

# Acknowledgement of Country

The University of Queensland (UQ) acknowledges the Traditional Owners and their custodianship of the lands on which we meet.

We pay our respects to their Ancestors and their descendants, who continue cultural and spiritual connections to Country.

We recognise their valuable contributions to Australian and global society.



# General Information:

- We are currently located in Building 69



Emergency evacuation point

- Food court and bathrooms are located in Building 63
- If you are experiencing cold/flu symptoms or have had COVID in the last 7 days please ensure you are wearing a mask for the duration of the module



# Data Agreement

To maximize your learning experience, we will be working with genuine human genetic data, during this module.

Access to this data requires agreement to the following in to comply with human genetic data ethics regulations

Please email [pctgadmin@imb.uq.edu.au](mailto:pctgadmin@imb.uq.edu.au) with your name and the below statement to confirm that you agree with the following:

“I agree that access to data is provided for educational purposes only and that I will not make any copy of the data outside the provided computing accounts.”

# Desktop Access

For non-UQ attendees, you are provided with a registration instruction for a guest account (A4 paper).

After you have completed the online registration, use the provided Username and the Password that you set to log into the desktop.



# Cluster Access

- You have all been provided with login details to computing resources needed for the practical component
- An SSH terminal is needed to connect to the computing:
  - Windows: Install PuTTY
    - Hostname: as provided (203.101.228.xxx)
    - User: as provided
    - Check Connection > SSH > X11 > Enable X11 forwarding
  - Mac/Linux: Use the terminal
    - `ssh -X <user>@203.101.228.xxx`
- If interactive R plotting does not work on your machine, you can generate plot on the server and then download
  - Windows: use WinSCP -> enter login information
  - Or use Command Prompt -> `sftp <user>@203.101.228.xxx`
    - `get xxx.pdf` and the file will be in your user directory

