REPORT ON EXPEDITION / PROJECT / CONFERENCE

Expedition/Project/ Conference Title:	Trees in the Desert Workshop
Travel Dates:	12 th – 14 th April 2019
Location:	Tucson, Arizona, USA
Group member(s):	Joseph C. Guscott
Aims:	Take part in a three-day workshop hosted by the University of Arizona

OUTCOME (not less than 300 words):-

Trees in the Desert is a workshop hosted at the University of Arizona's Biosphere 2 facility. It is an opportunity for instructors, postdocs, and PhD students to get together for a three-day workshop to communicate known approaches to the problems associated with the construction of large phylogenies, in addition to collating ideas for future directions, and demonstrations on some of the latest approaches and technologies. The instructors invited included world-leading researchers within the fields of phylogenetics, computational science, and mathematics, including Prof. Mike Steel (University of Canterbury, NZ), Prof. Mark Holder (University of Kansas, USA), Prof. Tandy Warnow (University of Illinois, USA), and Prof. Mike Sanderson (University of Arizona, USA).

The first day consisted of talks given by individual instructors regarding their recent research. Topics ranged from within the disciplines of phylogenetics, bioinformatics, mathematics, and computer science. Talks of particular interest included the rapid updating of large phylogenies, terraces within the tree space, and multiple sequence alignment estimation. Associated software for alleviating the problems discussed was also presented, including Terraphy, NJMerge, ASTRAL-III, and various pipelines (e.g. SuperCRUNCH). After the individual talks, we were presented with an opportunity to give our thoughts and experiences on issues we had faced, including software shortcomings, and potential future directions. These discussions acted as a guide for focused software demonstrations and practical sessions for the second day.

The practical sessions provided an opportunity for both PhD students and other instructors to test novel software on large datasets. Following the previous day's discussion, Terraphy, Treemerge, DupTree/DupLoss, Phlora, and SuperCrunch were all demonstrated. This provided a unique opportunity to analyse novel datasets with leading professionals, in addition to getting practical experience at the collection, manipulation, analysis, and visualisation of large datasets. Following on from the practical sessions, the PhD students were divided into groups each with an instructor to carry out mini projects which would be presented on the third day. The topics assigned covered the spectrum of phylogenetic analysis from data collection to visualisation. I took part in 'scalability of conventional phylogenetic tree building methods' and 'phylogeny visualisation'.

Having taken part in this workshop, I feel better equipped to communicate and address some of the problems directly influencing the construction large phylogenies within my PhD. I have also shared specific details relevant to others within my lab group. I am very grateful to the James Rennie Bequest for funding my travel to this workshop.