

Event title	WORKSHOP: Make your bioinformatics workflows findable and citable
Event type	Workshop
Date of event	21 March 2023
Time of event	3-5pm AEST
Topic description	Computational workflows are invaluable resources for research communities. They help us standardise common analyses, collaborate with other researchers, and support reproducibility. Bioinformatics workflow developers invest significant time and expertise to create, share, and maintain these resources for the benefit of the wider community and being able to easily find and access workflows is an essential factor in their uptake by the community.  Increasingly, the research community is turning to workflow registries to find and access public workflows that can be applied to their research. Workflow registries support workflow findability and citation by providing a central repository and allowing users to search for and discover them easily.  This workshop will introduce you to workflow registries and support attendees to register their workflows on the popular workflow registry, WorkflowHub. We'll kick off the workshop with an introduction to the concepts underlying workflow findability, how it can benefit workflow developers, and how you can make the most of workflow registries to share your computational workflows with the research community. You will then have the opportunity to register your own workflows in WorkflowHub with support from our trainers.
Format description	This interactive online workshop via Zoom included:
	Part 1: An introduction to the workflow registry WorkflowHub and live demo of workflow registration
	Part 2: An optional bring-your-own-workflow co-working session, where you can get assistance registering your own workflow(s)
	Expert trainers were available to provide support during the workshop.
	A breakdown of timings and topics is provided in the schedule.
	Approximate number of participants = 25
Identifier(s)/URL	https://www.biocommons.org.au/events/findable-workflows
Licence	Materials are shared under a Creative Commons Attribution 4.0



	International agreement unless otherwise stated on the materials
Keywords	Bioinformatics <a href="http://edamontology.org/topic">http://edamontology.org/topic</a> 0091 Analysis <a href="http://edamontology.org/operation_2945">http://edamontology.org/operation_2945</a> Workflows <a href="http://edamontology.org/topic">http://edamontology.org/topic</a> 0769 WorkflowHub Reproducibility Open Science FAIR
Contact	training@biocommons.org.au
Audience	The workshop is designed for anyone who is creating workflows, either via platforms like Galaxy Australia, or via the command line.
Prerequisites	Some knowledge of GitHub will be beneficial, but is not critical.
Technical requirements	Access to the internet, speakers, a webcam, microphone and Zoom.
Learning outcomes	By the end of the workshop you should be able to:  Register with WorkflowHub  Create and join teams and spaces on WorkflowHub  Register workflows manually  Register workflows by importing from a GitHub repository  Maintain your workflows  Understand the workflow metadata that is most useful to maintain  Create a workflow DOI  Cite workflows
Lead Trainers	Dr Johan Gustafsson, Bioinformatics Engagement Officer, Australian BioCommons
Facilitators	Dr Georgina Samaha, Senior Bioinformatician, Sydney Informatics Hub, University of Sydney
Related work	WorkflowHub documentation: <a href="https://about.workflowhub.eu/docs/registering-a-workflow/">https://about.workflowhub.eu/docs/registering-a-workflow/</a>