



PROJECT TITLE: Evaluating new data and methods to solve animal phylogeny

University of Bristol Theme: Climate and Environment Research Challenge Area Research Group(s): Bristol Palaeobiology

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Project keywords: Phylogenetics, Metazoa, Genomic Data Types, Synteny, Comparative genomics.

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Project Background

Understanding the phylogenetic relationships at the root of animal phylogeny has proven difficult. A diversity of approaches and data types have been used achieving different results. The core of the problem are the relative relationships of the sponges (Phylum porifera) and of the comb jellies (Phylum Ctenophora). Competing studies have alternately found sponges or comb jellies as the sister of all the other animals. A large amount of new data has been generated in recent years for phylogenetically key taxa, including the emergence of a new data type: chromosome fusions/fissions. While these chromosome data have been hailed as a very powerful new approach to phylogenetics, little investigation has been made into the phylogenetic potential of these data type. Furthermore, studies using these data present them as apomorphies without modelling their evolution. To solve the problem of the animal phylogeny, it is paramount we understand both the phylogenetic potential of these new data and how to model them, which is what this project intends to do.

Project Aims and Methods

You will be working with genome data, with the goal to clarify the relative relationships at the root of the animal tree. You will be focus on the study of the identification of syntenic patterns and their translation to phylogenetic characters that can be analysed in a phylogenetic framework. You will use a combination of analyses of real data and simulations to validate the utility of this new type of data. After that you will focus on modelling and how to test the robustness of phylogenetic trees inferred from syntenic data pattern. While the project focuses on early animals, as new genomes are being sequenced, chromosome fusions and fissions could be used to explore additional phylogenetic controversies, and you will be instrumental in determine the choice of hypotheses that will be explored using this approach. Furthermore, while the focus is on the use of syntenic pattern in phylogenetics, you will be welcome to investigate other novel approaches in phylogenetics, such as approaches using alpha-fold or other Al-based tools.

Candidate

The project is suited to a student with a bachelors or masters degree in Earth Sciences, Biological Sciences, Systematics, Palaeontology, Biochemistry, Zoology or Genetics. We do not anticipate that candidates will have the skills required to undertake this advertised project; a PhD is about training and you will be supported in the development of the required skills. However, some knowledge of computer programming would be welcome.





Training

You will be provided with training in phylogenetics and computer programming. There will be opportunities to undertake research visits to Barcelona to interact in person with Prof Jesus Lozano Fernandez and his research team.

Background reading and references

- Feuda R, Dohrmann M, Pett W, et al. 2017. Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. *Current Biology*: 3864-3870.e4. https://doi.org/10.1016/j.cub.2017.11.008.
- Giacomelli M, Rossi ME, Fernandez LJ, et al. 2022. Resolving Tricky Nodes in the Tree of Life through Amino Acid Recoding. *iScience* 25: 105594. <u>https://doi.org/10.1016/j.isci.2022.105594</u>.
- Kapli P, and Telford MJ. Topology-Dependent Asymmetry in Systematic Errors Affects Phylogenetic Placement of Ctenophora and Xenacoelomorpha. *Science Advances* 6: eabc5162. https://doi.org/10.1126/sciady.abc5162.
- Walker P, Adamski M, Adamska M, et al. 2019. The Role of Homology and Orthology in the Phylogenomic Analysis of Metazoan Gene Content. *Mol Biol Evol* 36: 643–49. https://doi.org/10.1093/molbev/msz013.
- Pisani D, Pett W, Dohrmann M et al. 2015. Genomic Data Do Not Support Comb Jellies as the Sister Group to All Other Animals. *PNAS* 112: 15402–7. <u>https://doi.org/10.1073/pnas.1518127112</u>.
- Schultz D, Haddock SHD, Bredeson JV, et al. 2023 Ancient Gene Linkages Support Ctenophores as Sister to Other Animals. *Nature* 618: 110–17. <u>https://doi.org/10.1038/s41586-023-05936-6</u>.
- Steenwyk JL and King N. The Promise and Pitfalls of Synteny in Phylogenomics. *PLOS Biology* 22, no. 5 (20 May 2024): e3002632. <u>https://doi.org/10.1371/journal.pbio.3002632</u>.

Useful links

http://www.bristol.ac.uk/earthsciences/courses/postgraduate/

Eligibility

UK and International students are eligible for a University of Bristol Scholarship. UoB Scholarships are fully funded for 4 years and cover university fees, living expenses at the UKRI standard rate, and an allowance of £2100 per year towards research expenses.