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FIRST PERSON

First person – Tom Carruthers

First Person is a series of interviews with the first authors of a selection of papers published in Biology Open, helping early-career researchers promote themselves alongside their papers. Tom Carruthers is first author on ‘exTREEmaTIME: a method for incorporating uncertainty into divergence time estimates’, published in BiO. Tom conducted the research described in this article while a PhD student in Professor Robert Scotland’s lab in the Department of Plant Sciences, University of Oxford. He is now a postdoc in the lab of Dr William Baker at the Royal Botanic Gardens, Kew, working on determining the extent to which large molecular phylogenies provide information about evolutionary history.

What is your scientific background?

I am a biologist who was lucky to receive a place to study biological sciences as an undergraduate at Oxford University. Having been interested in the natural world from a young age, studying at Oxford enabled me to develop these interests and approach them from a scientific and philosophical perspective. Upon completing my undergraduate degree in 2015, I received funding from NERC to undertake a PhD at Oxford, where I joined the Scotland group in the department of Plant Sciences. The primary focus of this group was to research the taxonomy of the megadiverse tropical plant genus *Ipomoea*. During the initial part of my PhD my sole focus was to bring an explicitly evolutionary focus to the group’s research – i.e., using the taxonomic and phylogenetic framework that was being developed by the group as a basis to investigate when and over what timescale *Ipomoea* diversified. Although I retained a focus on this topic, after around two years into my PhD I fundamentally shifted my research to theoretical issues concerning the estimation of evolutionary timescales. This shift began whilst I was attempting to justify assumptions of methods for estimating evolutionary timescales in *Ipomoea* (which in reality often seemed virtually impossible to justify), and when it became increasingly clear that our estimates were entirely sensitive to the assumptions of different methods. However, a key turning point was a new fossil discovery in 2017 named *Physalis infinemundi*, which completely overturned understanding of the timescale of evolution within the plant family Convolvulaceae (within which *Ipomoea* is nested). Since then, I have focused especially on how assumptions about biological data affect inferences of evolutionary timescales. With ever increasing data and computational resources, it is more important than ever to determine the theoretical limits of inferences that can be made about evolutionary history. Understanding these limits is what motivates my research.

> **“… it is more important than ever to determine the theoretical limits of inferences that can be made about evolutionary history.”**

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Tom Carruthers

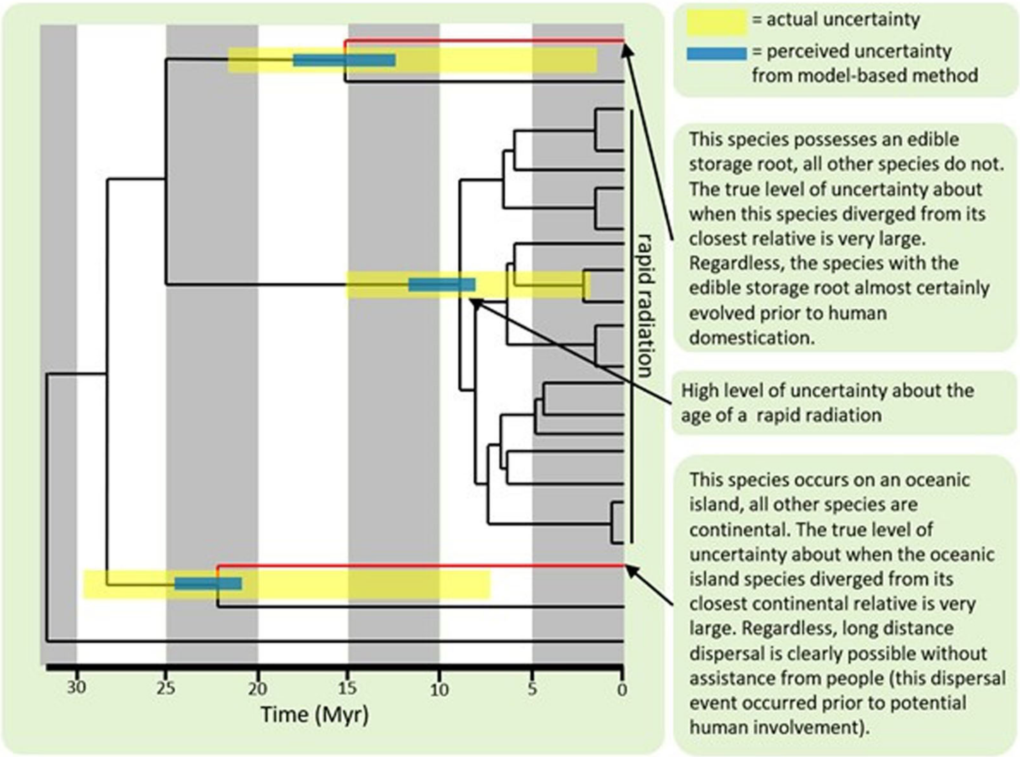
How would you explain the main findings of your paper to non-scientific family and friends?

