

2020 WEHI-Zhejiang University Online Bioinformatics Workshops on December 21st and 22nd

On the 21st and 22nd December four bioinformaticians from the Walter and Eliza Hall Institute for Medical Research (**WEHI**) will be running a series of training workshops on bioinformatics methods to analyse different kinds of data. This is an exciting opportunity for staff and students of the university to learn about bioinformatics analysis methods from experienced researchers with many years of experience in the analysis of data and the development of analysis methods.

Each workshop will have a limited attendance of 30 participants in order to have a good ratio between instructors and participants. Workshop participants should carefully review the installation instruction before attending.

Instructors



Dr Stefano Mangiola

Dr Stefano Mangiola is a dataoriented biologist at WEHI with experience in bulk and single cell RNA-seq analysis.



Mr Luyi Tian

Mr Luyi Tian is a PhD student working on single cell RNA-seq and nanopore data analysis and method development.



Ms Xueyi Dong

Mr Hongke Peng

Ms Xuey Dong is a PhD student at WEHI with experience in bulk RNA-seq and nanopore long read data analysis.



Mr Hongke Peng is a PhD student working on single cell RNA-seq and nanopore data analysis and method development.

Workshops Schedule

Monday 21 st December 11am – 1pm (Hangzhou Time 8am – 10am)	Associate Professor Matt Ritchie to deliver the welcome speech Workshop setup All attendees	Workshop participants are required to attend this session to check that R and the required packages have been installed correctly.
Monday 21 st December 2pm – 5pm (Hangzhou Time 11am – 2pm) Including lunch break	RNA-seq Analysis Workshop Maximum 30	In this workshop, you will be learning how to analyse RNA-seq count data using R and Bioconductor. We will run this workshop twice to allow for a larger number of participants.
Tuesday 22 nd December 11am – 3pm (Hangzhou Time 8am – 12pm)	Single cell RNA-seq Analysis Workshop Maximum 30 Professor Ming Chen to deliver the closing speech	In this workshop you will be introduced to the basics of analysing single-cell RNA sequencing data using R and Bioconductor.

To register for a workshop, contact Professor Ming Chen at <u>mchen@zju.edu.cn</u>. Workshops will be free, but places will be strictly limited so please ensure that you meet all the requirements for a workshop before you register, particularly with respect to setting up the required software on your computer. Please see detailed requirements for each workshop in the following detailed descriptions.