Omic Data Analysis & Visualisation Using R

Description:

Block 1: *Omic Data Analysis & Visualisation Using R* is the ideal place to begin to learn omics, bioinformatics and R coding. It is 100% entry level and aimed at wet-lab biologists with no prior experience of bioinformatics or R. It focuses on bioinformatic theory, how to use R, how to handle omic datasets in R, and most importantly, how to make any type of publication quality plot in R. This includes all of the most widely used omic plots and analysis, such as MA, volcano, PCA, heatmaps, box / violin / jitter, expression density and pathway analysis.

This course is recommended to anyone wanting to learn how to analyse omic datasets of any type for the first time. It is important to note, this is not a "theory course", it is 100% a skills based course. Designed ultimately to equip you with the skills needed to do your own omic analysis, of any dataset, on your own.

As a stand-alone this block will be sufficient for you to complete the data analysis of many typical omic projects, such as bulk RNA-seq, proteomics and metabolomics. For those that are intending to work with more complex experimental types or designs - such as multi-factor experiments, epigenomics, genomics or ssRNA-seq, this provides the essential foundation. Further blocks allow specialisation into these more advanced experimental types.

Learning objectives:

- A critical understanding different types of omic project and the steps within an omic project.
- A critical understanding of omic file types, including p and adjusted p-values.
- Practical experience of using R to handle omic datasets.
- Practical experience of using R to make custom plots of publication quality.
- A critical understanding of typical omic plot types, and practical experience of generating them in R.

Course outline:

Day 1 - Introduction to bioinformatics and R. Using R and R studio.
Day 2 - Sequencing, alignment and splice aware alignment. Handling omic datasets in R (part 1)
Day 3 - Fold change, p-values, and adjusted p-values. Handling omic datasets in R (part 2).
Day 4 - Using the GG plots package in R. Volcano and MA plots.
Day 5 - Colouring plots by groups. Legends. Using custom themes.
Day 6 - Expression density plots and principal component analysis (PCA)
Day 7 - Box, violin and jitter plots. Multi gene plots.
Day 8 - Heatmaps and clustering
Day 9 - Pathway analysis
Day 10 - When to stop, perfect scripts and new datasets