

<b>Event title</b>	WORKSHOP: R: fundamental skills for biologists
<b>Event type</b>	Workshop
<b>Date of event</b>	1, 8, 15 & 22 June 2022
<b>Time of event</b>	2-5pm AEST
<b>Topic description</b>	<p>Biologists need data analysis skills to be able to interpret, visualise and communicate their research results. While Excel can cover some data analysis needs, there is a better choice, particularly for large and complex datasets.</p> <p>R is a free, open-source software and programming language that enables data exploration, statistical analysis, visualisation and more. The large variety of R packages available for analysing biological data make it a robust and flexible option for data of all shapes and sizes.</p> <p>Getting started can be a little daunting for those without a background in statistics and programming. In this workshop we will equip you with the foundations for getting the most out of R and RStudio, an interactive way of structuring and keeping track of your work in R. Using biological data from a model of influenza infection, you will learn how to efficiently and reproducibly organise, read, wrangle, analyse, visualise and generate reports from your data in R.</p> <p>Topics covered in this workshop include:</p> <ul style="list-style-type: none"> <li>• Spreadsheets, organising data and first steps with R</li> <li>• Manipulating and analysing data with dplyr</li> <li>• Data visualisation</li> <li>• Summarized experiments and getting started with Bioconductor</li> </ul> <p>This workshop is presented by the <a href="#">Australian BioCommons</a> and Saskia Freytag from WEHI with the assistance of a network of facilitators from the national <a href="#">Bioinformatics Training Cooperative</a>.</p>
<b>Format description</b>	<p>Workshop, online via Zoom over a series of four three-hour sessions.</p> <p>Saskia Freytag, Brendan Ansell, Adele Barugahare and Maria Doyle led the training by introducing key concepts and demonstrating the steps involved in the analysis. Participants then moved into breakout rooms where they had the chance to apply these skills with support from facilitators. Participants were assigned homework between sessions and supported via Slack.</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>
<b>Identifier(s)/URL</b>	<a href="https://www.biocommons.org.au/events/fundamental-r">https://www.biocommons.org.au/events/fundamental-r</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>Statistics and probability <a href="http://edamontology.org/topic_2269">http://edamontology.org/topic_2269</a></p> <p>Data visualisation <a href="http://edamontology.org/topic_0092">http://edamontology.org/topic_0092</a></p> <p>R software</p> <p>RStudio</p>
<b>Contact</b>	Melissa Burke (melissa@biocommons.org.au)
<b>Audience</b>	<p>This workshop is for Australian life science researchers who are using, or intend to use, R to analyse their data.</p> <p>This workshop is suitable for absolute beginners or those who wish to go back to basics to ensure they are using R and RStudio effectively.</p>
<b>Prerequisites</b>	No prior knowledge of R is required.
<b>Technical requirements</b>	<ul style="list-style-type: none"> <li>• Slack was used to facilitate discussions.</li> <li>• Access to the internet, speakers, a webcam, microphone and Zoom.</li> <li>• Participants were provided with access to virtual machines running RStudio via a Nectar Cloud instance. Packages and data were preinstalled.</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>• Organise your data for effective use</li> <li>• Use RStudio to structure your work in R and run R packages</li> <li>• Make use of objects, vectors and functions in R</li> <li>• Load, inspect and manipulate data in R</li> <li>• Use dplyr and tidyr and packages to manipulate and reshape data</li> <li>• Produce and customise scatter plots, box plots, line plots, etc. using ggplot</li> <li>• Combine data spread across multiple tables</li> <li>• Use the SummarizedExperiment package to store and handle omics data</li> <li>• Have some familiarity with Bioconductor</li> <li>• Identify sources of help and support from the R community</li> </ul>

<b>Lead Trainers</b>	Saskia Freytag, WEHI Adele Barugahare, Monash Bioinformatics Platform Maria Doyle, Peter MacCallum Cancer Centre Brendan Ansell, WEHI
<b>Facilitators</b>	Akriti Varshney, Monash University Caitlin Bourke, WEHI Cara Conradsen, QCIF Chol-Hee Jung, Melbourne Bioinformatics Claudia Sandoval, Australian BioCommons Dineika Chandrananda, Peter MacCallum Cancer Centre Eden Zhang, Sydney Informatics Hub, University of Sydney Fernando Rosello, University of Melbourne Giulia Iacono, Monash University Ilariya Tarasova, WEHI Jessica Chung, Melbourne Bioinformatics Joel Moffet, WEHI Johan Gustafsson, Australian BioCommons Ke Ding, Australian National University Kirsten Feher, WEHI Laura Perlaza-Jimenez, Monash University Mark Crowe, QCIF Mengyao Ma, University of Melbourne Nitika Kandhari, Monash Bioinformatics Platform Sarah Williams, QCIF Tiffanie Nelson, Australian BioCommons Veronika Schreiber, QCIF William Pinzon Perez, QCIF
<b>Related work</b>	This workshop follows the tutorial 'Introduction to data analysis with R and Bioconductor'  <a href="https://saskiafreytag.github.io/biocommons-r-intro/">https://saskiafreytag.github.io/biocommons-r-intro/</a>  This is derived from material produced as part of The Carpentries Incubator project  <a href="https://carpentries-incubator.github.io/bioc-intro/">https://carpentries-incubator.github.io/bioc-intro/</a>