Title	Getting started with command line bioinformatics
Event type	Webinar
Date of event	22/06/2021
Time of event	12- 1pm AEST
Topic description	Bioinformatics skills are in demand like never before and biologists are stepping up to the challenge of learning to analyse large and ever growing datasets. Learning how to use the command line can open up many options for data analysis but getting started can be a little daunting for those without a background in computer science. Parice Brandies and Carolyn Hogg have recently put together ten simple rules for getting started with command-line bioinformatics to help biologists begin their computational journeys. In this webinar Parice walks you through their hints and tips for getting started with the command line. She covers topics like learning tech speak, evaluating your data and workflows, assessing computational requirements, computing options, the basics of software installation, curating and testing scripts, a bit of bash and keeping good records. The webinar will be followed by a short Q&A session.
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/command-line
Licence	Materials are shared under a Creative Commons Attribution 4.0 International unless otherwise stated on the materials
Keywords	Command line, bioinformatics, bash, data skills Bioinformatics http://edamontology.org/topic_0091 Workflows http://edamontology.org/topic_0769
Contact	Melissa Burke melissa@biocommons.org.au
Audience	Aspiring bioinformaticians and command line users from a variety of biological fields.
Prerequisites	None
Technical requirements	None

Learning outcomes	- Outline aspects of working with command line bioinformatics - Identify additional sources of training and support
Lead Trainer	Parice Brandies, University of Sydney
Facilitators	Not applicable
Related work	Ten simple rules for getting started with command-line bioinformatics https://doi.org/10.1371/journal.pcbi.1008645