

A statistical analysis of the relationship between transcription factor gene properties and eusocial evolution

Background: Eusociality has evolved across several lineages producing immense biodiversity and whose caste system provides an incredible example of polyphenism [1]. The influence of transcription factors on eusocial evolution has been little studied, particularly in *Blattodea* [2]. This project will compliment work on transcription factor selection, gene family and PFAM dynamics by looking at isoform number and intron properties. Intron size and alternative splicing have been found to have been correlated to organismal complexity [3] but this has not been looked at in relation to social evolution.

Objectives: The objective will be to investigate how intron size TF family and isoform number relate to eusocial evolution. This will involve phylogenetic generalised linear modelling to identify how intron size and isoform number relate to eusocial evolution.

Requirements:

- Interest evolutionary biology
- Knowledge / Interest in data analysis using either Python or R
- Ability to work independently

Methods:

- Basic coding and data handling
- Statistical analysis particularly Bayesian modelling
- Plotting using relevant packages / modules

Supervision: Dr Alun Jones, Room number 100.22, e-mail adress ajones@uni-muenster.de, Molecular Evolution and Bioinformatics Group (<http://bornberglab.org/>).

Selected Literature:

References

- [1] Sandra M. Rehan and Amy L. Toth. "Climbing the social ladder: the molecular evolution of sociality". en. In: *Trends in Ecology & Evolution* 30.7 (July 2015), pp. 426–433. ISSN: 01695347. DOI: 10.1016/j.tree.2015.05.004. URL: <https://linkinghub.elsevier.com/retrieve/pii/S0169534715001263> (visited on 01/19/2023).
- [2] Mark C. Harrison et al. "Hemimetabolous genomes reveal molecular basis of termite eusociality". en. In: *Nature Ecology & Evolution* 2.3 (Feb. 2018), pp. 557–566. ISSN: 2397-334X. DOI: 10.1038/s41559-017-0459-1. URL: <https://www.nature.com/articles/s41559-017-0459-1> (visited on 01/19/2023).
- [3] Pengcheng Yang, Depin Wang, and Le Kang. "Alternative splicing level related to intron size and organism complexity". en. In: *BMC Genomics* 22.1 (Dec. 2021), p. 853. ISSN: 1471-2164. DOI: 10.1186/s12864-021-08172-2. URL: <https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-021-08172-2> (visited on 01/17/2023).