Population Cycling Lab Protocol

2/26/2018

Part 1: Whole class

1) Download the lab materials from the course website (it's all in a single zip file).
2) Unzip the file.
3) Open population_cycling.Rproj. This will take you into Rstudio, and will avoid file path issues.
4) We will work with the script population_cycling_analysis.R to perform our analyses. Open this file in Rstudio, not in R! You can make sure you open it in Rstudio by using the Rstudio file navigation system.
5) Use data_analysis.R and follow along with the TA to conduct an analysis of the simulated dataset.
    a. Source the file with all the analysis functions
    b. Read in the data
    c. Plot the data
    d. Fit the first model
    e. Fit the second model
    f. Compare the fit of the two models
    g. Compare what the models are saying about the populations
    h. Assess whether either model could explain the data

Part 2: Work with your groups

1) As a group, choose two datasets to analyze. Feel free to plot them before committing to any of them. Your choices are:
    - lynx_hare.csv (This dataset is originally from the Hudson's Bay Company, counts are pelts sold of each species by the company. Data taken from http://www.math.tamu.edu/~phoward/m442/modbasics.pdf)
    - mink_muskrat.csv (This dataset is originally from the Hudson's Bay Company, counts are pelts sold of each species by the company. Data taken directly from Jones (1914), the relationship between mink and muskrat was suggested by Bulmer (1974))
    - Bonsall_moth_ragwood.csv (This dataset is from Bonsall *et al.* (2003), a study on whether interactions between species are consistent from location to location; spoilers: they are not. The data here were scraped from Figure 1i, data from Meijendel dune in the Netherlands, and are the numbers for a 4 square meter plot.)
    - Shertzer_algae_rotifers.csv (This dataset is from Shertzer *et al.* (2002), a study seeking to better explain cycling observed in previous work with new tests and better models. The data here scraped from Figure 1, converted from concentrations.)

2) As a group, decide on four models that you will fit to both datasets. Choose these based on the cycles you saw in plotting the data, biological knowledge, or personal curiosity!

   a. In this lab, we will define a model as a unique combination of four functions, one each for describing the birth and death rate of each population. One way to create a new model is to mix and match the functions given to you (scientists do this all the time!).w

   b. Not all combinations of all models may work on all datasets. If you have trouble fitting a model, there may be a workaround. Ask a TA for help!

   c. If you want, you can make your own function! It just has to look like the ones provided, so a good way to make it is to copy one, rename it, and make it do what you want. TAs can help with this! Two rules for making and using the functions:

      i. Every function must take at least one parameter.

      ii. If you have a constant birth rate for a population, do not choose a constant death rate for that population, and vice-versa (the model will not work well, or at all, and will run for a very, very long time).

3) Split into pairs. In each pair, analyze your dataset, modifying data_analysis.R to do what you need it to do here. Don't forget rename things, and don't overwrite a model or you won't be able to compare it later!

4) Rejoin your group-mates and make sense of what you all did.

   a. Did you choose the same models in both pairs? How different or similar are they qualitatively? Try to make statements like, "our best model says that the predator population size has a maximum, but your best model says it could grow indefinitely."

   b. How well did the best models fit in the absolute sense? How many models are plausible, in either the relative sense or the absolute sense?

   c. Do you think that your best model(s) are missing something? Is it something that you could account for with the tools at hand? Or is it something beyond the reach of these tools (*e.g.*, you think you need to account for what the prey eats and have a three level system)? In this case, is there a way you could approximate that with only the data at hand?

   d. What do the parameters of your best models mean? Consider the abstract ("this parameter tells us about…") and the concrete ("the value of this parameter means that, for this species, …") senses.

5) Implement an improvement to one of your models! Take an idea you discussed in (4c) (if you discussed improvements to two models, you can pick one) and write a function that will allow you to fit it. If there is an existing one that will do that, feel free to use it. Were you right, did it help?