



RNA-Seq Data Analysis Using R

*Draft Timetable - 3 Day Hands-on Bioinformatics Workshop
Monday 27th November -Wednesday 29th November 2017*

Day 1 – Introduction to R

Time	Topics
1000	Welcome and introduction
1030	Getting started <ul style="list-style-type: none">• Core R vs R studio• Ways to run R code Data types - simple data types
1200	Lunch
1500	Data types continue - complex data types Importing and exporting data from R
1500	Afternoon break
1530	Transforming User defined functions Vectorization, for loops and while loops
1700	Day 1 wrap-up

Day 2 - Functions in R and RNA-Seq Data Analysis

Time	Topics
0900	Day 1 review Data representation - plotting using native R functions Boxplot, barplot, scatter plot, histogram
1030	Morning break
1100	Reproducible reporting with R notebook

	Going further with R – documentations, installing and loading packages
1230	Lunch
1330	Introduction to NGS Loading data – understanding data Quality check (QC) of raw reads
1515	Afternoon break
1545	Mapping to reference, quantitation QC of mapping results
1720	Day 2 wrap-up

Day 3 - Biological Interpretation

Time	Topics
0900	Day 2 review Normalisation and QC
1030	Morning break
1100	Differential expression analysis
1230	Lunch
1130	Gene annotation
1515	Afternoon break
1545	Gene set enrichment
1720	Day 2 wrap-up

Please that this timetable subject to change.
Please contact Katherine Champ on kchamp@bioplatforms.com if you have any questions.