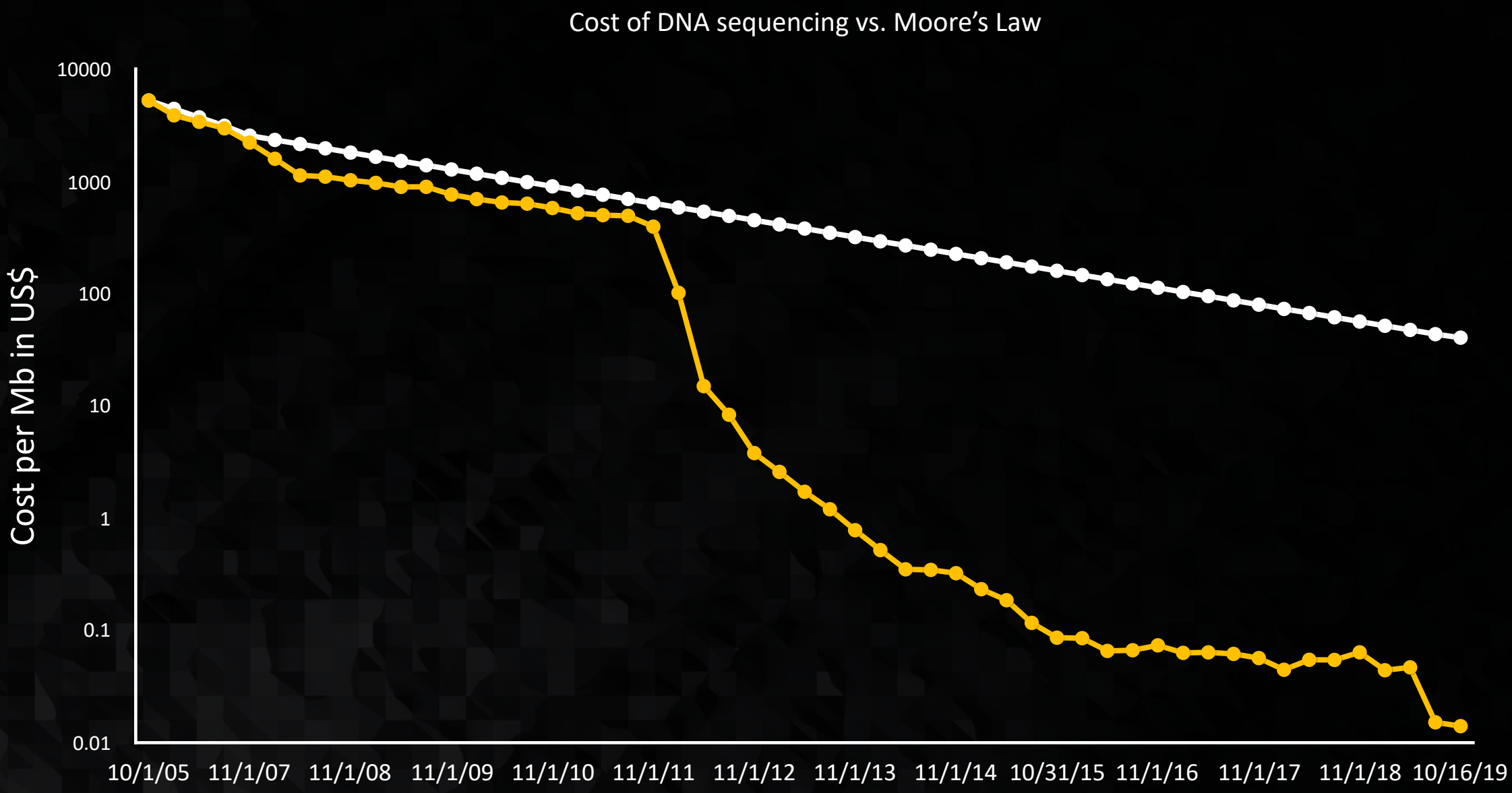
“Advice is a form of nostalgia. Dispensing it is a way of fishing the past from the disposal, and wiping it off, painting over the ugly parts, and recycling it for more than it’s worth.”

