

Firefly genomics and transcriptomics

Background

To investigate the evolutionary forces acting on genomes we need first to generate the genomic resources that will allow us to tackle specific questions on demography and adaptation. Therefore we are working on generating high quality genomes and transcriptomes of fireflies, which will allow us have a much deeper understanding on how firefly populations adapt to new environments or what is the role of transcriptome variation in trait evolution.

Project objectives

- Generation of high quality genomes using various technologies: Nanopore, PacBio, HiC, Illumina.
- Transcriptome assembly using short and long read sequencing.
- Population genomic analysis.
- Gene expression evolution.



Lamprohiza splendidula male.



illumina®

Arima-HiC⁺



Student requirements

- Basic bash / python / R
- High motivation.
- Commitment to the project.

Learning outcome

- Assembly of genomes and transcriptomes.
- Population genetics on whole genome data.
- Comparative transcriptomics.

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