**Phylogeography computer practical**

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**Software required:**

* PopArt
* Any text editor
* Any software where you can view/resize images (Open Office, Powerpoint, Word)

**Background**

In this practical we will produce and interpret a haplotype network for a species of frog endemic to the Philippines and Borneo (the species doesn’t actually exist, made-up for the purposes of this practical). We will use the software PopArt (Leigh and Bryant 2015).

The species was collected by researchers on several islands across the Philippines and also in Borneo. The aim was to cover most of its geographical range. 71 individuals were collected in total. The researches sequenced a mitochondrial gene for all 71 individuals. They then assigned haplotypes to each of the individuals. The researchers are interested in finding out what is the biogeographical history of the species, how genetic diversity is distributed, and whether there is some geographical structure in haplotypes.

**GOAL: Produce a figure with a haplotype network and a map with the haplotypes, using PopArt, and discuss the phylogeography of this frog species.**

1. Download and install PopArt. <http://popart.otago.ac.nz/index.shtml>
2. Open the nexus file ‘Frog mitochondrial seqs.nex’ using your text editor. The file includes the information on the haplotypes names (TAXA block), the sequences of each haplotye (CHARACTERS block) and the geographical information about the samples assigned to each haplotype (TRAITS block).
3. The TRAITS block includes the information on the latitude and longitude of each of the geographical regions where individuals were sampled. They are grouped by island or by location within an island. Eight regions are defined. The matrix in the traits block includes the number of individuals from each region that have each of the haplotypes.
4. Open PopArt and load the nexus file. On the left side under the traits tab you will see the different geographical regions and the summary of the number of different haplotypes and different samples for each. In the Alignment tab you can view the alignment.

1. Now let’s build a haplotype network. In the Network menu you can select TCS Network, which is a commonly used type of network. Select the best colour for your network.
2. Once you have your network, in the View menu select ‘Switch to map view’ to view the map. Zoom in to the focal geographical area to view your samples.
3. Play around with different options in PopArt to make the map and haplotype networks look how you want them. You can experiment with different types of network, moving around points and bar charts in the figures, and labels.
4. Export your map and network as images (using Export Graphics option, or using print screen) and open them in a program where you can resize images and write.
5. Discuss and hypothesize about the phylogeography of this species of frog taking into consideration that island may have been connected in the past or closer to each other.

Hypothesize on a potential biogeographical history for this species. There is no correct answer! But it needs to be consistent with the data. Questions/topics for discussion:

* Make sure you understand the difference between the map and the haplotype network. Colours mean different things!
* Is there geographical structure in this species?
* What are the most diverse regions in terms of haplotypes?
* How are haplotypes linked to each other?
* Has there been hybridization?
* Which island was colonised first, and last?
* Are there any unexpected/incongruent patterns?