

BIOINFORMATICS INTERNS

Session fourteen

REFRESHERS AND REVIEW

- 20 minute Q & A

FORK OUR FUNCTIONS

- See Github instructions

PROJECT UPDATE

- OUR NEW PROJECT OUTLINE!!
 - Exploring Genbank
 - The Gene-y Aligner:
 - Use cushaw
 - Rosalind examples
 - Make our own aligner
 - Compare and visualize

ALIGNMENT

- What is an aligner?

A method of arranging sequences to ID regions of similarity.

These regions may be caused by evolution, function or structure.

ALIGNMENT

- How does a short read aligner work?

The goal is to figure out where in the full sequence, a particular sequence (the short read) is from.

RUN CUSHAW WITH DATA

- Data is found on Github