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Figure S1. Long term trendsi n raw fish mercury concentrations for Walleye, Northern Pike and Lake Whitefish in Clay, Ball (North Basin), Separation and Tetu Lakes.

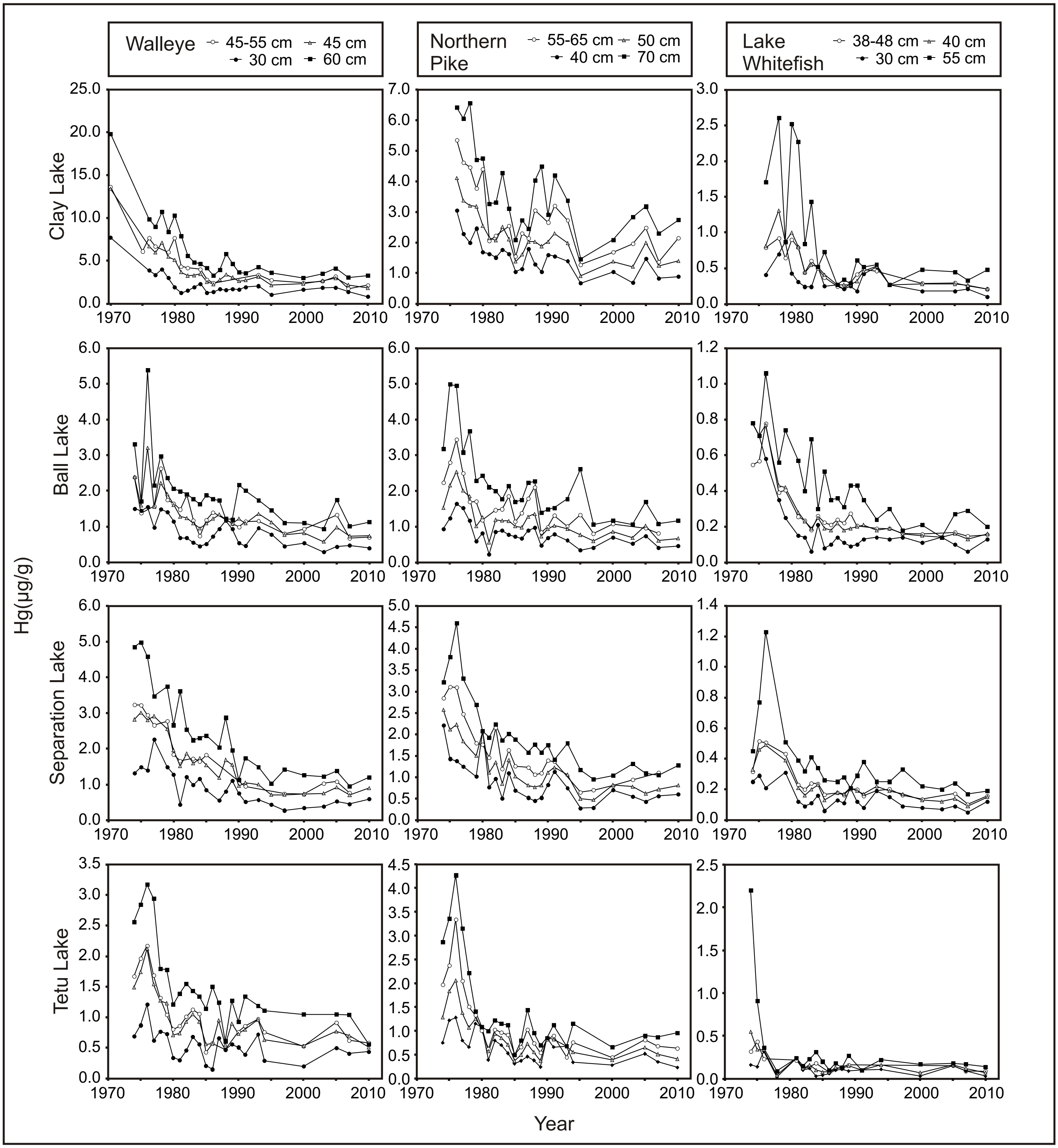

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Figure S2. Plots of fish length versus mercury concentration for recent (2000-2010) measurements of a) Yellow Perch, b) Sauger, c) White Sucker and d) Mooneye for each study lake, with the upper limit of each consumption guideline. Legends provide information on how to interpret each consumption guideline. For example, 0.26 µg/g and below is the range of mercury concentrations acceptable for 8 meals/month for those consumers in the sensitive population (i.e., children and women of childbearing age). 0.5 µg/g is the upper limit used by the Canadian Food Inspection Agency for commercial sale of fish.

