Event title	Getting started with whole genome mapping and variant calling on the command line
Event type	Webinar
Date of event	24/08/2022
Time of event	12pm AEST
Topic description	Life scientists are increasingly using whole genome sequencing (WGS) to ask and answer research questions across the tree of life. Before any of this work can be done, there is the essential but challenging task of processing raw sequencing data. Processing WGS data is a computationally challenging, multi-step process used to create a map of an individual's genome and identify genetic variant sites. The tools you use in this process and overall workflow design can look very different for different researchers, it all depends on your dataset and the research questions you're asking. Luckily, there are lots of existing WGS processing tools and pipelines out there, but knowing where to start and what your specific needs are is hard work, no matter how experienced you are. In this webinar we will walk through the essential steps and considerations for researchers who are running and building reproducible WGS mapping and variant calling pipelines at the command line interface. We will discuss how to choose and evaluate a pipeline that is right for your dataset and research questions, and how to get access to the compute resources you need.
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/wgs-command-line

Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Genome mapping Variant calling http://edamontology.org/operation_3227 Mapping http://edamontology.org/operation_2429 Workflows http://edamontology.org/topic_0769 Bioinformatics http://edamontology.org/topic_0091
Contact	Melissa Burke (melissa@biocommons.org.au)
Audience	This webinar is intended for life scientists who are using and building whole genome sequencing mapping and variant calling pipelines.
Prerequisites	Some familiarity with the concepts of whole genome sequencing is recommended.
Technical requirements	None
Learning outcomes	• Outline the steps in genome mapping and variant calling workflows • Outline how implementation of workflows can vary • Describe considerations for choosing the right pipeline • List sources of accessible compute
Speaker	Dr Georgina Samaha, Sydney Informatics Hub, University of Sydney
Related material	Evaluation of Mapping and Germline Variant Calling Pipelines on Australian High-Performance Computing Facilities Report. https://doi.org/10.5281/zenodo.6930813 Where to go when your bioinformatics outgrows your compute

	https://youtu.be/hNTbngSc-W0 High performance bioinformatics: submitting your best NCMAS application https://youtu.be/HeFGjguwS0Y