

Research project (Forschungsmodul/BSc/MSc)

Investigating the Molecular Footprints of Eusociality with Machine Learning

Background: Eusociality, in which colonies consist of overlapping generations performing cooperative brood-care and in which, importantly, reproductive labour is divided between sterile and fertile castes, has evolved independently in 3 orders of insects, Hymenoptera (ants, bees and wasps), Blattodea (termites) and beetles (one species of Ambrosia beetle). Little is known on the molecular level how eusociality evolves from solitary ancestors. The few molecular signatures of eusociality that have been discovered are clade-specific (e.g. in ants: Simola et al. 2013; in bees: Kapheim et al. 2015 and Shell et al. 2021; in termites: Harrison et al. 2018). No fundamental, convergent footprints of eusocial evolution have been found yet - machine learning techniques may be helpful in this search.

Overall objective: Investigate the genomic footprints of eusocial evolution across several insect clades using machine learning tools.

Potential hypotheses, to be supplemented and further developed within the project

1. Regulatory regions harbour similar patterns across eusocial genomes due to evolution of caste-specific gene expression.
2. Strength of the signal may differ by caste-specificity of corresponding genes.

Materials & methods

- Different genomic regions and their properties will be extracted from the genomes of social and non-social species.
- Established Python packages will be implemented, such as SciKit-learn, to develop a machine learning tool that can classify genomic regions and properties by sociality.

Requirements: This project can be scaled smaller or larger depending on the type of project and the experience of the student. But generally the following skills are necessary:

- Interest in genome evolution
- Experience working on the command line, at least basic Python skills
- Ability to work independently
- some basic knowledge of molecular evolution & selection

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References

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