

Event title	Detection of and phasing of hybrid accessions in a target capture dataset
Event type	Webinar
Date of event	10/06/2021
Time of event	12 - 1pm AEST
Topic description	<p>Hybridisation plays an important role in evolution, leading to the exchange of genes between species and, in some cases, generate new lineages. The use of molecular methods has revealed the frequency and importance of reticulation events is higher than previously thought and this insight continues with the ongoing development of phylogenomic methods that allow novel insights into the role and extent of hybridisation. Hybrids notoriously provide challenges for the reconstruction of evolutionary relationships, as they contain conflicting genetic information from their divergent parental lineages. However, this also provides the opportunity to gain insights into the origin of hybrids (including autopolyploids).</p> <p>This webinar explores some of the challenges and opportunities that occur when hybrids are included in a target capture sequence dataset. In particular, it describes the impact of hybrid accessions on sequence assembly and phylogenetic analysis and further explores how the information of the conflicting phylogenetic signal can be used to detect and resolve hybrid accessions. The webinar will showcase a novel bioinformatic workflow, HybPhaser, that can be used to detect and phase hybrids in target capture datasets and will provide the theoretical background and concepts behind the workflow.</p> <p>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.</p>
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/hybphaser
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	<ul style="list-style-type: none"> - Outline the challenges of including hybrids in phylogenetic analyses - Outline the HybPhaser workflow
Lead Trainer	Dr Lars Nauheimer, Australian Tropical Herbarium
Facilitators	Not applicable
Related work	HybPhaser: a workflow for the detection and phasing of hybrids in target capture datasets https://www.biorxiv.org/content/10.1101/2020.10.27.354589v2