

<b>Event title</b>	WEBINAR: Where to go when your bioinformatics outgrows your compute
<b>Event type</b>	Webinar
<b>Date of event</b>	19/08/2021
<b>Time of event</b>	12pm AEST
<b>Topic description</b>	<p>Bioinformatics analyses are often complex, requiring multiple software tools and specialised compute resources. "I don't know what compute resources I will need", "My analysis won't run and I don't know why" and "Just getting it to work" are common pain points for researchers. In this webinar, you will learn how to understand the compute requirements for your bioinformatics workflows. You will also hear about ways of accessing compute that suits your needs as an Australian researcher, including Galaxy Australia, cloud and high-performance computing services offered by the Australian Research Data Commons, the National Compute Infrastructure (NCI) and Pawsey. We also describe bioinformatics and computing support services available to Australian researchers.</p> <p>This webinar was jointly organised with the Sydney Informatics Hub at the University of Sydney.</p>
<b>Format description</b>	Webinar presentation followed by a brief question and answer session
<b>Identifier(s)/URL</b>	<a href="https://www.biocommons.org.au/events/compute-e-resources">https://www.biocommons.org.au/events/compute-e-resources</a>
<b>Licence</b>	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
<b>Keywords</b>	<ul style="list-style-type: none"> <li>● Computational Biology <a href="http://edamontology.org/topic_3307">http://edamontology.org/topic_3307</a></li> <li>● Computer Science <a href="http://edamontology.org/topic_3316">http://edamontology.org/topic_3316</a></li> <li>● Bioinformatics <a href="http://edamontology.org/topic_0091">http://edamontology.org/topic_0091</a></li> <li>● High Performance Computing</li> <li>● HPC</li> <li>● NCI</li> </ul>

	<ul style="list-style-type: none"> <li>• NCMAS</li> <li>• Pawsey Supercomputing Centre</li> <li>• Galaxy Australia</li> <li>• Nectar Research Cloud</li> </ul>
<b>Contact</b>	Melissa Burke (melissa@biocommons.org.au)
<b>Audience</b>	<p>This webinar is intended for Australian biological researchers who wish to understand what computational infrastructure is available outside their institution's compute facilities. Some familiarity with the concepts of high performance computing is recommended. We think you will enjoy this webinar if you have experienced one of the following:</p> <ul style="list-style-type: none"> <li>•Your high performance computing jobs fail because of walltime limits</li> <li>•Not having enough disk to process your data</li> <li>•Feeling intimidated by the compute resources and time required to process large datasets</li> </ul>
<b>Prerequisites</b>	Some familiarity with the concepts of high performance computing is recommended.
<b>Technical requirements</b>	None
<b>Learning outcomes</b>	<ul style="list-style-type: none"> <li>• Identify computing infrastructure available to Australian Researchers</li> <li>• Outline next steps for getting access to compute resources</li> <li>• Identify sources of training and assistance for accessing compute resources</li> </ul>
<b>Speakers</b>	<p>Dr Georgina Samaha, Sydney Informatics Hub  Dr Tracy Chew, Sydney Informatics Hub  Dr Rosemaire Sadsad, Sydney Informatics Hub  Dr Paul Coddington, ARDC  Simon Gladman, Melbourne Bioinformatics  Dr Roger Edberg, NCI  Dr Maciej Cytowski, Pawsey Supercomputing Centre</p>
<b>Realted work</b>	<p>WEBINAR: High performance bioinformatics: submitting your best NCMAS application  <a href="https://www.biocommons.org.au/events/ncmas">https://www.biocommons.org.au/events/ncmas</a></p> <p>A recording of this webinar is available on the Australian BioCommons YouTube Channel  <a href="https://youtu.be/HeFGjquwS0Y">https://youtu.be/HeFGjquwS0Y</a></p>