

Event metadata

Event title	Pro tips for scaling bioinformatics workflows to HPC
Event type	Webinar
Date of event	31/05/2023
Time of event	1pm AEST
Topic description	<p>High Performance Computing (HPC) infrastructures offer the computational scale and efficiency that life scientists need to handle complex biological datasets and multi-step computational workflows. But scaling workflows to HPC from smaller, more familiar computational infrastructures brings with it new jargon, expectations, and processes to learn. To make the most of HPC resources, bioinformatics workflows need to be designed for distributed computing environments and carefully manage varying resource requirements, and data scale related to biology.</p> <p>In this webinar, Dr Georgina Samaha from the Sydney Informatics Hub, Dr Matthew Downton from the National Computational Infrastructure (NCI) and Dr Sarah Beecroft from the Pawsey Supercomputing Research Centre help you navigate the world of HPC for running and developing bioinformatics workflows. They explain when you should take your workflows to HPC and highlight the architectural features you should make the most of to scale your analyses once you're there. You'll hear pro-tips for dealing with common pain points like software installation, optimising for parallel computing and resource management, and will find out how to get access to Australia's National HPC infrastructures at NCI and Pawsey.</p>
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/workflows-hpc
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Bioinformatics http://edamontology.org/topic_0091

	Workflows http://edamontology.org/topic_0769 High Performance Computing
Contact	training@biocommons.org.au
Audience	This webinar is intended for Australian life science researchers who wish to scale their research to HPC infrastructures or improve the computational efficiency of their existing workflows on HPCs.
Prerequisites	None
Technical requirements	None
Learning outcomes	By the end of this webinar you should be able to: <ul style="list-style-type: none"> • Describe when to move to HPC • Outline the basics of HPC architecture • List tips for software installation, managing your project, optimising workflows and managing workflows • List sources of support
Speakers	Dr Georgina Samaha, Senior Bioinformatician, Sydney Informatics Hub, University of Sydney Dr Sarah Beecroft, Life Sciences Applications Specialist, Pawsey Supercomputing Research Centre Dr Matthew Downton, Associate Director - Performance Optimisation, NCI Australia
Related material	None