



Event title	WEBINAR: Getting started with R
Event type	Webinar
Date of event	16/08/2021
Time of event	12pm AEST
Topic description	<p>Data analysis skills are now central to most biological experiments. While Excel can cover some of your data analysis needs, it is not always the best choice, particularly for large and complex datasets.</p> <p>R is an open-source software and programming language that enables data exploration, statistical analysis visualisation and more. While it is the tool of choice for data analysis, getting started can be a little daunting for those without a background in statistics.</p> <p>In this webinar Saskia Freytag, an R user with over a decade of experience and member of the Bioconductor Community Advisory Board, will walk you through their hints and tips for getting started with R and data analysis. She'll cover topics like R Studio and why you need it, where to get help, basic data manipulation, visualisations and extending R with libraries. The webinar will be followed by a short Q&A session.</p>
Format description	Webinar presentation followed by a brief question and answer session
Identifier(s)/URL	https://www.biocommons.org.au/events/r-intro
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	R statistical software Tidyverse RStudio Analysis http://edamontology.org/operation_2945
Contact	Melissa Burke melissa@biocommons.org.au
Audience	Aspiring data analysts from a variety of biological fields

Prerequisites	None
Technical requirements	None
Learning outcomes	<ul style="list-style-type: none"> • Outline types of applications that R can be used for • List advantages of using R Studio • Outline steps and packages for installing packages, data ingest, data wrangling and visualisation • Identify sources of help and support for using R
Lead Trainer	Dr Saskia Freytag, Harry Perkins Institute of Medical Research
Facilitators	Not applicable
Related work	