Event title	Conflict in multi-gene datasets: why it happens and what to do about it - deep coalescence, paralogy and reticulation
Event type	Webinar
Date of event	20/05/2021
Time of event	12 - 1pm AEST
Topic description	Multi-gene datasets used in phylogenetic analyses, such as those produced by the sequence capture or target enrichment used in the Genomics for Australian Plants: Australian Angiosperm Tree of Life project, often show discordance between individual gene trees and between gene and species trees. This webinar will explore three different forms of discordance: deep coalescence, paralogy, and reticulation. In each case, it will consider underlying biological processes, how discordance presents in the data, and what bioinformatic or phylogenetic approaches and tools are available to address these challenges. It will cover Yang and Smith paralogy resolution and general information on options for phylogenetic analysis. This webinar is part of a series of webinars and workshops developed by the Genomics for Australian Plants (GAP) Initiative that focuses on the analysis of target capture sequence data. In addition to two public webinars, the GAP bioinformatics working group is offering training workshops in the use of newly developed and existing scripts in an integrated workflow to participants in the 2021 virtual Australasian Systematic Botany Society Conference.
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/conflict-multigene-datasets
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Phylogenetics http://edamontology.org/topic_3293 Bioinformatics http://edamontology.org/topic_0091 Phylogeny http://edamontology.org/topic_0084 Genomics http://edamontology.org/topic_0622
Contact	Melissa Burke melissa@biocommons.org.au
Audience	Biologists working in the field of phylogenetics.
Prerequisites	Familiarity with basic terms and concepts used in the study of

	phylogenetics is recommended.
Technical requirements	None
Learning outcomes	- Outline common causes of conflict in gene tree data - Describe how deep coalescence, reticulation and parology present in the data - Identify methods for overcoming challenges of deep coalescence, reticulation and paralogy.
Lead Trainer	Dr Alexander Schmidt-Lebuhn, Centre for Australian National Biodiversity Research, CSIRO
Facilitators	Not applicable
Related work	