SIGNATURES OF SELECTION WITHIN CHROMOSOMAL INVERSIONS | MSc projects available

Supervisor/Contact

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Background/Introduction

Chromosomal inversions are structural mutations where a chromosome segment breaks at two points and reinserts in the opposite direction, altering genomic architecture. Driven by advancements in comparative genomics revealing that chromosomes are more structurally fluid than previously thought, there is a renewed interest in chromosomal inversions and their role in evolutionary processes ranging from mating strategies, through environmental adaptation, to speciation. Despite this growing interest, the mechanisms by which inversions drive adaptive evolution remain unclear. An important feature of inversions is that they suppress recombination in heterokaryotypes, linking alleles in a non-recombining genomic block. Theory suggests that inversions can therefore aid local adaptation by protecting sets of locally beneficial alleles from recombination. While ample empirical evidence is now linking inversion polymorphisms with local adaptation, we currently lack methods to identify selection targets within inversions.

Project description

This MSc project is part of a an ongoing SNF funded project to study chromosomal inversions, using mathematical modelling, individual based simulations and statistical analyses of data from stickleback and fruit flies (in collaboration with Profs. Katie Peichel, Uni Bern, and Thomas Flatt, Uni Fribourg). The project will be supervised by Karolina Wąchała and Stephan Peischl, but collaborations with other members of the group as well as the lab of Prof. Katie Peichel are possible. Depending on the interest and background of students, the project can cover one or more of the following subjects:

1) Performing individual-based simulations with parameters chosen to reflect the biological reality of the stickleback or fruit fly populations
2) Analysing and visualizing the output of simulations as well as empirical data
3) Developing new summary statistics to identify targets of selection within inversions
4) Building and training a supervised Machine Learning algorithm for detecting adaptive sites within inversion using simulated data
5) Extending and maintaining an existing Snakemake pipeline for efficient simulations and analysis of data (simulated as well as empirical)

Aim of the project

The overall aim of this project is twofold:

(a) Characterize the expected genomic signatures of selection within chromosomal inversions
(b) Develop methods to identify the targets of selection

Students working on this project will contribute to one or both of these aims, and the specific aims of the MSc project will be set at the beginning of the project together with the student.

Methods

SLiM, Machine Learning (either R or Python), Command line tools, High-Performance Computing (HPC), Snakemake

Literature/Further reading

Wellenreuther, M., & Bernatchez, L. (2018). Eco-evolutionary genomics of chromosomal inversions. *Trends in Ecology & Evolution*, 33(6), 427–440. https://doi.org/10.1016/j.tree.2018.04.002

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Schrider, D. R., & Kern, A. D. (2016). S/HIC: Robust identification of soft and hard sweeps using machine learning. *PLoS Genetics*, 12(3), e1005928. https://doi.org/10.1371/journal.pgen.1005928