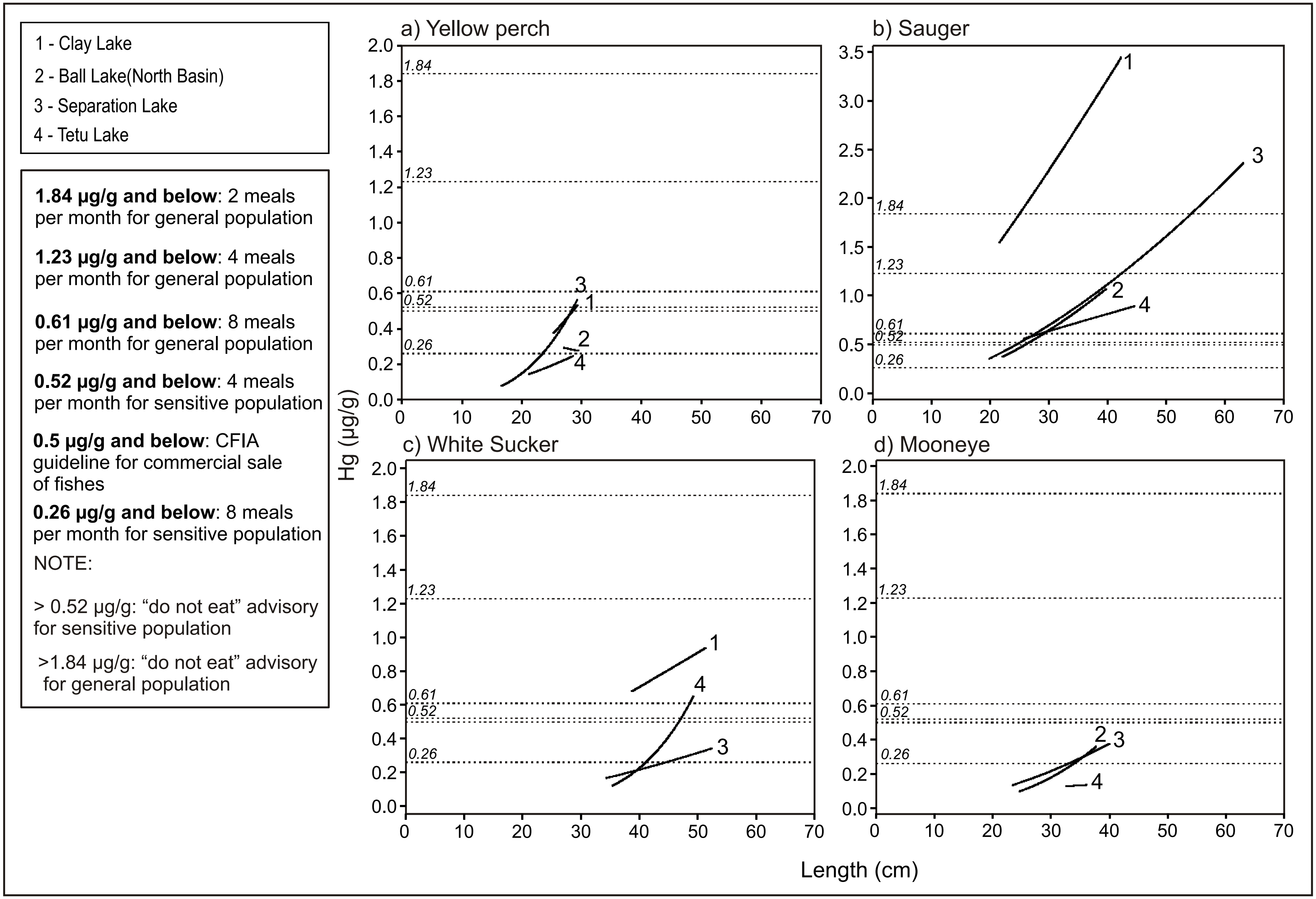

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Figure S3. Rate of decline as predicted by DLMs, for Walleye, Northern Pike and Lake Whitefish populations in a) Clay, b) Ball, c) Separation and d) Tetu Lakes.

