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| **Event title** | Making sense of phosphoproteomics data with Phosphomatics |
| **Event type** | Webinar |
| **Date of event** | 02/06/2021 |
| **Time of event** | 12 - 1pm AEST |
| **Topic description** | Mass spectrometry-based phosphoproteomics is one of the most powerful tools available for investigating the detailed molecular events that occur in response to cellular stimuli. Experiments can routinely detect and quantify thousands of phosphorylated peptides, and interpreting this data, and extracting biological meaning, remains challenging.<br><br>This webinar provides an overview of the phosphoproteomics data analysis website, Phosphomatics, that incorporates a suite of tools and resources for statistical and functional analysis that aim to simplify the process of extracting meaningful insights from experimental results.<br><br>Phosphomatics can natively import search and quantitation results from major search engines including MaxQuant and Proteome Discoverer and employs intuitive 'wizards' to guide users through data preprocessing routines such as filtering, normalization and transformation. A graphical platform of interactive univariate and multivariate analysis features is provided that allow subgroups of the uploaded data containing phosphosites of statistical interest to be created and interrogated through further functional analysis. A range of databases have been integrated that, for example, provide ligand and inhibitor information for key proteins or highlight key modification sites known to be involved in functional state regulation. At each step, published literature is natively incorporated along with a 'bibliography builder' that allows references of interest to be assembled and exported in various formats. Taken together, these expanded features aim to provide a 'one-stop-shop' for phosphoproteomics data analysis.<br><br>The webinar is followed by a short Q&A session. |

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| **Format description** | Webinar presentation followed by a brief question and answer session |
| **Identifier(s)/URL** | https://www.biocommons.org.au/events/phosphomatics |
| **Licence** | Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials |
| **Keywords** | Phosphoproteomics<br>Proteomics http://edamontology.org/topic_0121<br>Mass spectrometry data http://edamontology.org/data_2536 |
| **Contact** | Melissa Burke melissa@biocommons.org.au |
| **Audience** | Biologists and bioinformaticians with an interest in phosphoproteomics data. |
| **Prerequisites** | None |
| **Technical requirements** | None |
| **Learning outcomes** | • Describe the basic concepts of phosphoproteomics<br>• Outline the principles of mass spectrometry as applied to phosphoproteomics<br>• List features of Phosphomatics and how it can be used to analyse phosphoproteomics data |
| **Lead Trainer** | Dr Michael Leeming, Research Fellow, Mass Spectrometry and Proteomics Facility, University of Melbourne |
| **Facilitators** | Not applicable |
| **Related work** | Phosphomatics https://phosphomatics.com/ |