**Spatiotemporal Models for Ecologists**

**Retrospective skill testing and model mis-specification**

Goal: Practice and demonstrate ability to (1) estimate parameters for linear and nonlinear state-space models, and (2) explore forecast interval coverage using a parametric bootstrap given model mis-specification.

**Parametric bootstrap**

Start with the Week-2 laboratory assignment, where we obtain data for flathead sole (from Chap\_3/Biomass\_index.csv), and then fit a state-space Gompertz model estimating biomass given average CPUE data for all years 1982-2017:

while specifying that process errors and measurement errors have equal variance ()[[1]](#footnote-1), and record the maximum-likelihood estimates for this fitted model. We also introduce a state-space Ricker model:

Alternatively, we could use a linear model to make a linear forecast. Using lm formula syntax, we could fit:

Formula = y ~ x

And then use the predict(.) class to predict values for in-sample years, or when forecasting future years.

Finally, we could also fit these data using a generalized additive model (GAM) using mgcv. Using mgcv formula syntax, we could fit:

Formula = y ~ s(x)

And again use the predict(.) class to predict values for in-sample years, or when forecasting future years.

We will explore a 2x4 factorial cross of using the Gompertz and Ricker to simulate data, and using the Gompertz, Ricker, linear, or Generalized Additive models to fit these simulated data. This “self-and-cross” experiment shows model performance when mis-specifying the model. We will replicate each scenario 100 times to calculate the average forecast error in each box of the diagram below:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | Estimation model | | |  |
|  |  | Gompertz | Ricker | Linear model | GAM (using mgcv default options) |
| Simulation model | Gompertz | Average error in …  2013,  2014,  2015,  2016,  2017 | Average error in …  2013,  2014,  2015,  2016,  2017 | Average error in …  2013,  2014,  2015,  2016,  2017 | Average error in …  2013,  2014,  2015,  2016,  2017 |
| Ricker | Average error in …  2013,  2014,  2015,  2016,  2017 | Average error in …  2013,  2014,  2015,  2016,  2017 | Average error in …  2013,  2014,  2015,  2016,  2017 | Average error in …  2013,  2014,  2015,  2016,  2017 |

Specifically, to implement this experiment:

1. simulate new a new biomass time-series for all years 1982-2017, and simulate new CPUE data for these years, using the Gompertz state-space model and parameter values estimated previously.
2. re-fit the state-space Gompertz model to data for all years except the final five, i.e., 1982-2012, while estimating biomass for all years 1982-2017. Estimated biomass in 2013-2017 is the forecast for this replicate of the parametric bootstrap. Record forecasted biomass and its standard errors for 2013-2017, and record whether the true biomass for this bootstrap replicate is within the 50% forecast interval.
3. Re-fit the state-space Ricker model to these same data, and record estimated biomass for 2013-2017
4. Re-fit the linear model to these data, and record estimated biomass for 2013-2017;
5. Re-fit the Generalized Additive Model to these data, and record estimated biomass for 2013-2017
6. Repeat steps 1-5 to generate 100 replicates of the parametric bootstrap, and calculate the forecast interval coverage for each forecast year.
7. Repeat steps 1-6 but replacing the state-space Gompertz model used for simulating data in Step #1 with a state-space Ricker model for simulating data.

Questions:

1. What do you notice about forecast interval coverage when the model is correctly specified?
2. What do you notice about parameter estimates for each bootstrap replicate for the correctly specified model?
3. What do you notice about forecast interval coverage when the model is mis-specified? Do these patterns change for short forecasts (i.e., in 2013) vs. longer forecasts (i.e., in 2017)?

1. We impose this restriction during the simulation experiment to avoid having to deal with complications arising when the MLE for or . In practice, this assumption would likely be replaced with a more biologically meaningful restriction, although we do not explore this here. [↑](#footnote-ref-1)