

Experimental Biophysics the social distancing version!
Seppe Kuehn & Laura Troyer, March 19 2020

In light of the remote teaching requirements, we will be taking the Luria-Delbruck and Phylogenetics modules online for the remainder of the term. The computational aspects of both modules will be retained and we will add a reading assignment to both experiments as follows:

(1) Luria-Delbruck experiment.

- (a) Read the hand out on the experiment.
- (b) Use the data provided on colony counts to compute (for wild type and both mutant strains)
 - (i) N_0 (the number of cells put on the plate).
 - (ii) The mutation rate ("a")
 - (iii) The Fano Factor.
- (c) Perform the computational exercises in the writeup and proceed as if you had actually acquired the data provided in (b).
- (d) Read the following paper, write a summary of the papers conclusions, and answer the following questions:
 - (i) The paper is based on a long term evolution experiment by Lenski and co-workers. Do some research on the experiment and explain the basic premise.
 - (ii) What is the main finding of the paper?
 - (iii) How is the Luria-Delbruck experiment related to the paper? What do they use the technique to measure?
 - (iv) Is it believed that evolution should favor low or high mutation rates? When and why?
- (e) Evaluations:**
 - (i) Written report as you would have written if you had done the experiments + addressing the questions asked about the paper (d) above. Due at 5pm the last Thursday of the module.
 - (ii) 15-minute presentation given to the class via Zoom (schedule forthcoming)

Paper for Luria-Delbruck: Sniegowski, P., Gerrish, P. & Lenski, R. Evolution of high mutation rates in experimental populations of *E. coli*. *Nature* 387, 703–705 (1997).
<https://doi.org/10.1038/42701>
<https://www.nature.com/articles/42701>

(2) Phylogenetics experiment.

- (a) Read the hand out on the experiment.
- (b) Use the Sanger sequencing data for four strains (provided) to perform the analyses outlined in the hand out.
- (c) Complete the computational exercises in the hand out, including the extended computational investigation.
- (d) Read the following paper, write a summary of the conclusions and answer the following questions.
 - (i) What is the main point of the paper?
 - (ii) What is the definition of the distance S_{AB} in Table 1 based on? Do some detective work!
 - (iii) Manually enter the data in Table 1 into matlab or python. Use the tree building techniques you learned in this module to build a tree from these data. What does the tree look like? Does it support the main claim of the paper?
 - (iv) What do you think is the significance of the paper's conclusions?
- (e) **Evaluations:**
 - (i) Written report as you would have written had you done the experiments + addressing the questions asked about the paper (d) above. Due at 5pm the last Thursday of the module.
 - (ii) 15-minute presentation given to the class via Zoom (schedule forthcoming)

Paper for phylogenetics: **Phylogenetic structure of the prokaryotic domain: The primary kingdoms** Carl R. Woese and George E. Fox

PNAS November 1, 1977 74 (11) 5088-5090; <https://doi.org/10.1073/pnas.74.11.5088>
<https://www.pnas.org/content/pnas/74/11/5088.full.pdf>