**01/18/2017**  **P/BIO 381**

* Ecological Genomics
  + New field (from molecular ecology and population genetics)
  + “…field of study that seeks to understand the genetic mechanisms underlying adaptive responses of organisms to their environment” – Ecological Genomics Institute, KSU
  + \*Adaptation to environmental change
  + Next-gen sequencing is becoming more important
* Questions asked
  + Variation in gene expressed
  + Genetic variation within individuals vs. expressed phenotype
  + Genes giving rise to novel traits adapted to the environment
  + Speciation, hybridization, local adaptation, parasitism-mutualism life history genes, complex phenotypes, etc.
* Methods
  + De-novo genome assembly
    - Reads for evolutionary history and identification of parallel selection
  + RNA-seq
    - Single end 50bp for differential expression analysis
  + 16S metagenomics (MiSeq)
    - Microbial community diversity (variability across that sample)
  + RAD-Seq/GBS
    - Estimating diversity and population structure
* See handwritten notes for discussion of Pespeni and Keller’s research
* GitHub
  + Under your project:
    - Data/
      * Data file (csv)
    - Script/
      * R script
    - Results
      * Technical report
    - Docs/
      * Manuscript
    - Notebook (with dated entries)
    - Readme File
      * Documents all files wit description
  + GitHub can be used to **track all changes** (version control) to any file in the project
  + Share it (post it online). Good for collaboration and backing up files (can use your data on different computers).
  + DOI associated with your project that can be a citable unit