Australian BioCommons

Event metadata

Event title	WORKSHOP: Hello Nextflow!
Event type	Workshop
Date of event	24 - 25 September 2024
Time of event	2-5pm AEST
Topic description	The rise of big data has made it essential to be able to analyse and perform experiments on large datasets in a portable and reproducible manner. Nextflow is a popular bioinformatics workflow orchestrator that makes it easy to run data-intensive computational pipelines. It enables scalable and reproducible scientific workflows using software containers on any infrastructure. It allows the adaptation of workflows written in most languages and provides the ability to customise and optimise workflows for different computational environments, types and sizes of data. This workshop will put you on the path to writing your own reproducible and scalable scientific workflows using Nextflow. You will learn how to use core Nextflow components to build, run and troubleshoot a scalable multi-step workflow.
Format description	Workshop, online via Zoom over two three hour sessions. Chris Hakkaart and Fred Jaya led the training by introducing key concepts and demonstrating the steps involved in the analysis. Participants then completed code along exercises giving them a chance to apply these skills with support from facilitators. In parallel to the live session, Slack was used to answer questions as they arose, troubleshoot code and share tips and resources. A breakdown of timings and topics is provided in the schedule. Participation was free but subject to application with selection. Applications were reviewed by the organising committee. Number of participants = 43
Identifier(s)/URL	https://www.biocommons.org.au/events/hello-nextflow
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
Contact	training@biocommons.org.au
Audience	This is an intermediate-advanced workshop for people developing reproducible bioinformatics workflows.
Prerequisites	● You must be associated with an Australian organisation for your application to be considered ● Command line / linux experience is essential. The workshop will be conducted in a Unix environment ● Experience developing reproducible workflows (eg. bash, CWL, WDL, or Snakemake)
Technical requirements	Online Platform ● Zoom ● Slack was used to facilitate discussions. Participants required: ● Laptop with VSCode installed ● Access to the internet, speakers, a webcam, microphone and Zoom. Virtual Machines ● Participants were provided with access to virtual machines running on ARDC Nectar Cloud. Packages, workflows and data were preinstalled.
Learning outcomes	By the end of the workshop you should be able to: ● Describe and utilise core Nextflow components sufficient to build a simple multi-step workflow ● Describe next-step concepts such as operations and channels ● Launch a Nextflow workflow locally ● Find and interpret outputs and log files generated by Nextflow ● Troubleshoot basic issues ● Develop a scalable workflow that processes multiple samples and incorporates advanced features ● Assess the effectiveness of a workflow in handling multiple samples in parallel execution.
Lead Trainers	Dr Chris Hakkaart, Developer Advocate, Seqera Labs. Fred Jaya, Senior Bioinformatician (Australian BioCommons), Sydney Informatics Hub, University of Sydney.

	Dr Georgie Samaha - Product Owner of the Australian BioCommons BioCLI Project and Bioinformatics Group Lead at the Sydney Informatics Hub, The University of Sydney.
Facilitators	Dr Ziad Al Bkhetan, Australian BioCommons
Training materials	The materials were developed by the Sydney Informatics Hub, University of Sydney in partnership with Seqera. The workshop was enabled through the Australian BioCommons - BioCLI Platforms Project (NCRIS via Bioplatforms Australia). Training materials webpage: https://sydney-informatics-hub.github.io/hello-nextflow/ Data and documentation: https://github.com/Sydney-Informatics-Hub/hello-nextflow
Related work	These materials build Seqera's Hello Nextflow materials: https://training.nextflow.io/hello_nextflow/