuation and other plausible covariates. Further, individual lakes may have features that affect nesting success, including latent covariates such as prey availability and environmental contaminants. Therefore all models include lake-specific random effects to capture such latent sources of variation. Denote the numbers of chicks, mated pairs and adults counted on lake i during year j as Y_{ij}, X_{ij} and W_{ij}, respectively, and let $\mathbf{z}_{ij}$ denote a vector of covariates. Values of X_{ij} were not recorded by the MLMP, and we also assume a multiplicative measurement error structure given by $X_{ij} = \lambda_{X,ij} + \epsilon_i$ where $\lambda_{X,ij} = \mathrm{E}\left(X_{ij}\right)$ and ϵ_j is measurement error. Therefore we adopt a possibly over-dispersed Poisson model for pair counts X_{ij} given by

$$\begin{aligned}
X_{ij} &\sim \text{Po}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_i \\
\epsilon_i &\sim \text{N}\left(0, \tau_X\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_\theta\right) \\
\mathbf{\Omega}_\theta &\sim \text{Wishart}\left(\rho_\theta \mathbf{R}_\theta, \rho_\theta\right),
\end{aligned}$$

with the addition of an appropriate prior on τ_x. We allow for correlation among $\theta = (\theta_1 \theta_z)$ through the multivariate normal prior distribution having mean vector $\mathbf{0}$ and precision matrix $\mathbf{\Omega}_\theta$. We give $\mathbf{\Omega}_\theta$ the most vague hyperprior that is still proper by choosing the dimension of θ for ρ_θ and where $\mathbf{R}_\theta$ is a scaling matrix of the order of the covariance matrix $\mathbf{\Sigma}_\theta = \mathbf{\Omega}_\theta^{-1}$. The statistical models of reproductive success are elaborations on the general form

$$\begin{aligned}
Y_{ij} &\sim \text{Po}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,i} + \beta_z \mathbf{z}_{ij}\right) \\
\beta_{1,i} &\sim \text{f}\left(\beta_1, \tau_{\beta_1}\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_z) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_\beta\right) \\
\mathbf{\Omega}_\beta &\sim \text{Wishart}\left(\rho_\beta \mathbf{R}_\beta, \rho_\beta\right),
\end{aligned}$$

where $\beta_{1,i}$ are lake-specific random-effects parameters, β_z is a parameter vector associated with $\mathbf{z}_{ij}$. Note that the expected values of pair counts $\lambda_{X,ij}$ appear as offsets, so that the exponential function in $\lambda_{Y,ij}$ is a dimensionless model of the numbers of chicks per pair. We borrow strength across lakes by assuming that the $\beta_{1,i}$ share a common mean β_1 in the prior distribution $f\left(\beta_1, \tau_{\beta_1}\right)$, and allow for correlation among $\beta = (\beta_1, \beta_z)$ through the multivariate normal prior distribution having mean vector $\mathbf{0}$ and precision matrix $\mathbf{\Omega}_\beta$. The Gamma$(3, 1)$ distribution provides a reasonably vague hyperprior specification for the precision τ_{β_1} in the prior for β_1. We give $\mathbf{\Omega}_\beta$ the most vague hyperprior that is still proper by choosing the dimension of β for ρ_β and where $\mathbf{R}_\beta$ is a scaling matrix of the order of the covariance matrix $\mathbf{\Sigma}_\beta = \mathbf{\Omega}_\beta^{-1}$.

Covariates

Covariates are given in Table B-39

The covariate vector $\mathbf{z}$ comprises several variables (Table B-39). The production and survival of chicks through late July is likely influenced by several factors, including spring water-level rises. The hypothetical mechanism for the effect of water-level fluctuation is nest flooding. Mated pairs may respond to rising water levels by building up the elevation of the existing nest or, if inundation occurs, by abandoning the nest and, perhaps,

Table B-2. List of covariates

Covariate	Description
`max.dwdt`	Maximum of daily water-level rises ($\mathrm{cm \cdot day^{-1}}$), centered
`v.max.dwdt`	Variance of `max.dwdt`
`max.dw`	Maximum water-level rise (cm), centered
`v.max.dw`	Variance of `max.dw`
`eagleindex`	Standardized WI eagle nest counts
`doy_io`	Day of the year of ice-out, centered

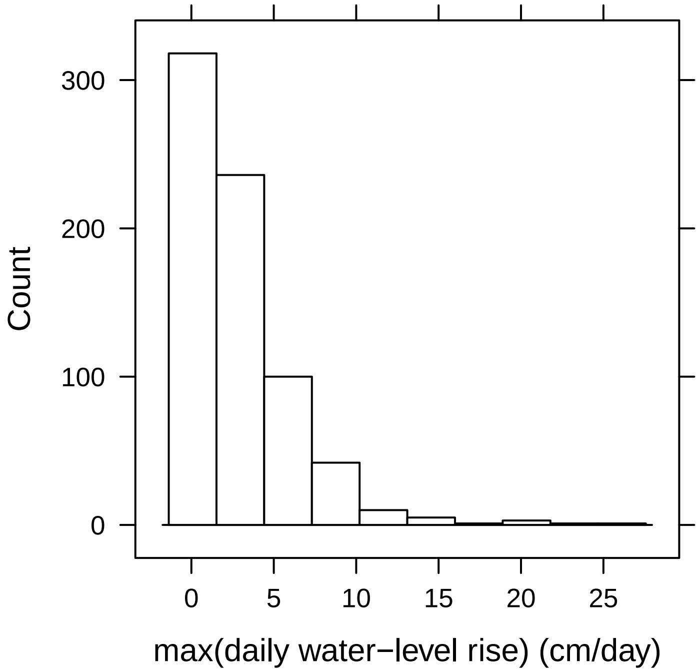

Figure B-1. Marginal distribution of the estimated maxima of daily rates of water-level increase ($\mathrm{cm \cdot day^{-1}}$), computed from presumptive 60-day nesting seasons, in combinations of lakes and years from which loon nesting data were selected.

attempting nesting at a higher elevation. Eggs or chicks may be lost during abandonment. Therefore our primary focus is on measures of rise in water-surface elevation. Two measures are obvious candidates. First, the *maximum rate of daily rise* `max.dwdt` (cm·day^{-1})measures the severity of the most-rapid increase (Fig. B-1). Rapid rates of rise may overwhelm the pairs ability to build-up the elevation of the existing nest. Second, the *maximum net increase in water-surface elevation* `max.dw` (cm) measures the severity of flooding during the 60-day nesting period regardless of the rate of increase (Fig. B-2). Large increases in water-surface elevation may eliminate entire nesting sites, especially where bank slopes become steep.

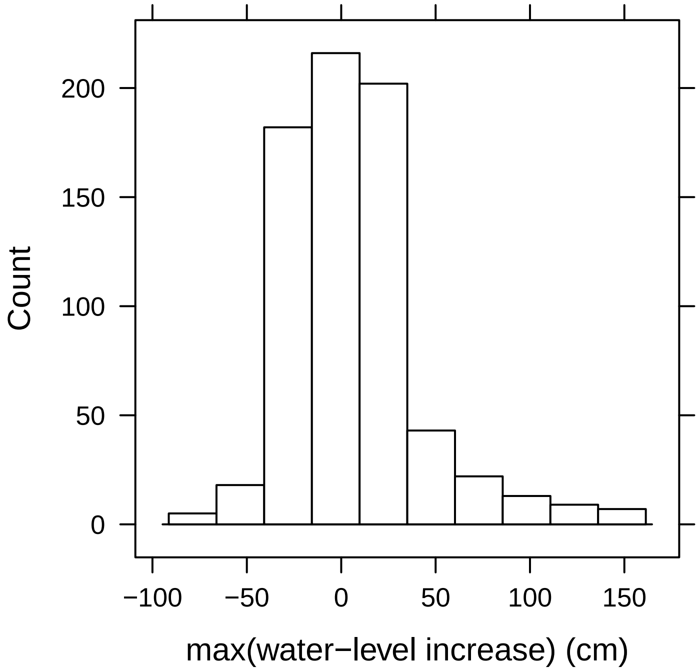

Figure B-2. Marginal distribution of the estimated maxima of water-level increases (cm) during the presumptive 60-day nesting seasons in combinations of lakes and years from which loon nesting data were selected.

Predation is also an important source of mortality in loon chicks. Potential predators include mink, racoons, bald eagles, foxes, wolves and bobcats. Among those, a regional abundance index, `eagleindex`, is available for bald eagles. Nest counts of bald eagles have been increasing steadily since at least 1979 (Fig. B-3). Therefore this regional eagle abundance index is correlated with any monotonic temporal trend, and cannot isolate any pure effect of eagle abundance. Inclusion in models serves as a marker for trend and may represent effects of predation by bald eagles.

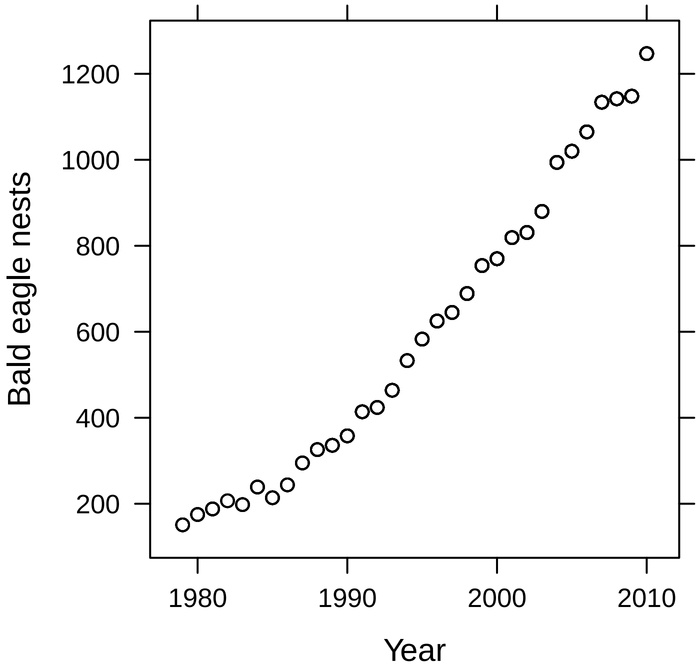

Figure B-3. Numbers of occupied bald eagle territories tabulated by the Wisconsin Bald Eagle and Osprey Surveys (`http://dnr.wi.gov/org/land/wildlife/harvest/harvest.htm`).

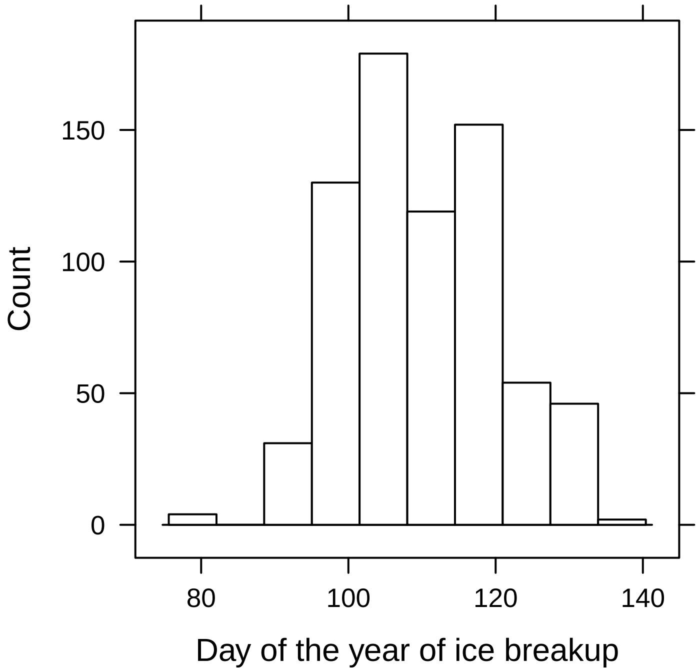

Figure B-4. Distribution of day-of-the year of spring ice breakup on for combinations of lakes and years represented in the Minnesota loon data.

The summer breeding range of common loons spans a climatic gradient. The earlier spring ice break up on southerly lakes provides loons with a longer nesting season that may influence nesting success. Therefore `doy_io`, the (centered) day of the year (counted from January 1) of ice break up (Fig. B-4) is a plausible covariate for prediction of nesting success.

Model Fitting and Assessment

Model 1: Maximum daily water level rise and normally distributed random effects

Description

Model 1 uses the estimated maxima of the daily rates of water-level increase as the water-level predictor covariate. A vague normal distribution is assumed for the latent random effect of lakes on nesting success.

Let $z_{1,ij}$ denote the *estimated maxima of daily rates of water-level increase during the 60-day nesting season* (variable `est_max_dwl_ddoy` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j \\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right) \\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_X\right) \\
\mathbf{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right) \\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right) \\
\beta_{1,j} &\sim \text{N}\left(\beta_1, \tau_{\beta_1}\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_Y\right) \\
\mathbf{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000         ##  Number of burn-in iterations
R> nsamps <- 5000         ##  Number of post-convergence iterations
R> Model <- 1             ##  Model number
R> ##modseed <- as.numeric(Sys.time())
```

```
R> modseed <- 2736736
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+                (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+                0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+               max.dwdt=max.dwdt, tau.max.dwdt=tau.max.dwdt,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx, doyio=doy_io,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                      beta.chicks=parm0[1,3:6],
+                      beta.chicks.j=re0[,1]),
+                 list(theta.pairs=parm0[2,1:2],
+                      beta.chicks=parm0[2,3:6],
+                      beta.chicks.j=re0[,3]),
+                 list(theta.pairs=parm0[3,1:2],
+                      beta.chicks=parm0[3,3:6],
+                      beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                            theta.pairs[2]*adults[i]*adults[i] +
+                            epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                             beta.chicks[2]*mu.max.dwdt.cut[i] +
+                             beta.chicks[3]*eagleindx[i] + beta.chicks[4]*doyio[i]
```

```
+                              )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dwdt[i] ~ dnorm(mu.max.dwdt[i],tau.max.dwdt[i])
+         mu.max.dwdt.cut[i] <- cut(mu.max.dwdt[i])
+         mu.max.dwdt[i]~dnorm(3,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dnorm(beta.chicks[1],tau.chicks)
+                         }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-5).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> ## Consider eliminating monitoring of Cov.theta and Cov.beta
R> samplesSet(c("theta.pairs", "sigma.pairs",
+              "beta.chicks", "sigma.chicks",
+              "lambda.chicks","post.chicks",
+              "cpp"))
```

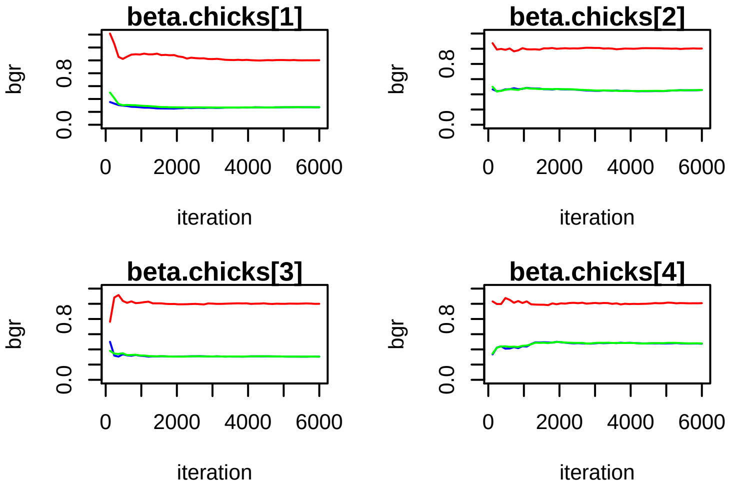

Figure B-5. Model 1: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod <- rbind(dicMod,dicTmp)
R> rm(dicTmp)
```

Table B-3. Model 1: Summary of the joint posterior distribution of the parameters.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3574	0.0114	7.6070E-04	0.3322	0.3571	0.3777
theta.pairs[2]	-0.0004	0.0001	3.9220E-06	-0.0005	-0.0004	-0.0003
sigma.pairs	0.9828	0.1635	6.5240E-03	0.6996	0.9699	1.3360
beta.chicks[1]	-0.3739	0.0745	2.0600E-03	-0.5155	-0.3746	-0.2227
beta.chicks[2]	-0.0201	0.0086	1.7020E-04	-0.0377	-0.0198	-0.0040
beta.chicks[3]	-0.0716	0.0254	6.6550E-04	-0.1214	-0.0718	-0.0218
beta.chicks[4]	-0.0009	0.0024	6.2920E-05	-0.0054	-0.0009	0.0038
sigma.chicks	0.4708	0.0531	1.0290E-03	0.3783	0.4669	0.5858

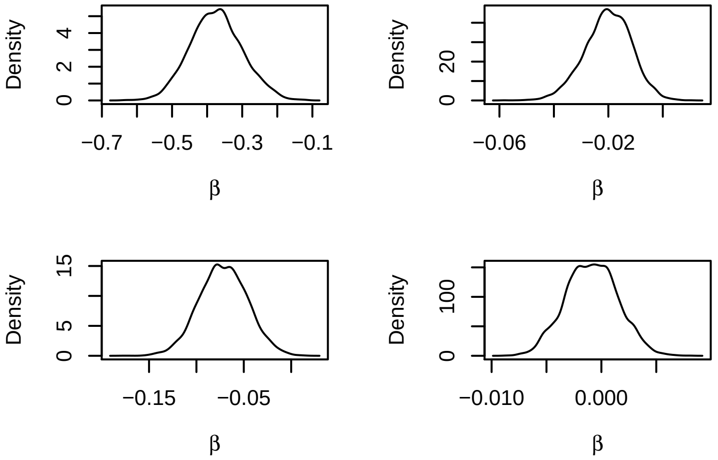

Figure B-6. Model 1: Posterior densities of the parameter vector β.

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                           chicks.holdouts,chicks.post.u,max.dwdt)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                    points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                        groups=post.chicks$survey,
+                        key=key.groups,
+                        panel=panel.bar,
+                        dyu=post.chicks$chicks.post.u,
+                        dyl=post.chicks$chicks.post.l,
+                        cex=1.0,col="black",fill=T,
+                        ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                        pch=c(15,17,16),ylab="Chick counts",xlab="",
+                        scales = list(x = list(draw = FALSE)))


R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dwdt=max.dwdt
R> resids <- resids[!is.na(resids$resid.raw),]
```

Table B-4. Model 1: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0444	-0.0900	0.0396
beta.chicks[2]	0.0444	1.0000	0.0180	0.0894
beta.chicks[3]	-0.0900	0.0180	1.0000	0.0112
beta.chicks[4]	0.0396	0.0894	0.0112	1.0000

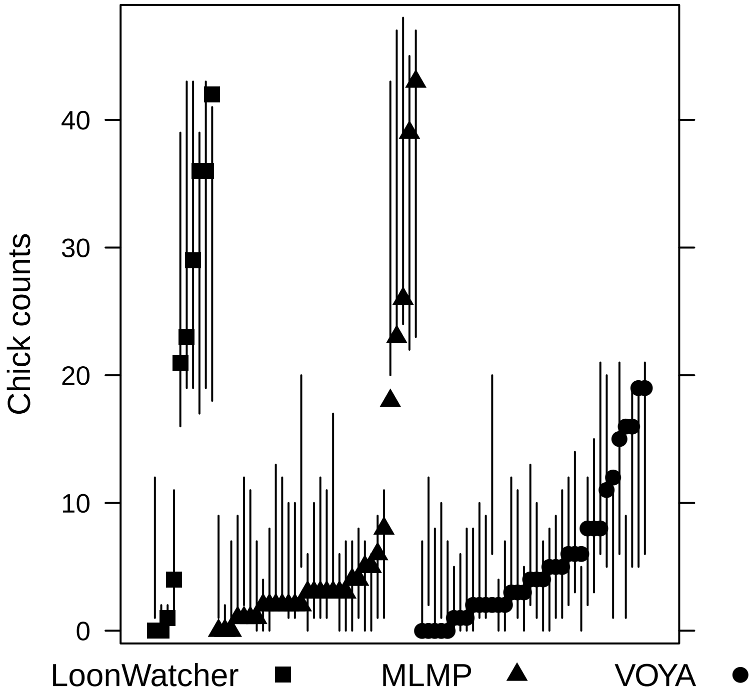

Figure B-7. Model 1: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]

R> binnedplot(resids$pred.chicks,resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Predicted chick counts",
+            ylab="Raw residuals")
```

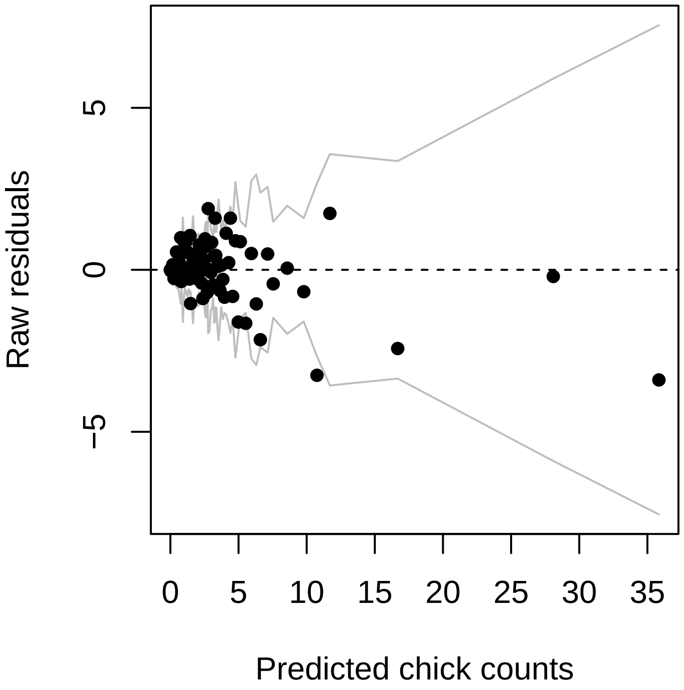

Figure B-8. Model 1: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                      quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
```

```
R> binnedplot((resids$max.dwdt+mean.max.dwdt),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max WL rise (cm/d)",
+            ylab="Raw residuals")
```

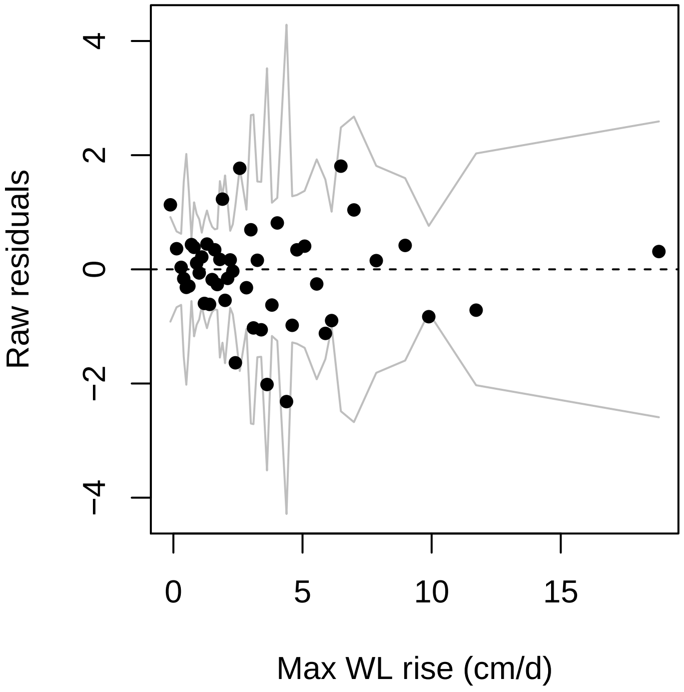

Figure B-9. Model 1: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                    quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                              "Maximum chicks/pair"),
+                      P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                      row.names=NULL)
```

Table B-5. Model 1: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.8482
Skewness of chick counts	0.9846
Maximum chicks/pair	0.937

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks-",sep=""), quiet=TRU
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                       probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                        q_025=as.numeric(beta2.cs[1]),
+                        q_05=as.numeric(beta2.cs[2]),
+                        q_10=as.numeric(beta2.cs[3]),
+                        q_25=as.numeric(beta2.cs[4]),
+                        q_50=as.numeric(beta2.cs[5]),
+                        q_75=as.numeric(beta2.cs[6]),
+                        q_90=as.numeric(beta2.cs[7]),
+                        q_95=as.numeric(beta2.cs[8]),
+                        q_975=as.numeric(beta2.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> Pr_beta2 <- round(sum((beta2.chains<0)/length(beta2.chains)),digits=4)
R> Pbeta2 <- data.frame(Value=Pr_beta2)
R> rm("beta2.chains","Pr_beta2")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_2 < 0)$.

The effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

```
R> zz <- seq(from=ceiling(min(max.dwdt)),to=floor(max(max.dwdt)),length.out=50) + mea
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q))
R> wl.effect <- data.frame(wl.var=zz,
+                       wl.mean=wl.tmp[,1],
+                       wl.q025=wl.tmp[,2],
+                       wl.q05=wl.tmp[,3],
+                       wl.q10=wl.tmp[,4],
+                       wl.q25=wl.tmp[,5],
+                       wl.q50=wl.tmp[,6],
+                       wl.q75=wl.tmp[,7],
+                       wl.q90=wl.tmp[,8],
+                       wl.q95=wl.tmp[,9],
+                       wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                      xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                             zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                             distribute.type=TRUE, col=c(rep("black",5)),
+                             xlab="Max(daily water-level rise) (cm/day)",
+                             ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

Table B-6. Model 1: Pr(beta2 < 0)

Value
0.9934

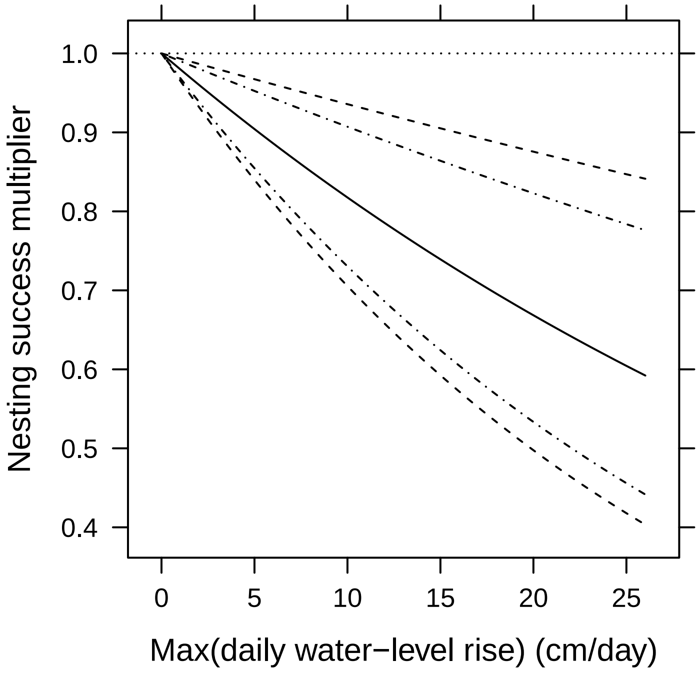

Figure B-10. Model 1: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model 2: Maximum daily water level rise and t-distributed random effects

Description

Model 2 uses the estimated maxima of the daily rates of water-level increase as the water-level predictor covariate. A vague Student-t distribution is assumed for the latent random effect of lakes on nesting success.

Let $z_{1,ij}$ denote the *estimated maxima of daily rates of water-level increase during the 60-day nesting season* (variable `est_max_dwl_ddoy` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j \\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right) \\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \boldsymbol{\Omega}_X\right) \\
\boldsymbol{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\ 2\right) \\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right) \\
\beta_{1,j} &\sim \text{t}\left(\beta_1, \tau_{\beta_1}, 3\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \boldsymbol{\Omega}_Y\right) \\
\boldsymbol{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\ 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> Model <- 2               ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
R> set.seed(modseed)
```

```
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+               paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+               paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+               (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+               0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+              max.dwdt=max.dwdt, tau.max.dwdt=tau.max.dwdt,
+              lkno=lkno, N=N, nlakes=nlakes,
+              eagleindx=eagleindx, doyio=doy_io,
+              zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+              nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+         datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                     beta.chicks=parm0[1,3:6],
+                     beta.chicks.j=re0[,1]),
+               list(theta.pairs=parm0[2,1:2],
+                     beta.chicks=parm0[2,3:6],
+                     beta.chicks.j=re0[,3]),
+               list(theta.pairs=parm0[3,1:2],
+                     beta.chicks=parm0[3,3:6],
+                     beta.chicks.j=re0[,3])),
+          numChains = 3, initfiles, digits=5)
R> write("model{
+    for (i in 1:N){
+
+        ##  Model for nesting pairs
+        pairs[i] ~ dpois(lambda.pairs[i])
+        lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                         theta.pairs[2]*adults[i]*adults[i] +
+                         epsilon.pairs[lkno[i]])
+
+        ##  Model for chicks
+        chicks[i] ~ dpois(lambda.chicks[i])
+        cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                         beta.chicks[2]*mu.max.dwdt.cut[i] +
+                         beta.chicks[3]*eagleindx[i] + beta.chicks[4]*doyio[i]
+                         )
+        lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
```

```
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dwdt[i] ~ dnorm(mu.max.dwdt[i],tau.max.dwdt[i])
+         mu.max.dwdt.cut[i] <- cut(mu.max.dwdt[i])
+         mu.max.dwdt[i]~dnorm(3,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dt(beta.chicks[1],tau.chicks,3)
+                         }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-11).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+             "beta.chicks", "sigma.chicks",
+             "lambda.chicks","post.chicks",
+             "cpp"))
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
```

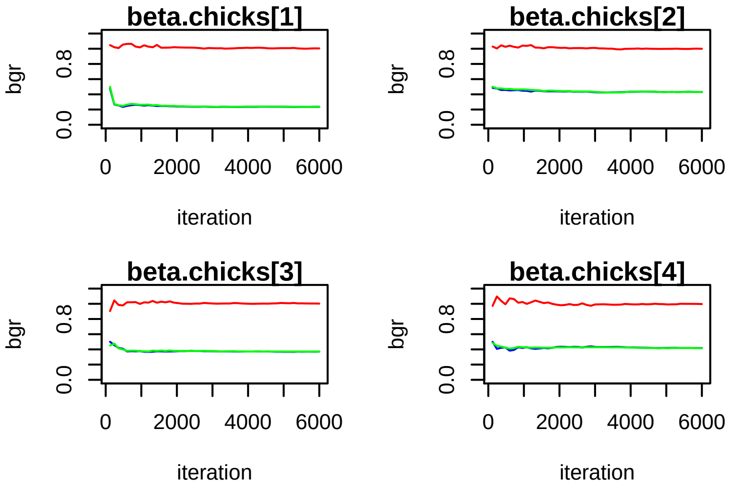

Figure B-11. Model 2: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod <- rbind(dicMod,dicTmp)
R> rm(dicTmp)
```

Table B-7. Model 2: Summary of the joint posterior distribution of the parameters.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3536	0.0144	9.6970E-04	0.3281	0.3550	0.3808
theta.pairs[2]	-0.0004	0.0001	4.6060E-06	-0.0005	-0.0004	-0.0002
sigma.pairs	1.0130	0.1759	7.7270E-03	0.7125	0.9975	1.3970
beta.chicks[1]	-0.3513	0.0772	2.6860E-03	-0.5086	-0.3497	-0.2066
beta.chicks[2]	-0.0194	0.0084	1.7610E-04	-0.0370	-0.0190	-0.0035
beta.chicks[3]	-0.0718	0.0254	6.7330E-04	-0.1211	-0.0716	-0.0223
beta.chicks[4]	-0.0010	0.0022	6.1970E-05	-0.0055	-0.0010	0.0033
sigma.chicks	0.4014	0.0513	9.4540E-04	0.3123	0.3975	0.5145

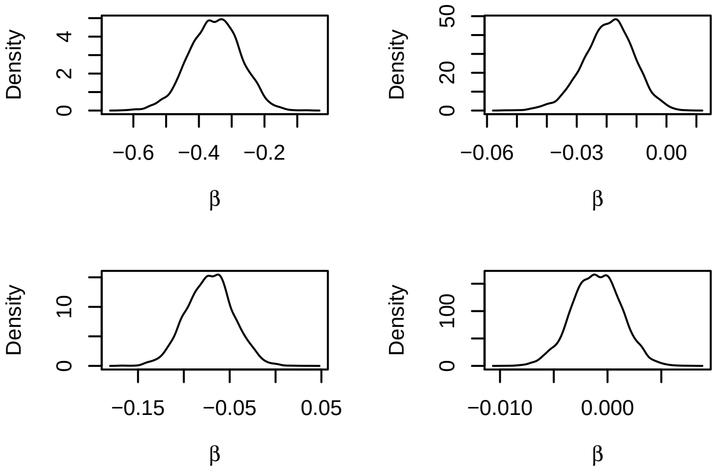

Figure B-12. Posterior densities of the parameter vector β.

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
```

```
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dwdt)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                     points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                         groups=post.chicks$survey,
+                         key=key.groups,
+                         panel=panel.bar,
+                         dyu=post.chicks$chicks.post.u,
+                         dyl=post.chicks$chicks.post.l,
+                         cex=1.0,col="black",fill=T,
+                         ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                         pch=c(15,17,16),ylab="Chick counts",xlab="",
+                         scales = list(x = list(draw = FALSE)))


R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dwdt=max.dwdt
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]
```

Table B-8. Model 2: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0362	-0.0760	0.0053
beta.chicks[2]	0.0362	1.0000	0.0078	0.0566
beta.chicks[3]	-0.0760	0.0078	1.0000	0.0296
beta.chicks[4]	0.0053	0.0566	0.0296	1.0000

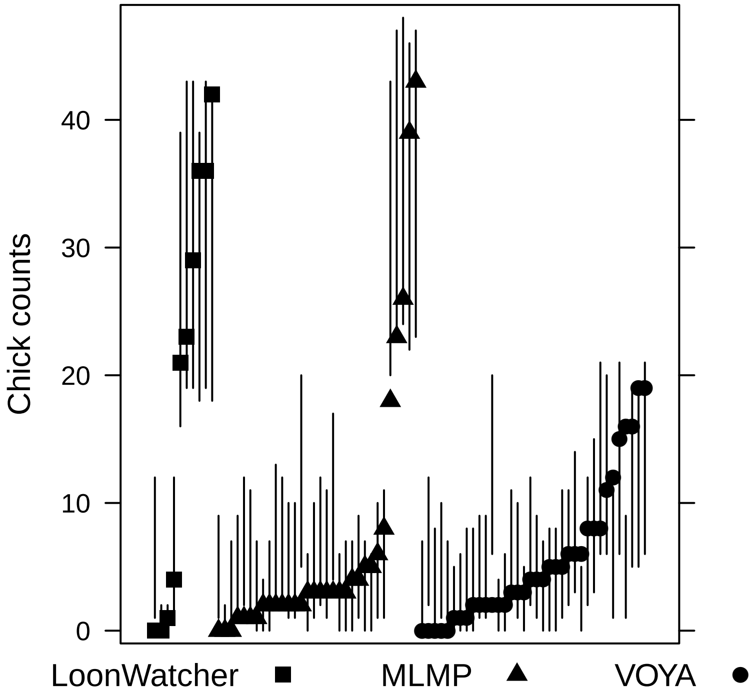

Figure B-13. Model 2: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> binnedplot(resids$pred.chicks,resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Predicted chick counts",
+            ylab="Raw residuals")
```

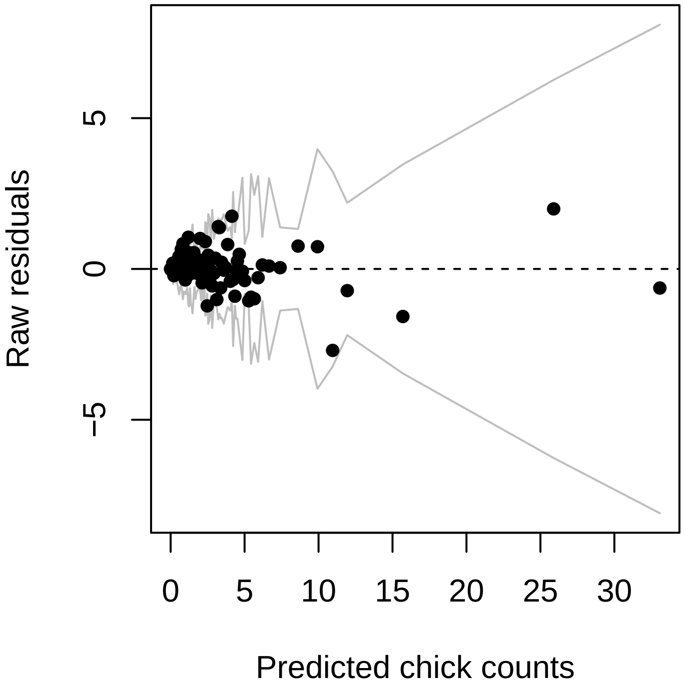

Figure B-14. Model 2: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> binnedplot((resids$max.dwdt+mean.max.dwdt),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max WL rise (cm/d)",
+            ylab="Raw residuals")
```

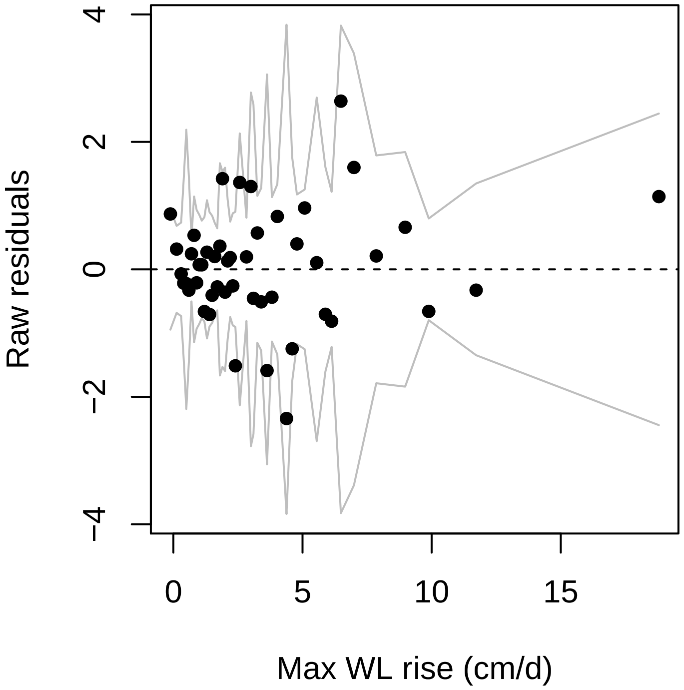

Figure B-15. Model 2: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                      quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                   quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                              "Maximum chicks/pair"),
+                      P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                      row.names=NULL)
```

Table B-9. Model 2: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.8118
Skewness of chick counts	0.9766
Maximum chicks/pair	0.5352

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks-",sep=""), quiet=TRU
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                       probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                        q_025=as.numeric(beta2.cs[1]),
+                        q_05=as.numeric(beta2.cs[2]),
+                        q_10=as.numeric(beta2.cs[3]),
+                        q_25=as.numeric(beta2.cs[4]),
+                        q_50=as.numeric(beta2.cs[5]),
+                        q_75=as.numeric(beta2.cs[6]),
+                        q_90=as.numeric(beta2.cs[7]),
```

```
+                       q_95=as.numeric(beta2.cs[8]),
+                       q_975=as.numeric(beta2.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> Pr_beta2 <- round(sum((beta2.chains<0)/length(beta2.chains)),digits=4)
R> Pbeta2 <- data.frame(Value=Pr_beta2)
R> rm("beta2.chains","Pr_beta2")
```

The marginal adverse effect of the water-level covariate on nesting success is given by Pr($\beta_2 < 0$).

The effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

Table B-10. Model 2: Pr(beta2 < 0)

Value
0.9945

```
R> zz <- seq(from=ceiling(min(max.dwdt)),to=floor(max(max.dwdt)),length.out=50) + mea
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q))
R> wl.effect <- data.frame(wl.var=zz,
+                         wl.mean=wl.tmp[,1],
+                         wl.q025=wl.tmp[,2],
+                         wl.q05=wl.tmp[,3],
+                         wl.q10=wl.tmp[,4],
+                         wl.q25=wl.tmp[,5],
+                         wl.q50=wl.tmp[,6],
+                         wl.q75=wl.tmp[,7],
+                         wl.q90=wl.tmp[,8],
+                         wl.q95=wl.tmp[,9],
+                         wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                        xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                               zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                               distribute.type=TRUE, col=c(rep("black",5)),
+                               xlab="Max(daily water-level rise) (cm/day)",
+                               ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

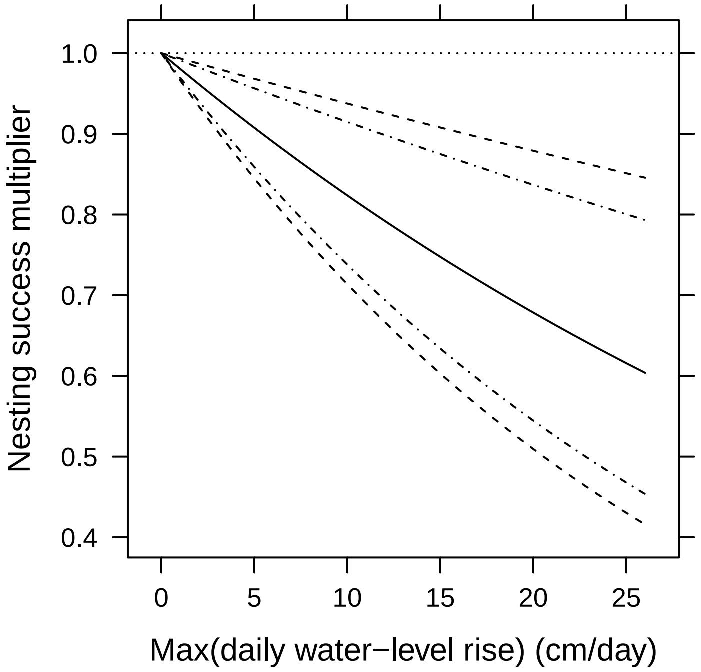

Figure B-16. Model 2: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model 3: Maximum 60-day water-level rise and normally distributed random effects

Description

Model 3 uses the estimated maximal increase in water level over the putative 60-day nesting season as the water-level predictor covariate. A vague normal distribution is assumed for the latent random effect of lakes on nesting success.

Let $z_{1,ij}$ denote the *estimated maxima of water-level increase during the 60-day nesting season* (variable `est_delta_wl` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j \\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right) \\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_X\right) \\
\mathbf{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right) \\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right) \\
\beta_{1,j} &\sim \text{N}\left(\beta_1, \tau_{\beta_1}\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_Y\right) \\
\mathbf{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> Model <- 3               ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
R> set.seed(modseed)
```

```
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+               paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+               paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+               (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+               0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+              max.dw=max.dw, tau.max.dw=tau.max.dw,
+              lkno=lkno, N=N, nlakes=nlakes,
+              eagleindx=eagleindx, doyio=doy_io,
+              zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+              nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+         datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                    beta.chicks=parm0[1,3:6],
+                    beta.chicks.j=re0[,1]),
+               list(theta.pairs=parm0[2,1:2],
+                    beta.chicks=parm0[2,3:6],
+                    beta.chicks.j=re0[,3]),
+               list(theta.pairs=parm0[3,1:2],
+                    beta.chicks=parm0[3,3:6],
+                    beta.chicks.j=re0[,3])),
+          numChains = 3, initfiles, digits=5)
R> write("model{
+    for (i in 1:N){
+
+        ##  Model for nesting pairs
+        pairs[i] ~ dpois(lambda.pairs[i])
+        lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                           theta.pairs[2]*adults[i]*adults[i] +
+                           epsilon.pairs[lkno[i]])
+
+        ##  Model for chicks
+        chicks[i] ~ dpois(lambda.chicks[i])
+        cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                            beta.chicks[2]*mu.max.dw.cut[i] +
+                            beta.chicks[3]*eagleindx[i] + beta.chicks[4]*doyio[i]
+                            )
+        lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
```

```
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dw[i]~dnorm(0,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dnorm(beta.chicks[1],tau.chicks)
+                          }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-17).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+             "beta.chicks", "sigma.chicks",
+             "lambda.chicks","post.chicks",
+             "cpp"))
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
```

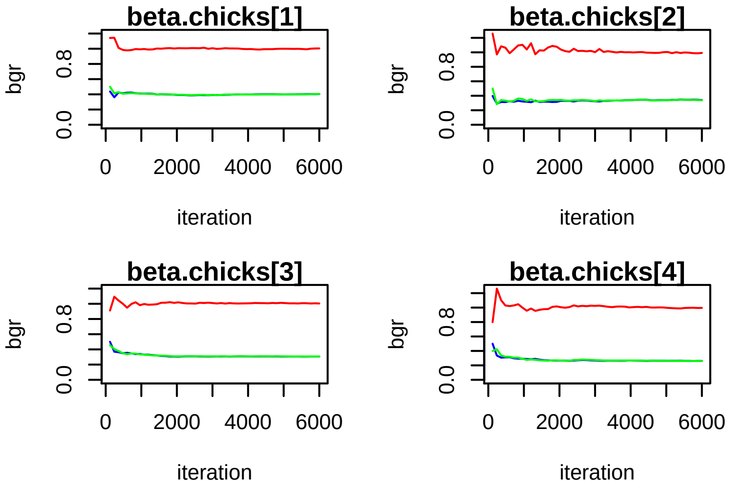

Figure B-17. Model 3: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod <- rbind(dicMod,dicTmp)
R> rm(dicTmp)
```

Table B-11. Model 3: Summary of the joint posterior distribution of the parameters.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3496	0.0131	8.8060E-04	0.3255	0.3488	0.3803
theta.pairs[2]	-0.0004	0.0001	4.8890E-06	-0.0005	-0.0004	-0.0002
sigma.pairs	1.0210	0.1727	7.2570E-03	0.7261	1.0060	1.4010
beta.chicks[1]	-0.3703	0.0723	2.0880E-03	-0.5110	-0.3707	-0.2254
beta.chicks[2]	-0.0030	0.0009	3.5630E-05	-0.0050	-0.0031	-0.0012
beta.chicks[3]	-0.0776	0.0256	6.8580E-04	-0.1278	-0.0778	-0.0273
beta.chicks[4]	-0.0036	0.0024	7.0490E-05	-0.0085	-0.0036	0.0010
sigma.chicks	0.4521	0.0523	1.0410E-03	0.3598	0.4484	0.5645

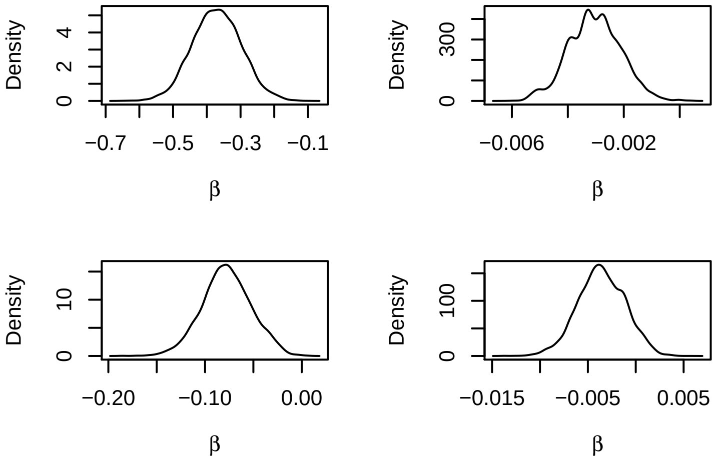

Figure B-18. Model 3: Posterior densities of the parameter vector β.

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
```

```
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dw)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                     points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                         groups=post.chicks$survey,
+                         key=key.groups,
+                         panel=panel.bar,
+                         dyu=post.chicks$chicks.post.u,
+                         dyl=post.chicks$chicks.post.l,
+                         cex=1.0,col="black",fill=T,
+                         ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                         pch=c(15,17,16),ylab="Chick counts",xlab="",
+                         scales = list(x = list(draw = FALSE)))


R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dw=max.dw)
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]
```

Table B-12. Model 3: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0567	-0.0932	0.0639
beta.chicks[2]	0.0567	1.0000	0.0732	0.3721
beta.chicks[3]	-0.0932	0.0732	1.0000	0.0179
beta.chicks[4]	0.0639	0.3721	0.0179	1.0000

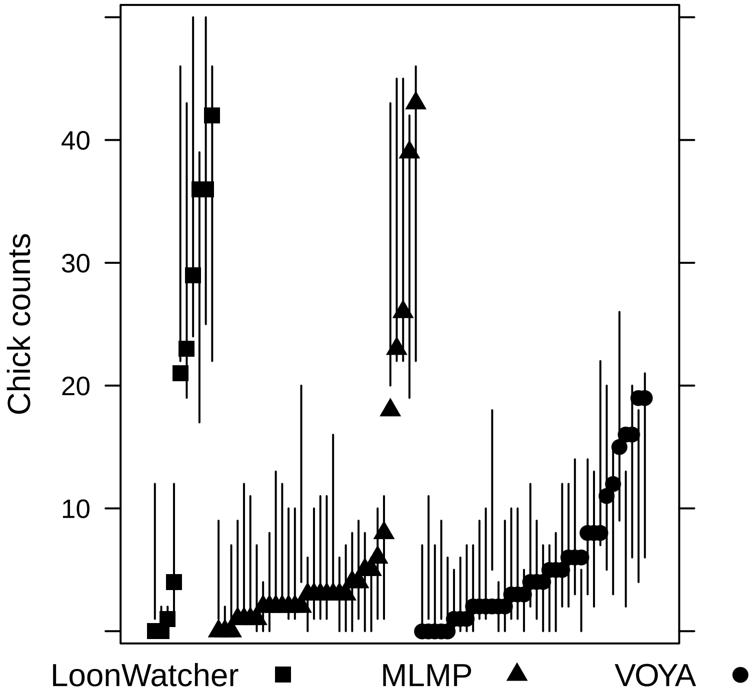

Figure B-19. Model 3: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> binnedplot(resids$pred.chicks,resids$resid.raw,
+           nclass=3*floor(sqrt(length(resids$pred.chicks))),
+           main=NULL,
+           xlab="Predicted chick counts",
+           ylab="Raw residuals")
```

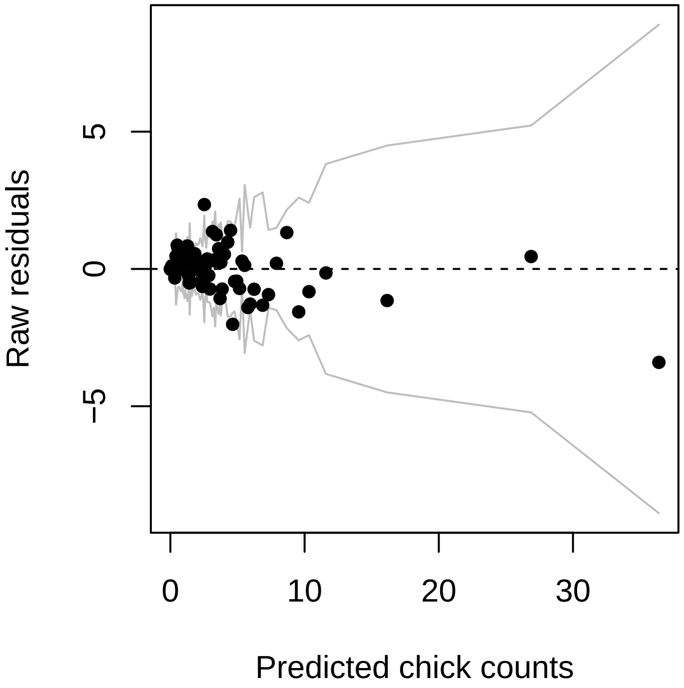

Figure B-20. Model 3: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> binnedplot((resids$max.dw+mean.max.dw),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max 60-d WL rise (cm)",
+            ylab="Raw residuals")
```