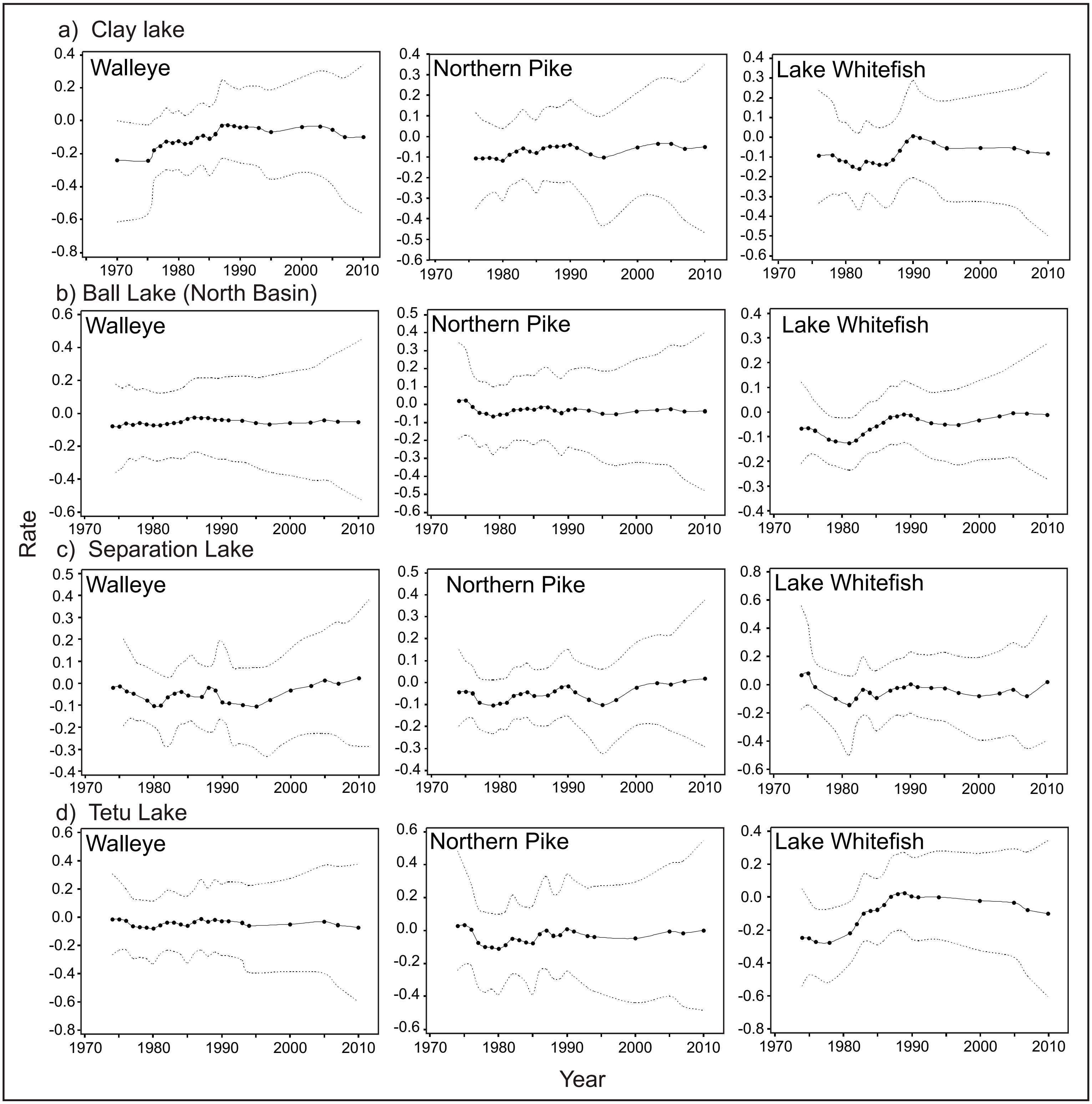

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Table S1. Code used for DLM analysis of long-term trends in mercury concentrations in Clay, Ball, Separation and Tetu Lake. Here, DLM code for a model which includes fish length (cm) as a covariate is presented. In the other two models, the code was modified to include fish weight as a covariate ("weight" model), or without any variables as covariates ("random walk" model). All DLM analyses were run using the WinBUGS software. Presented here is code for a model which includes fish length (cm) as a covariate with mercury concentration.

DLM Model Code

```
model {
for (I in 1:N) {
lengthstdev[i]<-(length[i]-###)/###
LogHgm[i]<-
level[time[i]+1]+beta[time[i]+1]*lengthstdev
[i]
LogHg[i]~dnorm(LogHgm[i],mtau[time[i]+1
])
LogPredHg[i]~dnorm(LogHgm[i],mtau[time
[i]+1])
PredHg[i]<-exp(LogHg[i])}
for (t in 2:#) {
beta[year[t]]~dnorm(beta[year[t-
1]],btau[year[t]])
growth[year[t]]~dnorm(growth[year[t-
1]],gtau[year[t]])
levelm[year[t]]<-level[year[t-
1]]+growth[year[t]]
level[year[t]]~dnorm(levelm[year[t]],ltau[ye
ar[t]])
ltau[year[t]]<-ltau.in*pow(0.95,year[t]-1)
lsigma[year[t]]<-sqrt(1/ltau[year[t]])
btau[year[t]]<-btau.in*pow(0.95,year[t]-1)
