The arthropod megaphylogeny and the origin of Earth’s biodiversity

Supervisory team:
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Project description:
Rationale: The Arthropoda (insects, spiders, centipedes, and crustaceans such as crabs and lobsters), includes millions of species and represents most animal biodiversity1. Arthropods also have an excellent fossil record (spanning most of the phanerozoic)2, when compared to that or other animal lineages, and abundant genomic information is available for this lineage, which includes model species such as the fruit fly Drosophila melanogaster. However, many questions in arthropod evolution remains unresolved, in particular it is unclear whether patterns of species diversity through time and across arthropod groups, correlate with changes in morphological disparity3, pattern of genomic change4 or both. A major limitation to study global pattern of arthropod evolution has traditionally been that the share taxonomic richness of this lineage has made it impossible to generate the densely sampled, dated, arthropod phylogenies representing the background information necessary to test hypotheses of arthropod diversification.

Objectives: This project proposes to combine methodological advances in phylogenetics, molecular clocks5, and fossil-based dating6 to derive the first, densely sampled (>1,000 taxa) Arthropod ‘megaphylogeny’ and use it to test hypotheses about Arthropod evolution. We shall focus on testing whether there is a direct correlation between changes in genome size and content across the arthropod tree and, (1) the emergence of arthropod diversity and (2) their morphological disparity. Training Opportunities: You will be responsible for integrating large-scale fossil and molecular datasets to test evolutionary hypotheses that cannot be addressed using only fossils or genomes. You will learn about phylogenomics, molecular clocks, genomics, arthropod diversity, and the fossil record. You will learn computer programming (Python, R and Shell scripting), and gain knowledge of the most advanced Bayesian and Maximum Likelihood approaches to infer and date phylogenies5,6. You will learn about genome evolution and software to reconstruct ancestral genomes7, and how to study morphological disparity3. Overall, these skill will prepare you for a career in the study of evolution. However, all the skills you will learn are highly transferrable data-science skills, that will be useful irrespective of what career path you will choose.

References
1. Giribet and Edgecombe (2019) Current Biology 29(12):R592–R602
2. Daley et al. (2018) PNAS 115:5323–5331
3. Delane et al. (2018) PNAS 115(38), E8909-E8918
4. Thomas et al. (2020) BMC Genome Biology 21:15
5. Álvarez-Carretero et al. (2022) Nature. 602:263–267
6. Carlisle et al. (2023) Current Biology 33:3073–3082
7. Ocaña-Pallarès et al. (2022) Nature 609:747–753

Our aim as the SWBio DTP is to support students from a range of backgrounds and circumstances. Where needed, we will work with you to take into consideration reasonable project adaptations (for example to support caring responsibilities, disabilities, other significant personal circumstances) as well as flexible working and part-time study requests, to enable greater access to a PhD. All our supervisors support us with this aim, so please feel comfortable in discussing further with the listed PhD project supervisor to see what is feasible.