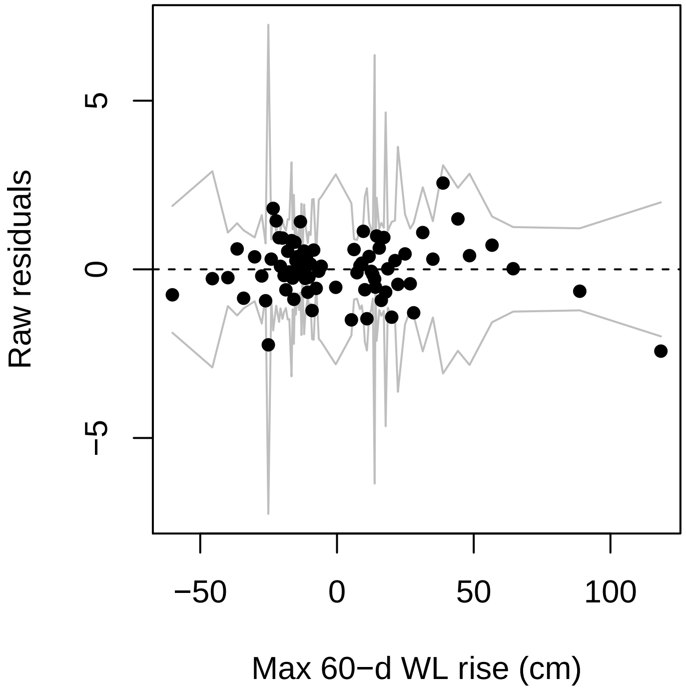

Figure B-21. Model 3: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                      quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                   quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                             "Maximum chicks/pair"),
+                     P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                     row.names=NULL)
```

Table B-13. Model 3: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.7982
Skewness of chick counts	0.9708
Maximum chicks/pair	0.9126

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks-",sep=""), quiet=TRU
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                      probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                       q_025=as.numeric(beta2.cs[1]),
+                       q_05=as.numeric(beta2.cs[2]),
+                       q_10=as.numeric(beta2.cs[3]),
+                       q_25=as.numeric(beta2.cs[4]),
+                       q_50=as.numeric(beta2.cs[5]),
+                       q_75=as.numeric(beta2.cs[6]),
+                       q_90=as.numeric(beta2.cs[7]),
```

```
+                        q_95=as.numeric(beta2.cs[8]),
+                        q_975=as.numeric(beta2.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> Pr_beta2 <- round(sum((beta2.chains<0)/length(beta2.chains)),digits=4)
R> Pbeta2 <- data.frame(Value=Pr_beta2)
R> rm("beta2.chains","Pr_beta2")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_2 < 0)$. The effect of the water-level covariate on nesting success is given by $\exp\left(\beta_1 z_{1,ij}\right)$.

Table B-14. Model 3: Pr(beta2 < 0)

Value
0.9987

```
R> zz <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=50) + mean.ma
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q))
R> wl.effect <- data.frame(wl.var=zz,
+                          wl.mean=wl.tmp[,1],
+                          wl.q025=wl.tmp[,2],
+                          wl.q05=wl.tmp[,3],
+                          wl.q10=wl.tmp[,4],
+                          wl.q25=wl.tmp[,5],
+                          wl.q50=wl.tmp[,6],
+                          wl.q75=wl.tmp[,7],
+                          wl.q90=wl.tmp[,8],
+                          wl.q95=wl.tmp[,9],
+                          wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                         xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                                zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                                distribute.type=TRUE, col=c(rep("black",5)),
+                                xlab="Max(water-level rise) (cm)",
+                                ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

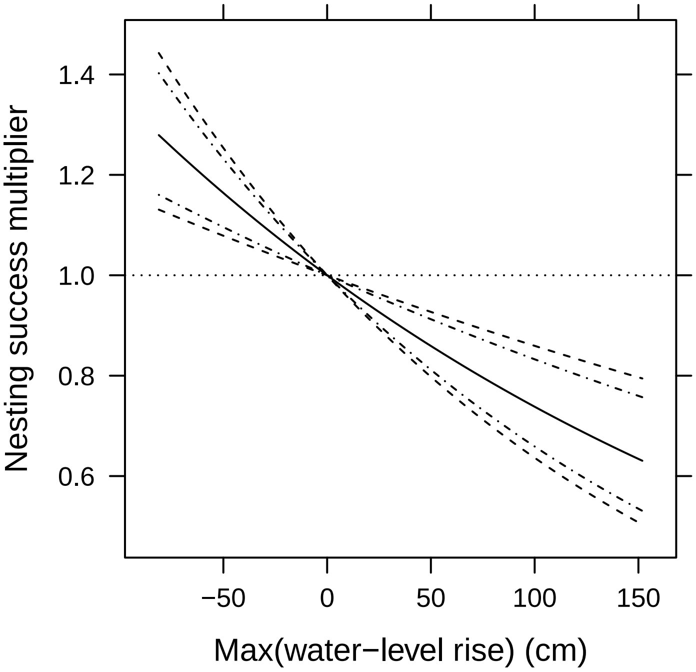

Figure B-22. Model 3: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model 4: Maximum 60-day water-level rise and t-distributed random effects

Description

Model 4 uses the estimated maximal increase in water level over the putative 60-day nesting season as the water-level predictor covariate. A vague long-tailed Student-t distribution is assumed for the latent random effect of lakes on nesting success.

Let $z_{1,ij}$ denote the *estimated maxima of water-level increase during the 60-day nesting season* (variable `est_delta_wl` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j \\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right) \\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_X\right) \\
\mathbf{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times2}(2),\, 2\right) \\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right) \\
\beta_{1,j} &\sim \text{t}\left(\beta_1, \tau_{\beta_1}, 3\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_Y\right) \\
\mathbf{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> Model <- 4               ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
R> set.seed(modseed)
```

```
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+                (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+                0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+               max.dw=max.dw, tau.max.dw=tau.max.dw,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx, doyio=doy_io,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                      beta.chicks=parm0[1,3:6],
+                      beta.chicks.j=re0[,1]),
+                 list(theta.pairs=parm0[2,1:2],
+                      beta.chicks=parm0[2,3:6],
+                      beta.chicks.j=re0[,3]),
+                 list(theta.pairs=parm0[3,1:2],
+                      beta.chicks=parm0[3,3:6],
+                      beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                                theta.pairs[2]*adults[i]*adults[i] +
+                                epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                                 beta.chicks[2]*mu.max.dw.cut[i] +
+                                 beta.chicks[3]*eagleindx[i] + beta.chicks[4]*doyio[i]
+                                 )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
```

```
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dw[i]~dnorm(0,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dt(beta.chicks[1],tau.chicks,3)
+                         }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-23).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+              "beta.chicks", "sigma.chicks",
+              "lambda.chicks","post.chicks",
+              "mu.max.dw","cpp"))
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
```

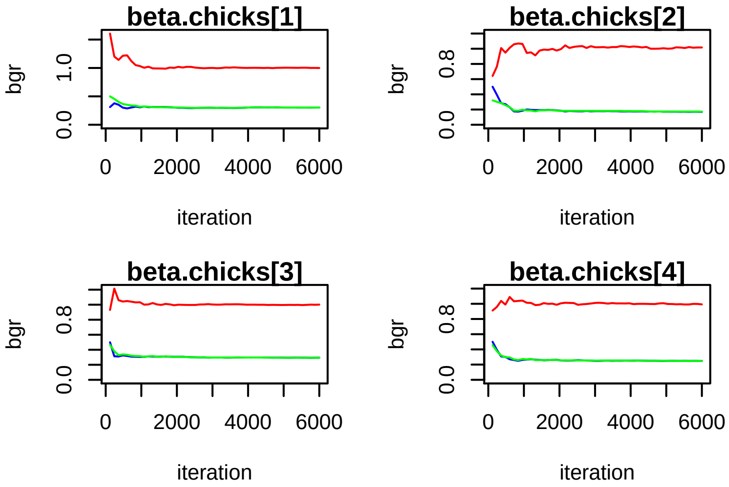

Figure B-23. Model 4: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod <- rbind(dicMod,dicTmp)
R> rm(dicTmp)
```

Table B-15. Model 4: Summary of the joint posterior distribution of the parameters

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3555	0.0121	8.1120E-04	0.3261	0.3565	0.3741
theta.pairs[2]	-0.0004	0.0001	3.9170E-06	-0.0005	-0.0004	-0.0002
sigma.pairs	1.0070	0.1654	6.6700E-03	0.7204	0.9928	1.3600
beta.chicks[1]	-0.3638	0.0751	2.6020E-03	-0.5096	-0.3633	-0.2181
beta.chicks[2]	-0.0027	0.0009	3.5720E-05	-0.0043	-0.0028	-0.0009
beta.chicks[3]	-0.0783	0.0253	6.8250E-04	-0.1283	-0.0783	-0.0283
beta.chicks[4]	-0.0032	0.0024	7.3180E-05	-0.0079	-0.0032	0.0017
sigma.chicks	0.3946	0.0492	1.0050E-03	0.3097	0.3907	0.5024

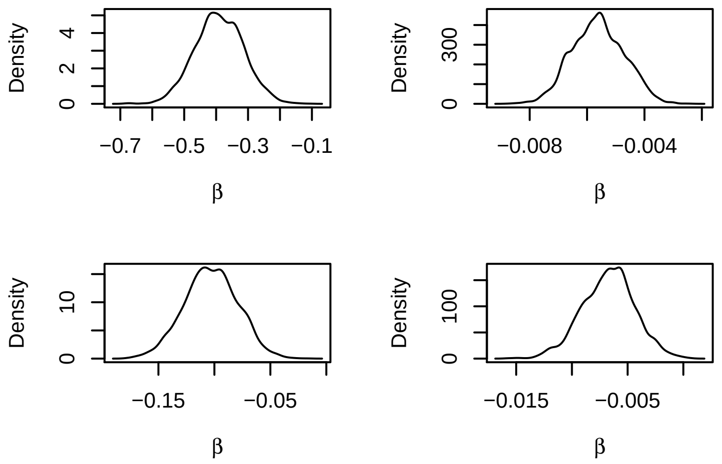

Figure B-24. Model 4: Posterior densities of the parameter vector β.

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
```

```
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dw)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                    points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                        groups=post.chicks$survey,
+                        key=key.groups,
+                        panel=panel.bar,
+                        dyu=post.chicks$chicks.post.u,
+                        dyl=post.chicks$chicks.post.l,
+                        cex=1.0,col="black",fill=T,
+                        ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                        pch=c(15,17,16),ylab="Chick counts",xlab="",
+                        scales = list(x = list(draw = FALSE)))

R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> samplesCoda("mu.max.dw",stem=paste(MCMCout,"mu-max-dw-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dw=max.dw)
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]
```

Table B-16. Model 4: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0826	-0.0778	0.0429
beta.chicks[2]	0.0826	1.0000	0.0747	0.3721
beta.chicks[3]	-0.0778	0.0747	1.0000	0.0431
beta.chicks[4]	0.0429	0.3721	0.0431	1.0000

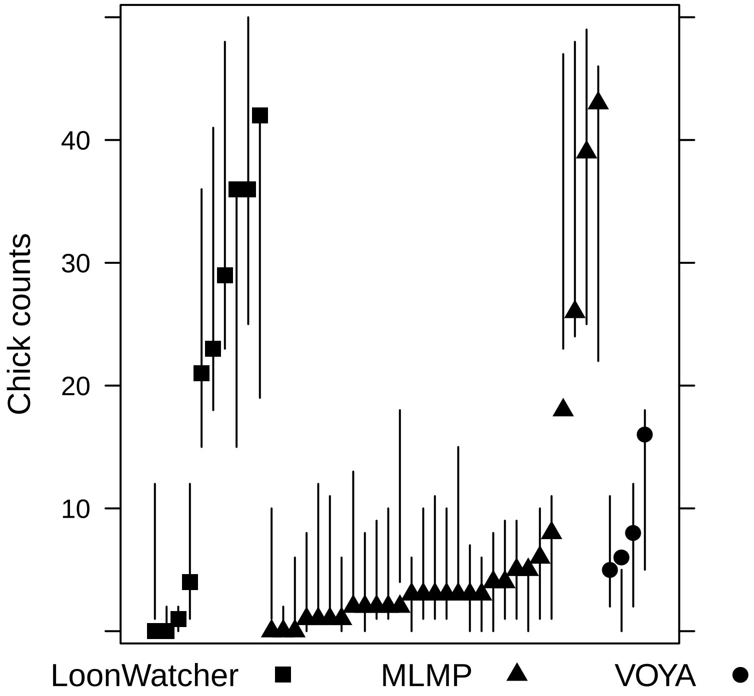

Figure B-25. Model 4: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> binnedplot(resids$pred.chicks,resids$resid.raw,
+             nclass=3*floor(sqrt(length(resids$pred.chicks))),
+             main=NULL,
+             xlab="Predicted chick counts",
+             ylab="Raw residuals")
```

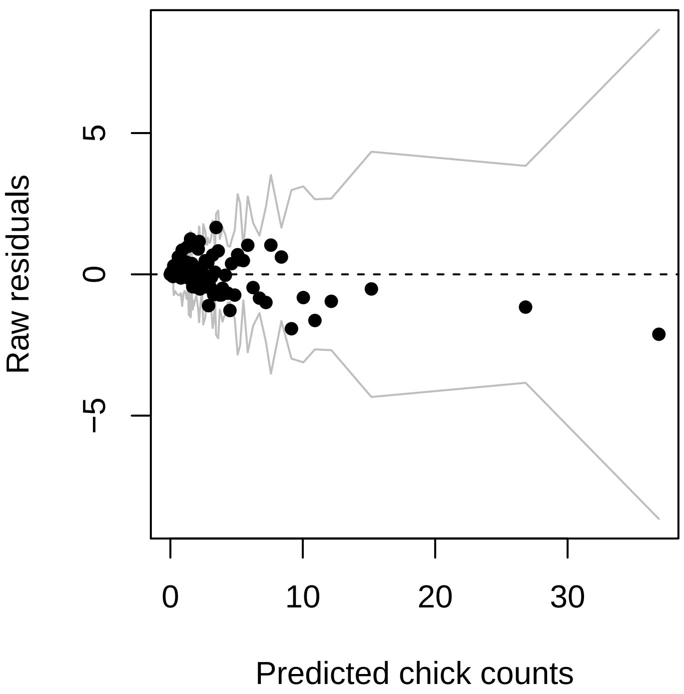

Figure B-26. Model 4: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> binnedplot((resids$max.dw+mean.max.dw),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max 60-d WL rise (cm)",
+            ylab="Raw residuals")
```

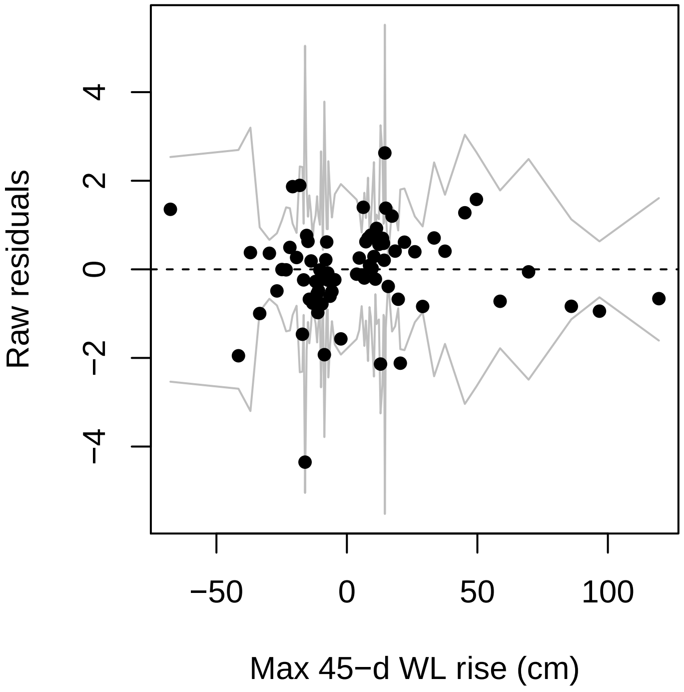

Figure B-27. Model 4: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                      quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                   quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                              "Maximum chicks/pair"),
+                      P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                      row.names=NULL)
```

Table B-17. Model 4: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.8258
Skewness of chick counts	0.982
Maximum chicks/pair	0.554

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks-",sep=""), quiet=TRU
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                       probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                        q_025=as.numeric(beta2.cs[1]),
+                        q_05=as.numeric(beta2.cs[2]),
+                        q_10=as.numeric(beta2.cs[3]),
+                        q_25=as.numeric(beta2.cs[4]),
+                        q_50=as.numeric(beta2.cs[5]),
+                        q_75=as.numeric(beta2.cs[6]),
+                        q_90=as.numeric(beta2.cs[7]),
```

```
+                        q_95=as.numeric(beta2.cs[8]),
+                        q_975=as.numeric(beta2.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> Pr_beta2 <- round(sum((beta2.chains<0)/length(beta2.chains)),digits=4)
R> Pbeta2 <- data.frame(Value=Pr_beta2)
R> rm("beta2.chains","Pr_beta2")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_2 < 0)$. The effect of the water-level covariate on nesting success is given by $\exp\left(\beta_1 z_{1,ij}\right)$.

Table B-18. Model 4: Pr(beta2 < 0)

Value
0.9989

```
R> zz <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=50)+mean.max.
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q))
R> wl.effect <- data.frame(wl.var=zz,
+                          wl.mean=wl.tmp[,1],
+                          wl.q025=wl.tmp[,2],
+                          wl.q05=wl.tmp[,3],
+                          wl.q10=wl.tmp[,4],
+                          wl.q25=wl.tmp[,5],
+                          wl.q50=wl.tmp[,6],
+                          wl.q75=wl.tmp[,7],
+                          wl.q90=wl.tmp[,8],
+                          wl.q95=wl.tmp[,9],
+                          wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                         xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                                zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                                distribute.type=TRUE, col=c(rep("black",5)),
+                                xlab="Max(water-level rise) (cm)",
+                                ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

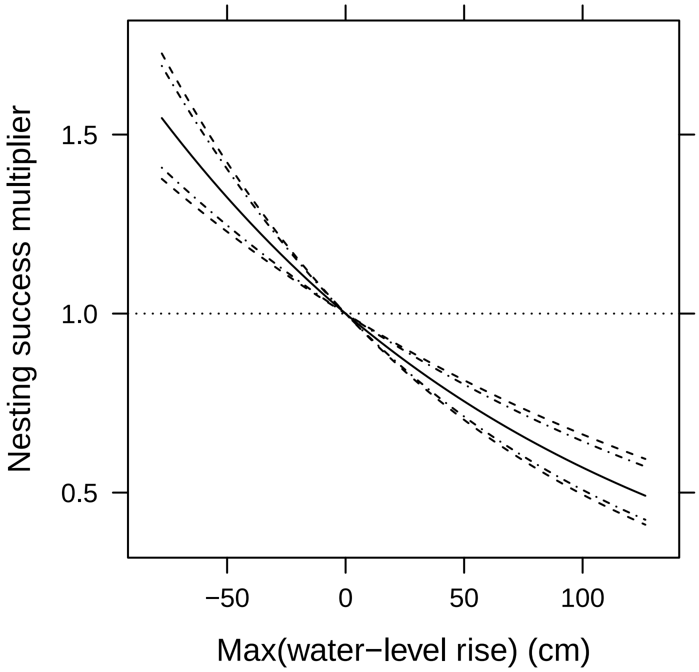

Figure B-28. Model 4: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model 5: Maximum daily water-level rise, maximum 60-day rise, and Student-t distributed random effects

Description

Model 5 uses the estimated maxima of the daily rates of water-level increase and the maximum rise over the putative 60-day nesting season as water-level predictor covariates. A vague, flat-tailed Student t distribution is assumed for the latent random effect of lakes on nesting success.

Let $z_{1,ij}$ denote the *estimated maxima of daily rates of water-level increase during the 60-day nesting season* (variable `est_max_dwl_ddoy` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j \\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right) \\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_X\right) \\
\mathbf{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right) \\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right) \\
\beta_{1,j} &\sim \text{t}\left(\beta_1, \tau_{\beta_1}, 3\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_Y\right) \\
\mathbf{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> modno <- 5              ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
```

```
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/mod",modno,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",modno,"-init1.txt", sep=""),
+                paste(bugsdir, "inputs/mod",modno,"-init2.txt", sep=""),
+                paste(bugsdir, "inputs/mod",modno,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",modno,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",modno,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+                (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+                0.1*rnorm(3,0),0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(62,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+               max.dwdt=max.dwdt, tau.max.dwdt=tau.max.dwdt,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx,
+               max.dw=max.dw, tau.max.dw=tau.max.dw,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                     beta.chicks=parm0[1,3:6],
+                     beta.chicks.j=re0[,1]),
+                list(theta.pairs=parm0[2,1:2],
+                     beta.chicks=parm0[2,3:6],
+                     beta.chicks.j=re0[,3]),
+                list(theta.pairs=parm0[3,1:2],
+                     beta.chicks=parm0[3,3:6],
+                     beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                            theta.pairs[2]*adults[i]*adults[i] +
+                            epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                             beta.chicks[2]*mu.max.dwdt.cut[i] +
+                             beta.chicks[3]*eagleindx[i] +
```

```
+                              beta.chicks[4]*mu.max.dw.cut[i]
+                              )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dwdt[i] ~ dnorm(mu.max.dwdt[i],tau.max.dwdt[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dwdt.cut[i] <- cut(mu.max.dwdt[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dwdt[i]~dnorm(3,0.001)
+         mu.max.dw[i]~dnorm(0,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dt(beta.chicks[1],tau.chicks,3)
+                         }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-29).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
```

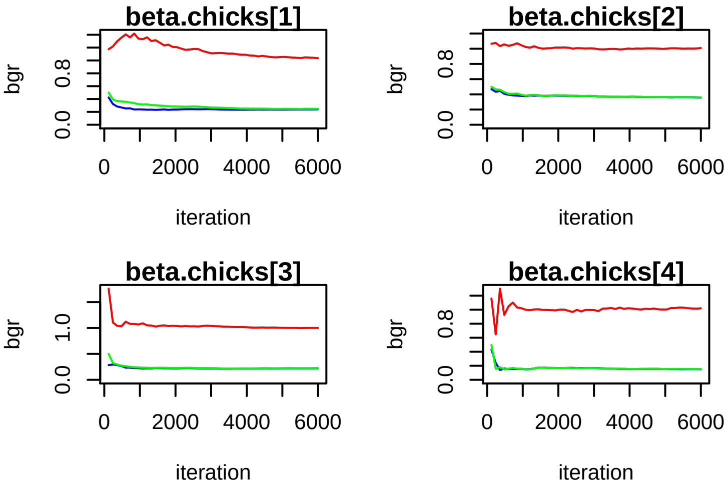

Figure B-29. Model 5: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
+               "beta.chicks", "sigma.chicks",
+               "lambda.chicks","post.chicks",
+               "cpp"))
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod <- rbind(dicMod,dicTmp)
R> rm(dicTmp)
```

Table B-19. Model 5: Summary of the joint posterior distribution of the parameters from Model 1.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3437	0.0097	6.5270E-04	0.3269	0.3426	0.3627
theta.pairs[2]	-0.0004	0.0001	3.5540E-06	-0.0005	-0.0003	-0.0002
sigma.pairs	1.0780	0.1721	6.5430E-03	0.7753	1.0660	1.4500
beta.chicks[1]	-0.3480	0.0759	2.5800E-03	-0.4964	-0.3467	-0.2002
beta.chicks[2]	-0.0137	0.0087	2.1110E-04	-0.0313	-0.0135	0.0028
beta.chicks[3]	-0.0746	0.0265	7.8330E-04	-0.1274	-0.0745	-0.0246
beta.chicks[4]	-0.0017	0.0010	3.7930E-05	-0.0037	-0.0017	0.0002
sigma.chicks	0.3973	0.0494	9.7240E-04	0.3113	0.3937	0.5064

Table B-20. Model 5: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0308	-0.0976	0.0867
beta.chicks[2]	0.0308	1.0000	-0.0105	-0.3450
beta.chicks[3]	-0.0976	-0.0105	1.0000	0.0912
beta.chicks[4]	0.0867	-0.3450	0.0912	1.0000

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dwdt)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
```

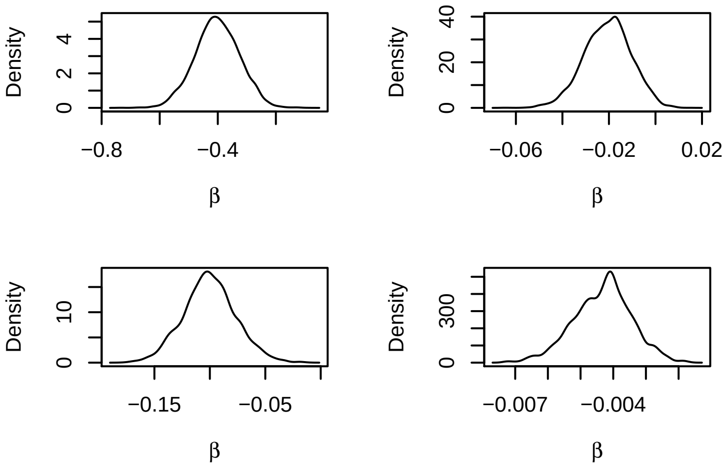

Figure B-30. Posterior densities of the parameter vector β.

```
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                    points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                        groups=post.chicks$survey,
+                        key=key.groups,
+                        panel=panel.bar,
+                        dyu=post.chicks$chicks.post.u,
+                        dyl=post.chicks$chicks.post.l,
+                        cex=1.0,col="black",fill=T,
+                        ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                        pch=c(15,17,16),ylab="Chick counts",xlab="",
+                        scales = list(x = list(draw = FALSE)))
```

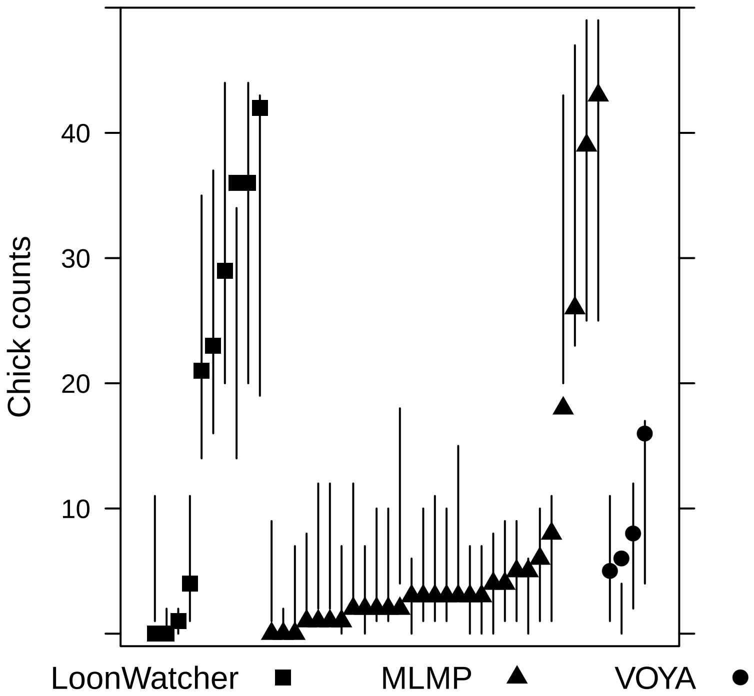

Figure B-31. Model 5: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
```

```
+                                   quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dw=max.dw,max
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]