bsigma[year[t]]<-sqrt(1/btau[year[t]])
gtau[year[t]]<-gtau.in*pow(0.95,year[t]-1)
gsigma[year[t]]<-sqrt(1/gtau[year[t]])
mtau[year[t]]<-mtau.in*pow(0.95,year[t]-1)
msigma[year[t]]<-sqrt(1/mtau[year[t]])
}
```

```
beta[year[1]]~dnorm(beta[1],btau[year[1]])
growth[year[1]]~dnorm(growth[1],gtau[year[
1]])
levelm[year[1]]<-level[1]+growth[year[1]]
level[year[1]]~dnorm(levelm[year[1]],ltau[ye
ar[1]])
ltau[year[1]]<-ltau.in*pow(0.95,year[1]-1)
lsigma[year[1]]<-sqrt(1/ltau[year[1]])
btau[year[1]]<-btau.in*pow(0.95,year[1]-1)
bsigma[year[1]]<-sqrt(1/btau[year[1]])
gtau[year[1]]<-gtau.in*pow(0.95,year[1]-1)
gsigma[year[1]]<-sqrt(1/gtau[year[1]])
mtau[year[1]]<-mtau.in*pow(0.95,year[1]-1)
msigma[year[1]]<-sqrt(1/mtau[year[1]])
beta[1]~dnorm(0,0.0001)
growth[1]~dnorm(0,0.0001)
level[1]~dnorm(0,0.0001)
ltau.in~dgamma(0.001,0.001)
ltau[1]<-ltau.in
btau.in~dgamma(0.001,0.001)
btau[1]<-btau.in
gtau.in~dgamma(0.001,0.001)
gtau[1]<-gtau.in
mtau.in~dgamma(0.001,0.001)
mtau[1]<-mtau.in
}
```

DLM Model Run Details

The amount of information the model discounts is determined by a discount factor, which ranges between 0 and 1. A discount factor = 1 corresponds to a static linear model where no information is disregarded. The literature suggests that discount

