Deliverable 2B: Aligning another set of reads

Apply what you learned in Deliverable 2A to this tutorial, where you'll align reads to the lambda phage genome.

Note that you already have access to Bowtie through the modules on Discovery, so you do not need to download the program or set a path, you only need to load the module.

Pro-tip extra:
Set up aliases (on your machine)

I recommend going through each deliverable twice, start to finish, and keeping two windows open .

Upon satisfactory completion of Deliverables 2A and 2B you will earn access to real sequencing reads generated recently by Tovah Day's lab. Your work with these data will comprise Deliverable 3C.

All Unit 2 work is due by Mar 10.

Each deliverable is complete when you have:
- answered each question
- saved a terminal session or screenshots demonstrating your performance of the commands (on Discovery or posted on GitHub)
- indicated in a "TOC" (table of contents) file where your work is found (GitHub repo or specific path/name_of_file on the cluster).