R> binnedplot(resids$pred.chicks,resids$resid.raw,
+           nclass=3*floor(sqrt(length(resids$pred.chicks))),
+           main=NULL,
+           xlab="Predicted chick counts",
+           ylab="Raw residuals")
```

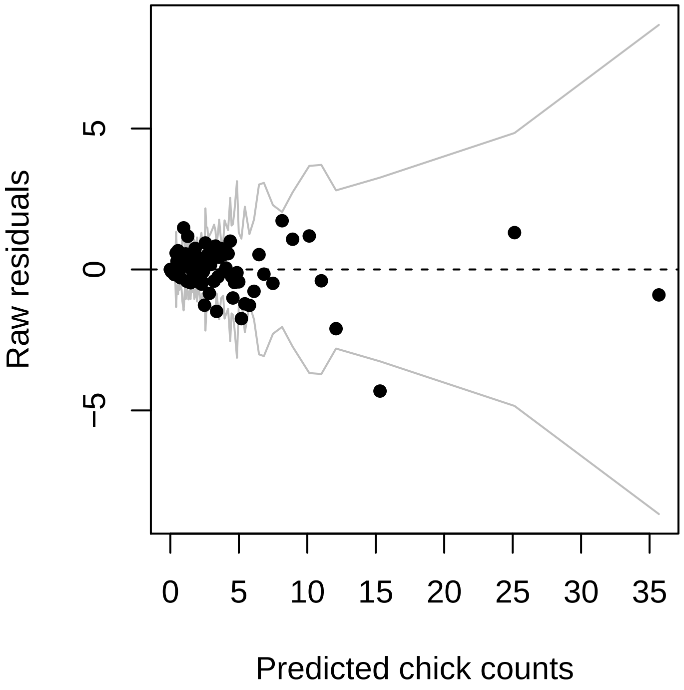

Figure B-32. Model 5: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                      quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
```

```
R> binnedplot((resids$max.dw+mean.max.dw),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max 60-d WL rise (cm)",
+            ylab="Raw residuals")
```

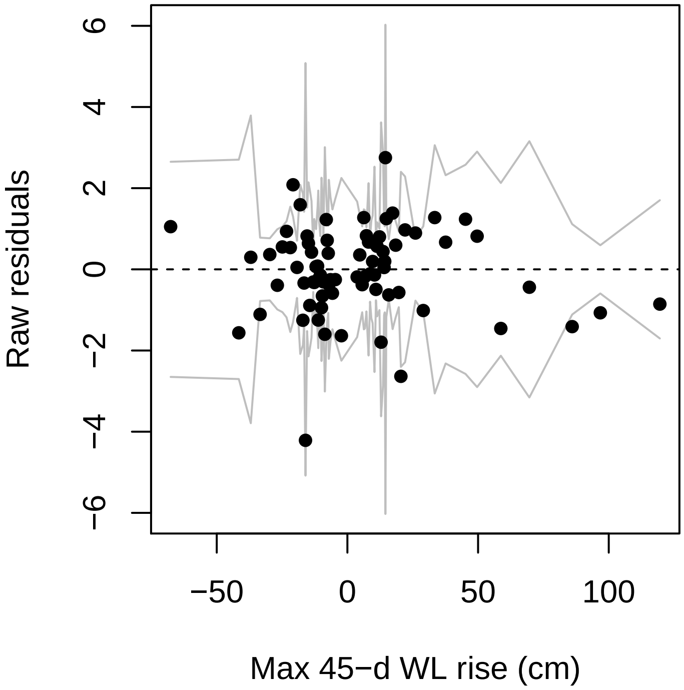

Figure B-33. Model 5: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> binnedplot((resids$max.dwdt+mean.max.dwdt),resids$resid.raw,
+           nclass=3*floor(sqrt(length(resids$pred.chicks))),
+           main=NULL,
+           xlab="Max daily rise (cm/day)",
+           ylab="Raw residuals")
```

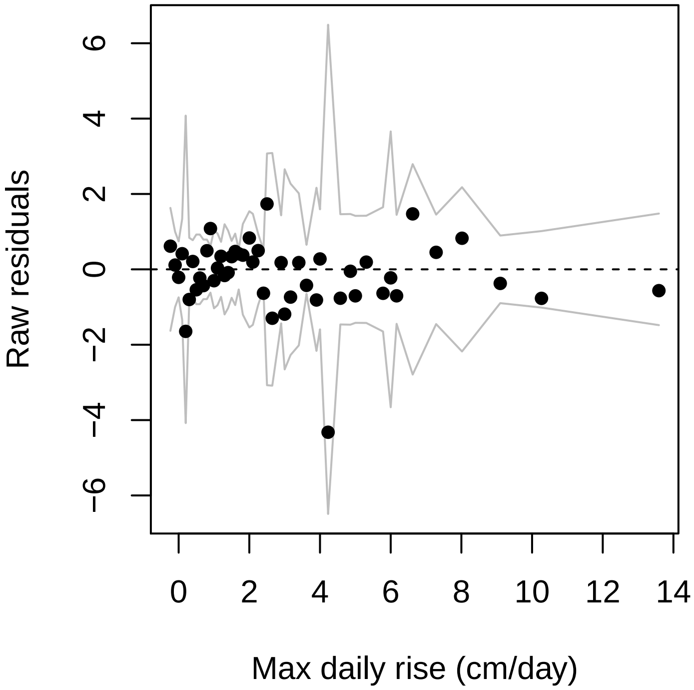

Figure B-34. Model 5: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                    quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                             "Maximum chicks/pair"),
+                     P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                     row.names=NULL)
```

Table B-21. Model 5: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.8268
Skewness of chick counts	0.9692
Maximum chicks/pair	0.536

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> beta4.mean <- samplesStats("beta.chicks[4]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta2-chicks-",sep=""))
R> samplesCoda("beta.chicks[4]", stem=paste(MCMCout,"beta4-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta2-chicks-",sep=""), quiet=TR
R> beta4.chains <- read.openbugs(stem=paste(MCMCout,"beta4-chicks-",sep=""), quiet=TR
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                      probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta4.cs <- quantile(as.vector(as.array(beta4.chains)),
+                      probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                       q_025=as.numeric(beta2.cs[1]),
+                       q_05=as.numeric(beta2.cs[2]),
+                       q_10=as.numeric(beta2.cs[3]),
+                       q_25=as.numeric(beta2.cs[4]),
+                       q_50=as.numeric(beta2.cs[5]),
+                       q_75=as.numeric(beta2.cs[6]),
+                       q_90=as.numeric(beta2.cs[7]),
+                       q_95=as.numeric(beta2.cs[8]),
```

```
+                        q_975=as.numeric(beta2.cs[9]))
R> beta4.q <- data.frame(mean=as.numeric(beta4.mean),
+                        q_025=as.numeric(beta4.cs[1]),
+                        q_05=as.numeric(beta4.cs[2]),
+                        q_10=as.numeric(beta4.cs[3]),
+                        q_25=as.numeric(beta4.cs[4]),
+                        q_50=as.numeric(beta4.cs[5]),
+                        q_75=as.numeric(beta4.cs[6]),
+                        q_90=as.numeric(beta4.cs[7]),
+                        q_95=as.numeric(beta4.cs[8]),
+                        q_975=as.numeric(beta4.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> beta4.chains <- unlist(beta4.chains)
R> Pr_beta <- c(round(sum((beta2.chains<0)/length(beta2.chains)),digits=4),
+              round(sum((beta4.chains<0)/length(beta4.chains)),digits=4))
R> Pbeta <- data.frame(beta=c(1,4),Value=Pr_beta)
R> rm("beta2.chains","beta4.chains","Pr_beta")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_k < 0)$, $k \in \{1, 5\}$.

Table B-22. Model 5: Pr(beta < 0)

beta	Value
1	0.9461
4	0.9646

The linear effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

```
R> v1 <- seq(from=ceiling(min(max.dwdt)),to=floor(max(max.dwdt)),length.out=20)
R> v2 <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=20)
R> zz <- expand.grid(v1,v2)
R> wl.tmp <- exp(zz$Var1%o%as.numeric(beta2.q) + zz$Var2%o%as.numeric(beta4.q))
R> wl.effect <- data.frame(max.dwdt=zz$Var1,
+                          max.dw=zz$Var2,
+                          wl.mean=wl.tmp[,1],
+                          wl.q025=wl.tmp[,2],
+                          wl.q05=wl.tmp[,3],
+                          wl.q10=wl.tmp[,4],
+                          wl.q25=wl.tmp[,5],
+                          wl.q50=wl.tmp[,6],
+                          wl.q75=wl.tmp[,7],
+                          wl.q90=wl.tmp[,8],
+                          wl.q95=wl.tmp[,9],
+                          wl.q975=wl.tmp[,10])
```

```
R> write.csv(wl.effect,file=paste(predir,"mod",modno,"_wl.effect.csv",sep=""))
R> wl.effect.plot.mean <- levelplot(wl.mean ~ max.dwdt + max.dw, data=wl.effect,
+                                   cuts=100,pretty=TRUE,col.regions=terrain.colors)
R> wl.effect.plot.l <- levelplot(wl.q05 ~ max.dwdt + max.dw, data=wl.effect,
+                                   cuts=100,pretty=TRUE,col.regions=terrain.colors)
R> wl.effect.plot.u <- levelplot(wl.q95 ~ max.dwdt + max.dw, data=wl.effect,
+                                   cuts=100,pretty=TRUE,col.regions=terrain.colors)
```

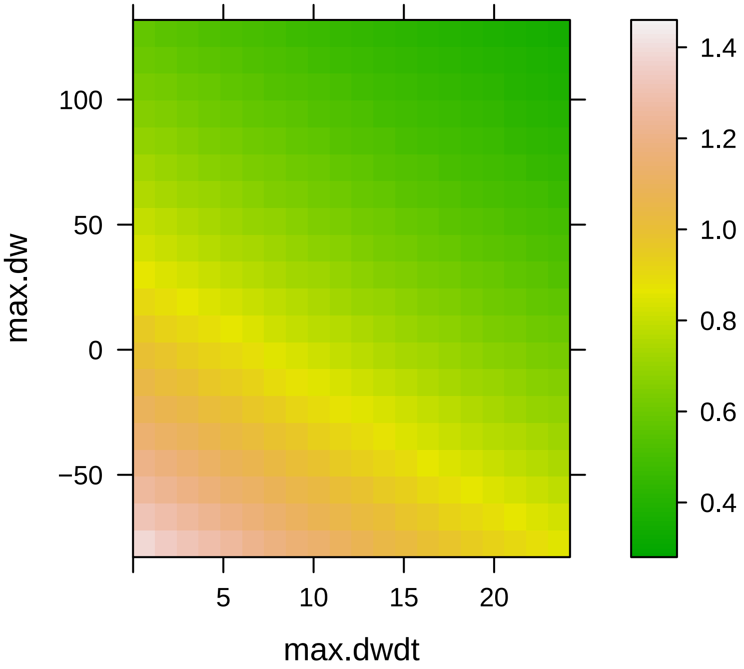

Figure B-35. Model 5: Estimated effects of the peak daily rate of water-level increase and peak 60-day increase on expected nesting success of loons.

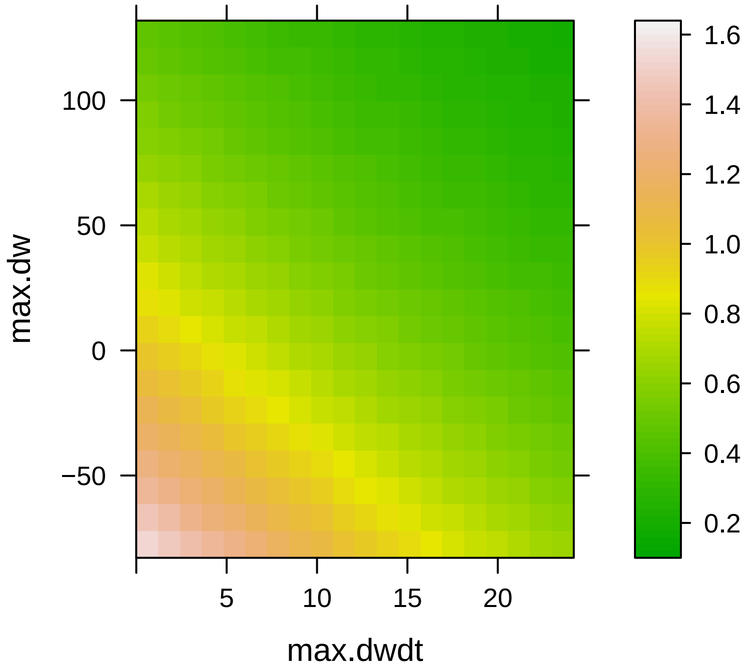

Figure B-36. Model 5: Estimated effects of the peak daily rate of water-level increase and peak 60-day increase on lower bound of Pr=0.90 credible set.

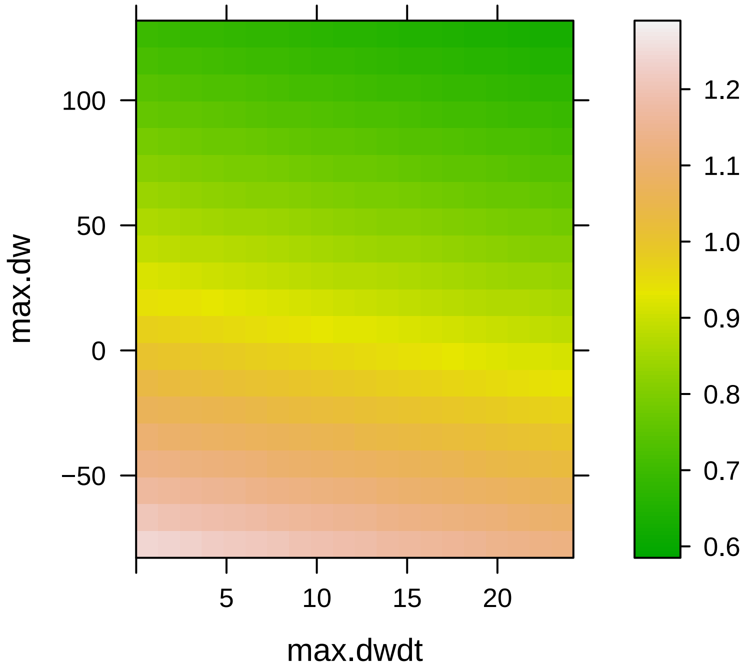

Figure B-37. Model 5: Estimated effects of the peak daily rate of water-level increase and peak 60-day increase on upper bound of Pr=0.90 credible set.

Model 6: Quadratic maximum 60-day water-level rise and normally distributed random effects

Description

Model 6 uses the estimated maximal increase in water level over the putative 60-day nesting season as the water-level predictor covariate. A vague normal distribution is assumed for the latent random effect of lakes on nesting success.

Let $z_{1,ij}$ denote the *estimated maxima of water-level increase during the 60-day nesting season* (variable `est_delta_wl` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right)\\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j\\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right)\\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right)\\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \boldsymbol{\Omega}_X\right)\\
\boldsymbol{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right)\\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right)\\
\lambda_{Y,ij} &= \lambda_{X,ij}\exp\left(\frac{\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{1,ij}^2}{100}\right)\\
\beta_{1,j} &\sim \text{N}\left(\beta_1, \tau_{\beta_1}\right)\\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right)\\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \boldsymbol{\Omega}_Y\right)\\
\boldsymbol{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively. The exponential function on the right-hand side of the equation for $\lambda_{Y,ij}$ is rescaled by the denominator of 100 for numerical convenience.

Initialization

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> Model <- 6              ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
```

```
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+                (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+                0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+               max.dw=max.dw, tau.max.dw=tau.max.dw,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                     beta.chicks=parm0[1,3:6],
+                     beta.chicks.j=re0[,1]),
+                list(theta.pairs=parm0[2,1:2],
+                     beta.chicks=parm0[2,3:6],
+                     beta.chicks.j=re0[,3]),
+                list(theta.pairs=parm0[3,1:2],
+                     beta.chicks=parm0[3,3:6],
+                     beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                             theta.pairs[2]*adults[i]*adults[i] +
+                             epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                              beta.chicks[2]*mu.max.dw.cut[i] +
+                              beta.chicks[3]*eagleindx[i] +
+                              beta.chicks[4]*mu.max.dw.cut[i]*mu.max.dw.cut[i]/100 )
```

```
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dw[i]~dnorm(0,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dnorm(beta.chicks[1],tau.chicks)
+                         }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-38).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+              "beta.chicks", "sigma.chicks",
+              "lambda.chicks","post.chicks",
+              "cpp"))
R> dicSet()
R> modelUpdate(nsamps)
```

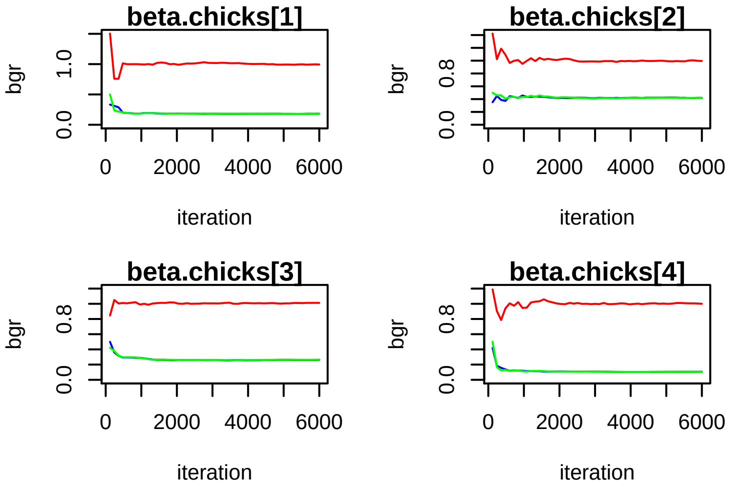

Figure B-38. Model 6: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> dicTmp <- dicStats()
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod <- rbind(dicMod,dicTmp)
R> rm(dicTmp)
```

Table B-23. Model 6: Summary of the joint posterior distribution of the parameters.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3554	0.0117	7.8960E-04	0.3322	0.3544	0.3766
theta.pairs[2]	-0.0004	0.0001	4.1630E-06	-0.0005	-0.0004	-0.0003
sigma.pairs	1.0020	0.1609	6.1950E-03	0.7181	0.9911	1.3460
beta.chicks[1]	-0.3294	0.0717	2.2570E-03	-0.4668	-0.3293	-0.1870
beta.chicks[2]	-0.0016	0.0009	3.3240E-05	-0.0034	-0.0016	0.0000
beta.chicks[3]	-0.0718	0.0248	6.0950E-04	-0.1202	-0.0714	-0.0226
beta.chicks[4]	-0.0056	0.0016	6.1490E-05	-0.0090	-0.0056	-0.0024
sigma.chicks	0.4408	0.0500	1.0490E-03	0.3532	0.4373	0.5494

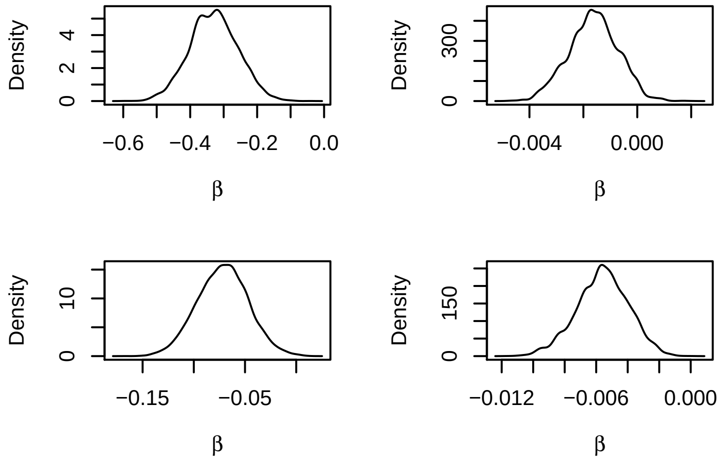

Figure B-39. Model 6: Posterior densities of the parameter vector β.

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
```

```
R> chicks.post.l <- post.chicks$val2.5pc
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dw)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                    points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                         groups=post.chicks$survey,
+                         key=key.groups,
+                         panel=panel.bar,
+                         dyu=post.chicks$chicks.post.u,
+                         dyl=post.chicks$chicks.post.l,
+                         cex=1.0,col="black",fill=T,
+                         ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                         pch=c(15,17,16),ylab="Chick counts",xlab="",
+                         scales = list(x = list(draw = FALSE)))


R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resid.std <- resid.raw/sd(resid.raw,na.rm=TRUE)
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,
+                       resid.std=resid.std,max.dw=max.dw)
R> resids <- resids[!is.na(resids$resid.raw),]
```

Table B-24. Model 6: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0484	-0.0502	-0.2215
beta.chicks[2]	0.0484	1.0000	0.1145	-0.1889
beta.chicks[3]	-0.0502	0.1145	1.0000	-0.0327
beta.chicks[4]	-0.2215	-0.1889	-0.0327	1.0000

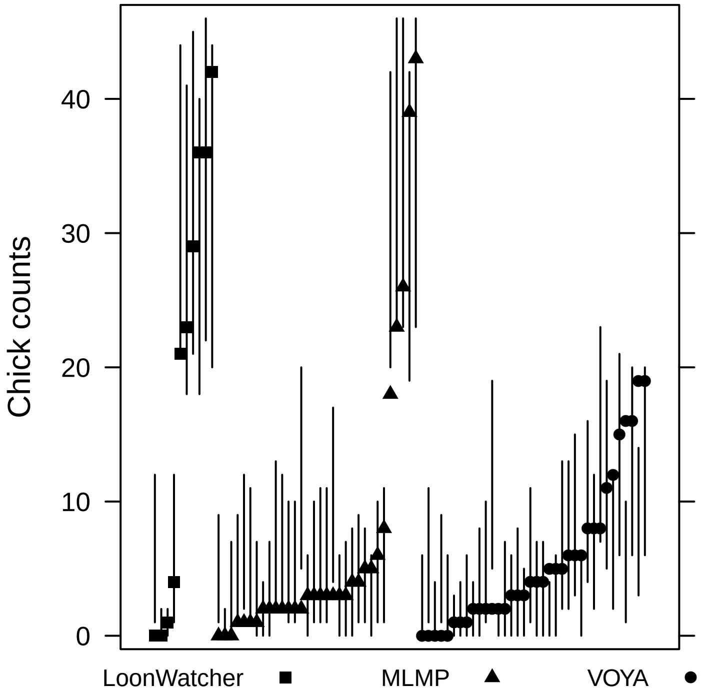

Figure B-40. Model 6: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]

R> binnedplot(resids$pred.chicks,resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Predicted chick counts",
+            ylab="Raw residuals")
```

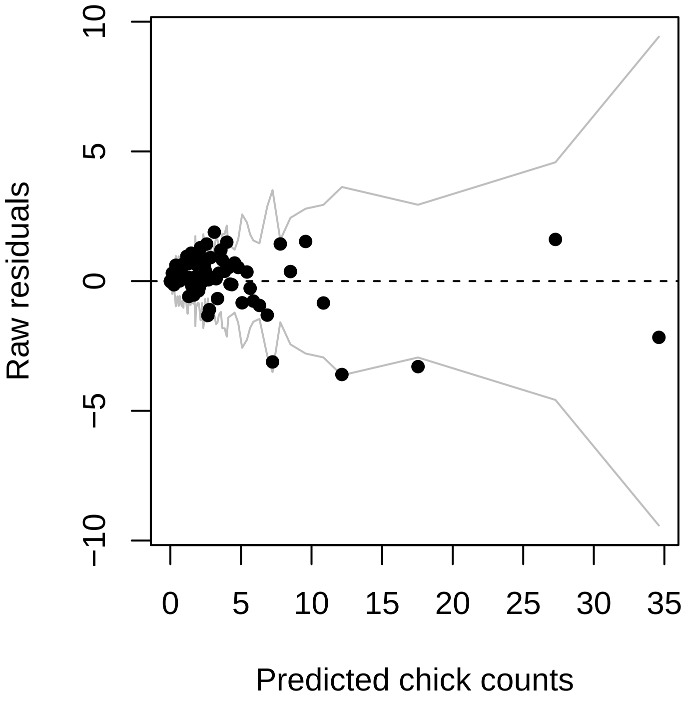

Figure B-41. Model 6: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                        quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
```

```
R> binnedplot(resids$max.dw,resids$resid.raw,
+           nclass=3*floor(sqrt(length(resids$pred.chicks))),
+           main=NULL,
+           xlab="Max 60-d WL rise (cm)",
+           ylab="Raw residuals")
```

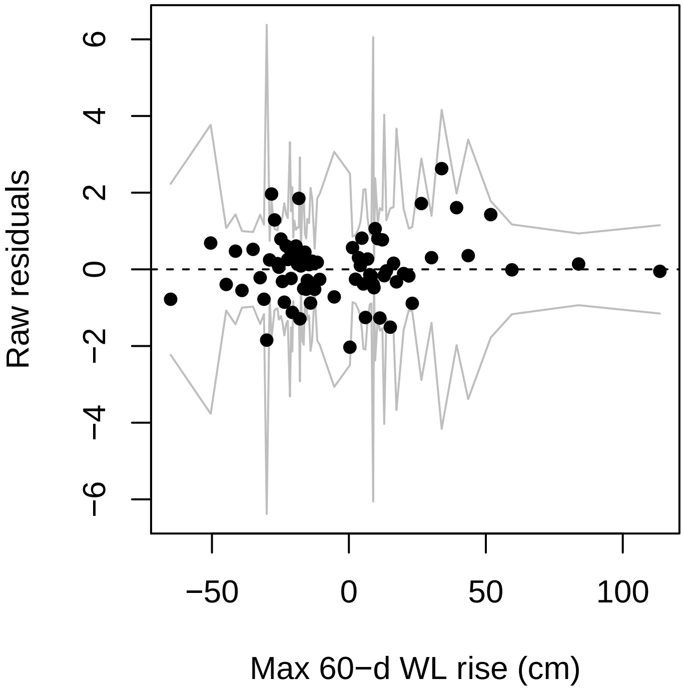

Figure B-42. Model 6: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                   quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                              "Maximum chicks/pair"),
+                        P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                        row.names=NULL)
```

Table B-25. Model 6: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.8254
Skewness of chick counts	0.982
Maximum chicks/pair	0.9574

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> beta4.mean <- samplesStats("beta.chicks[4]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks2-",sep=""))
R> samplesCoda("beta.chicks[4]", stem=paste(MCMCout,"beta-chicks4-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks2-",sep=""), quiet=TR
R> beta4.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks4-",sep=""), quiet=TR
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                       probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta4.cs <- quantile(as.vector(as.array(beta4.chains)),
+                       probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                        q_025=as.numeric(beta2.cs[1]),
+                        q_05=as.numeric(beta2.cs[2]),
+                        q_10=as.numeric(beta2.cs[3]),
+                        q_25=as.numeric(beta2.cs[4]),
+                        q_50=as.numeric(beta2.cs[5]),
+                        q_75=as.numeric(beta2.cs[6]),
+                        q_90=as.numeric(beta2.cs[7]),
+                        q_95=as.numeric(beta2.cs[8]),
+                        q_975=as.numeric(beta2.cs[9]))
R> beta4.q <- data.frame(mean=as.numeric(beta4.mean),
+                        q_025=as.numeric(beta4.cs[1]),
+                        q_05=as.numeric(beta4.cs[2]),
+                        q_10=as.numeric(beta4.cs[3]),
```