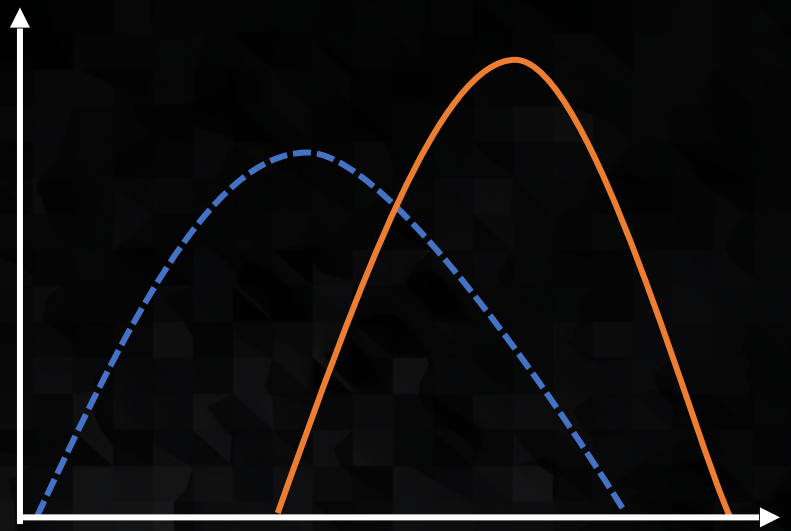
-Baz Luhrmann

The genomic era: powered by NGS

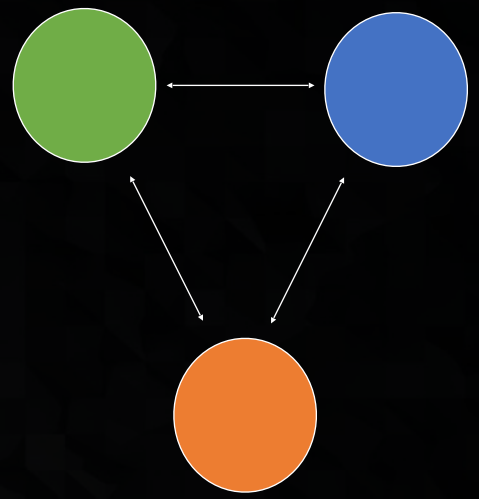


Fundamental biological questions

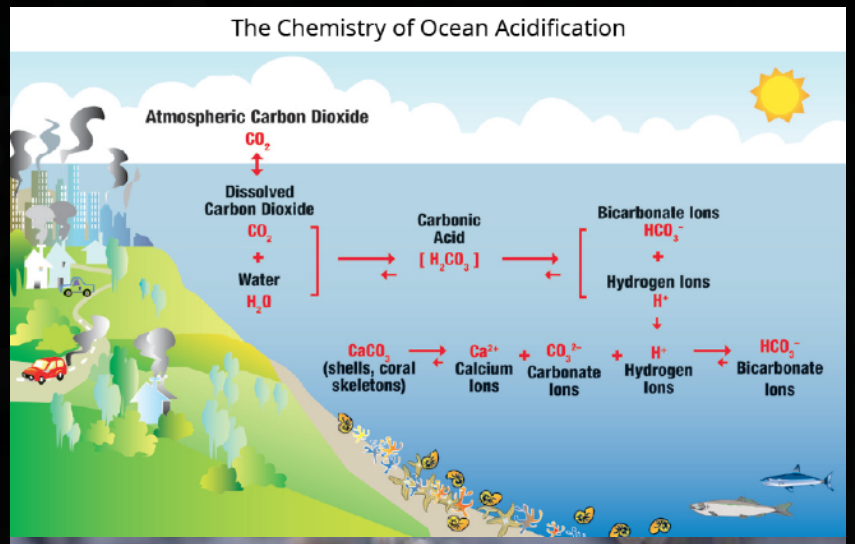
Selection



Connectivity



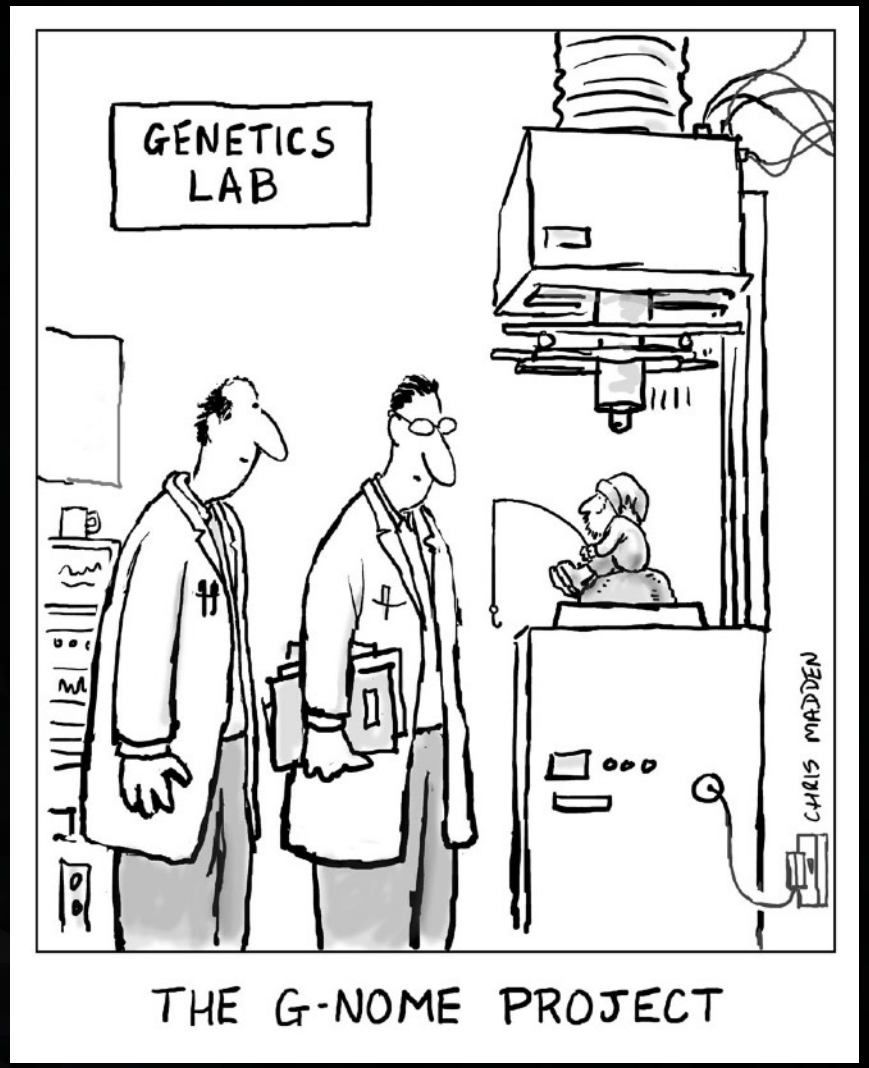
Evolutionary trajectory of species/populations



For population level inference, genome reduction is needed.

Genome reduction options

- No existing genomic resources
  - RADseq
  - RNAseq
  - Exome capture?
  - EpiRAD
- With genomic resources
  - Pool-seq
  - Low coverage WGS



Goals

- Effectively work in a command-line Linux environment
- Visualize and manipulate multiple next-generation sequencing data formats
- Use and apply the tools and analyses covered in class
- Knowledgeably filter data sets for statistical and bioinformatic artifacts
- Determine loci potentially under selection and estimate population genetic parameters with both neutral and putatively adaptive loci
- **Produce a completely open and repeatable documentation** of a complete population genomic analysis

Syllabus and Course Repository

- https://github.com/jpuritz/BIO_594_2019

Goals for today

- Setup your personal computer for ssh
- Setup an RSA key for sshing into the class server
- Clone the class git repository to both your server account
- Test out terminal functionality in RStudio

Final thought of the day...