

Genomics for evolution and ecology – techniques and applications

In this 2-week section, we will discuss the use of genomic technologies to address evolutionary and ecological questions. We will focus on both methods and experimental designs, and discuss each of these aspects separately as we go through the literature. The emphasis will be on the “wet-bench” side of genomics and the basics of data acquisition and processing. The subsequent sections of PBG200 will go much more deeply into the analyses and uses of the processed data.

Techniques:

- Sequencing technologies, library preps, and barcoding
 - Several mature and emerging technologies
- Sequence assembly
 - de novo assembly
 - reference mapping
 - RNA to DNA mapping
- Genome sequencing and assembly
 - Genomic libraries
 - Impact of polymorphism
 - Whole genome amplification
- Transcriptome sequencing and assembly
 - RNA isolation and library preps
 - Normalization
 - Non-stranded and stranded sequencing
 - transcriptome analysis
- Reduced representation libraries
 - RAD tags
 - Sequence capture techniques
- Polymorphisms and genetic analysis
 - SNP identification
 - High-throughput genotyping
 - SNP arrays
 - bead arrays
 - mass-spec arrays
 - sequencing-based genotyping
 - Bulk segregant analysis and hitchhiking mapping
 - Genome-wide association studies
- Gene expression analysis
 - RNA isolation, library construction, and amplification
 - Microarrays
 - RNA-seq
 - Tag sequencing
 - Allele-specific expression analysis
 - ChIP-chip and ChIP-sequencing

Applications:

Population genetics
Evolutionary and ecological genetics (evolution of phenotypes)
Phylogeny reconstruction
Speciation genetics
Phylogeography
Molecular evolution
Comparative genomics
Metagenomics

Lecture plan:

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| Lecture 1 | Sequencing and assembly technologies |
| Lecture 2 | Genome and transcriptome sequencing |
| Lecture 3 | Reduced representation approaches |
| Lecture 4 | SNP identification and genotyping |
| Lecture 5 | Gene expression analysis |
| Lecture 6 | Metagenomics |