```
+                       q_25=as.numeric(beta4.cs[4]),
+                       q_50=as.numeric(beta4.cs[5]),
+                       q_75=as.numeric(beta4.cs[6]),
+                       q_90=as.numeric(beta4.cs[7]),
+                       q_95=as.numeric(beta4.cs[8]),
+                       q_975=as.numeric(beta4.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> beta4.chains <- unlist(beta4.chains)
R> Pr_beta <- c(round(sum((beta2.chains<0)/length(beta2.chains)),digits=4),
+              round(sum((beta4.chains<0)/length(beta4.chains)),digits=4))
R> Pbeta <- data.frame(beta=c(1,4),Value=Pr_beta)
R> rm("beta2.chains","beta4.chains","Pr_beta")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_2 < 0)$. The effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

Table B-26. Model 6: Pr(beta < 0)

beta	Value
1	0.9717
4	0.9999

```
R> zz <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=50) + mean.ma
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q) + (zz*zz/100)%o%as.numeric(beta4.q))
R> wl.effect <- data.frame(wl.var=zz,
+                         wl.mean=wl.tmp[,1],
+                         wl.q025=wl.tmp[,2],
+                         wl.q05=wl.tmp[,3],
+                         wl.q10=wl.tmp[,4],
+                         wl.q25=wl.tmp[,5],
+                         wl.q50=wl.tmp[,6],
+                         wl.q75=wl.tmp[,7],
+                         wl.q90=wl.tmp[,8],
+                         wl.q95=wl.tmp[,9],
+                         wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                        xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                               zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                               distribute.type=TRUE, col=c(rep("black",5)),
+                               xlab="Max(water-level rise) (cm)",
+                               ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

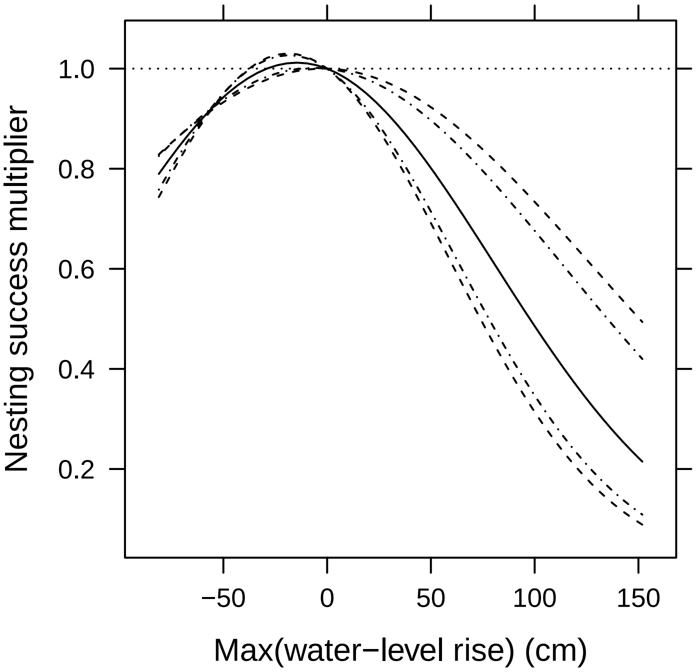

Figure B-43. Model 6: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model 7: Quadratic maximum 45-day water-level rise and Student's t- distributed random effects

Description

Model 7 uses the estimated maximal increase in water level over the putative 45-day nesting season as the water-level predictor covariate. A vague long-tailed Student's t is assumed for the latent random effect of lakes on nesting success. Model 7 informs the possibility of a quadratic effect in the maxima of 45-day water-level rises; a similar model based on 60-day nesting seasons failed. **Note: This model uses a subset of the data used by Models 1–6 and is therefore not comparable with those models.**

Let $z_{1,ij}$ denote the *estimated maxima of water-level increase during the 45-day nesting season* (variable `est_delta_wl` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right) \\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j \\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right) \\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right) \\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \boldsymbol{\Omega}_X\right) \\
\boldsymbol{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right) \\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right) \\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\frac{\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{1,ij}^2}{100}\right) \\
\beta_{1,j} &\sim \text{t}\left(\beta_1, \tau_{\beta_1}, 3\right) \\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right) \\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \boldsymbol{\Omega}_Y\right) \\
\boldsymbol{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively. The exponential function on the right-hand side of the equation for $\lambda_{Y,ij}$ is rescaled by the denominator of 100 for numerical convenience.

The Data

Get the data corresponding to 45-day putative nesting windows.

```
R> loondata2 <- read.csv(paste(datdir, "loon_comb.csv", sep=""))
R> loondata2 <- loondata2[(!loondata2$adults == 0 & loondata2$ret2 == 1),]
```

```
R> loondata2 <- loondata2[, c("lkcode","lake","year","source","adults",
+                             "pairs","chicks","hectares","date",
+                             "doy_io","n_wlobs45","est_max_dwl_ddoy45",
+                             "est_delta_wl45","est_delta_wl45",
+                             "v_est_w_diffwl45","v_est_max_dwl_ddoy45",
+                             "ret2","holdout")]
R> ## Omit records having implausible chick and/or pair counts:
R> ## -------------------------------------------------------------------
R> ##   9 chicks and 1 pair were reported from Birch Lake (Todd Co.)
R> ##     during 2002.  That is impossible and the data are omitted.
R> loondata2 <- loondata2[!(loondata2$lkcode==770084 & loondata2$year==2002),]
R> ##   14 chicks and 3 pairs were reported from Kabekona L. (Hubbard Co.)
R> ##     during 1997.  4.6 chicks/pair is implausible, and data omitted.
R> loondata2 <- loondata2[!(loondata2$lkcode==290075 & loondata2$year==1997),]
R> ##   4 chicks from 1 pair was reported from Cross L. (Crow Wing Co.)
R> ##     during 1980.  That ratio has not been reported elsewhere, and
R> ##     the next highest ratio is 3:1, which is known to be possible, but
R> ##     rare.  The 1980 Cross Lake record is omitted.
R> loondata2 <- loondata2[!(loondata2$lkcode==180312 & loondata2$year==1980),]
R> ## -------------------------------------------------------------------
R> loondata2 <- merge(loondata2, eagledata, by.x="year", by.y="year")
R> loondata2 <- loondata2[order(loondata2$source, loondata2$lkcode, loondata2$year),]
R> ## Hold out selected data from model fitting to enable out-of-sample
R> ## predictive evaluation by setting chicks <- NA.
R> chicks.temp <- rep(0,nrow(loondata2))
R> chicks.holdouts <- rep(0,nrow(loondata2))
R> loondata2$chicks.all <- loondata2$chicks
R> loondata2$pairs.all <- loondata2$pairs
R> for(i in 1:nrow(loondata2)){
+          if(loondata2$holdout[i]==1){
+                  chicks.holdouts[i] <- loondata2$chicks[i]
+                  chicks.temp[i] <- NA}
+          else{ chicks.holdouts[i] <- NA
+               chicks.temp[i] <- loondata2$chicks[i]}
+ }
R> loondata2$chicks <- chicks.temp
R> loondata2$chicks.holdouts <- chicks.holdouts
R> rm("chicks.temp")
R> year <- loondata2$year
R> yr <- as.factor(year-1978)
R> lake <- as.factor(loondata2$lake)
R> lkcode <- as.factor(loondata2$lkcode)
R> lkno <- charmatch(lkcode, unique(lkcode))
R> adults <- loondata2$adults
R> pairs <-  loondata2$pairs
R> chicks <- loondata2$chicks
```

```
R> ix <- (!is.na(loondata2$pairs.all)) & loondata2$pairs.all>0
R> cpp.obs <- loondata2$chicks.all[ix]/loondata2$pairs.all[ix]
R> max.cpp.obs <- max(cpp.obs,na.rm=TRUE)
R> eagleindx <- (loondata2$eaglenests -
+              mean(loondata2$eaglenests))/sd(loondata2$eaglenests)
R> survey <- as.factor(loondata2$source)
R> mean.doy.io <- round(mean(loondata2$doy_io))
R> doy_io <-  loondata2$doy_io - mean.doy.io
R> max.dwdt <- loondata2$est_max_dwl_ddoy45
R> mean.max.dwdt <- mean(max.dwdt)
R> max.dwdt <- max.dwdt - mean.max.dwdt
R> v.max.dwdt <- loondata2$v_est_max_dwl_ddoy45
R> v.max.dwdt[v.max.dwdt==0] <- 0.001
R> tau.max.dwdt <- 1/v.max.dwdt
R> max.dw <- loondata2$est_delta_wl45
R> mean.max.dw <- mean(max.dw)
R> max.dw <- max.dw - mean.max.dw
R> v.max.dw <- loondata2$v_est_w_diffwl45
R> v.max.dw[v.max.dw==0] <- 0.0001
R> tau.max.dw <- 1/v.max.dw
R> N <- length(adults)
R> nlakes <- max(lkno)
```

Initialization

Initialize the model:

```
R> burnin <- 6000         ##  Number of burn-in iterations
R> nsamps <- 5000         ##  Number of post-convergence iterations
R> Model <- 7             ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+               paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+               paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+              (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+               0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
```

```
+               max.dw=max.dw, tau.max.dw=tau.max.dw,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                     beta.chicks=parm0[1,3:6],
+                     beta.chicks.j=re0[,1]),
+                list(theta.pairs=parm0[2,1:2],
+                     beta.chicks=parm0[2,3:6],
+                     beta.chicks.j=re0[,3]),
+                list(theta.pairs=parm0[3,1:2],
+                     beta.chicks=parm0[3,3:6],
+                     beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                            theta.pairs[2]*adults[i]*adults[i] +
+                            epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                             beta.chicks[2]*mu.max.dw.cut[i] +
+                             beta.chicks[3]*eagleindx[i] +
+                             beta.chicks[4]*mu.max.dw.cut[i]*mu.max.dw.cut[i]/100 )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dw[i]~dnorm(0,0.001)
+                 }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dt(beta.chicks[1],tau.chicks,3)
+                       }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
```

```
+      Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+      tau.chicks ~ dgamma(3,1)
+      sigma.chicks <- pow(tau.chicks,-0.5)
+      beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+      Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

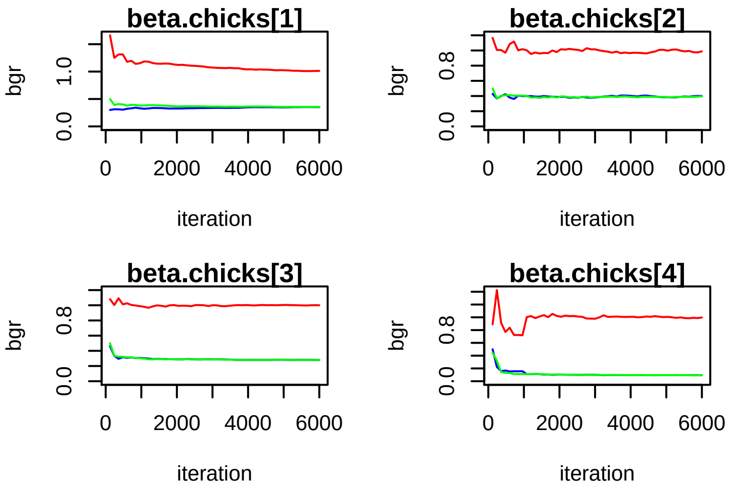

Figure B-44. Model 7: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-44).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+              "beta.chicks", "sigma.chicks",
+              "lambda.chicks","post.chicks",
+              "cpp"))
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod2 <- rbind(dicMod2,dicTmp)
R> rm(dicTmp)
```

Table B-27. Model 7: Summary of the joint posterior distribution of the parameters.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3522	0.0141	9.4620E-04	0.3240	0.3523	0.3808
theta.pairs[2]	-0.0004	0.0001	4.7010E-06	-0.0005	-0.0004	-0.0002
sigma.pairs	1.0270	0.1733	7.5180E-03	0.7302	1.0130	1.4100
beta.chicks[1]	-0.3341	0.0758	2.7970E-03	-0.4824	-0.3346	-0.1834
beta.chicks[2]	-0.0027	0.0011	4.1850E-05	-0.0050	-0.0027	-0.0005
beta.chicks[3]	-0.0755	0.0255	7.4960E-04	-0.1271	-0.0748	-0.0253
beta.chicks[4]	-0.0081	0.0022	7.5740E-05	-0.0129	-0.0081	-0.0040
sigma.chicks	0.3945	0.0495	9.8920E-04	0.3081	0.3909	0.5014

Table B-28. Model 7: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.1203	-0.0373	-0.1624
beta.chicks[2]	0.1203	1.0000	-0.0076	-0.2236
beta.chicks[3]	-0.0373	-0.0076	1.0000	-0.0073
beta.chicks[4]	-0.1624	-0.2236	-0.0073	1.0000

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dw)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
```

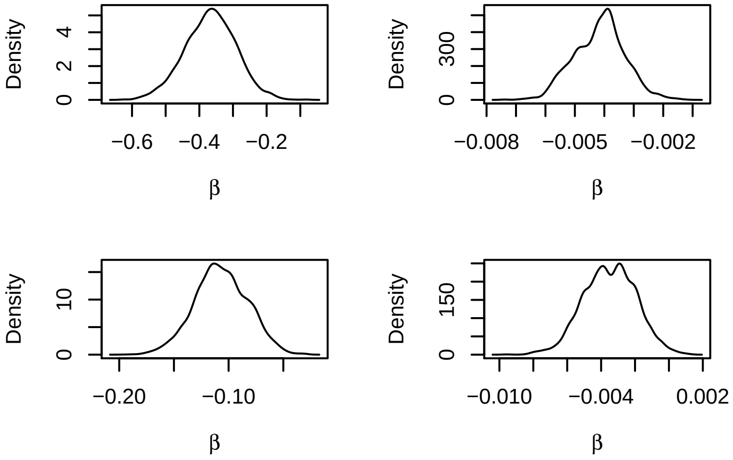

Figure B-45. Model 7: Posterior densities of the parameter vector β.

```
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                    points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                        groups=post.chicks$survey,
+                        key=key.groups,
+                        panel=panel.bar,
+                        dyu=post.chicks$chicks.post.u,
+                        dyl=post.chicks$chicks.post.l,
+                        cex=1.0,col="black",fill=T,
+                        ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                        pch=c(15,17,16),ylab="Chick counts",xlab="",
+                        scales = list(x = list(draw = FALSE)))


R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resid.std <- resid.raw/sd(resid.raw,na.rm=TRUE)
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,
+                      resid.std=resid.std,max.dw=max.dw)
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]


R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                     quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata2$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
```

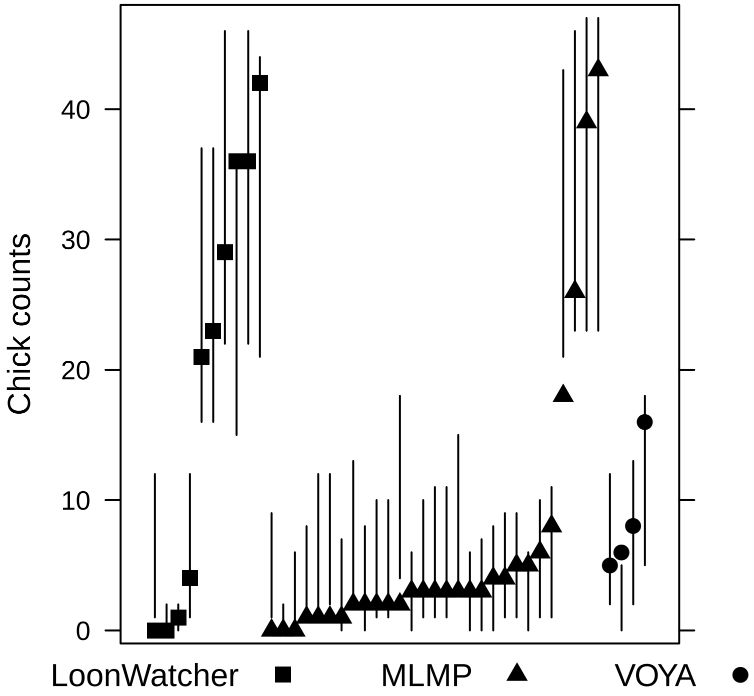

Figure B-46. Model 7: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> binnedplot(resids$pred.chicks,resids$resid.raw,
+           nclass=3*floor(sqrt(length(resids$pred.chicks))),
+           main=NULL,
+           xlab="Predicted chick counts",
+           ylab="Raw residuals")
```

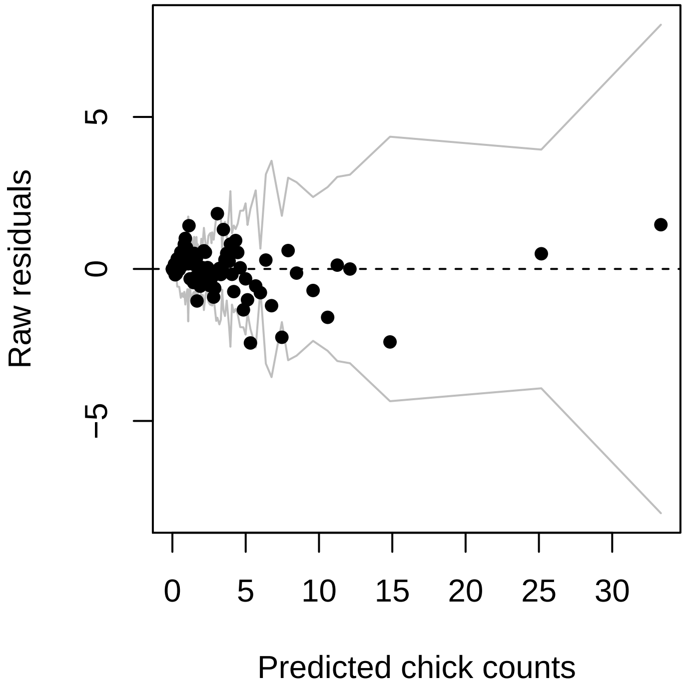

Figure B-47. Model 7: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> binnedplot(resids$max.dw,resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max 60-d WL rise (cm)",
+            ylab="Raw residuals")
```

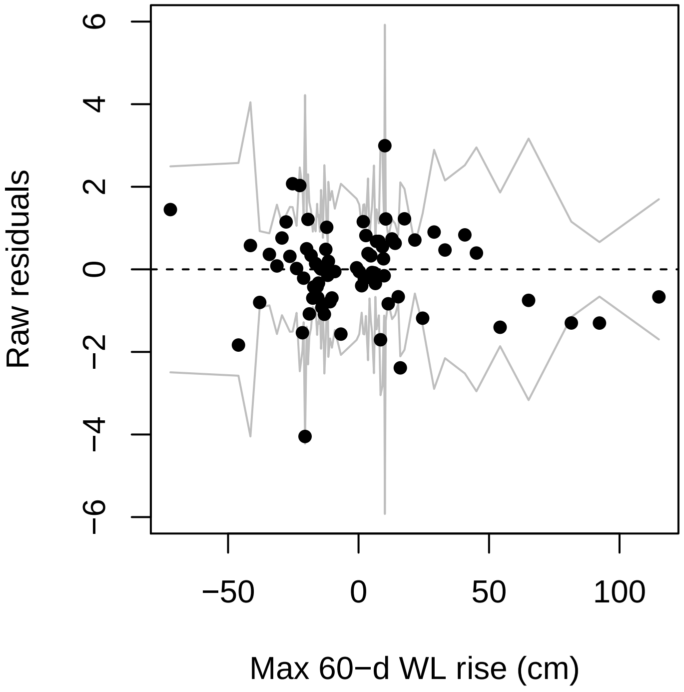

Figure B-48. Model 7: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                  quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                             "Maximum chicks/pair"),
+                     P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                     row.names=NULL)
```

Table B-29. Model 7: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.7118
Skewness of chick counts	0.949
Maximum chicks/pair	0.5332

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> beta4.mean <- samplesStats("beta.chicks[4]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks2-",sep=""))
R> samplesCoda("beta.chicks[4]", stem=paste(MCMCout,"beta-chicks4-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks2-",sep=""), quiet=TR
R> beta4.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks4-",sep=""), quiet=TR
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                      probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta4.cs <- quantile(as.vector(as.array(beta4.chains)),
+                      probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                       q_025=as.numeric(beta2.cs[1]),
+                       q_05=as.numeric(beta2.cs[2]),
+                       q_10=as.numeric(beta2.cs[3]),
+                       q_25=as.numeric(beta2.cs[4]),
+                       q_50=as.numeric(beta2.cs[5]),
+                       q_75=as.numeric(beta2.cs[6]),
+                       q_90=as.numeric(beta2.cs[7]),
+                       q_95=as.numeric(beta2.cs[8]),
+                       q_975=as.numeric(beta2.cs[9]))
R> beta4.q <- data.frame(mean=as.numeric(beta4.mean),
+                       q_025=as.numeric(beta4.cs[1]),
+                       q_05=as.numeric(beta4.cs[2]),
+                       q_10=as.numeric(beta4.cs[3]),
```

```
+                       q_25=as.numeric(beta4.cs[4]),
+                       q_50=as.numeric(beta4.cs[5]),
+                       q_75=as.numeric(beta4.cs[6]),
+                       q_90=as.numeric(beta4.cs[7]),
+                       q_95=as.numeric(beta4.cs[8]),
+                       q_975=as.numeric(beta4.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> beta4.chains <- unlist(beta4.chains)
R> Pr_beta <- c(round(sum((beta2.chains<0)/length(beta2.chains)),digits=4),
+              round(sum((beta4.chains<0)/length(beta4.chains)),digits=4))
R> Pbeta <- data.frame(beta=c(1,4),Value=Pr_beta)
R> rm("beta2.chains","beta4.chains","Pr_beta")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_2 < 0)$. The effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

Table B-30. Model 7: Pr(beta < 0)

beta	Value
1	0.9887
4	0.9999

```
R> zz <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=50) + mean.ma
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q) + (zz*zz/100)%o%as.numeric(beta4.q))
R> wl.effect <- data.frame(wl.var=zz,
+                         wl.mean=wl.tmp[,1],
+                         wl.q025=wl.tmp[,2],
+                         wl.q05=wl.tmp[,3],
+                         wl.q10=wl.tmp[,4],
+                         wl.q25=wl.tmp[,5],
+                         wl.q50=wl.tmp[,6],
+                         wl.q75=wl.tmp[,7],
+                         wl.q90=wl.tmp[,8],
+                         wl.q95=wl.tmp[,9],
+                         wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                        xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                               zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                               distribute.type=TRUE, col=c(rep("black",5)),
+                               xlab="Max(water-level rise) (cm)",
+                               ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

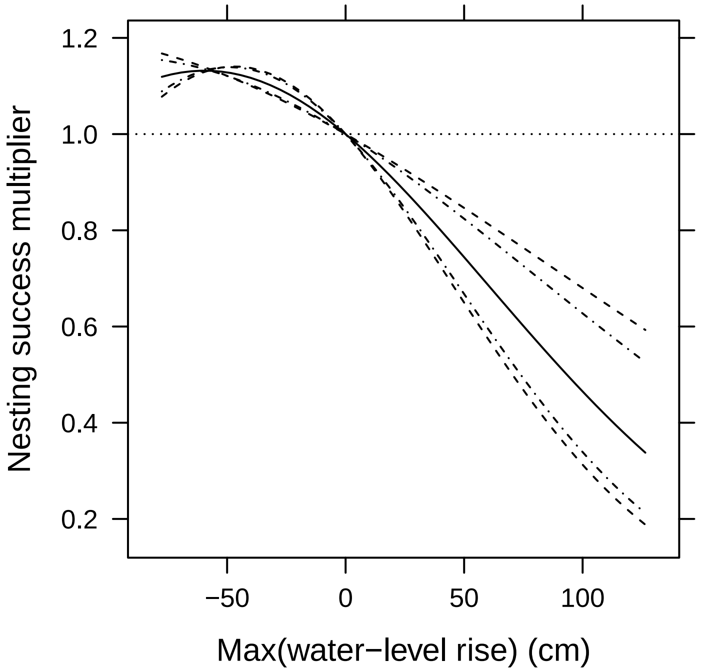

Figure B-49. Model 7: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model 8: Maximum daily water-level rise, maximum 45-day rise, and normally distributed random effects

Description

Model 8 uses the estimated maxima of the daily rates of water-level increase and the maximum rise over the putative 45-day nesting season as water-level predictor covariates. A vague normal distribution is assumed for the latent random effect of lakes on nesting success. Model 8 is identical to Model 5, apart from the data used to fit it. **Note: This model uses a subset of the data used by Models 1–6 and is therefore not comparable with those models.**

Let $z_{1,ij}$ denote the *estimated maxima of daily rates of water-level increase during the 45-day nesting season* (variable `est_max_dwl_ddoy` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right)\\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j\\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right)\\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right)\\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_X\right)\\
\mathbf{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right)\\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right)\\
\lambda_{Y,ij} &= \lambda_{X,ij}\exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right)\\
\beta_{1,j} &\sim \text{N}\left(\beta_1, \tau_{\beta_1}\right)\\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right)\\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_Y\right)\\
\mathbf{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\tau_X = 1/\sigma_X^2$ and $\tau_{\beta_1} = 1/\sigma_{\beta_1}^2$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X^2 and $\sigma_{\beta_1}^2$, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000           ##  Number of burn-in iterations
R> nsamps <- 5000           ##  Number of post-convergence iterations
```

```
R> Model <- 8             ##  Model number
R> ##modseed <- as.numeric(Sys.time())
R> modseed <- 2736736
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+                (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+                0.1*rnorm(3,0),0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+               max.dwdt=max.dwdt, tau.max.dwdt=tau.max.dwdt,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx,
+               max.dw=max.dw, tau.max.dw=tau.max.dw,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                     beta.chicks=parm0[1,3:6],
+                     beta.chicks.j=re0[,1]),
+                list(theta.pairs=parm0[2,1:2],
+                     beta.chicks=parm0[2,3:6],
+                     beta.chicks.j=re0[,3]),
+                list(theta.pairs=parm0[3,1:2],
+                     beta.chicks=parm0[3,3:6],
+                     beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                              theta.pairs[2]*adults[i]*adults[i] +
+                              epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
```

```
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                             beta.chicks[2]*mu.max.dwdt.cut[i] +
+                             beta.chicks[3]*eagleindx[i] +
+                             beta.chicks[4]*mu.max.dw.cut[i]
+                             )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dwdt[i] ~ dnorm(mu.max.dwdt[i],tau.max.dwdt[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dwdt.cut[i] <- cut(mu.max.dwdt[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dwdt[i]~dnorm(3,0.001)
+         mu.max.dw[i]~dnorm(0,0.001)
+                   }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dt(beta.chicks[1],tau.chicks,3)
+                         }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-50).

