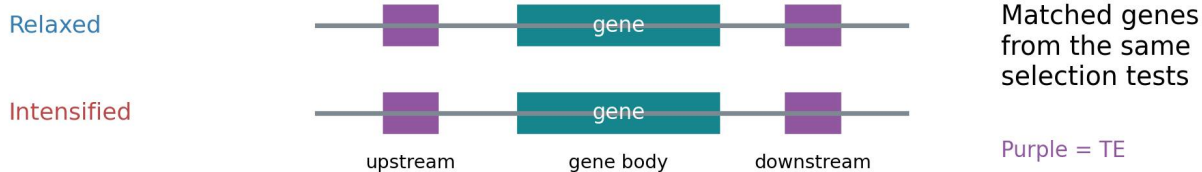


TE neighbourhoods of genes under changing selection

Background

Socially parasitic ants rely on their hosts for colony tasks, creating an opportunity to study changes in selection on genes. Transposable elements (TEs), or jumping DNA, may also alter the surrounding genome. This project asks whether genes showing relaxed or intensified selection have different TE neighbourhoods after differences in gene structure and genomic context are taken into account.

Compare the same genomic compartments



Schematic examples only; the diagrams show comparisons, not observed results.

The project

You will use existing annotations and selection results for *Temnothorax americanus* and its host *T. longispinosus*. Within each species, you will measure TE coverage in gene bodies and fixed 2 kb upstream and downstream windows. Comparison genes will come from the same successfully tested gene set, matched for gene length, GC content and local gene density. Simple repeats will be analysed separately. The core test is whether a TE association remains after matching, and whether it differs among genomic compartments.

Expected outcome

A reproducible analysis, effect sizes with uncertainty, and figures showing whether the association persists. This extends an initial overlap analysis; it does not assume that TEs caused changes in selection.

Possible MSc thesis extension

Test whether the pattern recurs in *T. pilagens* and *T. ambiguus*, then examine selected TE families or corresponding loci. The first pair alone cannot establish a general effect of social parasitism.

Methods

Genomic interval analysis, matched comparisons, resampling and plots in R or Python.

Requirements

- Interest in evolutionary genomics and willingness to learn command-line analysis and R or Python.
- Basic coding experience is helpful. Existing datasets will be provided.

Supervision

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Selected literature

- Harrison et al. (2025). Convergent Evolutionary Traces of Genomic Innovations and Depletions in Socially Parasitic Ants. *bioRxiv* [Preprint]. doi:10.1101/2024.12.31.630940
- Schrader et al. (2021). Relaxed selection underlies genome erosion in socially parasitic ant species. *Nature Communications* 12:2918. doi:10.1038/s41467-021-23178-w