



Methods in Ecological Genomic Analysis

MEGA2018

GENOMICS WORKSHOPS

Hands-on workshops designed for science professionals ready to apply the acquired knowledge in their ongoing projects: senior graduate students, postdocs, researchers and faculty. Prior molecular biology (DNA isolation, PCR, gel electrophoresis) and bioinformatic (Linux, R) experience will be helpful but is not required.

Workshops Offered: Population genomics | June 3–9, 2018
Gene expression | June 10–16, 2018

Workshop Location: Mote’s Elizabeth Moore International Center for Coral Reef Research & Restoration (IC2R3) in Summerland Key, Florida

Workshop Fees: \$1500 each OR \$2500 for both

For full workshop titles and descriptions, see back of flyer.

Registration and additional information at:
ecogeno.weebly.com/contact

Workshop Descriptions

Population genomics using low-coverage RAD data

During this workshop, you will learn:

- RNA isolation and sample prep
- Deriving gene counts
- Finding differentially expressed genes
- Functional summaries
- Pathway analysis
- Functional meta-analysis
- Gene co-expression networks

Utilizing the wet lab at IC2R3:

- preparation of 2bRAD libraries

Within the dry lab at IC2R3:

- read processing using HPC computer cluster (Linux/bash);
- population structure (PCA, ADMIXTURE, EEMS)
- demographic analysis based on allele frequency spectrum (Moments, stairwayPlot)
- genome scanning

Throughout the workshop, probabilistic genotyping with ANGSD will be used, which is designed for low-coverage data.

Functional genomics and gene network analysis with TagSeq

This workshop will teach RNA isolation and library prep (wet lab), mapping to transcriptome and deriving transcript counts (using HPC cluster of the Texas Advanced Computing Center, TACC). You will also learn how to make sense of such data using DESeq2 or, alternatively, with Weighted Gene Co-expression Network Analysis (WGCNA). Understand the Principal Coordinate Analysis (PCoA), making heatmaps and venn diagrams, and master how to summarize functional information based on Gene Ontology (GO), euKaryotic Orthologous Groups (KOG), or KEGG pathways. Finally, discover how to assemble and annotate a transcriptome of your own model organism. Throughout the workshop you will use probabilistic genotyping with ANGSD, which is designed for low-coverage data.

Utilizing the wet lab at IC2R3:

- preparation of TagSeq libraries

Within the dry lab at IC2R3:

- read processing using HPC computer cluster (Linux/bash);
- analysis of broad-scale patterns (PCA, DAPC)
- finding differentially expressed genes using generalized linear models (DESeq2)
- functional summaries (GO_MWU, KOGMWU)
- gene co-expression network analysis (WGCNA)