Results

Draw 5,000 additional samples to obtain the following results:

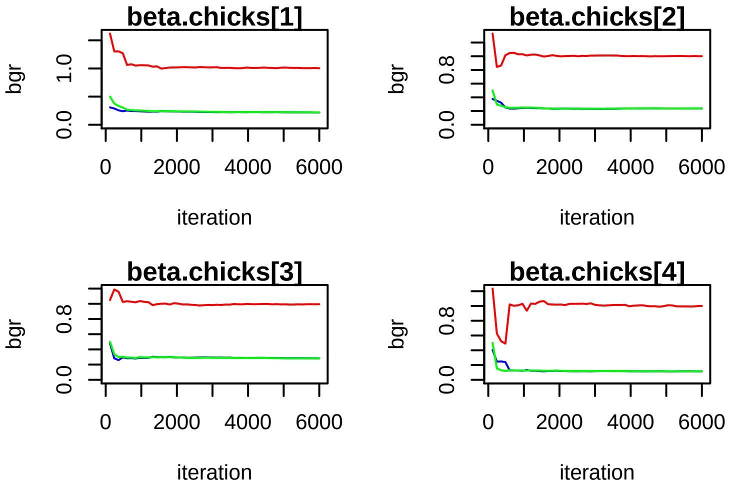

Figure B-50. Model 8: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+              "beta.chicks", "sigma.chicks",
+              "lambda.chicks","post.chicks",
+              "cpp"))
R> dicSet()
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod2 <- rbind(dicMod2,dicTmp)
R> rm(dicTmp)
```

Table B-31. Model 8: Summary of the joint posterior distribution of the parameters

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3469	0.0129	8.6770E-04	0.3118	0.3492	0.3675
theta.pairs[2]	-0.0004	0.0001	4.8480E-06	-0.0005	-0.0004	-0.0002
sigma.pairs	1.0520	0.1886	8.5770E-03	0.7403	1.0320	1.4800
beta.chicks[1]	-0.3801	0.0762	2.4760E-03	-0.5305	-0.3796	-0.2340
beta.chicks[2]	-0.0307	0.0113	2.7070E-04	-0.0530	-0.0307	-0.0091
beta.chicks[3]	-0.0724	0.0260	7.1710E-04	-0.1228	-0.0717	-0.0229
beta.chicks[4]	-0.0028	0.0012	5.0490E-05	-0.0051	-0.0029	-0.0004
sigma.chicks	0.3986	0.0507	1.0570E-03	0.3086	0.3948	0.5100

Table B-32. Model 8: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0466	-0.1234	0.0547
beta.chicks[2]	0.0466	1.0000	-0.0412	-0.2908
beta.chicks[3]	-0.1234	-0.0412	1.0000	0.0221
beta.chicks[4]	0.0547	-0.2908	0.0221	1.0000

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
R> chicks.post.l <- post.chicks$val2.5pc
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dwdt)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
```

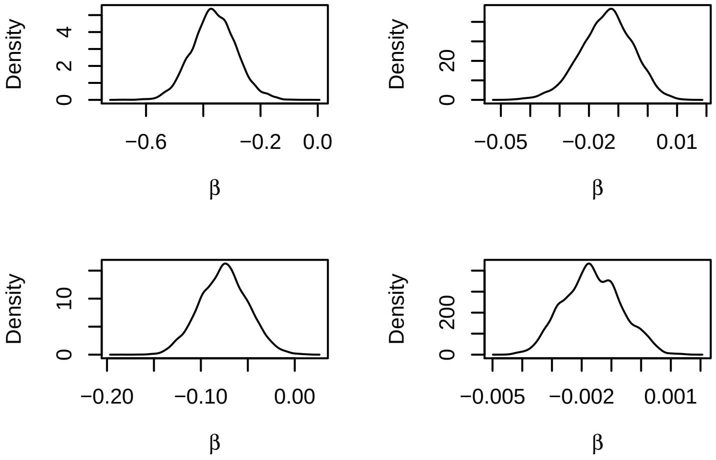

Figure B-51. Posterior densities of the parameter vector β.

```
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                     points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                         groups=post.chicks$survey,
+                         key=key.groups,
+                         panel=panel.bar,
+                         dyu=post.chicks$chicks.post.u,
+                         dyl=post.chicks$chicks.post.l,
+                         cex=1.0,col="black",fill=T,
+                         ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                         pch=c(15,17,16),ylab="Chick counts",xlab="",
+                         scales = list(x = list(draw = FALSE)))
```

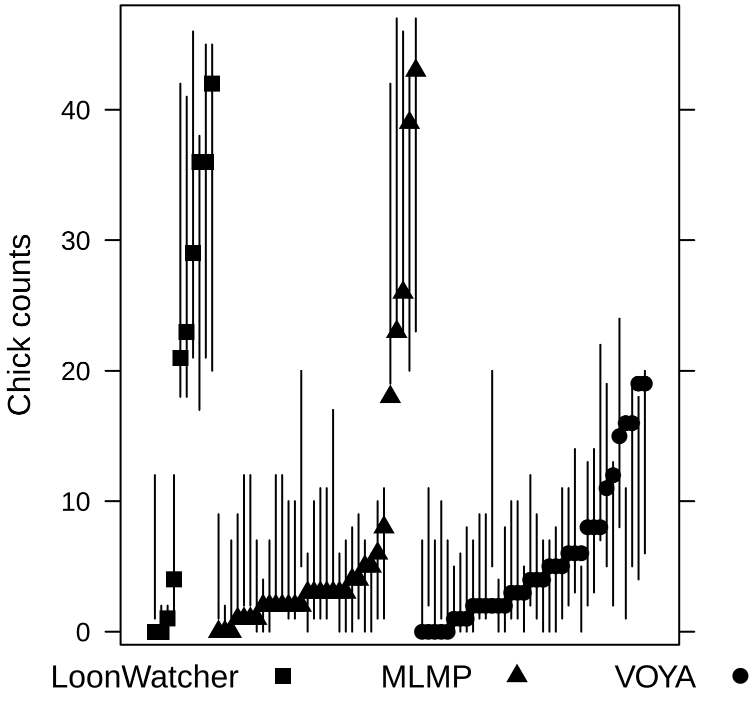

Figure B-52. Model 8: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
```

```
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dw=max.dw,max
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]
```

```
R> binnedplot(resids$pred.chicks,resids$resid.raw,
+           nclass=3*floor(sqrt(length(resids$pred.chicks))),
+           main=NULL,
+           xlab="Predicted chick counts",
+           ylab="Raw residuals")
```

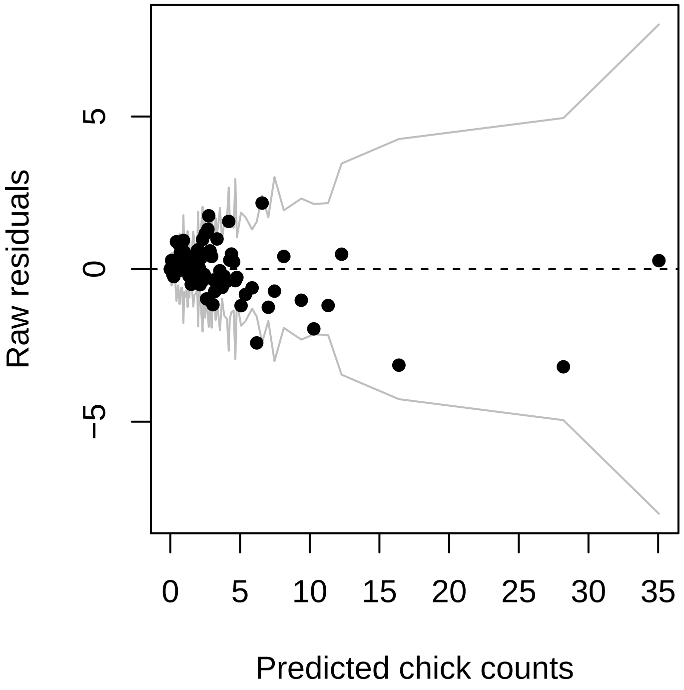

Figure B-53. Model 8: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                      quiet=TRUE)
```

```
R> binnedplot((resids$max.dw+mean.max.dw),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max 45-d WL rise (cm)",
+            ylab="Raw residuals")
```

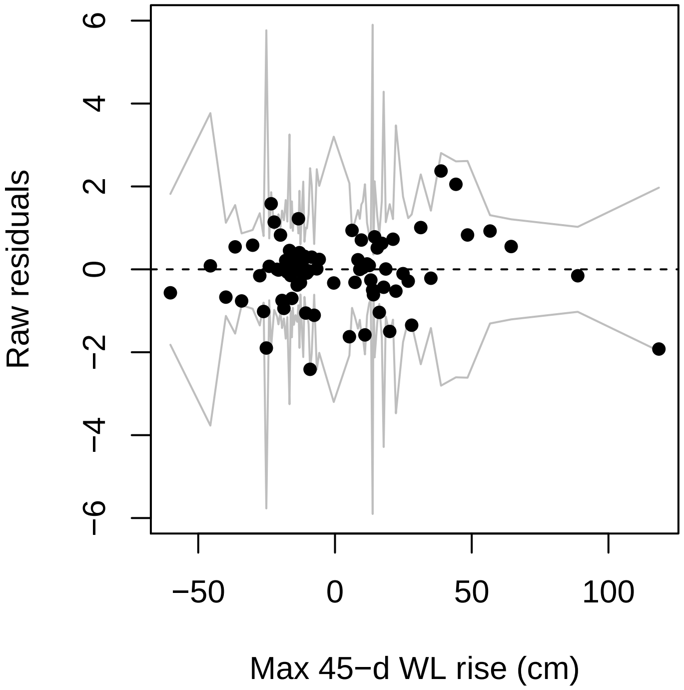

Figure B-54. Model 8: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> binnedplot((resids$max.dwdt+mean.max.dwdt),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max daily rise (cm/day)",
+            ylab="Raw residuals")
```

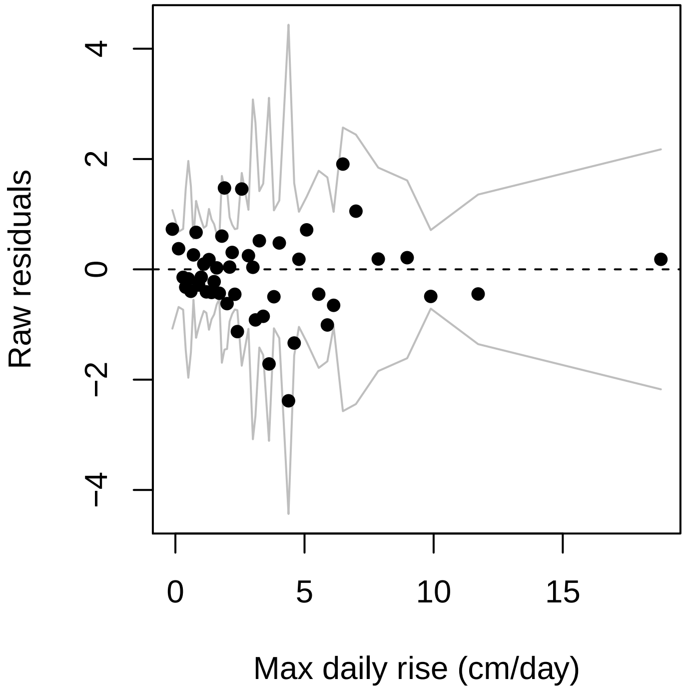

Figure B-55. Model 8: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                  quiet=TRUE)
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                             "Maximum chicks/pair"),
+                    P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                    row.names=NULL)
```

Table B-33. Model 8: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.657
Skewness of chick counts	0.8866
Maximum chicks/pair	0.6142

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> beta4.mean <- samplesStats("beta.chicks[4]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta2-chicks-",sep=""))
R> samplesCoda("beta.chicks[4]", stem=paste(MCMCout,"beta4-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta2-chicks-",sep=""), quiet=TR
R> beta4.chains <- read.openbugs(stem=paste(MCMCout,"beta4-chicks-",sep=""), quiet=TR
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                    probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta4.cs <- quantile(as.vector(as.array(beta4.chains)),
+                    probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                     q_025=as.numeric(beta2.cs[1]),
+                     q_05=as.numeric(beta2.cs[2]),
+                     q_10=as.numeric(beta2.cs[3]),
+                     q_25=as.numeric(beta2.cs[4]),
+                     q_50=as.numeric(beta2.cs[5]),
+                     q_75=as.numeric(beta2.cs[6]),
+                     q_90=as.numeric(beta2.cs[7]),
```

```
+                       q_95=as.numeric(beta2.cs[8]),
+                       q_975=as.numeric(beta2.cs[9]))
R> beta4.q <- data.frame(mean=as.numeric(beta4.mean),
+                       q_025=as.numeric(beta4.cs[1]),
+                       q_05=as.numeric(beta4.cs[2]),
+                       q_10=as.numeric(beta4.cs[3]),
+                       q_25=as.numeric(beta4.cs[4]),
+                       q_50=as.numeric(beta4.cs[5]),
+                       q_75=as.numeric(beta4.cs[6]),
+                       q_90=as.numeric(beta4.cs[7]),
+                       q_95=as.numeric(beta4.cs[8]),
+                       q_975=as.numeric(beta4.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> beta4.chains <- unlist(beta4.chains)
R> Pr_beta <- c(round(sum((beta2.chains<0)/length(beta2.chains)),digits=4),
+              round(sum((beta4.chains<0)/length(beta4.chains)),digits=4))
R> Pbeta <- data.frame(beta=c(1,5),Value=Pr_beta)
R> rm("beta2.chains","beta4.chains","Pr_beta")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_k < 0)$, $k \in \{1, 5\}$.

Table B-34. Model 8: Pr(beta < 0)

beta	Value
1	0.9982
5	0.9847

The effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

```
R> v1 <- seq(from=ceiling(min(max.dwdt)),to=floor(max(max.dwdt)),length.out=20) + mea
R> v2 <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=20) + mean.ma
R> zz <- expand.grid(v1,v2)
R> wl.tmp <- exp(zz$Var1%o%as.numeric(beta2.q) + zz$Var2%o%as.numeric(beta5.q))
R> wl.effect <- data.frame(max.dwdt=zz$Var1,
+                         max.dw=zz$Var2,
+                         wl.mean=wl.tmp[,1],
+                         wl.q025=wl.tmp[,2],
+                         wl.q05=wl.tmp[,3],
+                         wl.q10=wl.tmp[,4],
+                         wl.q25=wl.tmp[,5],
+                         wl.q50=wl.tmp[,6],
+                         wl.q75=wl.tmp[,7],
+                         wl.q90=wl.tmp[,8],
+                         wl.q95=wl.tmp[,9],
```

```
+                          wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot.mean <- levelplot(wl.mean ~ max.dwdt + max.dw, data=wl.effect,
+                               cuts=100,pretty=TRUE,col.regions=terrain.colors)
R> wl.effect.plot.l <- levelplot(wl.q05 ~ max.dwdt + max.dw, data=wl.effect,
+                               cuts=100,pretty=TRUE,col.regions=terrain.colors)
R> wl.effect.plot.u <- levelplot(wl.q95 ~ max.dwdt + max.dw, data=wl.effect,
+                               cuts=100,pretty=TRUE,col.regions=terrain.colors)
```

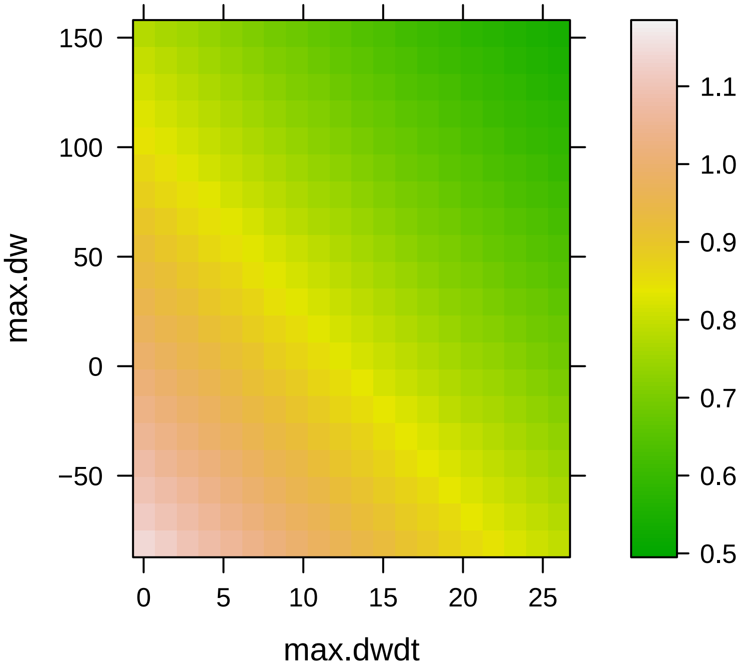

Figure B-56. Model 8: Estimated effects of the peak daily rate of water-level increase and peak 45-day increase on expected nesting success of loons.

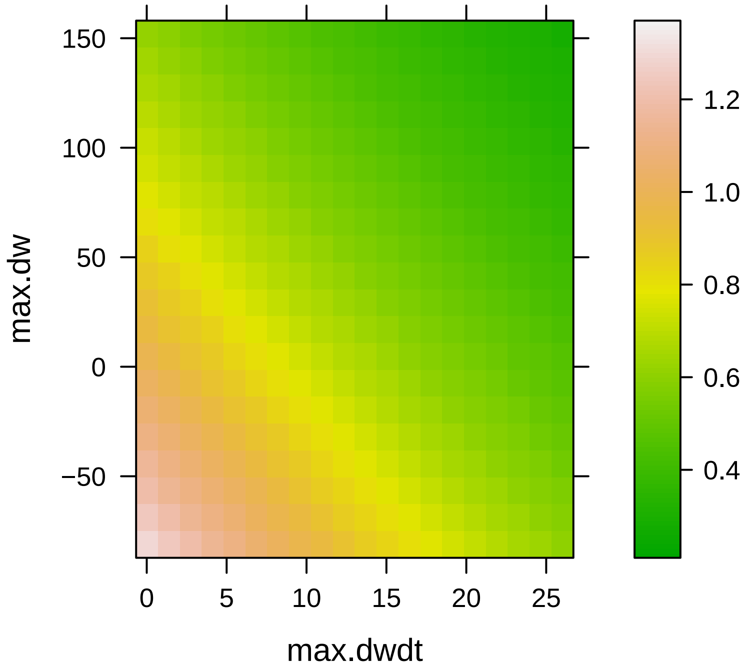

Figure B-57. Model 8: Estimated effects of the peak daily rate of water-level increase and peak 45-day increase on lower bound of Pr=0.90 credible set.

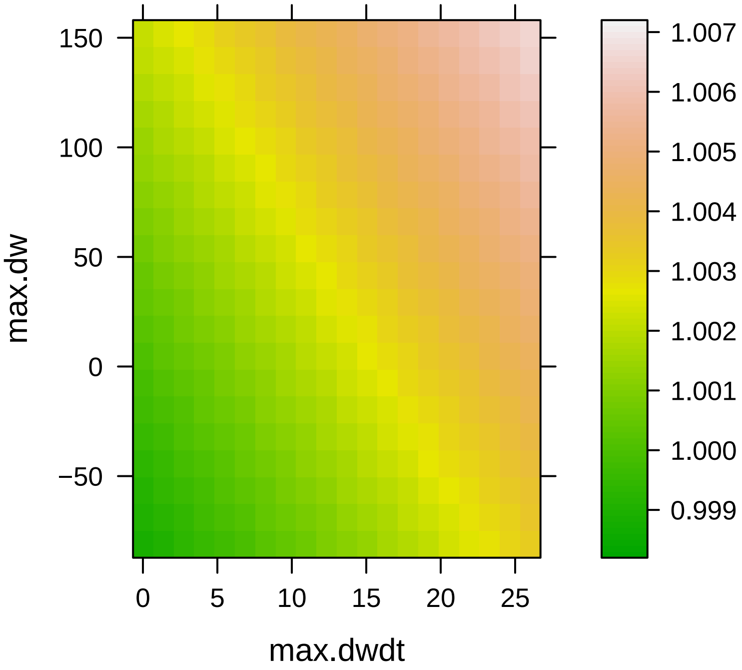

Figure B-58. Model 8: Estimated effects of the peak daily rate of water-level increase and peak 45-day increase on upper bound of Pr=0.90 credible set.

Model 9: Maximum 45-day water-level rise and t-distributed random effects

Description

Model 9 uses the estimated maximal increase in water level over the putative 45-day nesting season as the water-level predictor covariate. A vague long-tailed Student-t distribution is assumed for the latent random effect of lakes on nesting success. Model 9 is identical to Model 4, apart from use of 45-day water-level estimates. **Note: This model uses a subset of the data used by Models 1–6 and is therefore not comparable with those models.**

Let $z_{1,ij}$ denote the *estimated maxima of water-level increase during the 45-day nesting season* (variable `est_delta_wl` in `loon-comb.csv`) on lake i during year j, let $z_{2,j}$ denote the (zero-centered) regional bald eagle abundance index during year j, and let $z_{3,ij}$ denote the (zero-centered) day of the year of ice breakup. Counts of nesting pairs were not made by the MLMP so those counts, X_{ij}, must be estimated from counts of adult loons, denoted W_{ij}. The first model assumes normal distributions for the lake-specific latent random-effects parameters ϵ_j and $\beta_{1,j}$ and is given by

$$\begin{aligned}
X_{ij} &\sim \text{Poisson}\left(\lambda_{X,ij}\right)\\
\lambda_{X,ij} &= \theta_1 W_{ij} + \theta_2 {W_{ij}}^2 + \epsilon_j\\
\epsilon_j &\sim \text{N}\left(0, \tau_X\right)\\
\tau_X &\sim \text{Gamma}\left(3, 1.6\right)\\
(\theta_1, \theta_2) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_X\right)\\
\mathbf{\Omega}_X &\sim \text{Wishart}\left(2\,\text{diag}_{2\times 2}(2),\, 2\right)\\
Y_{ij} &\sim \text{Poisson}\left(\lambda_{Y,ij}\right)\\
\lambda_{Y,ij} &= \lambda_{X,ij} \exp\left(\beta_{1,j} + \beta_2 z_{1,ij} + \beta_3 z_{2,j} + \beta_4 z_{3,ij}\right)\\
\beta_{1,j} &\sim \text{t}\left(\beta_1, \tau_{\beta_1}, 3\right)\\
\tau_{\beta_1} &\sim \text{Gamma}\left(3, 1\right)\\
(\beta_1, \beta_2, \beta_3, \beta_4) &\sim \text{N}\left(\mathbf{0}, \mathbf{\Omega}_Y\right)\\
\mathbf{\Omega}_Y &\sim \text{Wishart}\left(4\,\text{diag}_{4\times 4}(3),\, 4\right),
\end{aligned}$$

where $\sigma_X = 1/\sqrt{\tau_X}$ and $\sigma_{\beta_1} = 1/\tau_{\beta_1}$. The Gamma priors on τ_X and τ_{β_1} are equivalent to vague but proper inverse (reciprocal) priors on σ_X and σ_{β_1}, respectively.

Initialization

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> Model <- 9              ##  Model number
R> ##modseed <- as.numeric(Sys.time())
```

```
R> modseed <- 2736736
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/mod",Model,"-init1.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init2.txt", sep=""),
+                paste(bugsdir, "inputs/mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+                (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+                0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+               max.dw=max.dw, tau.max.dw=tau.max.dw,
+               lkno=lkno, N=N, nlakes=nlakes,
+               eagleindx=eagleindx, doyio=doy_io,
+               zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+               nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+          datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                      beta.chicks=parm0[1,3:6],
+                      beta.chicks.j=re0[,1]),
+                 list(theta.pairs=parm0[2,1:2],
+                      beta.chicks=parm0[2,3:6],
+                      beta.chicks.j=re0[,3]),
+                 list(theta.pairs=parm0[3,1:2],
+                      beta.chicks=parm0[3,3:6],
+                      beta.chicks.j=re0[,3])),
+           numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                             theta.pairs[2]*adults[i]*adults[i] +
+                             epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                              beta.chicks[2]*mu.max.dw.cut[i] +
+                              beta.chicks[3]*eagleindx[i] + beta.chicks[4]*doyio[i]
```

```
+                              )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dw[i]~dnorm(0,0.001)
+                  }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dt(beta.chicks[1],tau.chicks,3)
+                       }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. B-59).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("theta.pairs", "sigma.pairs",
+             "beta.chicks", "sigma.chicks",
+             "lambda.chicks","post.chicks",
+             "mu.max.dw","cpp"))
R> dicSet()
```

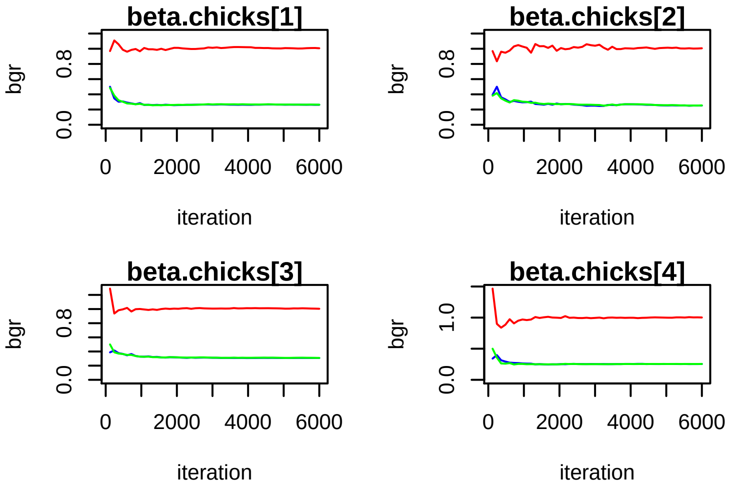

Figure B-59. Model 9: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

```
R> modelUpdate(nsamps)
R> dicTmp <- dicStats()
R> dicTmp <- dicTmp[c(1,3),]
R> dicTmp <- data.frame(rbind(dicTmp,apply(dicTmp,2,sum)),row.names=NULL)
R> dicTmp <- (cbind(Model,dicNode,dicTmp))
R> dicMod2 <- rbind(dicMod2,dicTmp)
R> rm(dicTmp)
```

Table B-35. Model 9: Summary of the joint posterior distribution of the parameters

	mean	sd	MC_error	val2.5pc	median	val97.5pc
theta.pairs[1]	0.3527	0.0146	9.8810E-04	0.3209	0.3539	0.3772
theta.pairs[2]	-0.0004	0.0001	4.6430E-06	-0.0006	-0.0004	-0.0003
sigma.pairs	1.0320	0.1860	8.5420E-03	0.7216	1.0130	1.4410
beta.chicks[1]	-0.3787	0.0750	2.5010E-03	-0.5263	-0.3778	-0.2337
beta.chicks[2]	-0.0044	0.0011	4.2800E-05	-0.0066	-0.0044	-0.0022
beta.chicks[3]	-0.0763	0.0258	7.2800E-04	-0.1264	-0.0760	-0.0274
beta.chicks[4]	-0.0038	0.0025	6.7690E-05	-0.0087	-0.0038	0.0011
sigma.chicks	0.3965	0.0503	1.0210E-03	0.3101	0.3921	0.5062

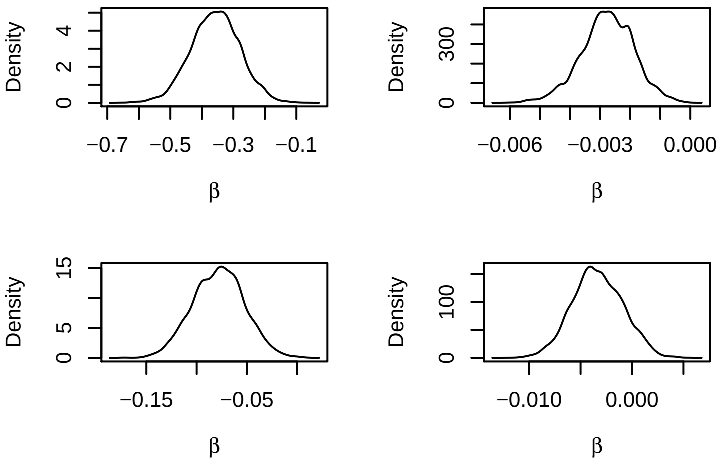

Figure B-60. Model 9: Posterior densities of the parameter vector β.

