

## Event metadata

<b>Event title</b>	WORKSHOP: Translating workflows into Nextflow with Janis
<b>Event type</b>	Workshop
<b>Date of event</b>	19 June 2023
<b>Time of event</b>	1:00 - 4:30pm AEST
<b>Topic description</b>	<p>Bioinformatics workflows are critical for reproducibly transferring methodologies between research groups and for scaling between computational infrastructures. Research groups currently invest a lot of time and effort in creating and updating workflows; the ability to translate from one workflow language into another can make them easier to share, and maintain with minimal effort. For example, research groups that would like to run an existing Galaxy workflow on HPC, or extend it for their use, might find translating the workflow to Nextflow more suitable for their ongoing use-cases.</p> <p><a href="#">Janis</a> is a framework that provides an abstraction layer for describing workflows, and a tool that can translate workflows between existing languages such as CWL, WDL, Galaxy and Nextflow. Janis aims to translate as much as it can, leaving the user to validate the workflow and make small manual adjustments where direct translations are not possible. Originating from the Portable Pipelines Project between <a href="#">Melbourne Bioinformatics</a>, the <a href="#">Peter MacCallum Cancer Centre</a>, and the <a href="#">Walter and Eliza Hall Institute of Medical Research</a>, this tool is now available for everyone to use.</p> <p>This workshop provides an introduction to Janis and how it can be used to translate Galaxy and CWL based tools and workflows into Nextflow. Using hands-on examples we'll step you through the process and demonstrate how to optimise, troubleshoot and test the translated workflows.</p> <p>This workshop event and accompanying materials were developed by the Melbourne Bioinformatics and the Peter MacCallum Cancer Centre. The workshop was enabled through the Australian BioCommons - Bring Your Own Data Platforms project funded by the Australian Research Data Commons and NCRIS via Bioplatforms Australia.</p>
<b>Format description</b>	<p>Workshop, online via Zoom as outlined in the schedule.</p> <p>Grace led the training by introducing key concepts and demonstrating the steps involved in translating workflows. Participants were invited to code along and try out activities as outlined in the training materials.</p> <p>Questions were answered in Zoom chat in real time.</p> <p>The workshop followed the tutorial linked in the 'Related work' section.</p>

	<p>A breakdown of timings and topics is provided in the schedule.</p> <p>Participation was free but subject to application with selection.</p> <p>Applications were reviewed by the organising committee.</p> <p>Number of participants = 14</p>
<b>Identifier(s)/URL</b>	<a href="https://www.biocommons.org.au/events/janis-workshop">https://www.biocommons.org.au/events/janis-workshop</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>	<p>Bioinformatics <a href="http://edamontology.org/topic_0091">http://edamontology.org/topic_0091</a></p> <p>Analysis <a href="http://edamontology.org/operation_2945">http://edamontology.org/operation_2945</a></p> <p>Workflows <a href="http://edamontology.org/topic_0769">http://edamontology.org/topic_0769</a></p> <p>Nextflow</p> <p>CWL</p> <p>Galaxy</p>
<b>Contact</b>	training@biocommons.org.au
<b>Audience</b>	This workshop is for Australian researchers and bioinformaticians who are using and/or customising workflows.
<b>Prerequisites</b>	<p>The workshop will be conducted in a Unix environment. Command line experience is required. Prior experience with developing, running, and troubleshooting Nextflow workflows is strongly recommended. You may wish to attend our workshop <a href="#">Unlocking nf-core - customising workflows for your research</a> in advance.</p> <p>If you're looking for an introduction to the fundamentals of Nextflow and nf-core you can watch our webinar <a href="#">Portable, reproducible and scalable bioinformatics workflows using Nextflow and Pawsey Nimbus Cloud</a> or recordings of recent <a href="#">nf-core training</a>.</p>
<b>Technical requirements</b>	<ul style="list-style-type: none"> <li>• Zoom chat used to facilitate discussions.</li> <li>• Access to the internet, speakers, a webcam, microphone and Zoom.</li> <li>• Visual Studio Code (VSC)</li> <li>• Nextflow and Remote-SSH VSC extensions (below)</li> <li>• Participants were provided with access to virtual machines running on <a href="#">NCI's Nirin cloud infrastructure</a>.</li> </ul>
<b>Learning outcomes</b>	<p>By the end of the workshop you should be able to:</p> <ul style="list-style-type: none"> <li>• Recognise the main aspects and benefits of workflow translation</li> <li>• Use Janis to translated Galaxy / CWL tools &amp; workflows to Nextflow</li> <li>• Configure Nextflow to run translated tools &amp; workflows</li> </ul>

	<ul style="list-style-type: none"> <li>• Troubleshoot translated Nextflow tools &amp; workflow</li> <li>• Adjust the translated Nextflow tools / workflows &amp; complete missing translations manually</li> </ul>
<b>Lead Trainers</b>	Grace Hall, Software Engineer, Melbourne Bioinformatics
<b>Facilitators</b>	Richard Lapat, Senior Bioinformatics Software Engineer, Peter MacCallum Cancer Centre
<b>Related work</b>	<p>This workshop follows the accompanying training materials:</p> <p><a href="https://www.melbournebioinformatics.org.au/tutorials/tutorials/janis_translate/janis_translate">https://www.melbournebioinformatics.org.au/tutorials/tutorials/janis_translate/janis_translate</a></p>