With current methods for estimating evolutionary timescales from molecular phylogenies (divergence time estimation), it is very hard to avoid making assumptions that are difficult to justify yet estimates have extreme sensitivity to these assumptions. Therefore, we present exTREEmaTIME as a new method that allows users to avoid making unjustifiable assumptions. We show that exTREEmaTIME leads to highly uncertain estimates, far more uncertain than has been represented in previous studies. By avoiding assumptions that are difficult to justify, exTREEmaTIME enables researchers to better understand the true extent of uncertainty underlying estimates of evolutionary timescales, and to determine the implications of the more complex assumptions that are inherent to other methods.

> **“… we present exTREEmaTIME as a new method that allows users to avoid making unjustifiable assumptions.”**

What are the potential implications of these results for your field of research?

Ideally, this research will give researchers a clearer indication of the true extent of uncertainty that underlies their research. This will enable them to understand the implications of the more complex and often unjustifiable assumptions inherent to other methods. This not only has implications for understanding when different parts of the tree of life evolved, but also for understanding a whole range of



Summary of Carruthers' research focus with respect to divergence time estimation. Representing the actual uncertainty, and in light of this uncertainty, demonstrating that important biological conclusions are still possible.

other evolutionary variables, the inference of which are highly dependent on the accurate estimation of evolutionary timescales. This includes diversification rate estimation, estimates of niche evolution, or historical biogeographical processes.

What has surprised you the most while conducting your research?

Whilst conducting research into divergence time estimation more generally, I have been surprised about the extent to which different methodological assumptions are difficult to justify, and the extent to which estimates are entirely sensitive to these assumptions. It was with this in mind that I sought to develop exTREEmaTIME. As such, in developing exTREEmaTIME, I was not at all surprised by the highly uncertain age estimates that are generated by this method – when you remove the different unjustifiable assumptions that are inherent to most other methods, there is very little information left upon which to determine evolutionary timescales. Estimates are therefore very uncertain.

What, in your opinion, are some of the greatest achievements in your field and how has this influenced your research?

The greatest recent achievements in the field are undoubtedly the discovery of new fossils. These have provided a 'wake-up call' to those attempting to estimate evolutionary timescales from molecular phylogenies and highlighted the fundamental unreliability of current methods. Several further achievements have also been important to the intellectual development of the field over previous years. First, Mike Sanderson's work in the late 90's on 'relaxed clock' methodologies provided a foundation for estimating evolutionary timescales when rates of molecular evolution vary and was fundamental for demonstrating how different divergence time estimates result from differing assumptions about rates of molecular evolution. Meanwhile, Susanna Magallón and Mike Sanderson's work on the fundamental uncertainty of the age of angiosperms stands to this day. Although the uncertainty surrounding the age of angiosperms is widely thought of as an exception, uncertainty surrounding the age of this clade was an important trigger for me to undertake a broader critique of the reliability of divergence time estimation. An additional important achievement in this field is the work of Tom Britton in 2005, who demonstrated with a simple mathematical model how regardless of the availability of molecular sequence data, variation in rates of molecular evolution leads to error in divergence time estimates. This study was important whilst I was initially developing ideas and approaches to assess the reliability of divergence time estimates, although it should have perhaps had a bigger influence than it has done on the field more generally.

What changes do you think could improve the professional lives of early-career scientists?

There should be more support for the exploration and development of new ideas by early-career researchers that fundamentally challenge current approaches to research. Some aspects of scientific research are overly conservative, and it can be hard for early-career researchers to propose radically new ideas (that challenge approaches used by established researchers) if they want to establish their career. Changing this will require a cultural shift in the scientific community, as well as a change in the emphasis of funding such that support is given to those developing new theoretical ideas, rather than always those analysing ever-larger datasets.

Reference

Carruthers, T. and Scotland, R. W. (2022). exTREEmaTIME: a method for incorporating uncertainty into divergence time estimates. *Biology Open*, **11** bio.059181.