Event title	WEBINAR: High performance bioinformatics: submitting your best NCMAS application
Event type	Webinar
Date of event	20/08/2021
Time of event	12pm AEST
Topic description	Bioinformaticians are increasingly turning to specialised compute infrastructure and efficient, scalable workflows as their research becomes more data intensive. Australian researchers that require extensive compute resources to process large datasets can apply for access to national high performance computing facilities (e.g. Pawsey and NCI) to power their research through the National Computational Merit Allocation Scheme (NCMAS). NCMAS is a competitive, merit-based scheme and requires applicants to carefully consider how the compute infrastructure and workflows will be applied. This webinar provides life science researchers with insights into what makes a strong NCMAS application, with a focus on the technical assessment, and how to design and present effective and efficient bioinformatic workflows for the various national compute facilities. It will be followed by a short Q&A session.
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/ncmas
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Keywords	- Computational Biology http://edamontology.org/topic_3307 - Computer Science http://edamontology.org/topic_3316 - Bioinformatics http://edamontology.org/topic_0091 - High Performance Computing - HPC - NCMAS

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Audience	This webinar is intended for biologists and bioinformaticians who wish to apply for the NCMAS 2022 allocation.
Prerequisites	Familiarity with HPC is recommended.
Technical requirements	None
Learning outcomes	- Determine if NCMAS is right for you - Address technical requirements in the NCMAS application - Outline key technical concepts - Describe strategies used to achieve computationally performant bioinformatics workflows - Describe the landscape and use of HPC as it relates to bioinformatics and NCMAS
Lead Trainer	Dr Tracy Chew, Sydney Informatics Hub Dr Georgina Samaha, Sydney Informatics Hub
Related work	WEBINAR: Where to go when your bioinformatics outgrows your compute https://www.biocommons.org.au/events/compute-resources A recording of this webinar is available on the Australian BioCommons YouTube Channel https://youtu.be/hNTbngSc-W0