



Australian
BioCommons



Event metadata

Event title	WORKSHOP: Genetic Outlier Analysis
Event type	Workshop
Date of events	Online: 27 - 28 February 2024 Melbourne: 10 -11 April 2024 Sydney: 4 - 5 July 2024
Topic description	<p>There are many interesting patterns that you can extract from genetic variant data. This can include patterns of linkage, balancing selection, or even inbreeding signals. One of the most common approaches is to find sites on the genome that are under selection.</p> <p>This workshop introduces the basics of genetic selection analysis. It will step you through the process of identifying signals of selection using your own data (or an example genomic dataset) using the outlier analysis method.</p>
Format description	<p>Three versions of the same workshop were delivered between February and July 2024.</p> <p>Online version: Via Zoom over two three and a half hour sessions.</p> <p>Melbourne/Sydney versions: In person over two 5 and half hour sessions (including breaks)</p> <p>Dr Katarina Stuart led the training by introducing key concepts and demonstrating the steps involved in the analysis. Participants then completed code along exercises giving them a chance to apply these skills with support from facilitators.</p> <p>Facilitators provided assistance troubleshooting code and answering questions. For the online version of the workshop this support was provided via Slack in parallel to the main session.</p> <p>The content and exercises covered in the workshop are detailed in the materials developed by Dr Stuart and linked in the 'Materials' section.</p> <p>A breakdown of timings and topics is provided in the schedules.</p> <p>Participation was free but subject to application with selection.</p> <p>Applications were reviewed by the organising committee.</p>
Identifier(s)/URL	Online workshop: https://www.biocommons.org.au/events/genetic-outlier



Australian
BioCommons



	Melbourne workshop: https://www.biocommons.org.au/events/genetic-outlier-apr24 Sydney workshop: https://www.biocommons.org.au/events/genetic-outlier-jul24
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials
Keywords	Bioinformatics http://edamontology.org/topic_0091 Analysis http://edamontology.org/operation_2945 Genetics http://edamontology.org/topic_3053 Genetic Outlier Analysis
Contact	training@biocommons.org.au
Audience	These workshops were for researchers associated with an Australian organisation and/or members of the Genetics Society of AustralAsia who use genetic selection analysis as part of their projects.
Prerequisites	<p>This workshop requires:</p> <ul style="list-style-type: none">• (Preferred) Your own data variant files in VCF format and a tab delimited sample metadata file containing individual ID and other important info for your samples.• Some familiarity with biological concepts, including the concept of selection.• Basic command line (bash) knowledge. You must know how to navigate the directory structure and copy files between the computers. If you need a refresher on Unix/Linux try this online tutorial.• Basic knowledge of R. You must know how to set up directories, run commands, reading in and outputting files. If you need a refresher on R try the Introduction to R and RStudio section of this online tutorial.
Technical requirements	<p>All workshops</p> <ul style="list-style-type: none">• Laptop with access to the internet• Participants were provided with access to virtual machines running on Pawsey Nimbus infrastructure. Packages, workflows and data were preinstalled <p>Online workshop</p> <ul style="list-style-type: none">• The workshop was delivered using Zoom• Slack was used to facilitate discussions and troubleshooting of code



Australian
BioCommons



Learning outcomes	<p>By the end of the workshop you should be able to:</p> <ul style="list-style-type: none">• Download example genomic data (or prepare your own)• Use the PCAdapt tool to identify outlier loci within a genome.• Use VCFtools to identify outlier SNPs in pairwise population comparisons.• Use Bayescan and Baypass to identify outlier SNPs based on allele frequencies across multiple populations.• Use Baypass to identify SNPs that are related to phenotype (GWAS)• Compare the results of the different methods and discuss the results.
Lead Trainers	Dr Katarina Stuart, Research Fellow, University of Auckland.
Facilitators	<p>Online workshop:</p> <p>Adele Barugahare, Monash Genomics and Bioinformatics Platform Dr Georgina Samaha, Sydney Informatics Hub, University of Sydney Dr Ching-Yu Lu, Sydney Informatics Hub, University of Sydney Soleille Miller, University of NSW</p> <p>Melbourne workshop: Adele Barugahare, Monash Genomics and Bioinformatics Platform</p> <p>Sydney Workshop: Soleille Miller, University of NSW Dr Nandan Deshpande, Sydney Informatics Hub, University of Sydney</p>
Infrastructure support	Audrey Stott, Pawsey Supercomputing Centre Dr Georgina Samaha, Sydney Informatics Hub, University of Sydney
Workshop administration	Dr Melissa Burke, Australian BioCommons Dr Christina Hall, Australian BioCommons
Materials	<p>Included in this Zenodo record:</p> <p>Schedules describing the timing of sessions for the in person and online events</p> <p>Shared elsewhere:</p> <p>These workshops followed the materials developed by Dr Katarina Stuart https://github.com/katarinastuart/Ev1_SelectionMetaAnalysis</p>