

Title:

Uncovering signatures of selection from experimentally evolved populations with Machine Learning

Authors:

Diogo Ribeiro, Rui Borges, Christian Schlötterer

- 1. Institute of Population Genetics, University of Veterinary Medicine Vienna, Austria**

Abstract:

The rapid progress in high-throughput sequencing technologies has led to massive population genomic datasets characterized by their high dimensionality and complexity. The latter in particular is challenging to study as it represents the interplay of various evolutionary forces (e.g, genetic drift, selection and recombination) that leave traces in the genome. Nevertheless, distinguishing between the different forces based on the genomic patterns has remained a major challenge of the field. Machine Learning (ML) allows to extract information from raw data, capturing intricate patterns and hierarchical structures and thus provides a promising alternative to classic population genetic tests. We employed ML techniques to explore the adaptive architecture of a *Drosophila melanogaster* experimental population founded by combining two inbred strains and undergoing adaptation to hot temperatures for 210 generations. This experiment permits us to study the evolution of a complex trait that is influenced by multiple genetic factors. Through the analysis of time series data of allele frequencies along the genome, we aim to infer the number of selection targets and their selection coefficients using ML. Given the extensive data demands, we trained our models using simulated genomic data replicating the experimental design. Finally, we compared strategies that analyze entire chromosomes or employ a moving window with multiple different models in terms of their computational performance and predictive power. Our study will provide valuable insights on the number of players involved, their relative contribution and better our understanding of the genomic response to adaptation.

(242 / 250 words)

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