



Australian  
**BioCommons**



# Genetic outlier analysis

In person events April and July 2024

## Schedule

This schedule gives you an idea of the topics to be covered and how long we will spend on them. Timings are flexible and subject to change.

## Day 1

Time (AEDT)	Activity
10:00	Welcome and housekeeping
10:10	Introductory slides
10:40	Log into Nimbus
10:55	<b>Download data</b> 1. Define working directory 2. Download data 3. Convert data formats 4. Install PCA 5. Load in data 6. Produce K plot
12:30	<b>Lunch</b>
13:00	<b>PCAdapt</b> 1. Investigate axis projections 2. Investigate Manhattan and Q-Qplot. 3. Plot and adjust the p-values. 4. Mapping Outliers: PCAdapt 5. Subset metadata file 6. SNP-based Fst comparison. Lemon and War 7. Sliding windows
14:45	<b>Break</b>
15:00	<b>VCFtools &amp; Bayescan</b> 1. Plot the Fst across the chromosome. 2. Generate a list of outlier SNP IDs 3. Bayescan conversion 4. Run Bayescan  Note: Stop point is flexible depending on where discussions lead. We will pick up where we left off on day 2.

Time (AEDT)	Activity
10:00	Welcome and housekeeping
10:10	Introductory slides
16:20	Questions and wrap up of day 1
<b>16:30</b>	End of session

## Day 2

Time (AEST)	Activity
10:00	Welcome and Housekeeping
10:05	<b>Log into Nimbus</b>
10:15	<b>Bayescan &amp; Baypass</b> 1. Identify bayescan outliers 2. Check convergence 3. Map outliers 1. PLINK File + making baypass file type
12:30	<b>Lunch</b>
13:00	<b>Baypass continued</b> 2. Run Baypass and generate simulated data 3. XtX statistic threshold 4. Filtering/identifying SNPs and plotting 5. Generate a list of phenotype associated SNPs
14:30	<b>Break</b>
14:45	<b>Baypass (continued)</b>
16:15	<b>Compile results</b> Group discussions
16:20	Wrap up and feedback
<b>16:30</b>	End of workshop