

## Cambridge IB Ecology

### Field Course in Molecular Ecology

#### Project:

#### **Investigating diversity and population structure in western chimpanzees using genomic data from fecal samples**

Collecting genetic data from wild populations is often extremely difficult, particularly from species which are endangered or whose habitat is difficult to access. Often, genetic studies must make use of zoo animals or a very limited number of wild individuals. This is a particular problem for studies of molecular ecology and conservation genetics.

One way to increase our chances of getting larger numbers of sampled individuals – and therefore a better representation of wild population diversity – would be if we could extract useful genetic data from fecal matter. Such samples would be far easier to collect than blood samples from live individuals.

This project explores the potential for successful analyses based on such data, using data from a pilot study of fecal sample sequencing in western chimpanzees. This study collected DNA both from fecal samples and from blood for several individuals. Your aims are as follows:

- a) Obtain data (e.g. from <http://giladlab.uchicago.edu/fecalcode.html>), and find the files representing autosomal genotype data.
- b) Import this data into R and carry out simple initial analyses, e.g. calculate heterozygosity in each individual, compare data from fecal and blood samples.
- c) Develop an analysis of population structure – ie differences between based on this data, e.g. using trees, principal component analysis or other approaches. What conclusions can you draw about western chimpanzee genetic diversity and structure?
- d) Consider the effectiveness and potential difficulties in a fecal sampling approach if extended to a larger scale, given what you have found.
- e) Explore the mtDNA sequences for these samples – do they show a similar pattern? Can you make a tree from them and mtDNA sequences from other nearby or more distant species?