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**Foundation Masterclasses 2021-2022**

**Primer for Advanced ‘Omics’ Approaches**

*optional for first- and second-year EASTBIO PhD students*

**Workshop leader**: **Dr Simon Tomlinson** (University of Edinburgh, Centre for Regenerative Medicine)

**Date: 6th & 7th June 2023**

**Location**

Day one of the course will be delivered online (via Zoom). Day two will be delivered in person in Edinburgh.

**Workshop description**:

The workshop aims to teach students how to carry out the analysis and interpretation of RNA-seq data. The course focused on RNA-seq data from mixed cell populations rather than single cell data, although the analysis concepts taught are common to both types of data. The course is taught from first principles and so is suitable for someone who is new to RNA-seq analysis. Basic knowledge of applied statistics and molecular biology is assumed although extra reading is provided for students who need to refresh their knowledge of these subjects. In the course, we make extensive use of R and Unix but no prior knowledge is required although basic computer literacy is assumed. We make use of a generic server on the course so that the skills taught can be applied easily outside the local environment.

The course will cover the skills necessary to analyse and interpret RNA-seq data. The typical student on the course may be interested in using skills gained on the course for analysis of data available online or analysing and interpreting their own lab data. The aim is to get students over the most difficult part of the learning curve and then provide a platform for further exploration of these techniques. We make use of several data sets on the course downloaded from public databases. The example data used will be mouse embryonic stem cell data but the skills taught are directly applicable to other biological domains.

**Learning outcomes**:

At the end of the course students will:

* be familiar with Unix and R and how to access resources hosted on remote servers.
* be able to perform an RNA-seq analysis and interpret the analysis outcomes.
* learn how to use the most commonly used analysis methods; they will gain an understanding of the underlying concepts so they will be ready to adapt their knowledge to related technologies not explicitly covered by the course.

**Background reading**

A good textbook for Data Analysis using R.
Bioinformatics and Computational Biology Solutions Using R and Bioconductor
Editors: Robert Gentleman, Vincent J. Carey, Wolfgang Huber, Rafael A. Irizarry, Sandrine Dudoit
ISBN: 978-0-387-25146-2 (Print) 978-0-387-29362-2 (Online)
(<https://link-springer-com.ezproxy.is.ed.ac.uk/book/10.1007/0-387-29362-0> )

A good general article covering many of the R technologies discussed on the course...
<http://manuals.bioinformatics.ucr.edu/home/R_BioCondManual>

This is quite an accessible review for basic molecular biology
<https://www.sciencedirect.com/science/article/pii/B9780080918655000035?via%3Dihub>

This is a good RNA-seq review
<https://www.annualreviews.org/doi/abs/10.1146/annurev-biodatasci-072018-021255>

Useful extra materials for learning R
<https://rstudio.com/resources/cheatsheets/>

**Training web-page:** <http://www.eastscotbiodtp.ac.uk/foundation-masterclasses>

For **further info**, please email enquiries@eastscotbiodtp.ac.uk