

Galaxy Australia  Event type Webinar  Date of event 26/10/2022	
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Time of event 1pm AEDT	
Topic description  Have you discovered a brilliant bioinformatics workflow but you're not construction and (re)use of reproducible workflows, whether building workflows scratch, recreating them from published descriptions and/or extracting from Galahistories.  Using an established bioinformatics	vill From
<ul> <li>method, we'll show you how to:</li> <li>Use the workflows creator in Ga Australia</li> <li>Build a workflow based on a published method</li> </ul>	<u>laxy</u>
<ul> <li>Annotate workflows so that you others) can understand them</li> <li>Make workflows finable and cita (important and very easy to do!)</li> </ul>	ble
Format description  Webinar presentation followed by a brie question and answer session	f
Identifier(s)/URL <a href="https://www.biocommons.org.au/events-axy-workflows">https://www.biocommons.org.au/events-axy-workflows</a>	/gal
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Contact	http://edamontology.org/topic_0769 Bioinformatics http://edamontology.org/topic_0091 Galaxy training@biocommons.org.au
Audience	This webinar is for life scientists and bioinformaticians who need to use and recreate reproducible data analysis workflows.
Prerequisites	None
Technical requirements	None
Learning outcomes	<ul> <li>Use the workflows creator in Galaxy Australia</li> <li>Build a workflow based on a published method</li> <li>Annotate workflows so that you (and others) can understand them</li> <li>Make workflows finable and citable (important and very easy to do!)</li> </ul>
Speaker	Dr Gareth Price, Head of Computational Biology, QCIF Bioinformatics Dr Johan Gustafsson, Bioinformatics Engagement Officer, Australian BioCommons
Related material	None