

Contribution ID: 408

Type: **Poster Presentation**

Can we future-proof phylogenetic consensus trees?

Monday, 9 July 2018 19:45 (15 minutes)

Consensus methods are widely used for combining phylogenetic trees into a single estimate of the evolutionary tree for a group of species. But how robust are these methods to future information? If additional species are added to the original set of trees, will the expanded consensus tree simply be an expansion of the original consensus tree? In this talk I will formalise and answer this question. Joint work with David Bryant (Otago, NZ) and Mike Steel (Canterbury, NZ).

Primary author: Prof. FRANCIS, Andrew (Western Sydney University)

Co-authors: Prof. BRYANT, David (Otago University); Prof. STEEL, Mike (Canterbury University)

Presenter: Prof. FRANCIS, Andrew (Western Sydney University)

Session Classification: Poster Session

Track Classification: Evolutionary biology and Genetics