**UQ IMB Genetics and Genomics Winter School 2024**

**Timetable for Module 6 - Systems Genomics and Pharmacogenomics**

Though we have identified hundreds of variants associated with many diseases through genome-wide association studies (GWAS), identifying the causal variants, genes and drug candidates is a major bottleneck. In this module we will take you through some of the downstream analytical approaches after conducting a GWAS that can be used to prioritise variants, genes and drug candidates for further wet-lab investigation.

**If you are not familiar with GWAS, we recommend attending Module 1 before attending this Module.**

27th June 2024: This session will cover expression quantitative trait loci (eQTL) analysis for prioritising genes within GWAS regions, as well as using an online tool FUMA to extract biologically meaningful information from GWAS results.

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| 1 – 1.50pm | Lecture: Making sense of GWAS signals |
| 1.50 - 2pm | Short break |
| 2 – 2.45pm | **Practical:** eQTL mapping and introduction to the GTEx resource |
| 2.45 - 3pm | Coffee break |
| 3 - 3.30pm | **Lecture:** Downstream GWAS analysis (integration of omic data,  gene-based test, tissue and functional enrichment analysis) |
| 3.30 - 4pm | **Practical:** Using FUMA for functional annotation of GWAS |

28th June 2024: In this session we will go through analyses that can be used to identify drug repurposing candidates from GWAS summary data. We will cover tools such as SMR and Connectivity Map.

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| 9 – 9.50am | Lecture: Human genomics for drug target validation and safety evaluation |
| 9.50 - 10am | Short break |
| 10 – 10.45am | **Lecture:** Summary-based Mendelian randomisation analysis |
| 10.45 -11am | Coffee break |
| 11 - 12pm | **Practical:** Summary-based Mendelian randomisation analysis |
| 12 - 1pm | Lunch |
| 1 - 2pm | **Lecture:** Introduction to Connectivity Map |
| 2 - 2.10pm | Short break |
| 2.10 - 2.45pm | **Lecture:** How to query Connectivity Map |
| 2.45 - 3pm | Coffee break |
| 3 - 4pm | **Practical:** Using CMap for identifying drug repurposing candidates |