```
R> ## Out-of-sample posterior predictive assessment
R> post.chicks <- samplesStats("post.chicks")[,1:6]
```

```
R> chicks.post.l <- post.chicks$val2.5pc
R> chicks.post.u <- post.chicks$val97.5pc
R> post.chicks <- data.frame(survey,lake,lkcode,year,chicks.post.l,
+                            chicks.holdouts,chicks.post.u,max.dw)
R> o <- order(post.chicks$survey,post.chicks$chicks.holdouts,post.chicks$lake)
R> post.chicks <- post.chicks[o,]
R> post.chicks <- post.chicks[!is.na(post.chicks$chicks.holdouts),]
R> write.csv(post.chicks,file=paste(predir,"post.chicks-m",Model,".csv",sep=""))
R> panel.bar <- function(x,y,dyu=NULL,dyl=NULL,...){
+     panel.xyplot(x,y,...)
+     for(i in 1:length(x)){
+         panel.segments(x[i],dyl[i],x[i],dyu[i])
+     }
+ }
R> key.groups <- list(space="bottom",columns=3,text=list(levels(post.chicks$survey)),
+                     points=list(pch=c(15,17,16)),col="black")
R> holdout.plot <- xyplot(post.chicks$chicks.holdouts~1:dim(post.chicks)[1],
+                         groups=post.chicks$survey,
+                         key=key.groups,
+                         panel=panel.bar,
+                         dyu=post.chicks$chicks.post.u,
+                         dyl=post.chicks$chicks.post.l,
+                         cex=1.0,col="black",fill=T,
+                         ylim=c(-1,(1+max(post.chicks$chicks.post.u))),
+                         pch=c(15,17,16),ylab="Chick counts",xlab="",
+                         scales = list(x = list(draw = FALSE)))

R> ## Plot binned residuals
R> samplesCoda("lambda.chicks",stem=paste(MCMCout,"lambda-chicks-",sep=""))
R> samplesCoda("mu.max.dw",stem=paste(MCMCout,"mu-max-dw-",sep=""))
R> lambda.chicks <- read.openbugs(stem=paste(MCMCout,"lambda-chicks-",sep=""),
+                                 quiet=TRUE)
R> pred.chicks <- as.vector(lambda.chicks[[1]][nsamps,])
R> resid.raw <- chicks - pred.chicks
R> resids <- data.frame(pred.chicks=pred.chicks,resid.raw=resid.raw,max.dw=max.dw)
R> resids <- resids[!is.na(resids$resid.raw),]
R> o <- order(resids$pred.chicks,resids$resid.raw)
R> resids <- resids[o,]
```

Table B-36. Model 9: Correlation matrix for the posterior distribution of key parameters.

	beta.chicks.1.	beta.chicks.2.	beta.chicks.3.	beta.chicks.4.
beta.chicks[1]	1.0000	0.0822	-0.0835	0.0009
beta.chicks[2]	0.0822	1.0000	0.0131	0.2978
beta.chicks[3]	-0.0835	0.0131	1.0000	0.0213
beta.chicks[4]	0.0009	0.2978	0.0213	1.0000

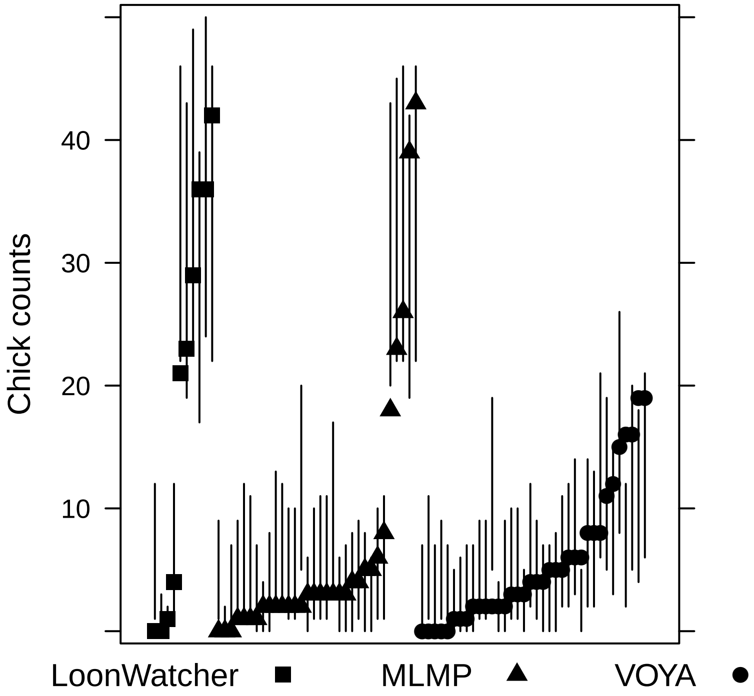

Figure B-61. Model 9: Posterior predictive performance against chick counts that were withheld from model fitting (solid symbols). Vertical bars denote Pr = 0.95 posterior-predictive credible sets for chick counts.

```
R> binnedplot(resids$pred.chicks,resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Predicted chick counts",
+            ylab="Raw residuals")
```

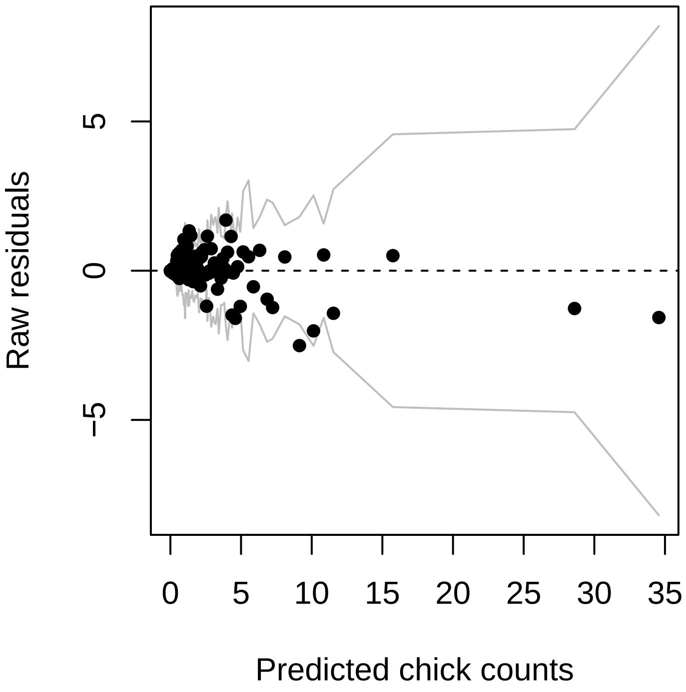

Figure B-62. Model 9: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> ## Bayesian P-values for max(chicks)
R> samplesCoda("cpp",stem=paste(MCMCout,"post-cpp-",sep=""))
R> samplesCoda("post.chicks",stem=paste(MCMCout,"post-chicks-",sep=""))
R> post.chicks.chains <- read.openbugs(stem=paste(MCMCout,"post-chicks-",sep=""),
+                                       quiet=TRUE)
R> post.chicks.mat <- as.matrix(post.chicks.chains[,][1])
R> post.chicks.max <- apply(post.chicks.mat,1,max)
R> max.chicks <- max(na.omit(chicks))
R> Pval.max <- mean(max.chicks >= post.chicks.max)
R> skew.chicks <- skewness(loondata$chicks.all, na.rm=TRUE)
R> post.chicks.skew <- apply(post.chicks.mat,1,skewness)
R> Pval.skew <- mean(skew.chicks >= post.chicks.skew)
R> post.cpp.chains <- read.openbugs(stem=paste(MCMCout,"post-cpp-",sep=""),
+                                   quiet=TRUE)
```

```
R> binnedplot((resids$max.dw+mean.max.dw),resids$resid.raw,
+            nclass=3*floor(sqrt(length(resids$pred.chicks))),
+            main=NULL,
+            xlab="Max 45-d WL rise (cm)",
+            ylab="Raw residuals")
```

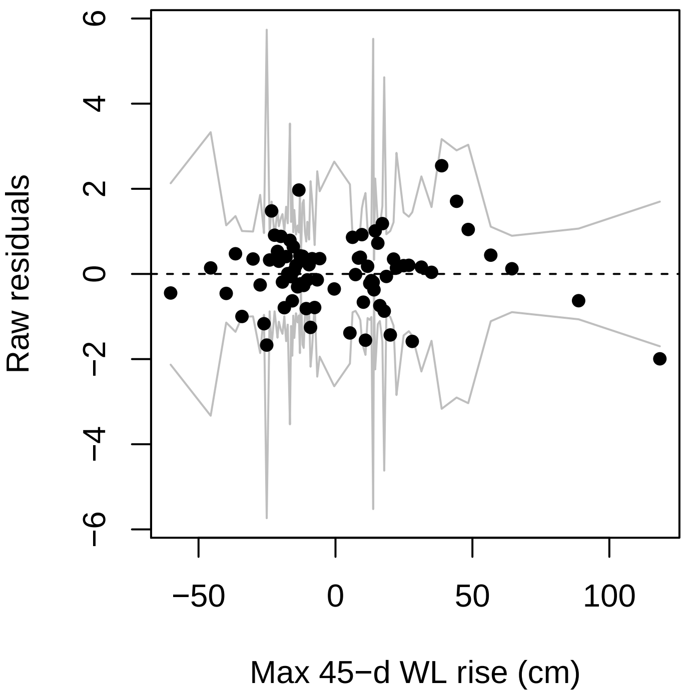

Figure B-63. Model 9: Plot of binned residuals from the final MCMC iteration. Grey lines enclose ±2 standard errors.

```
R> post.cpp.mat <- as.matrix(post.cpp.chains[,][1])
R> post.cpp.max <- apply(post.cpp.mat,1,max)
R> Pval.max.cpp <- mean(max.cpp.obs >= post.cpp.max)
R> pvals <- data.frame(cbind(Statistic=c("Maximum chick count","Skewness of chick cou
+                               "Maximum chicks/pair"),
+                      P_value=c(Pval.max,Pval.skew,Pval.max.cpp)),
+                      row.names=NULL)
```

Table B-37. Model 9: Bayesian P-values for posterior assessment of model performance against selected statistics.

Statistic	P_value
Maximum chick count	0.7156
Skewness of chick counts	0.9102
Maximum chicks/pair	0.5372

```
R> ## Pr(beta[2] < 0)
R> beta2.mean <- samplesStats("beta.chicks[2]")["mean"]
R> samplesCoda("beta.chicks[2]", stem=paste(MCMCout,"beta-chicks-",sep=""))
R> beta2.chains <- read.openbugs(stem=paste(MCMCout,"beta-chicks-",sep=""), quiet=TRU
R> beta2.cs <- quantile(as.vector(as.array(beta2.chains)),
+                       probs=c(0.025,0.05,0.1,0.25,0.5,0.75,0.9,0.95,0.975))
R> beta2.q <- data.frame(mean=as.numeric(beta2.mean),
+                        q_025=as.numeric(beta2.cs[1]),
+                        q_05=as.numeric(beta2.cs[2]),
+                        q_10=as.numeric(beta2.cs[3]),
+                        q_25=as.numeric(beta2.cs[4]),
+                        q_50=as.numeric(beta2.cs[5]),
+                        q_75=as.numeric(beta2.cs[6]),
+                        q_90=as.numeric(beta2.cs[7]),
+                        q_95=as.numeric(beta2.cs[8]),
+                        q_975=as.numeric(beta2.cs[9]))
R> beta2.chains <- unlist(beta2.chains)
R> Pr_beta2 <- round(sum((beta2.chains<0)/length(beta2.chains)),digits=4)
R> Pbeta2 <- data.frame(Value=Pr_beta2)
R> rm("beta2.chains","Pr_beta2")
```

The marginal adverse effect of the water-level covariate on nesting success is given by $\Pr(\beta_2 < 0)$. The effect of the water-level covariate on nesting success is given by $\exp(\beta_1 z_{1,ij})$.

```
R> zz <- seq(from=ceiling(min(max.dw)),to=floor(max(max.dw)),length.out=50)+mean.max.
R> wl.tmp <- exp(zz%o%as.numeric(beta2.q))
R> wl.effect <- data.frame(wl.var=zz,
+                          wl.mean=wl.tmp[,1],
```

```
+                       wl.q025=wl.tmp[,2],
+                       wl.q05=wl.tmp[,3],
+                       wl.q10=wl.tmp[,4],
+                       wl.q25=wl.tmp[,5],
+                       wl.q50=wl.tmp[,6],
+                       wl.q75=wl.tmp[,7],
+                       wl.q90=wl.tmp[,8],
+                       wl.q95=wl.tmp[,9],
+                       wl.q975=wl.tmp[,10])
R> write.csv(wl.effect,file=paste(predir,"mod",Model,"_wl.effect.csv",sep=""))
R> wl.effect.plot <- with(wl.effect,
+                      xyplot(wl.mean + wl.q05 + wl.q95 + wl.q10 + wl.q90 ~
+                             zz, type=rep("l",5), lty=c(1,2,2,4,4),
+                             distribute.type=TRUE, col=c(rep("black",5)),
+                             xlab="Max(water-level rise) (cm)",
+                             ylab="Nesting success multiplier"))
R> wl.effect.plot <- wl.effect.plot + layer(panel.abline(h=1,lty=3))
```

Table B-38. Model 9: Pr(beta2 < 0)

Value
1.0000

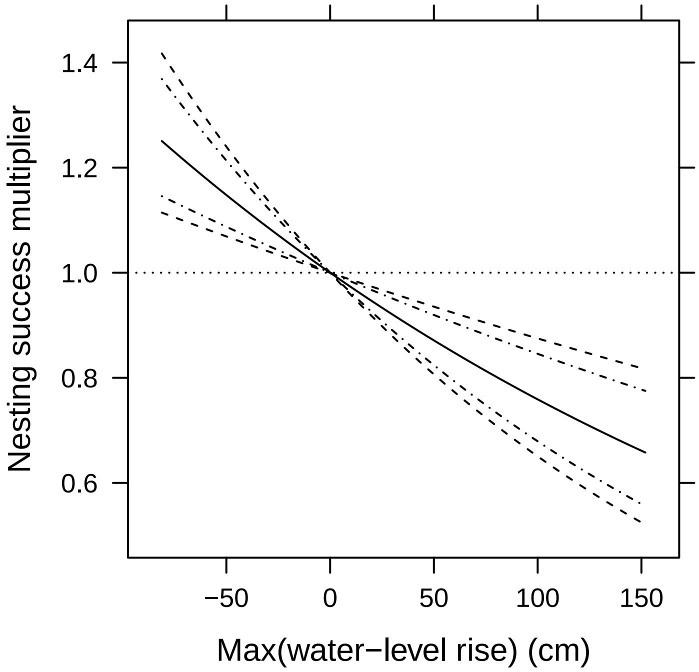

Figure B-64. Model 9: Estimated effect of the peak daily rate of water-level increase on nesting success of loons. The solid line is the mean response and the outer and inner sets of dashed lines enclose Bayesian credible sets having 0.80 and 0.90 posterior probability.

Model Comparison

The Deviance Information Criterion (DIC; Spiegelhalter et al. (2002)) is used to compare models. Models having small values of DIC have better predictive capability than models having larger values. DIC values from models based on presumptive 60-day nesting windows are *not* comparable with DIC values from models based on presumptive 45-day nesting windows because the data differ. Therefore DIC summaries are presented separately.

Models Based on Presumptive 60-day Nesting Seasons

Table B-39. Deviance Information Criterion (DIC) and associated statistics for comparison among models based on 60-day nesting seasons. Dbar is the posterior mean deviance, Dhat is the deviance measured at the posterior mean and pD is the number of effective parameters in the models.

Model	Node	Dbar	Dhat	DIC	pD
1	chicks	2533	2470	2597	63.24
1	pairs	1783	1756	1810	26.88
1	total	4316	4226	4407	90.12
2	chicks	2532	2467	2596	64.36
2	pairs	1780	1753	1808	27.44
2	total	4312	4220	4404	91.80
3	chicks	2534	2472	2596	61.95
3	pairs	1779	1752	1807	27.67
3	total	4313	4224	4403	89.62
4	chicks	2531	2468	2593	62.70
4	pairs	1781	1753	1808	27.14
4	total	4312	4221	4401	89.84
5	chicks	2528	2464	2592	64.01
5	pairs	-410	-1125	306	715.90
5	total	2118	1339	2898	779.91
6	chicks	2526	2464	2587	61.46
6	pairs	1782	1755	1809	27.06
6	total	4308	4219	4396	88.52

Models Based on Presumptive 45-day Nesting Seasons

Table B-40. Deviance Information Criterion (DIC) and associated statistics for comparison among models based on 45-day nesting seasons. Dbar is the posterior mean deviance, Dhat is the deviance measured at the posterior mean and pD is the number of effective parameters in the models.

Model	Node	Dbar	Dhat	DIC	pD
7	chicks	2462	2397	2526	64.22
7	pairs	1748	1720	1775	27.34
7	total	4210	4117	4301	91.56
8	chicks	2465	2400	2531	65.68
8	pairs	-122	-822	577	699.20
8	total	2343	1578	3108	764.88
9	chicks	2473	2408	2537	64.31
9	pairs	1748	1720	1775	27.58
9	total	4221	4128	4312	91.89

Appendix C
Evaluation of Effects of the 2000 Rule Curve on the Nesting Success of Loons on Rainy Lake and the Namakan Reservoir

This appendix is an image of the Reproducible Research Record for evaluation of the statistical properties of alternative estimators of water-level extremes. This reproducible research record (Ince et al., 2012) was implemented by the R noweb file `loon-rulecurvepred.Rnw`. Execution of that file from R replicates the analysis and produces the LaTeX source file from which this appendix was generated. Thus, this appendix contains the printed record of the analysis.

Objective

The objective of this analysis is to compare posterior predictions of common loons *Gavia immer* on Rainy Lake and the Namakan Reservoir complex under the 1970 and 2000 Rule Curves. This analysis uses Model 6.

The model does not include temporal dynamics of the Minnesota-Ontario breeding population. Therefore the approach used here is to hold the counts of adults and pairs fixed at the values observed during 2005. The results are conditional predictions of differences in nesting success between the 2000 and 1970 Rule Curves, assuming a constant breeding population.

Implementation

This analysis used R version 2.15.0 (R Development Core Team, 2011). Bayesian Markov Chain Monte Carlo sampling was implemented using the R package BRugs version 0.7-7 (Thomas et al., 2006). Computations were performed on `umesc-250.er.usgs.gov` running under Ubuntu Gnu Linux 10.04.

Data Description

The 2005 counts of adult loons and loon pairs from the National Park Service Voyageurs National Park (VOYA) are treated as a fixed basis for comparison, and are replicated over the years 1970 through 2010. The water-level covariates are computed from the observed hydrographs for each of those years. The system was operated under the 1970 Rule Curve from 1970–1999, and under the 2000 Rule curve from 2000–2010. The data construction was performed by the SAS program `Loon_Data-6.sas`.

These analyses re-computed Model 6 (retaining the original RNG seed) with the addition of the replicated data, as described above. Because there are no chick counts for those hypothetical data, they do not inform the model fit. However, the MCMC sampling produces posterior predictions of chick counts and the numbers of chicks per pair, which are the basis for comparison of nesting success predicted under the 1970 and 2000 rule curves.

Data extraction

Extract the loon-count and water-level data from `rulecurvepred.csv` and extract the Wisconsin bald eagle nest index from `EagelNestSurvey.csv`:

```
R> library(BRugs)
R> library(xtable)
R> library(moments)
R> library(latticeExtra)
R> library(arm)
R> setwd("/home/sgutreuter/projects/NRPP-Voya/R/loons")
R> old.par <- par
R> options(SweaveHooks = list(fig=function() par(mar=c(5.1,4.1,1.1,2.1))))
R> datdir <- paste((Sys.getenv("DATA")), "/projects/NRPP-Voya/Loons/", sep="")
R> bugsdir <- paste((Sys.getenv("HOME")),
+                  "/projects/NRPP-Voya/R/loons/BUGS/", sep="")
R> ruledata <- read.csv(paste(datdir, "rulecurvepred.csv", sep=""))
R> eagledata <- read.csv(paste(datdir, "EagleNestSurvey.csv", sep=""))
R> loondata <- read.csv(paste(datdir, "loon_comb.csv", sep=""))
R> loondata <- loondata[(!loondata$adults == 0 & loondata$ret1 == 1),]
R> ## Omit records having implausible chick and/or pair counts:
R> ## ---------------------------------------------------------------
R> ##   9 chicks and 1 pair were reported from Birch Lake (Todd Co.)
R> ##     during 2002.  That is impossible and the data are omitted.
R> loondata <- loondata[!(loondata$lkcode==770084 & loondata$year==2002),]
R> ##   14 chicks and 3 pairs were reported from Kabekona L. (Hubbard Co.)
R> ##     during 1997.  4.6 chicks/pair is implausible, and data omitted.
R> loondata <- loondata[!(loondata$lkcode==290075 & loondata$year==1997),]
R> ##   4 chicks from 1 pair was reported from Cross L. (Crow Wing Co.)
R> ##     during 1980.  That ratio has not been reported elsewhere, and
R> ##     the next highest ratio is 3:1, which is known to be possible, but
```

```
R> ##     rare.  The 1980 Cross Lake record is omitted.
R> loondata <- loondata[!(loondata$lkcode==180312 & loondata$year==1980),]
R> ## ------------------------------------------------------------------
R>
R> loondata <- merge(loondata, eagledata, by.x="year", by.y="year")
R> ## Hold out selected data from model fitting to enable out-of-sample
R> ## predictive evaluation by setting chicks <- NA.
R> chicks.temp <- rep(0,nrow(loondata))
R> chicks.holdouts <- rep(0,nrow(loondata))
R> loondata$chicks.all <- loondata$chicks
R> loondata$pairs.all <- loondata$pairs
R> for(i in 1:nrow(loondata)){
+        if(loondata$holdout[i]==1){
+                chicks.holdouts[i] <- loondata$chicks[i]
+                chicks.temp[i] <- NA}
+        else{ chicks.holdouts[i] <- NA
+             chicks.temp[i] <- loondata$chicks[i]}
+ }
R> loondata$chicks <- chicks.temp
R> loondata$chicks.holdouts <- chicks.holdouts
R> rm("chicks.temp")
R> year <- loondata$year
R> yr <- as.factor(year-1978)
R> lake <- as.factor(loondata$lake)
R> lkcode <- as.factor(loondata$lkcode)
R> lkno <- charmatch(lkcode, unique(lkcode))
R> adults <- loondata$adults
R> pairs <-  loondata$pairs
R> chicks <- loondata$chicks
R> ix <- (!is.na(loondata$pairs.all)) & loondata$pairs.all>0
R> cpp.obs <- loondata$chicks.all[ix]/loondata$pairs.all[ix]
R> max.cpp.obs <- max(cpp.obs,na.rm=TRUE)
R> eagleindx <- (loondata$eaglenests -
+              mean(loondata$eaglenests))/sd(loondata$eaglenests)
R> survey <- as.factor(loondata$source)
R> mean.doy.io <- round(mean(loondata$doy_io))
R> doy_io <-  loondata$doy_io - mean.doy.io
R> max.dwdt <- loondata$est_max_dwl_ddoy60
R> mean.max.dwdt <- mean(max.dwdt)
R> max.dwdt <- max.dwdt - mean.max.dwdt
R> v.max.dwdt <- loondata$v_est_max_dwl_ddoy60
R> v.max.dwdt[v.max.dwdt==0] <- 0.0001
R> tau.max.dwdt <- 1/v.max.dwdt
R> max.dw <- loondata$est_delta_wl60
R> mean.max.dw <- mean(max.dw)
R> max.dw <- max.dw - mean.max.dw
```

```
R> v.max.dw <- loondata$v_est_w_diffwl60
R> v.max.dw[v.max.dw==0] <- 0.0001
R> tau.max.dw <- 1/v.max.dw
R> N0 <- length(adults)
R> nlakes <- max(lkno)
R> base.idx <- 1 + sum(as.numeric(is.na(chicks)))
R> ruledata$rcurve <- as.factor((ruledata$year < 2000)*1970 +
+                               (ruledata$year >= 2000)*2000)
R> doy_io.1970 <- ruledata$doy_io[ruledata$rcurve == 1970]
R> doy_io.2000 <- ruledata$doy_io[ruledata$rcurve == 2000]
R> N.1970 <- length(ruledata$pairs[ruledata$rcurve == 1970])
R> N.2000 <- length(ruledata$pairs[ruledata$rcurve == 2000])
R> doy_io.1970 <- ruledata$doy_io[ruledata$rcurve == 1970] - mean.doy.io
R> doy_io.2000 <- ruledata$doy_io[ruledata$rcurve == 2000] - mean.doy.io
R> eagleindx.1970 <- rep(0, N.1970)
R> eagleindx.2000 <- rep(0, N.2000)
R> v.max.dwdt.1970 <- rep(0.0001, N.1970)
R> tau.max.dwdt.1970 <- 1/v.max.dwdt.1970
R> v.max.dw.1970 <- rep(0.0001, N.1970)
R> tau.max.dw.1970 <- 1/v.max.dw.1970
R> v.max.dwdt.2000 <- rep(0.0001, N.2000)
R> tau.max.dwdt.2000 <- 1/v.max.dwdt.2000
R> v.max.dw.2000 <- rep(0.0001, N.2000)
R> tau.max.dw.2000 <- 1/v.max.dw.2000
R> max.dwdt.1970 <- ruledata$est_max_dwl_ddoy60[ruledata$rcurve == 1970]
R> max.dwdt.2000 <- ruledata$est_max_dwl_ddoy60[ruledata$rcurve == 2000]
R> max.dw.1970 <- ruledata$est_delta_wl60[ruledata$rcurve == 1970]
R> max.dw.2000 <- ruledata$est_delta_wl60[ruledata$rcurve == 2000]
R> adults.1970 <- ruledata$adults[ruledata$rcurve == 1970]
R> adults.2000 <- ruledata$adults[ruledata$rcurve == 2000]
R> pairs.1970 <- ruledata$pairs[ruledata$rcurve == 1970]
R> pairs.2000 <- ruledata$pairs[ruledata$rcurve == 2000]
R> lkcode.1970 <- ruledata$lkcode[ruledata$rcurve == 1970]
R> lkcode.2000 <- ruledata$lkcode[ruledata$rcurve == 2000]
R> year.1970 <- ruledata$year[ruledata$rcurve == 1970]
R> year.2000 <- ruledata$year[ruledata$rcurve == 2000]
R> yr.1970 <- as.factor(year.1970 - 1978)
R> yr.2000 <- as.factor(year.2000 - 1978)
R> nlakes.rc <- 4
R> lkno.1970 <- c(rep(56,30),rep(57,30),rep(58,30),rep(59,30))
R> lkno.2000 <- c(rep(56,11),rep(57,11),rep(58,11),rep(59,11))
R> chicks.rc <- as.numeric(rep(NA,dim(ruledata)[1]))
R> predir <- paste(bugsdir,"preds/",sep="")
R> doy_io <- c(doy_io,doy_io.1970,doy_io.2000)
R> eagleindx <- c(eagleindx,eagleindx.1970,eagleindx.2000)
R> max.dwdt <- c(max.dwdt,max.dwdt.1970,max.dwdt.2000)
```

```
R> tau.max.dwdt <- c(tau.max.dwdt,tau.max.dwdt.1970,tau.max.dwdt.2000)
R> max.dw <- c(max.dw,max.dw.1970,max.dw.2000)
R> tau.max.dw <- c(tau.max.dw,tau.max.dw.1970,tau.max.dw.2000)
R> adults <- c(adults,adults.1970,adults.2000)
R> pairs <- c(pairs,pairs.1970,pairs.2000)
R> chicks <- c(chicks,chicks.rc)
R> lkno <- c(lkno,lkno.1970,lkno.2000)
R> N <- N0 + N.1970 + N.2000
R>
```

Model 6: Quadratic maximum 60-day water-level rise and lognormally distributed lake-specific random effects.

