



# RNA-Seq Data Analysis Using R

*2.5 Day Hands-on Bioinformatics Training Workshop*

*Draft Timetable*

*Wednesday 19<sup>th</sup> April -Friday 21<sup>st</sup> April 2017*

## *Day 1 – Introduction to R*

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

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

<b>Time</b>	<b>Topics</b>
0900	Day 1 review Data representation - plotting using native R functions Boxplot, barplot, scatter plot, histogram Introduction to NGS
1030	Morning break
1100	Loading data – understanding data Quality check (QC) of raw reads
1230	Lunch
1330	Quality check of raw reads continue Mapping to reference, quantitation QC of mapping results
1515	Afternoon break
1545	Normalisation and QC
1720	Day 2 wrap-up

## *Day 3 - Biological Interpretation*

<b>Time</b>	<b>Topics</b>
0900	Day 2 review Differential expression analysis
1030	Morning break
1100	Gene annotation Gene set enrichment
1230	Wrap-up and close

Please that this timetable subject to change.

Please contact Katherine Champ on [kchamp@bioplatforms.com](mailto:kchamp@bioplatforms.com) if you have any questions.