Measuring and interpreting convergence in molecular data Supervisors: Davide Pisani (University of Bristol), Matthew Wills (University of Bath), and Mark Wilkinson (The Natural History Museum, London) **Deadline for application: 31st March.**

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In biology, convergent similarity is a form of correspondence (e.g. between morphological features or of molecular sequences/structures from different species) not caused by common ancestry. Two species that display a convergent feature therefore acquired it starting from distinct ancestral features. At the least at the morphological level convergence is generally considered a consequence of evolutionary adaptation, and is generally achieved in species that adapted to a common lifestyle. An example is the evolution of fins in dolphins (mammals) and ichthyosaurs (reptiles). Convergence happens also at the molecular level and stricking examples have been discovered in the prestin gene in bats and dolphins. Prestin plays a key role in echolocation and convergence of this molecule was achieved in these two echolocating lineages. However, the extent to which convergence affect molecular data is not clear, and the forces underpinning molecular convergence are often equally unclear. Further on, how we should measure molecular convergence is not fully clear. Sequence similarity should obviously be included in the equation, but whether this similarity should be weighted, for example based on the phylogenetic distance between the considered species, is not known. Yet this can significantly impact our perception of the pervasiveness of convergence in genomic evolution. Generally, evolutionary convergence is assumed to be more common and more detailed in more closely related species, simply because closely related species tend to be more similar and tend to have more similar evolutionary constraints and potentialities. Further to that, it is often argued that molecular (i.e. genetic) data tend to be less affected by homoplasy than morphological data. We would argue that these expectations or believes are the closest thing we currently have to any 'Law of Convergence' and that a sensible and promising way of investigating the importance of convergence and its broader significance is by testing these expectations. If patterns of convergence are not so constrained and data-dependent, this would provide a powerful novel insight into the nature of evolutionary change. This PhD project is part of a larger Templeton Foundation founded research programme, the aim of which is investigating the pervasiveness of convergence in biology and its role in the process of adaptation. In specific, the student working on this project will investigate how to measure convergence in molecular data sets, and investigate how common is molecular convergence. In particular the student will: (1) develop measures to quantify convergence and address the following questions. (2) How common is convergence in molecular datasets? (2) Is molecular convergence more common within specific lineages (e.g. mammals versus birds)? (3) Are specific parts of the genome more prone to convergent evolution (e.g. protein coding genes versus regulatory non-coding sequences like microRNA)? (4) Are alternative forms of the same data (e.g. amino acid versus nucleotide sequences) differently prone to undergo convergent processes? (4) To what extent is adaptive evolution underpinning the origin of molecular convergences? The project is entirely computational and will fit a mathematically-inclined student with some experience in computer programming (or the will to learn about computational methods and programming). You will be based at the University of

Bristol, in the newly built 'Life Sciences Building', where you will join the Palaeobiology and Biodiversity Research Group. However, more broadly, you will be the member of a diverse, Templeton funded, research group spread between the University of Bristol, Bath, and the Natural History Museum of London, and interactions and visits to Bath and London will be common. Dr Davide Pisani Reader in Phylogenomics School of Biological Sciences and School of Earth Sciences University of Bristol Life Sciences Building 24 Tyndall Avenue Bristol, BS8 1TG Email:
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