

The Genetics of Conservation:

An Introductory Course on Data Collection and Analysis

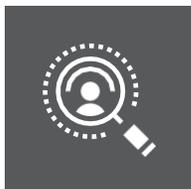
UTPL

Unidad de
Educación
Continua



2019

Para seguir este curso:



ESTÁ DIRIGIDO A *It is aimed at*

- **Professionals in biological sciences or equivalents who are interested in conservation genetics.**



REQUISITOS DE INGRESO *Entry requirements*

- **Minimum prerequisites for the course are a B.S. in Biological Sciences (or equivalent) and good computer skills.**



PERFIL DE SALIDA *Output profile*

- **After the course, participants will be able to perform a basic analysis of their own data and be better prepared to interpret the conservation genetics literature.**



METODOLOGÍA *Methodology*

In the development of this course, we will use:

- **Lectures.**
- **Review of journal articles.**
- **In class analysis of data.**
- **In class exercises.**



EVALUACIÓN *Evaluation*

The grading of the course will be:

In class exercises	35%
Homeworks (CANVAS platform)	30%
Final project	35%



MODALIDAD *Modality*

El curso se desarrollará bajo la modalidad de estudios:

SEMIPRESENCIAL

Presentación

Presentation

The exponential growth of the human population since the mid-19th century has caused terrible damage to the Earth's environment and its non-human inhabitants. Deforestation, overharvesting, agricultural expansion, pollution, climate change, introduction of invasive species and other destructive practices have resulted in severe habitat loss and population declines in countless plant and animal species. As these populations are fragmented and reduced in size, the subsequent loss of genetic diversity makes adaptation to changing conditions more difficult and can ultimately contribute to their extinction. Conservation geneticists identify species that are threatened by this genetic erosion and then suggest policies that will halt, and hopefully reverse, the trend.

This intensive, 5-day course (taught in English) will focus on how data are collected and analyzed by conservation geneticists in their study of threatened species. Designed for working conservation biologists, the course will first explore the challenges of sample collection, DNA isolation, and the more common problems associated with amplifying genetic loci. The majority of the course, however, will focus on two of the most widely used methods of acquiring genetic data: DNA sequencing and microsatellite analysis.

Nuclear, mitochondrial and plastid loci will be examined as sources of DNA sequence variation at the species, subspecies and population levels. By generating sequence alignments, statistics, phylogenetic trees and haplotype networks, students will analyze data taken from the conservation genetics literature. Brief discussions of microsatellite loci identification, amplification, and scoring issues will be followed by calculation of genetic diversity indices, null allele frequencies, and the likelihood of bottlenecks. Various phylogenetic tree-building models and the popular Bayesian clustering method Structure will be used to assess population structure from microsatellite data. Throughout the course, the biological and phylogeographical interpretation of results and their application to conservation will be stressed.

Objetivo

Objective



To introduce non-geneticists (or those new to conservation genetics) to the common data analysis methods and software used in the discipline.

Certificación y aprobación

Certification and Approval



El curso tiene una duración de 40 horas, distribuidas en 25 horas presenciales, 6 horas virtuales y 9 horas de trabajo autónomo del participante.

El presente curso se aprueba con el 70% como mínimo de la nota total y el 75% de asistencia a las jornadas presenciales. Al finalizar el curso se entregará un Certificado aprobatorio en *The Genetics of Conservation: An Introduction to Data Collection and Analysis*, avalado por la Universidad Técnica Particular de Loja (UTPL).

The structure to be developed is the one presented below:

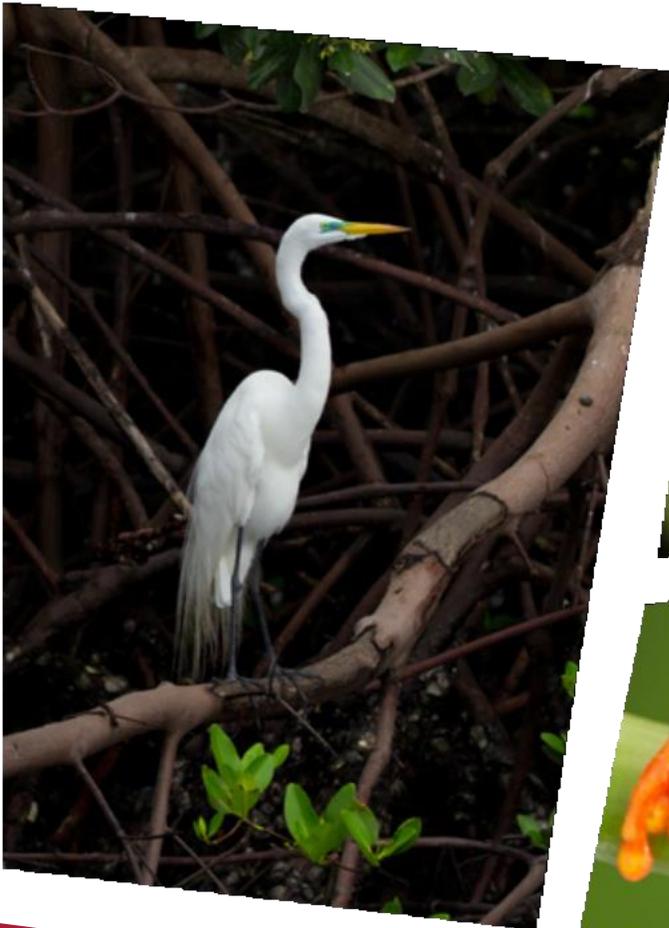
1. Sampling, DNA isolation and PCR issues
 - 1.1. Brief overview of genetic analysis for conservation purposes.
 - 1.2. Sampling considerations (number of populations, number of individuals).
 - 1.3. Sample storage.
 - 1.4. Choice of DNA isolation methods and kits.
 - 1.5. PCR inhibitors and sequencing problems.
 - 1.6. Review of journal articles.
2. Mitochondrial and chloroplast sequence analysis
 - 2.1. Relative evolution rates vs. nuclear loci.
 - 2.2. Commonly used loci and universal PCR primers.
 - 2.3. Sequence alignment (CLUSTAL).
 - 2.4. Statistics and phylogenetic tree construction (MEGA).
 - 2.5. Haplotype network analysis (TCS).
 - 2.6. GenBank retrieval of sequences and in-class analysis.
 - 2.7. Review of journal articles.
3. Microsatellite data collection
 - 3.1. Use of loci from related species.
 - 3.2. Loci discovery (Illumina sequencing).
 - 3.3. Number of loci needed for analysis; probability of identity.
 - 3.4. PCR multiplexing.

Estructura de contenidos

Structure of Contents



- 3.5. **Electropherogram analysis.**
- 3.6. **Null allele detection.**
- 3.7. **Review of journal articles.**
- 4. **Microsatellite data analysis I**
 - 4.1. **Data organization and format conversion (CONVERT).**
 - 4.2. **Basic population genetics statistics (GenePop, GenAlex).**
 - 4.3. **Null allele frequency determination (FreeNA).**
 - 4.4. **In-class analysis of sample data.**
 - 4.5. **Review of journal articles.**
- 5. **Microsatellite data analysis II**
 - 5.1. **Population assignments using Bayesian analysis (STRUCTURE, DISTRUCT).**
 - 5.2. **Frequency model vs mutation model-based phylogenetic trees (PopTree2).**
 - 5.3. **Do the data make biological and phylogeographical sense?**
 - 5.4. **In-class analysis of sample data.**
 - 5.5. **Review of journal articles.**



Prueba de recuperación

Recovery Test



The evaluation tools considered are:

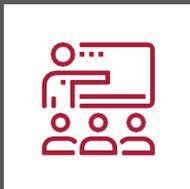
- Attendance to face-to-face classes.
- Final project delivery.

Nota: El curso será dictado en el idioma inglés.

The course will be taught in the English language.

Cuerpo de instructores

Instructor



La Unidad de Educación Continua de la UTPL, cuenta con instructores de gran experiencia en su área del conocimiento, tanto a nivel profesional como de enseñanza a nivel superior.

La asignación de docentes a cada ciudad es potestad exclusiva de la UTPL.



Dr. Chris Brinegar

Obtained his Ph.D in 1983 from the University of Wisconsin and did post-doctoral work at the Plant Cell Research Institute in California before serving as a professor in the Department of Biological Sciences at San José State University for 20 years. He has been Adjunct Professor of Natural Sciences at the University of Maine in Farmington since 2006. He specializes in the study of plants and animals of the West Coast of the United States. His projects have included the genetic characterization of redwoods (*Sequoia sempervirens*), redwood sorrel (*Oxalis oregana*), spineflowers (*Chorizanthe spp.*) and spotted owls (*Strix occidentalis*). Current projects include population genetics studies of the threatened Ecuadorian tree species *Cinchona officinalis* and *Vasconcellea stipulata* with colleagues at UTPL. He resides in Crescent City, California.



Forma de pago

Los pagos se pueden hacer en cualquier banco o pagar con su tarjeta de crédito preferida:



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SIEMPRE SEGURO Y NUESTRO



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