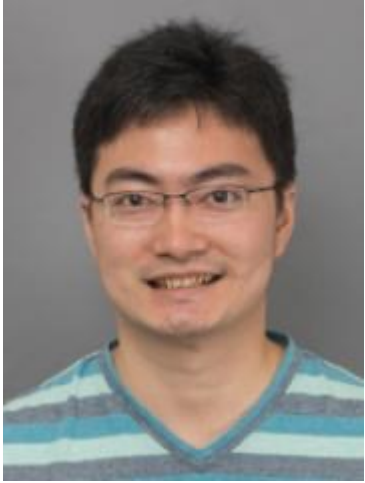
# Module 4 Quantitative Genetics

Room 304, Building 69

**Slides and Practical notes:**

<https://cnsgenomics.com/data/teaching/GNGWS22/model4/>

## Teaching Team



**Jian Zeng**



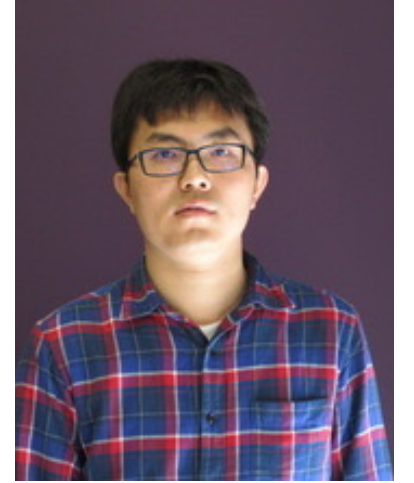
**Loic Yengo**



**Valentin Hivert**



**Kathryn Kemper**



**Huanwei Wang**

## Guest Lecturers



**Prof. Naomi Wray**



**Prof. Ben Hayes**



Day 1 (June 23 <sup>rd</sup> Thursday): Polygenic Prediction		
9-9:30am	<b>Lecture 1: Introduction to polygenic prediction.</b> We will introduce the concept, applications, and perspective of polygenic prediction for complex traits and common diseases.	Naomi Wray (Guest Lecturer)
9:30-9:50am	<i>Practical 1: Calculation of polygenic scores using C+PT.</i> Software: R and PLINK.	Jian Zeng
9:50-10am	Break	
10-10:30am	<b>Lecture 2: Prediction accuracy and pitfalls.</b> We will introduce the criteria and methods to assess the prediction accuracy in quantitative and disease traits, and discuss factors affecting prediction accuracy as well as traps and pitfalls when conducting prediction analysis.	Huanwei Wang
10:30-10:50am	<i>Practical 2: Calculation of prediction accuracy and demonstration for Winner's curse in in-sample prediction.</i> Software: R.	Huanwei Wang
10:50-11am	Break	
11-11:30am	<b>Lecture 3: Best linear unbiased prediction (BLUP).</b> We will introduce mixed linear model, genomic relationship matrix (GRM), and two equivalent models for BLUP prediction.	Jian Zeng
11:30-11:50am	<i>Practical 3: Calculation of GRM and solving BLUP equations.</i> Software: R and GCTA.	Jian Zeng
11:50am-12pm	<b>Questions and discussions</b>	
12-1pm	<b>Lunch break</b>	
1-1:30pm	<b>Lecture 4: Bayesian methods for genomic prediction (30min).</b> We will introduce BayesA, B, C and R methods for genomic prediction and the properties of these methods.	Ben Hayes (Guest Lecturer)
1:30-1:50pm	<i>Practical 4: Application of Bayesian methods to simulated data.</i> Software: R and GCTB.	Jian Zeng
1:50-2pm	Break	
2-2:30pm	<b>Lecture 5: Summary-data-based methods for polygenic prediction.</b> We will introduce the variations of BLUP and Bayesian methods that only require GWAS summary statistics.	Jian Zeng
2:30-2:50pm	<i>Practical 5: Application of summary-data-based methods to simulated data.</i> Software: R, GCTA and GCTB.	Jian Zeng
2:50-3pm	Break	
3-3:30pm	<b>Lecture 6: Additional sources of information to improve prediction within and between ancestries.</b> We will introduce methods that integrate genome variations with other sources of information, including family history, biomarkers or covariates, and functional genomic annotations, and discuss challenges in trans-ancestry prediction.	Loic Yengo
3:30-3:50pm	<i>Practical 6.</i> Software: R and PLINK	Loic Yengo
3:50-4pm	<b>Questions and discussions</b>	

Day 2 (June 24 <sup>th</sup> Friday): Heritability Estimation		
9-9:30am	<b>Lecture 7: Methods for variance estimation.</b> We will introduce two classes of methods for variance estimation, ANOVA and REML, and discuss their pros and cons.	Jian Zeng
9:30-9:50am	<i>Practical 7: Comparison between ANOVA and REML estimations using a sire model.</i> Software: R.	Jian Zeng
9:50-10am	Break	
10-10:30am	<b>Lecture 8: Heritability and GREML.</b> We will introduce the concept of pedigree-based heritability and SNP-based heritability, discuss the difference between them, and the commonly used methods for estimation, including Haseman–Elston regression and Genomic REML (GREML).	Kathryn Kemper
10:30-10:50am	<i>Practical 8: Estimation of heritability using HE regression and GREML.</i> Software: R and GCTA.	Kathryn Kemper
10:50-11am	Break	
11-11:30am	<b>Lecture 9: Heritability estimation for diseases.</b> We will introduce the liability threshold model for conceptualising and estimating the heritability of diseases.	Loic Yengo
11:30-11:50am	<i>Practical 9: Estimation of heritability at liability scale.</i> Software: R.	Loic Yengo
11:50am-12pm	<b>Questions and discussions</b>	
12-1pm	<b>Lunch break</b>	
1-1:25pm	<b>Lecture 10: Non-additive genetic variance and genetic correlation between traits.</b> We will introduce the concept of non-additive genetic variance and genetic correlation between traits, and methods to estimate the variance components and genetic correlation.	Valentin Hivert
1:25-1:45pm	<i>Practical 10: Estimation of dominance variance component and genetic correlation.</i> Software: R and GCTA.	Valentin Hivert
1:45-1:50pm	Break	
1:50-2:15pm	<b>Lecture 11: Heritability estimation using summary-data-based methods and genome partitioning.</b> We will introduce LD score regression, a family of methods that only requires GWAS summary statistics for heritability estimation, genome partitioning and genetic correlation estimation.	Loic Yengo
2:15-2:35pm	<i>Practical 11: Estimation of heritability using LD score regression.</i> Software: R and ldsc.	Loic Yengo
2:35-2:40pm	Break	
2:40-3:05pm	<b>Lecture 12: Evolutionary forces influencing genetic variance.</b> We will introduce key concepts in population genetics about quantifying genetic variance within and between populations, including Fst, Qst, impact of genetic drift and natural selection on genetic variance.	Valentin Hivert
3:05-3:25pm	<i>Practical 12.</i> Software: R and slim.	Valentin Hivert
3:25-3:30pm	Break	
3:30-3:45pm	<b>Lightning talks about our research</b>	3min/speaker
3:45-4pm	<b>Summary and questions</b>	