Initialize the model:

```
R> burnin <- 6000          ##  Number of burn-in iterations
R> nsamps <- 5000          ##  Number of post-convergence iterations
R> Model <- 6              ##  Model number
R> modseed <- 2736736
R> set.seed(modseed)
R> datafile <- paste(bugsdir, "inputs/rc-mod",Model,"-data.txt", sep="")
R> initfiles <- c(paste(bugsdir, "inputs/rc-mod",Model,"-init1.txt", sep=""),
+               paste(bugsdir, "inputs/rc-mod",Model,"-init2.txt", sep=""),
+               paste(bugsdir, "inputs/rc-mod",Model,"-init3.txt", sep=""))
R> modelfile <- paste(bugsdir, "inputs/rc-model-",Model,".bug", sep="")
R> MCMCout <- paste(bugsdir,"chains/rc-m",Model,"_",sep="")
R> zerovec <- rep(0,4)
R> nuR.chicks <- 3*diag(1, nrow=4)
R> nuR.pairs <- 2*diag(1, nrow=2)
R> parm0 <- cbind((0.33 + 0.1*rnorm(3,0)), (-0.0003+0.001*rnorm(3,0)),
+               (0.2*rnorm(3,0)-0.8), 0.001*rnorm(3,0), 0.1*rnorm(3,0),
+               0.1*rnorm(3,0) )
R> re0 <- outer(0.1*rnorm(nlakes,0), parm0[,1], FUN="+")
R> bugsData(list(pairs=pairs, adults=adults, chicks=chicks,
+              max.dw=max.dw, tau.max.dw=tau.max.dw,
+              lkno=lkno, N=N, nlakes=nlakes,
+              eagleindx=eagleindx,
+              zerovec.chicks=zerovec, zerovec.pairs=zerovec[1:2],
+              nuR.chicks=nuR.chicks, nuR.pairs=nuR.pairs),
+         datafile, digits=5)
R> bugsInits(list(list(theta.pairs=parm0[1,1:2],
+                     beta.chicks=parm0[1,3:6],
+                     beta.chicks.j=re0[,1]),
+               list(theta.pairs=parm0[2,1:2],
```

```
+                      beta.chicks=parm0[2,3:6],
+                      beta.chicks.j=re0[,3]),
+                 list(theta.pairs=parm0[3,1:2],
+                      beta.chicks=parm0[3,3:6],
+                      beta.chicks.j=re0[,3])),
+            numChains = 3, initfiles, digits=5)
R> write("model{
+     for (i in 1:N){
+
+         ##  Model for nesting pairs
+         pairs[i] ~ dpois(lambda.pairs[i])
+         lambda.pairs[i] <- max(0.0001, theta.pairs[1]*adults[i] +
+                             theta.pairs[2]*adults[i]*adults[i] +
+                             epsilon.pairs[lkno[i]])
+
+         ##  Model for chicks
+         chicks[i] ~ dpois(lambda.chicks[i])
+         cpp[i] <- exp(beta.chicks.j[lkno[i]] +
+                              beta.chicks[2]*mu.max.dw.cut[i] +
+                              beta.chicks[3]*eagleindx[i] +
+                              beta.chicks[4]*mu.max.dw.cut[i]*mu.max.dw.cut[i]/100 )
+         lambda.chicks[i] <- (max(0.0001,lambda.pairs[i]))*cpp[i]
+         post.chicks[i] ~ dpois(lambda.chicks[i])
+         max.dw[i] ~ dnorm(mu.max.dw[i],tau.max.dw[i])
+         mu.max.dw.cut[i] <- cut(mu.max.dw[i])
+         mu.max.dw[i]~dnorm(0,0.001)
+                  }
+
+     for (j in 1:nlakes) {
+         epsilon.pairs[j] ~ dnorm(0,tau.pairs)
+         beta.chicks.j[j] ~ dnorm(beta.chicks[1],tau.chicks)
+                        }
+
+     tau.pairs ~ dgamma(3,1.6)
+     sigma.pairs <- pow(tau.pairs,-0.5)
+     theta.pairs[1:2] ~ dmnorm(zerovec.pairs[],Omega.theta[,])
+     Omega.theta[1:2 , 1:2] ~ dwish(nuR.pairs[,],2)
+
+     tau.chicks ~ dgamma(3,1)
+     sigma.chicks <- pow(tau.chicks,-0.5)
+     beta.chicks[1:4] ~ dmnorm(zerovec.chicks[],Omega.beta[,])
+     Omega.beta[1:4, 1:4] ~ dwish(nuR.chicks[,],4)
+
+ }", modelfile)
R> modelCheck(modelfile)
R> modelData(datafile)
```

```
R> modelCompile(numChains=3)
R> modelInits(initfiles)
R> modelGenInits()
R> samplesSet(c("beta.chicks"))
R> modelUpdate(burnin)
```

Convergence diagnostics

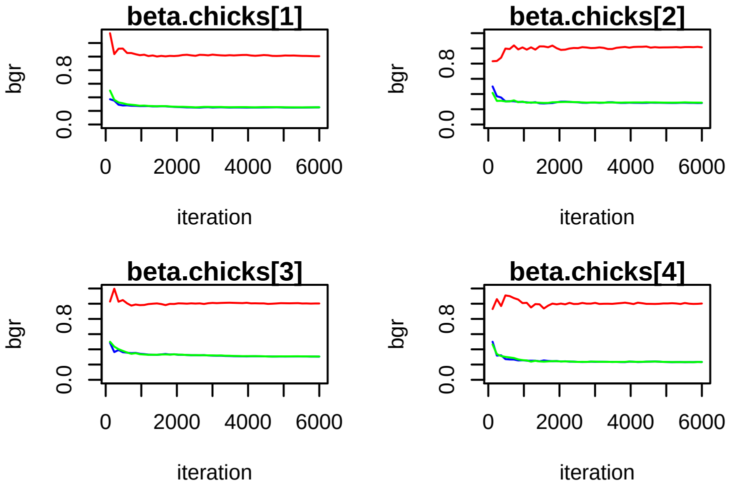

Figure C-1. Model 6: BGR plot of parameter vector beta. The chains have likely converged when the ratio of among-chain to within-chain variances (red line) equals one.

Verify convergence using Brooks-Gelman-Rubin plots. The chains for $\boldsymbol{\beta}$ clearly converged within the 10,000-iteration burn in (Fig. C-1).

Results

Draw 5,000 additional samples to obtain the following results:

```
R> samplesClear("beta.chicks")
R> samplesSet(c("beta.chicks", "chicks", "cpp"))
R> modelUpdate(nsamps)
```

Compute the differences of means (over years) between the 2000 and 1970 Rule Curves. The intermediate result is a set of `nsamps` × 3 differences from the MCMC output, which are used to compute posterior summaries. The final results are the overall predicted mean differences between Rule Curves from each lake and Pr = 0.90 and Pr = 0.95 Bayesian credible sets.

```
R> samplesCoda("chicks",stem=paste(MCMCout,"chicks-rc-",sep=""))
R> samplesCoda("cpp",stem=paste(MCMCout,"cpp-rc-",sep=""))
R> chicks.rc <- read.openbugs(stem=paste(MCMCout,"chicks-rc-",sep=""),
+                             quiet=TRUE)
R> cpp.rc <- read.openbugs(stem=paste(MCMCout,"cpp-rc-",sep=""),
+                          quiet=TRUE)
R> chicks.rc.array <- as.array(chicks.rc)
R> chicks.rc.array <- chicks.rc.array[,(base.idx:(base.idx+N.1970+N.2000-1)),]
R> chicks.sandpoint.1970 <- chicks.rc.array[,1:30,]
R> chicks.namakan.1970 <- chicks.rc.array[,31:60,]
R> chicks.rainy.1970 <- chicks.rc.array[,61:90,]
R> chicks.kabetogama.1970 <- chicks.rc.array[,91:120,]
R> chicks.sandpoint.2000 <- chicks.rc.array[,121:131,]
R> chicks.namakan.2000 <- chicks.rc.array[,132:142,]
R> chicks.rainy.2000 <- chicks.rc.array[,143:153,]
R> chicks.kabetogama.2000 <- chicks.rc.array[,154:164,]
R> q.chicks.sandpoint.1970 <- round(quantile(chicks.sandpoint.1970,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.namakan.1970 <- round(quantile(chicks.namakan.1970,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.rainy.1970 <- round(quantile(chicks.rainy.1970,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.kabetogama.1970 <- round(quantile(chicks.kabetogama.1970,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.sandpoint.2000 <- round(quantile(chicks.sandpoint.2000,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.namakan.2000 <- round(quantile(chicks.namakan.2000,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.rainy.2000 <- round(quantile(chicks.rainy.2000,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.chicks.kabetogama.2000 <- round(quantile(chicks.kabetogama.2000,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> mean.chicks.sandpoint.1970 <- as.vector(apply(chicks.sandpoint.1970,
+                                               c(1,3), mean))
```

Table C-1. Model 6: Summary of the joint posterior distribution of the parameters.

	mean	sd	MC_error	val2.5pc	median	val97.5pc
beta.chicks[1]	-0.4468	0.0709	1.9870E-03	-0.5869	-0.4490	-0.3029
beta.chicks[2]	-0.0016	0.0009	3.6520E-05	-0.0033	-0.0015	0.0002
beta.chicks[3]	-0.0771	0.0254	7.1620E-04	-0.1272	-0.0763	-0.0278
beta.chicks[4]	-0.0053	0.0016	6.0920E-05	-0.0086	-0.0053	-0.0021

```
R> mean.chicks.sandpoint.2000 <- as.vector(apply(chicks.sandpoint.2000,
+                                               c(1,3), mean))
R> mean.chicks.namakan.1970 <- as.vector(apply(chicks.namakan.1970,
+                                             c(1,3), mean))
R> mean.chicks.namakan.2000 <- as.vector(apply(chicks.namakan.2000,
+                                             c(1,3), mean))
R> mean.chicks.rainy.1970 <- as.vector(apply(chicks.rainy.1970,
+                                             c(1,3), mean))
R> mean.chicks.rainy.2000 <- as.vector(apply(chicks.rainy.2000,
+                                             c(1,3), mean))
R> mean.chicks.kabetogama.1970 <- as.vector(apply(chicks.kabetogama.1970,
+                                             c(1,3), mean))
R> mean.chicks.kabetogama.2000 <- as.vector(apply(chicks.kabetogama.2000,
+                                             c(1,3), mean))
R> gm.chicks.sandpoint.1970 <- mean(mean.chicks.sandpoint.1970)
R> gm.chicks.namakan.1970 <- mean(mean.chicks.namakan.1970)
R> gm.chicks.rainy.1970 <- mean(mean.chicks.rainy.1970)
R> gm.chicks.kabetogama.1970 <- mean(mean.chicks.kabetogama.1970)
R> gm.chicks.sandpoint.2000 <- mean(mean.chicks.sandpoint.2000)
R> gm.chicks.namakan.2000 <- mean(mean.chicks.namakan.2000)
R> gm.chicks.rainy.2000 <- mean(mean.chicks.rainy.2000)
R> gm.chicks.kabetogama.2000 <- mean(mean.chicks.kabetogama.2000)
R> mdif.chicks.sandpoint <- mean.chicks.sandpoint.2000 -
+                          mean.chicks.sandpoint.1970
R> mdif.chicks.namakan <- mean.chicks.namakan.2000 -
+                        mean.chicks.namakan.1970
R> mdif.chicks.rainy <- mean.chicks.rainy.2000 -
+                      mean.chicks.rainy.1970
R> mdif.chicks.kabetogama <- mean.chicks.kabetogama.2000 -
+                      mean.chicks.kabetogama.1970
R> cpp.rc.array <- as.array(cpp.rc)
R> cpp.rc.array <- cpp.rc.array[,((N0+1):(N0+N.1970+N.2000)),]
R> cpp.sandpoint.1970 <- cpp.rc.array[,1:30,]
R> cpp.namakan.1970 <- cpp.rc.array[,31:60,]
R> cpp.rainy.1970 <- cpp.rc.array[,61:90,]
R> cpp.kabetogama.1970 <- cpp.rc.array[,91:120,]
R> cpp.sandpoint.2000 <- cpp.rc.array[,121:131,]
R> cpp.namakan.2000 <- cpp.rc.array[,132:142,]
R> cpp.rainy.2000 <- cpp.rc.array[,143:153,]
R> cpp.kabetogama.2000 <- cpp.rc.array[,154:164,]
R> q.cpp.sandpoint.1970 <- round(quantile(cpp.sandpoint.1970,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.namakan.1970 <- round(quantile(cpp.namakan.1970,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.rainy.1970 <- round(quantile(cpp.rainy.1970,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
```

```
R> q.cpp.kabetogama.1970 <- round(quantile(cpp.kabetogama.1970,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.sandpoint.2000 <- round(quantile(cpp.sandpoint.2000,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.namakan.2000 <- round(quantile(cpp.namakan.2000,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.rainy.2000 <- round(quantile(cpp.rainy.2000,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.kabetogama.2000 <- round(quantile(cpp.kabetogama.2000,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> mean.cpp.sandpoint.1970 <- as.vector(apply(cpp.sandpoint.1970,
+                                            c(1,3), mean))
R> mean.cpp.sandpoint.2000 <- as.vector(apply(cpp.sandpoint.2000,
+                                            c(1,3), mean))
R> mean.cpp.namakan.1970 <- as.vector(apply(cpp.namakan.1970,
+                                            c(1,3), mean))
R> mean.cpp.namakan.2000 <- as.vector(apply(cpp.namakan.2000,
+                                            c(1,3), mean))
R> mean.cpp.rainy.1970 <- as.vector(apply(cpp.rainy.1970,
+                                            c(1,3), mean))
R> mean.cpp.rainy.2000 <- as.vector(apply(cpp.rainy.2000,
+                                            c(1,3), mean))
R> mean.cpp.kabetogama.1970 <- as.vector(apply(cpp.kabetogama.1970,
+                                            c(1,3), mean))
R> mean.cpp.kabetogama.2000 <- as.vector(apply(cpp.kabetogama.2000,
+                                            c(1,3), mean))
R> gm.cpp.sandpoint.1970 <- mean(mean.cpp.sandpoint.1970)
R> gm.cpp.namakan.1970 <- mean(mean.cpp.namakan.1970)
R> gm.cpp.rainy.1970 <- mean(mean.cpp.rainy.1970)
R> gm.cpp.kabetogama.1970 <- mean(mean.cpp.kabetogama.1970)
R> gm.cpp.sandpoint.2000 <- mean(mean.cpp.sandpoint.2000)
R> gm.cpp.namakan.2000 <- mean(mean.cpp.namakan.2000)
R> gm.cpp.rainy.2000 <- mean(mean.cpp.rainy.2000)
R> gm.cpp.kabetogama.2000 <- mean(mean.cpp.kabetogama.2000)
R> mdif.cpp.sandpoint <- mean.cpp.sandpoint.2000 -
+                            mean.cpp.sandpoint.1970
R> mdif.cpp.namakan <- mean.cpp.namakan.2000 -
+                            mean.cpp.namakan.1970
R> mdif.cpp.rainy <- mean.cpp.rainy.2000 - mean.cpp.rainy.1970
R> mdif.cpp.kabetogama <- mean.cpp.kabetogama.2000 -
+                            mean.cpp.kabetogama.1970
R> q.cpp.sandpoint <- round(quantile(mdif.cpp.sandpoint,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.namakan <- round(quantile(mdif.cpp.namakan,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.rainy <- round(quantile(mdif.cpp.rainy,
```

```
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> q.cpp.kabetogama <- round(quantile(mdif.cpp.kabetogama,
+                             probs=c(0.025,0.05,0.95,0.975)), digits=3)
R> m.cpp.sandpoint <- round(mean(mdif.cpp.sandpoint), digits=3)
R> m.cpp.namakan <- round(mean(mdif.cpp.namakan), digits=3)
R> m.cpp.rainy <- round(mean(mdif.cpp.rainy), digits=3)
R> m.cpp.kabetogama <- round(mean(mdif.cpp.kabetogama), digits=3)
R> p.cpp.sandpoint <- round((100*mean(mdif.cpp.sandpoint))/gm.cpp.sandpoint.1970,
+                          digits=1)
R> p.cpp.namakan <- round((100*mean(mdif.cpp.namakan))/gm.cpp.namakan.1970,
+                         digits=1)
R> p.cpp.rainy <- round((100*mean(mdif.cpp.rainy))/gm.cpp.rainy.1970,
+                         digits=1)
R> p.cpp.kabetogama <- round((100*mean(mdif.cpp.kabetogama))/gm.cpp.kabetogama.1970,
+                         digits=1)
R> table1 <- data.frame(pct.chg=c(p.cpp.rainy,p.cpp.namakan,p.cpp.kabetogama,p.cpp.sa
+             mean.cpp=c(m.cpp.rainy,m.cpp.namakan,m.cpp.kabetogama,m.cpp.sandpoint),
+            cs90=c(paste(q.cpp.rainy[2],"--",q.cpp.rainy[3],sep=""),
+                   paste(q.cpp.namakan[2],"--",q.cpp.namakan[3],sep=""),
+                   paste(q.cpp.kabetogama[2],"--",q.cpp.kabetogama[3],sep=""),
+                   paste(q.cpp.sandpoint[2],"--",q.cpp.sandpoint[3],sep="")),
+            cs95=c(paste(q.cpp.rainy[1],"--",q.cpp.rainy[4],sep=""),
+                   paste(q.cpp.namakan[1],"--",q.cpp.namakan[4],sep=""),
+                   paste(q.cpp.kabetogama[1],"--",q.cpp.kabetogama[4],sep=""),
+                   paste(q.cpp.sandpoint[1],"--",q.cpp.sandpoint[4],sep="")),
+            row.names=c("Rainy","Namakan","Kabetogama","Sand Point"))
R> table2 <- data.frame(lake=c("Rainy"," ","Kabetogama"," ","Namakan"," ","Sand Point
+                     rc=c(1970,2000,1970,2000,1970,2000,1970,2000),
+                      obscpp=c(0.43,0.27,0.16,0.22,0.36,0.20,0.26,0.34),
+                      postmean=c(gm.cpp.rainy.1970,gm.cpp.rainy.2000,
+                                 gm.cpp.kabetogama.1970,gm.cpp.kabetogama.2000,
+                                 gm.cpp.namakan.1970,gm.cpp.namakan.2000,
+                                 gm.cpp.sandpoint.1970,gm.cpp.sandpoint.2000),
+                      cs5=c(paste(q.cpp.rainy.1970[1],"--",q.cpp.rainy.1970[4],sep="
+                            paste(q.cpp.rainy.2000[1],"--",q.cpp.rainy.2000[4],sep="
+                            paste(q.cpp.kabetogama.1970[1],"--",q.cpp.kabetogama.197
+                            paste(q.cpp.kabetogama.2000[1],"--",q.cpp.kabetogama.200
+                            paste(q.cpp.namakan.1970[1],"--",q.cpp.namakan.1970[4],s
+                            paste(q.cpp.namakan.2000[1],"--",q.cpp.namakan.2000[4],s
+                            paste(q.cpp.sandpoint.1970[1],"--",q.cpp.sandpoint.1970[
+                            paste(q.cpp.sandpoint.2000[1],"--",q.cpp.sandpoint.2000[
R> mdif.chicks.sandpoint <- mean.chicks.sandpoint.2000 -
+                              mean.chicks.sandpoint.1970
R> mdif.chicks.namakan <- mean.chicks.namakan.2000 -
+                              mean.chicks.namakan.1970
R> mdif.chicks.rainy <- mean.chicks.rainy.2000 - mean.chicks.rainy.1970
```

```
R> mdif.chicks.kabetogama <- mean.chicks.kabetogama.2000 -
+                               mean.chicks.kabetogama.1970
R> q.chicks.sandpoint <- round(quantile(mdif.chicks.sandpoint,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=1)
R> q.chicks.namakan <- round(quantile(mdif.chicks.namakan, probs=c(0.025,0.05,0.95,0.
R> q.chicks.rainy <- round(quantile(mdif.chicks.rainy,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=1)
R> q.chicks.kabetogama <- round(quantile(mdif.chicks.kabetogama,
+                              probs=c(0.025,0.05,0.95,0.975)), digits=1)
R> m.chicks.sandpoint <- round(mean(mdif.chicks.sandpoint), digits=1)
R> m.chicks.namakan <- round(mean(mdif.chicks.namakan), digits=1)
R> m.chicks.rainy <- round(mean(mdif.chicks.rainy), digits=1)
R> m.chicks.kabetogama <- round(mean(mdif.chicks.kabetogama), digits=1)
R> table3 <- data.frame(mean.chicks=c(m.chicks.rainy,m.chicks.namakan,m.chicks.kabeto
+            cs90=c(paste(q.chicks.rainy[2],"--",q.chicks.rainy[3],sep=""),
+                   paste(q.chicks.namakan[2],"--",q.chicks.namakan[3],sep=""),
+                   paste(q.chicks.kabetogama[2],"--",q.chicks.kabetogama[3],sep=""),
+                   paste(q.chicks.sandpoint[2],"--",q.chicks.sandpoint[3],sep="")),
+            cs95=c(paste(q.chicks.rainy[1],"--",q.chicks.rainy[4],sep=""),
+                   paste(q.chicks.namakan[1],"--",q.chicks.namakan[4],sep=""),
+                   paste(q.chicks.kabetogama[1],"--",q.chicks.kabetogama[4],sep=""),
+                   paste(q.chicks.sandpoint[1],"--",q.chicks.sandpoint[4],sep="")),
+            row.names=c("Rainy","Namakan","Kabetogama","Sand Point"))
```

Table C-2. Model 6: Posterior predictions of differences between mean chicks per pair under the 2000 and 1970 Rule Curves.

	pct.chg	mean.cpp	cs90	cs95
Rainy	-6.2	-0.030	-0.046—0.014	-0.05—0.011
Namakan	45.3	0.157	0.097–0.228	0.088–0.245
Kabetogama	45.4	0.119	0.078–0.163	0.071–0.174
Sand Point	45.4	0.078	0.05–0.111	0.045–0.119

Table C-3. Model 6: Observed mean chicks per pair and posterior predictions under the 2000 and 1970 Rule Curves.

	lake	rc	obscpp	postmean	cs5
1	Rainy	1970.0000	0.43000	0.47877	0.296–0.694
2		2000.0000	0.27000	0.44919	0.139–0.692
3	Kabetogama	1970.0000	0.16000	0.26199	0.061–0.493
4		2000.0000	0.22000	0.38086	0.207–0.599
5	Namakan	1970.0000	0.36000	0.34611	0.078–0.685
6		2000.0000	0.20000	0.50284	0.255–0.838
7	Sand Point	1970.0000	0.26000	0.17164	0.04–0.329
8		2000.0000	0.34000	0.24955	0.13–0.403

Table C-4. Model 6: Posterior predictions of differences between mean numbers of chicks under the 2000 and 1970 Rule Curves.

	mean.chicks	cs90	cs95
Rainy	-1.3	-4–1.3	-4.5–1.8
Namakan	4.2	1.7–7.1	1.3–7.7
Kabetogama	4.0	1.6–6.5	1.2–7.1
Sand Point	0.5	-0.2–1.3	-0.3–1.5