Learn about current generation sequencing technologies:
- Capabilities
- Costs
- Types of data generated

A brief Unix “boot-camp” to get you comfortable driving a computer from a command-line interface

Learn how to assess the quality of your sequences and “clean” them before use in other applications like reference genome comparisons (single nucleotide polymorphisms) and de novo genome assembly

OPEN TO ALL GRADUATES AND QUALIFIED UNDERGRADUATES
Permission number: Contact Elaine Mirken (elaine.mirken@uconn.edu)