

Learning outcomes

Participants who complete this workshop will:

- 1) understand methods used to quantify genetic diversity within and among populations;
- 2) gain experience using software to quantify concepts such as genetic divergence, gene flow, and genetically effective population size;
- 3) be familiar with genetic methods for delineating populations and species;
- 4) be introduced to state-of-the-art advances and techniques in conservation genetics.

Workshop Schedule

Both days of the Workshop will include presentations on concepts of conservation genetics and laboratory sessions where participants will gain experience analyzing genetic data with user-friendly software. All sessions will emphasize the use of genetic data to inform management of imperiled species.

Tuesday, February 16: arrival at NCTC, registration, dinner, and social

Wednesday, February 17

Morning Session: *Introduction to Conservation Genetics*

Dr. David J. Berg, Department of Biology, Miami University
Dr. Kentaro Inoue, Department of Ecology and Ecosystem Management,
Technical University of Munich

- Introduction and genetics refresher
- Genetic structure within and among populations
allelic richness, heterozygosity, F_{ST} , and gene flow
- Laboratory Session I
use of GenAlEx (Genetic Analysis in Excel)

Afternoon Session: *Big Trouble in Little Populations*

Dr. Curt L. Elderkin, Department of Biology, The College of New Jersey
Dr. Emy M. Monroe, Whitney Genetics Lab, U.S. Fish & Wildlife Service

- Loss of genetic variation in populations of conservation concern
inbreeding, genetic drift, genetically effective population size (N_e)
- Laboratory Session II
quantifying inbreeding, genetic drift, and N_e

Evening Session

- Poster session: *Advances in Freshwater Mollusk Conservation*
- Social (concurrent with poster session)

Thursday, February 18

Morning Session: *Phylogenetics and Species Delineation*

Dr. Kevin J. Roe, Department of Natural Resource Ecology and Management,
Iowa State University

Dr. David M. Hayes, Department of Biological Sciences, Eastern Kentucky
University

- Population and species delineation
distinct populations and management units, phylogeography
- Laboratory Session III
use of phylogeographic tools

Afternoon Session: *New Directions in Conservation Genetics*

- Environmental DNA (eDNA) for detecting biodiversity
Emy Monroe & David Hayes
- Genetics and Captive Propagation of Freshwater Mollusks
David Berg
- PLENARY PRESENTATION: Introduction to Conservation Genomics
Dr. Gordon Luikart, Division of Biological Sciences, University of Montana
- “Review session”: How can these tools be used?

Evening Session

- Social, discussion of all the cool things learned

Friday, February 19: departure after breakfast

The Plenary Speaker for this workshop is Dr. Gordon Luikart. After receiving his Ph.D. under Drs. Fred Allendorf and J.T. Hogg at the University of Montana, he held several postdoctoral fellowships and research scientist appointments at the National Center for Scientific Research in Grenoble, France. In 2005, Dr. Luikart returned to the University of Montana, where he is now Professor of Conservation Ecology and Genetics at Flathead Lake Biological Station in the Division of Biological Sciences. In 2014, he was named one of “The World’s Most Influential Scientific Minds” by Thomson Reuters for being one of the most highly-cited authors of peer-reviewed scientific papers published between 2002 and 2013.

Continuing to collaborate with Fred Allendorf and other colleagues at Flathead Lake Biological Station, Dr. Luikart’s research uses genetic principles and tools to address questions of conservation in natural, domesticated, and invasive populations. Recently, much of this work has focused on the application of genomics to questions of conservation. He has authored a seminal book, *Conservation and the Genetics of Populations*, the third edition of which will be released in 2016. Dr. Luikart has authored well over 100 papers in peer-reviewed journals such as *Science*, *Trends in Ecology & Evolution*, *Proceedings of the National Academy of Sciences*, *Conservation Biology*, and *Molecular Ecology*.