**Masters Project 2022-2023**

**Starts in Sept 2022**

**(duration: 9 - 12 months)**

**Project title:** Fluctuations in gene flow and their impact on parapatric speciation

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**Abstract:**

Migration plays a crucial role in evolution in general, as a source of diversity as well as a homogenizing force. Unless speciation happens between fully isolated populations, migration will have a determining role in shaping the fate of incipient species. However, migration is almost always assumed to be constant through time. This is true both for a theoretical perspective and when reconstructing demographic histories. Only a few studies have investigated the effect of fluctuations migrations rates, but not in the context of speciation. Here, we aim to address this issue and investigate how having fluctuations in the migration rate will affect the build up of reproductive isolation. One goal is to calculate the corresponding (constant) effective migration rate that will produce the same amount of reproductive isolation between the two incipient species. In addition, we will test whether this effective migration rate also matches the one obtained when considering patterns of diversity at a neutral marker (FST for example). Such system can be described by a system of ordinary differential equations. An initial exploration of this question will be conducted through simulations of the deterministic dynamics of the model. Depending on the outcomes, the results may be completed by an analytical analysis or large-scale simulations using SLiM. The student will gain knowledge of evolutionary and theoretical biology and develop skills in bioinformatics. Some knowledge of one programming language (R or others) would be an advantage to the student.

 References:

* Butlin et al. (2012) What do we need to know about speciation? Trends Ecol. Evol. **27**, 27–39.

(doi:10.1016/j.tree.2011.09.002)

* Bank at al. (2012) The limits to parapatric speciation: Dobzhansky–Muller incompatibilities in a continent–island model. *Genetics* **191**, 845–863. (doi:10.1534/genetics.111.137513)