

## Event metadata

<b>Event title</b>	Making sense of gene and protein lists with functional enrichment analysis
<b>Event type</b>	Workshop
<b>Date of event</b>	20/11/2024 - 21/11/2024
<b>Time of event</b>	1 - 4 pm AEDT
<b>Topic description</b>	<p>Omics experiments often generate long lists of genes or proteins. Functional enrichment analysis identifies biological trends in the data by assessing these lists against gene ontology and pathway information. This can help interpret the experimental results in the context of larger biological systems.</p> <p>This workshop continues from our introductory webinar and provides a practical introduction to functional enrichment analysis. Using example data you will get hands-on with some of the most commonly used databases and tools for over representation (ORA) and gene set enrichment analysis (GSEA) and for identifying enriched biological functions in a list of genes or proteins. We'll focus on tools available online and in R.</p>
<b>Format description</b>	<p>Workshop, online via Zoom over two 3 hours sessions.</p> <p>Hossein Valipour Kahrood and Cali Willet led the training by introducing key concepts and live coding sessions where participants had a chance to apply their skills with support from facilitators.</p> <p>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 timing 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 = 32.</p>
<b>Identifier(s)/URL</b>	<a href="https://www.biocommons.org.au/events/funct-enrich-workshop">https://www.biocommons.org.au/events/funct-enrich-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>Enrichment analysis <a href="http://edamontology.org/operation_3501">http://edamontology.org/operation_3501</a></p>
<b>Contact</b>	training@biocommons.org.au

<b>Audience</b>	This workshop is for Australian researchers and bioinformaticians working with omics experiments (e.g. RNA-Seq, protein expression) that generate gene or protein lists.
<b>Prerequisites</b>	<ul style="list-style-type: none"> <li>• You must be associated with an Australian organisation for your application to be considered.</li> <li>• (Recommended) Basics of R/RStudio. We'll start at a beginner level but you will get more from the workshop if you know the basics of setting up directories, running commands, reading in and outputting files. If you need a refresher on R/RStudio try the <a href="#">Introduction to R and RStudio</a> section of this online tutorial.</li> <li>• (Recommended) Watch the <a href="#">introductory webinar</a> for a primer on how functional enrichment analysis methods work.</li> </ul>
<b>Technical requirements</b>	<p>Online Platform</p> <ul style="list-style-type: none"> <li>• Zoom</li> <li>• Slack was used to facilitate discussions.</li> </ul> <p>Participants required</p> <ul style="list-style-type: none"> <li>• Laptop</li> <li>• Access to the internet, speakers, a webcam, microphone and Zoom.</li> </ul> <p>Virtual Machines</p> <ul style="list-style-type: none"> <li>• Participants were provided with access to virtual machines running on ARDC Nectar Cloud. Packages 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>• Explain the purpose of functional enrichment analysis and its role in biological experiments</li> <li>• Identify the key challenges and factors to consider when applying functional enrichment analysis in biological research</li> <li>• Describe the statistical methods underpinning enrichment analysis, including the use of p-values, false discovery rates (FDR), and multiple testing corrections</li> <li>• Apply functional enrichment methods/tools (e.g. over representation analysis, GSEA methods) in the browser and with R to:             <ul style="list-style-type: none"> <li>○ Get a systems perspective of gene functions</li> <li>○ Discover pathways that are enriched in a gene list</li> </ul> </li> <li>• Visualise and interpret the results of enrichment analysis to gain biological insights</li> <li>• Use different types of functional databases - GO, KEGG and Reactome</li> </ul>



<b>Lead Trainer</b>	Dr Hossein Valipour Kahrood, Monash Genomics and Bioinformatics Platform Dr Cali Willet, Sydney Informatics Hub
<b>Facilitators</b>	Dr Georgina Samaha, Australian BioCommons Dr Laura Perlaza-Jimenez, Monash Genomics and Bioinformatics Platform
<b>Related work</b>	WEBINAR: Making sense of gene and protein lists with functional enrichment analysis (DOI: 10.5281/zenodo.14032116)