

Event metadata

Event title	Introduction to Machine Learning in R - from data to knowledge
Event type	Workshop
Date of event	09/12/2024
Time of event	1 - 5 pm AEDT
Topic description	With the rise in high-throughput sequencing technologies, the volume of omics data has grown exponentially. A major issue is to mine useful knowledge from these heterogeneous collections of data. The analysis of complex high-volume data is not trivial and classical tools cannot be used to explore their full potential. Machine Learning (ML), a discipline in which computers perform automated learning without being programmed explicitly and assist humans to make sense of large and complex data sets, can thus be very useful in mining large omics datasets to uncover new insights that can advance the field of bioinformatics.
	taxonomy and the applications of common ML algorithms to health data. The workshop will cover the foundational concepts and common methods being used to analyse omics data sets by providing a practical context through the use of basic but widely used R libraries. Participants will acquire an understanding of the standard ML processes, as well as the practical skills in applying them on familiar problems and publicly available real-world data sets.
Format description	 Workshop, online via Zoom over one 4 hours session. Fotis Psomopoulos led the training by introducing key concepts and live coding sessions where participants had a chance to apply their skills with support from facilitators. 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 <u>schedule</u>. Participation was free but subject to application with selection. Applications were reviewed by the organising committee.
	Number of participants = 26.
Identifier(s)/URL	https://www.biocommons.org.au/events/mlr2024
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Keywords	Bioinformatics http://edamontology.org/topic_0091 Machine Learning http://edamontology.org/topic_0091
Contact	training@biocommons.org.au
Audience	This workshop is for Australian researchers who are or will apply ML to the analysis of omics data as part of their projects. It is suitable for beginners in ML.
Prerequisites	 You must be associated with an Australian organisation for your application to be considered No previous knowledge of ML is required or expected (please note, that this will be an introductory course to ML) Familiarity with the R programming language
Technical requirements	 Online Platform Zoom Slack was used to facilitate discussions.
	 Participants required Laptop Access to the internet, speakers, a webcam, microphone and Zoom.
	 Virtual Machines Participants were provided with access to virtual machines running on ARDC Nectar Cloud. Packages were preinstalled.
Learning outcomes	 By the end of the workshop you should be able to: Understand key ML concepts, common algorithms and terminology Understand the importance of ML in analysing complex, high-volume health-related data Use R packages to implement an ML workflow on real-world dataset, from data preparation to model application and evaluation
Lead Trainer	Dr Fotis Psomopoulos, Senior Researcher, Institute of Applied Biosciences (INAB), Center for Research and Technology Hellas (CERTH)
Facilitators	Dr Giorgia Mori, Australian BioCommons Dr Eden Zhang, Sydney Informatics Hub (SIH) Dr Erin Graham, Queensland Cyber Infrastructure Foundation (QCIF)
Related work	