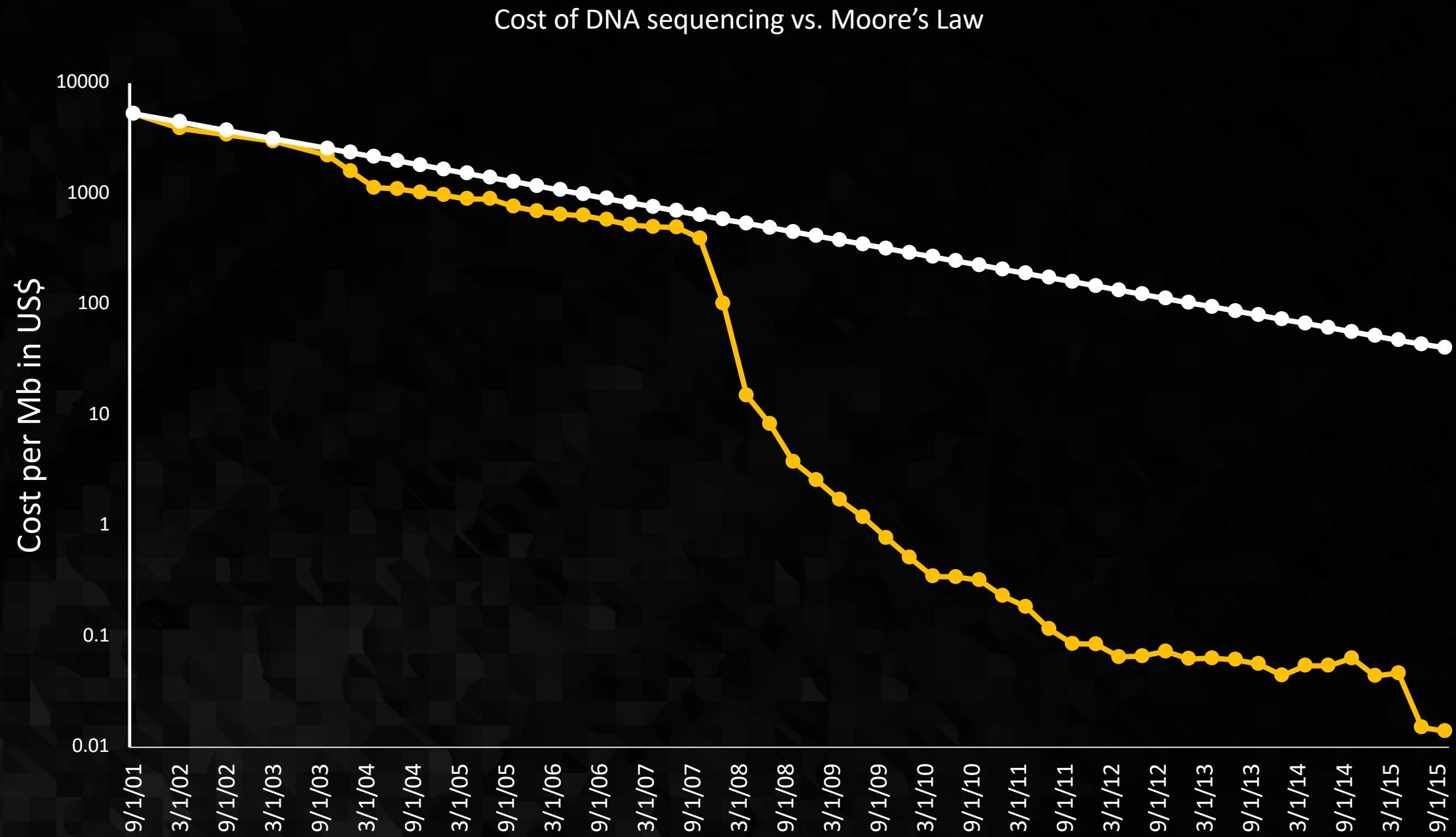


“Advice is a form of nostalgia. Dispensing it is a way of fishing the past from the disposal, and wiping it off, painting over the ugly parts, and recycling it for more than it’s worth.”

