



Australian  
**BioCommons**



# Genetic outlier analysis

## Online event

### 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	Presenter
10:55	Zoom opened for participants	
11:00	Welcome and housekeeping	Melissa
11:10	Introductory slides	Kat
11:40	Log into Nimbus	Kat
11:55	Download data  1. Define working directory 2. Download data 3. Convert data formats 4. Install PCA 5. Load in data 6. Produce K plot	Kat
12:25	Break	
12:55	PCAdapt  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	Kat
14:40	Break	

14:55	VCFtools & Bayescan  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.	Kat
15:45	Questions	All
15:55	Wrap up and reminders	Melissa
16:00	End of session	

## Day 2

Time (AEDT)	Activity	Presenter
10:55	Zoom opened for participants	
11:00	Welcome and Housekeeping	Melissa
11:05	Log into Nimbus	Kat
11:15	Bayescan & Baypass  1. Identify bayescan outliers 2. Check convergence 3. Map outliers 1. PLINK File + making baypass file type	Kat
12:15	Break	
12:45	Baypass continued  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	Kat
14:30	Break	
14:45	Baypass (continued)	Kat
15:45	Compile results Group discussions	Kat
15:55	Wrap up and feedback	Melissa
16:00	End of workshop	