Event title	Variant interpretation: from the clinic to the lab… and back again
Event type	Webinar
Date of event	07/12/2022
Time of event	1pm AEDT
Topic description	The use of genomic testing is increasing rapidly as the cost of genome sequencing decreases. Many areas of the health workforce are upskilling in genomics to help meet the increased demand. From clinicians learning how to use the right test, for the right patient, at the right time, to medical scientists learning how to interpret and classify variants, and data scientists to learning how to better create and continuously refine the pipelines and software to handle and curate big data. In this webinar, we'll hear from two people working at the coalface of variant interpretation – one in a diagnostic laboratory and the other in a cancer research laboratory. Naomi Baker is Medical Scientist at Victorian Clinical Genetics Services. She helps process hundreds of genomic tests per year to find the variants that cause rare diseases. She'll explain the clinical variant interpretation processes she uses, the pipelines, professions and people involved. Joep Vissers is a Curation Team Leader, at the University of Melbourne Centre for Cancer Research, Department of Clinical Pathology. Joep, who also teaches cancer biology at the University, will describe how he uses variant interpretation in his work at the research/clinical interface, and the shift in mindset required when working with data for these different purposes. Amy Nisselle, Genomics Workforce Lead at Melbourne Genomics, will then briefly outline some of the education programs available in clinical variant interpretation. This webinar is co-presented by Australian BioCommons and Melbourne Genomics
Format description	Webinar presentation followed by a brief question and answer session

Identifier(s)/URL	https://www.biocommons.org.au/events/clinical-variant-interpretation
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Clinical genomics Variant interpretation Professional development Continuing Professional Development Bioinformatics http://edamontology.org/topic_0091 Genomics http://edamontology.org/topic_0622 Variant Calling http://edamontology.org/operation_3227
Contact	training@biocommons.org.au
Audience	This webinar is for anyone interested in how genomics technologies and workflows are used to inform clinical practice. Whether you're wanting to get started in translational research, curating big data in a clinical setting or just curious about careers and opportunities in clinical genomics there is something in this webinar for you.
Prerequisites	None
Technical requirements	None
Learning outcomes	By the end of this webinar you should be able to: ● Provide examples of how variant interpretation is being used in a clinical setting ● Identify opportunities for continuing professional development in the field of variant interpretation and curation.
Speakers	Naomi Baker, Medical Scientist, Victorian Clinical Genetics Services Joep Vissers, Curation Team Leader, The University of Melbourne Centre for Cancer Research, Department of Clinical Pathology Amy Nisselle, Genomics Workforce Lead, Melbourne Genomics
Related material	None