

Predicting Evolution

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It is one of the greatest challenges of biology today to understand to what extent evolution may be predictable. This project will focus on assessing whether we can identify molecular characteristics of a gene that limit or increase the chance that it may undergo sequence divergence under positive selective pressure.

Specifically, the project will focus on the amount of evolutionary change that genes have undergone within the *Drosophila* genus, and whether this correlates with how many regulatory interactions a gene has; the expectation being that genes with many regulatory interactions are more conserved. This project will make use of the huge databases that have been developed in the latest years on whole-genome sequences for multiple species and populations, functional gene annotations, co-expression, and protein-protein interactions. These databases contain a large body of research on the molecular mapping of the interactions between genes in *Drosophila*.

Methods: Programming, R.

Starting date: open

