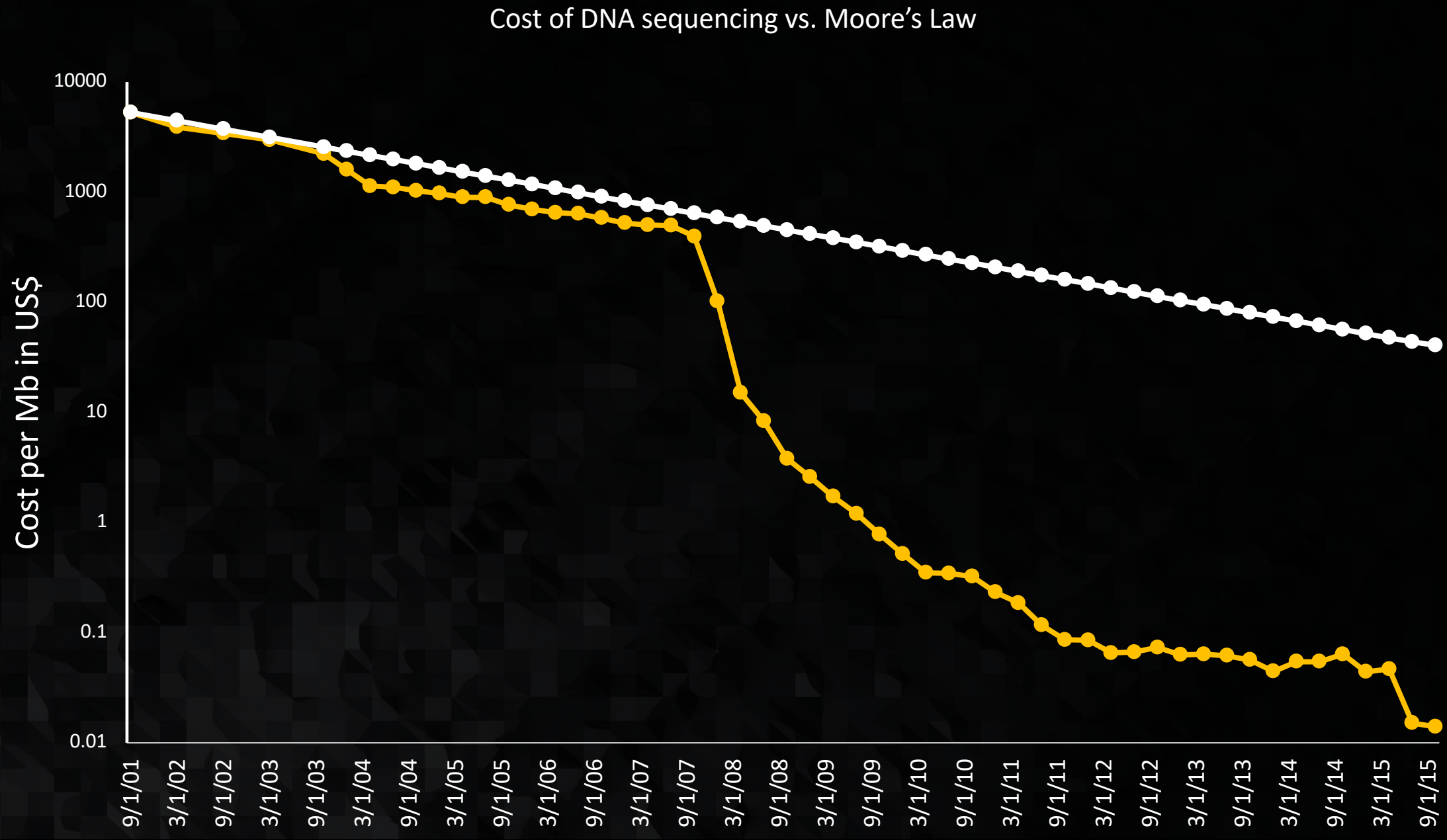


BIO 594

Conservation and Population  
Genomics: theory and practice

# The genomic era: powered by NGS



# The importance of theory

## MOLECULAR ECOLOGY

News and Views | [Free Access](#)

### Genetics and the conservation of natural populations: allozymes to genomes

Fred W. Allendorf 

First published: 09 December 2016 | <https://doi.org/10.1111/mec.13948> | Citations: 168

Today, it is relatively easy to obtain and analyze enormous amounts of information on genetic variation in any species. A wide variety of software programs are available to analyze data and estimate parameters of interest. However, the ease of collecting and analyzing data has led to an unfortunate and potentially dangerous reduction in the emphasis on understanding theory in the training of population and conservation geneticists. I am concerned that current training focuses too much on techniques and too little on understanding the conceptual basis needed to interpret these data.

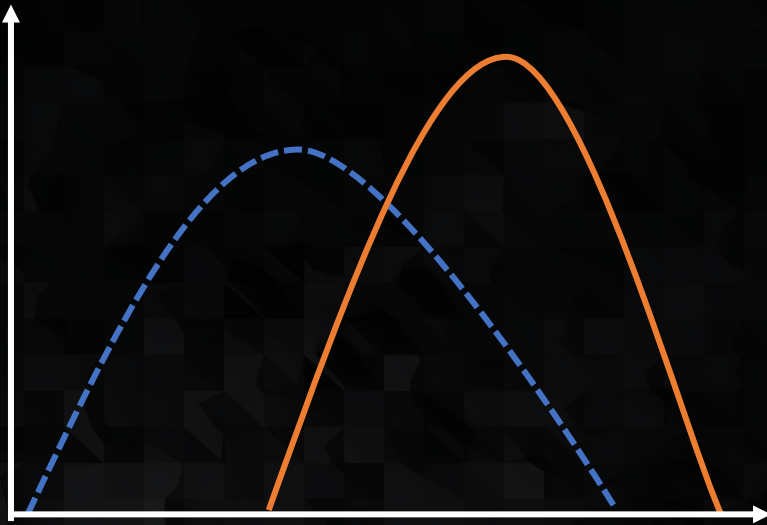
Understanding theory is crucial for correctly interpreting outputs from computer programs and statistical analyses. The most powerful software programs that estimate important parameters, such as effective population size, are not useful if their assumptions and limitations are not understood.



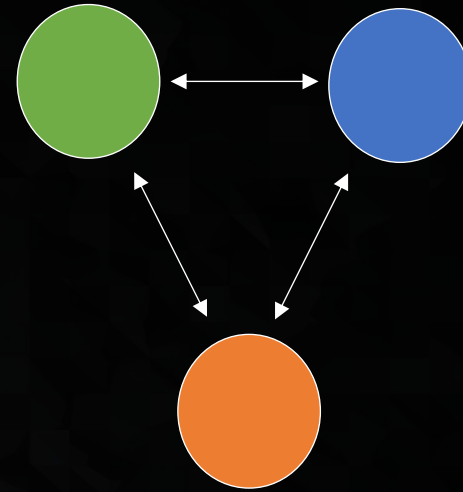
# Fundamental biological questions

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**Selection**



**Connectivity**



# Goals

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- Understand the basic theoretical principles of population genomics
- Effectively work in a command-line Linux environment
- 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

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- [https://github.com/jpuritz/BIO\\_594](https://github.com/jpuritz/BIO_594)



# Goals for today

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- 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 and personal computer
- Test out terminal functionality in Rstudio and/or VSCode