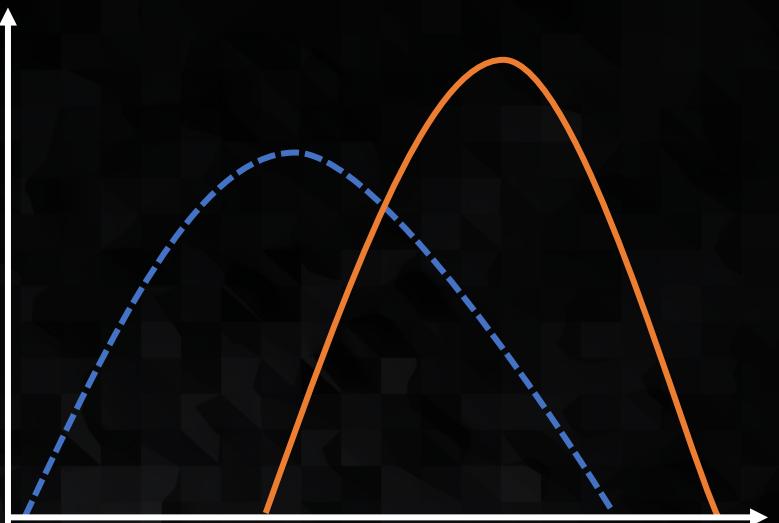
-Baz Luhrmann

The genomic era: powered by NGS

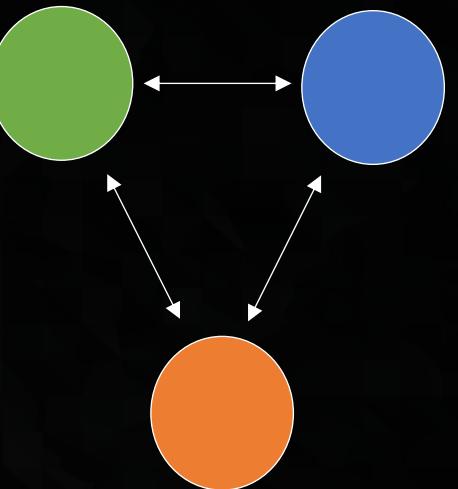


Fundamental biological questions

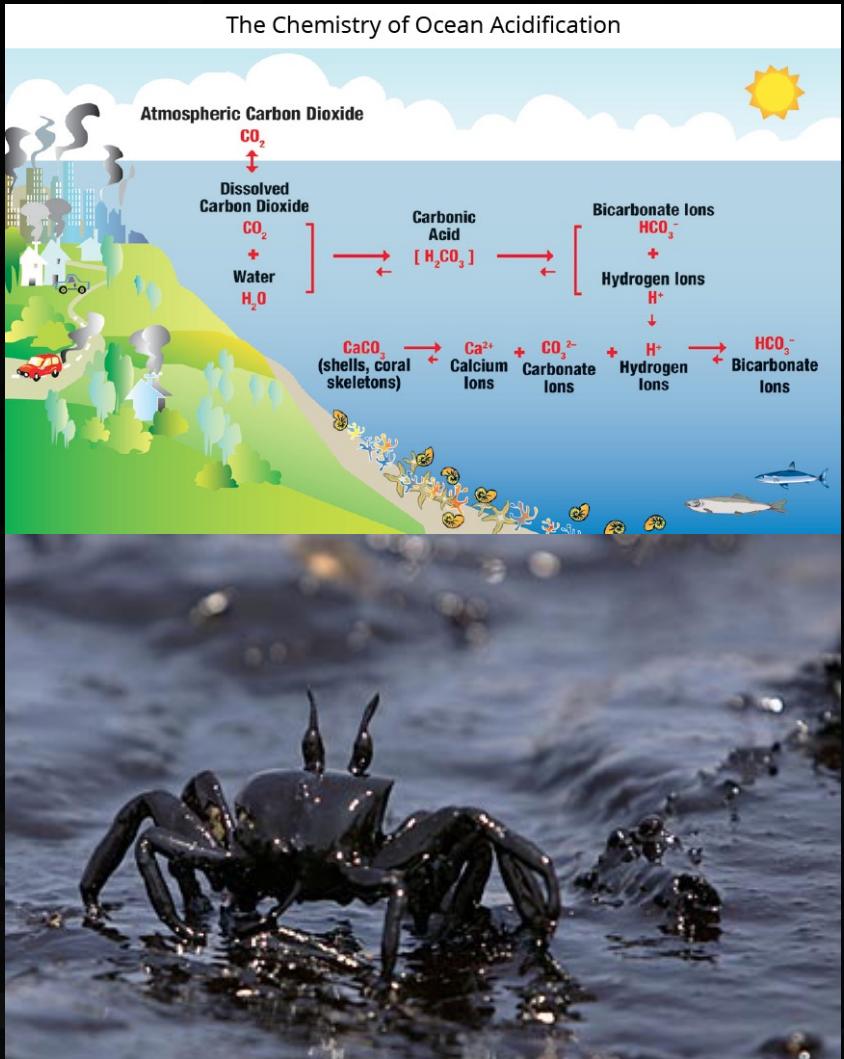
Selection



Connectivity



Evolutionary trajectory of species/populations



For population level inference, genome reduction is needed.

