Introductory workshop on environmental DNA studies

6th and 7th of July 2026

Department of Zoology and Entomology, Rhodes University
Makhanda, South Africa

Environmental DNA (eDNA) analyses represent a versatile suite of methods that can be used in fields as diverse as the discovery of new species, community analysis, detection of rare taxa (e.g. threatened species or non-native species before they become invasive), and dietary analysis when the examination of gut contents or faeces is needed.

Sterivex filter being used to collect environmental DNA from seawater

COURSE OVERVIEW

This workshop offers an introduction to environmental DNA (eDNA) methods (from theory to practice) and their applications for biodiversity conservation and species detection, including the use of metabarcoding to identify both metazoan and non-metazoan species within a sampled community.

TARGET AUDIENCE

The workshop is designed for researchers and students interested in learning the basic genetic and analytical techniques commonly used to undertake ecological and biogeographical studies that use eDNA data. No prior experience in genomics or bioinformatics is required, but each workshop participant needs to bring their own laptop computer for the bioinformatics session.

The course will be divided into three parts:

- A broad introduction of eDNA studies and their importance for several scientific disciplines.
- Sessions presenting methodologies for collecting and processing various types of eDNA samples.
- A bioinformatics session on how to use specific software for processing and analysing eDNA data.

Day 1

Session 1. Welcome and Introduction

- What is eDNA? Types of environmental samples
- How to design a metabarcoding or qPCR survey depending on the focus of the study
- Need for field and laboratory controls
- Pre-amplification laboratory procedures

Session 2. Main approaches

- Metabarcoding markers, universal vs taxon-specific markers, commonly used primers
- Database coverage and gaps, taxonomic resolution
- Qualitative and quantitative values of the different metabarcoding approaches

Day 2

Session 1. Basic bioinformatics

- Metabarcoding pipeline: main steps of sequence processing, demultiplexing and dereplicating, chimera filtering
- Denoising and clustering, applications of ASVs and OTUs
- Controls, abundance-based and occurrence-based filters
- Taxonomic assignment, reference databases

Session 2. Data analysis

- Analysis of metabarcoding datasets. Rarefaction curves, alpha and beta-diversities, community analyses, indicator species
- Metaphylogeography and genetic differentiation
- Applications of eDNA-based research: Studies on biodiversity patterns, invasive species, endangered species, diet analysis, biogeographic patterns, marine protected areas, etc.

Day 3 (morning). Practical

- Processing of a mock dataset

INSTRUCTORS

Xavier Turon and Marc Rius, CEAB-CSIC, Spain
Peter Teske, University of Johannesburg, South Africa

COST AND REGISTRATION

This workshop is financially supported by a research grant from the Spanish government (COOPB24022) and is free of charge to all participants, but travel and accommodation are not covered. Please ensure that you organise your accommodation long in advance, as the workshop takes place immediately after the National Arts Festival (June 25 - July 5), and accommodation may be limited.

Please register using the link below. If the number of applicants exceeds the available spaces, we will select individuals on the basis of the motivations provided in the registration form.

WORKSHOP REGISTRATION LINK