



$$\log_{10} N(t) = \log_{10} N_0 + C \left(\exp \left(- \exp \left(\frac{e \cdot \mu}{C} (\lambda - t) + 1 \right) \right) \right)$$

This lab will take the programming and plotting basics we have touched on in R so far and apply them in a new problem area. Microbial growth modeling. Under controlled conditions, the population of a microbe will grow along a curve that is predictable. These predictions can be represented as mathematical models and implemented within your program. The equation above shows the modified Gompertz growth model that we will implement in this lab. ($\exp(x) = e^x$) The math involved may seem intimidating at first but ideally, once the math has been represented within the program the meaning and impact of each of the parameters should become visible.

Our goal for this lab will be to implement the first example of the `predict_growth` function of the `biogrowth` package by associating each parameter with a slider input. This will allow us to see how changing the inputs will impact the final prediction.

Part 0: Create a new Rshiny app called “[yourLastName]Biogrowth.R”

Lab 12: Modeling Microbial Growth

Biol135: Introduction to Bioinformatics Programming

Part 1: Place the code from example 1 from `predict_growth()` within the call to `renderPlot()` in the example.

Part 2: Modify the example code so that each of the parameters (`LogN0`, `C`, `Mu`, and `Lambda`) are each associated with their own slider input in your app. Adjust the range and interval of the slider input to reflect appropriate potential values for each parameter. The final output should feature only the growth curve which should reactively update when the parameters are adjusted. Modify the title of the app to reflect its new purpose. The time interval on the x axis will remain constant. The axis labels may remain the

Part 3: Review the paper below and add a description to each parameter inside the corresponding Slider input so that the user has an idea what they are changing.

Part 4: Upload your app to the MyCourses Dropbox.

Bonus: Select another example model type from the list and create a new app that applies that one instead. The parameters will have different names and there may be more of them but the workflow should be the same.

References:

[Garre, A., Koomen, J., den Besten, H. M., & Zwietering, M. H. \(2023\). Modeling population growth in R with the biogrowth package. *Journal of Statistical Software*, 107, 1-51.](#)