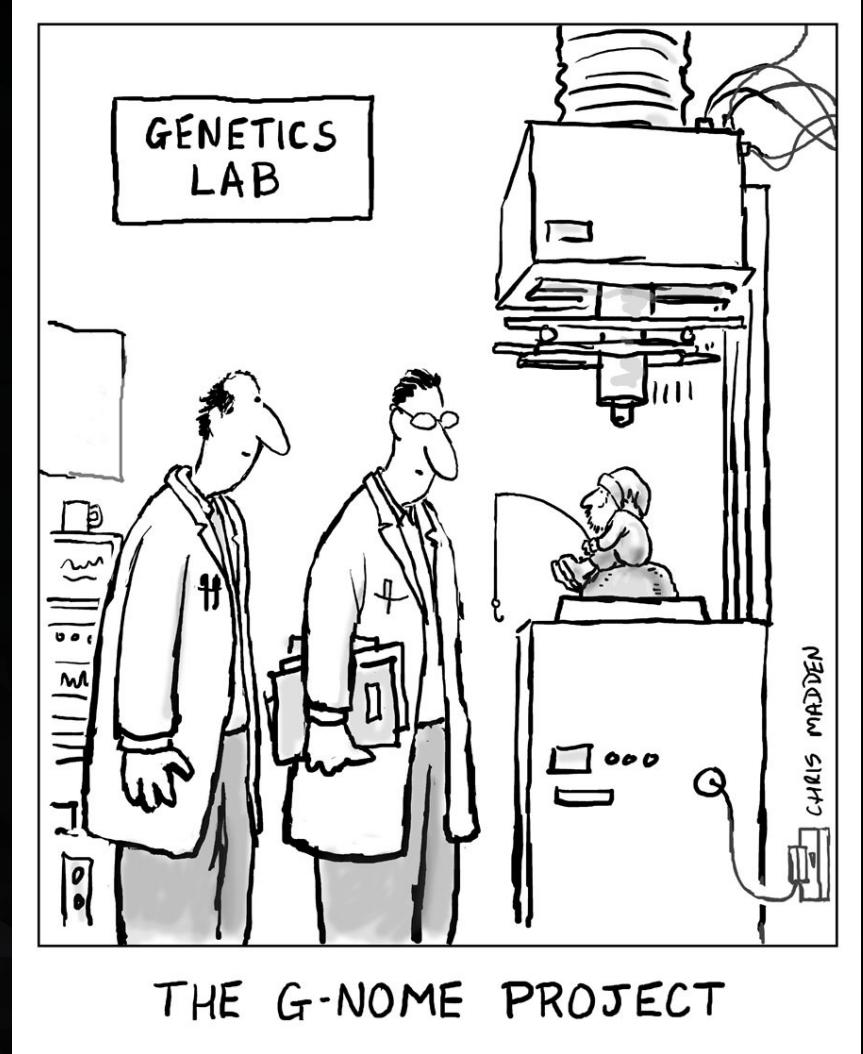
Genome reduction options

- 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 2022>

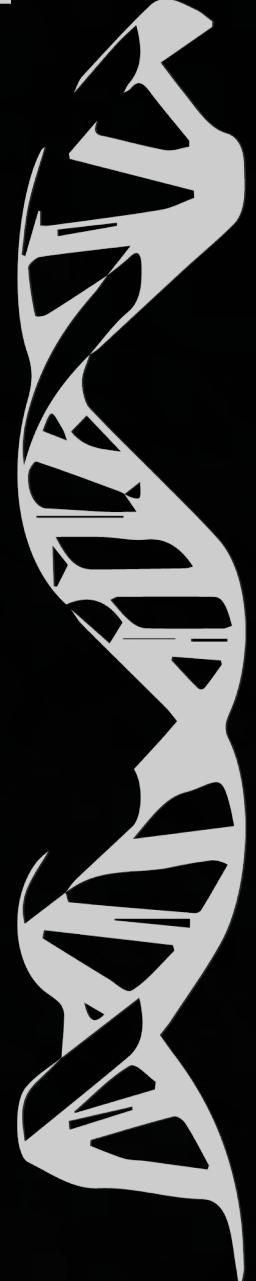


Goals for today

- 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...



 **Jon Puritz** 🦀🔬🧪🧬💻📄

@JonPuritz

The only best practice is an exhaustive exploration of all practices.

PopGenGoogling @poggengooling
is it ok to determine best practices by exhaustive exploration of worst practices

5:42 AM - 23 Jan 2019 from Kingston, RI

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