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factors >0.8 are the most useful; here, we used a discount factor = 0.95, as per the recommendation of Sadraddini et al.[1] Sequence of realizations from the model posterior distributions were obtained using Markov Chain Monte Carlo (MCMC) simulations.[2] Specifically, we used the general normal-proposal Metropolis algorithm as implemented in the WinBUGS software; this algorithm is based on a symmetric normal proposal distribution, whose standard deviation is adjusted over the first 4,000 iterations, such as the acceptance rate ranges between 20% and 40%. We used two chain runs of 80,000 iterations and samples were taken after the MCMC simulation converged to the true posterior distribution. Convergence was assessed using the modified Gelman-Rubin convergence statistic.[3] Generally, we noticed that the sequences converged very rapidly (1,000 iterations), and the summary statistics reported in this study were based on the last 75,000 draws by keeping every 20th iteration (thin=20) to avoid serial correlation. The accuracy of the posterior parameter values was inspected by assuring that the Monte Carlo error for all parameters was less than 5% of the sample standard deviation.

[1] Sadraddini, S., M.E. Azim, Y. Shimoda, S.P. Bhavsar, S.M. Backus and G.B. Arhonditsis. 2011. Temporal PCB and mercury concentrations in Lake Erie fish communities: a dynamic linear modeling analysis. Ecotoxicology and Environmental Safety 74: 2203-2214

[2] Gilks, W., G.O. Roberts and S.K. Sahu. 1998. Adaptive Markov Chain Monte Carlo through regeneration. Journal of the American Statistical Association 93: 1045-1054.

[3] Brooks, S.P., and A. Gelman. 1998. General methods for monitoring convergence of iterative simulations. Journal of Computational and Graphical Statistics 7: 434-455.

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Table S2. Summary of model performance using fish length or fish weight compared to a random walk model which incorporates no covariate. Like AIC, ΔDIC indicates the difference in DIC values between the "best" model (i.e., that with the lowest DIC value) and the other models. When the difference in DIC values is less than 2, then the two models explain the data equally well. For each lake and species, the model with the lowest DIC value is highlighted in bold. When comparing models of equal complexity, such as models with a single covariate (e.g., "length and "weight" models), it is more appropriate to compare Dbar values, and so these are also included. Dbar is the posterior mean of the deviance, which equals DIC minus the the effective number of parameters, pD - thus, DIC = Dbar + pD.

a) Clay Lake

	Walleye			Northern Pike			Lake Whitefish		
Model	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC
Random walk	750.451	771.984	326.326	1153.93	1174.9	651.577	653.438	668.997	58.522
Length	414.312	**445.658**	--	492.079	**523.323**	--	584.384	**610.475**	--
Weight	456.609	487.683	42.025	530.257	561.726	38.403	632.164	653.853	43.378

b) Ball Lake

	Walleye			Northern Pike			Lake Whitefish		
Model	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC
Random walk	1205.93	1225.54	153.92	1156.97	1173.13	245.34	982.681	993.904	39.861
Length	1042.48	**1071.62**	--	903.138	**927.79**	--	936.823	954.31	0.267
Weight	1082.97	1110.45	38.83	939.938	966.428	38.638	935.399	**954.043**	--

c) Separation Lake

	Walleye			Northern Pike			Lake Whitefish		
Model	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC
Random walk	680.672	702.189	337.1889	862.065	878.348	294.551	396.291	415.44	132.439
Length	337.814	**365.0001**	–	550.444	**583.797**	–	257.419	**283.001**	--
Weight	368.353	400.525	35.5249	839.746	863.14	279.343	398.394	422.239	139.238

d) Tetu Lake

	Walleye			Northern Pike			Lake Whitefish		
Model	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC	Dbar	DIC	ΔDIC
Random walk	786.391	806.948	300.518	954.917	974.736	309.781	620.665	633.078	21.435
Length	476.887	**506.43**	–	632.869	**664.955**	–	596.392	**611.643**	–
Weight	504.969	534.763	28.333	659.461	692.779	27.824	603.727	619.906	8.263