

3I Bioinformatics Course 22/01/2018-26/01/2018

Thank you for participating in the course. Here is some information about the course.

Pre course stuff - important

Please apply before the 15 of January for those two accounts, as also indicated in the email.

HPC account: On page <https://www.gla.ac.uk/myglasgow/it/hpcc/> see link IT Services Compute Cluster account registration form (docx). Please follow the instructions. Thomas Otto can sign the form if you are a student. Staff do not need the head of department to sign.

A Galaxy account. Please email to David.Meltzer@glasgow.ac.uk with the subject: GALAXY USER ACTIVATION.

For those bringing their own computers, you need to install [mobaxterminal](#) and [R-studio](#). In order to run RStudio you also need to have a recent version of [R](#) installed. Alternatively, you could install a virtual machine, if you have a modern notebook (> 2 threads, > 2GB of mem and >50GB of free disc). If so download the [virtual machine](#) and follow [the instruction](#).

Connecting to the HPC

[Here are instructions](#) for connecting to the HPC.

Make sure this works before the start of the workshop.

Venue and times

We are going to have course in the
**West medical Building,
Room 515**

As there is a lot of material to go through, we aim to start sharp at **9am every day**. We would appreciate if you could come a bit early, start the computer, so that we can make most out of the time.

As you can see on the program, Monday and Friday afternoon we will be in another room, to be confirmed. At the moment it is on level 2 in the GBRC.

Draft program

	Monday 22/01/2018	Tuesday 23/01/2018	Wednesday 24/01/2018	Thursday 25/01/2018	Friday 26/01/2018	
09:00	Overview of Courses - Thomas	Genomic viewer - Artemis Kathryn	RNA-Seq I Mapping and differential expression Malaria Knock out analysis including GO enrichment Kathryn	Galaxy analysis	Group task	09:00
09:30	Introduction to Linux Thomas	NGS Mapping exercise Malaria drug, CNV, SNP, databases Thomas / Kathryn		ChipSeq Kathryn		09:30
10:00						10:00
10:30	Break	Break	Break	Break	Break	10:30
11:00	Introduction to Linux	NGS Mapping exercise continued	RNA-Seq I continued	ChipSeq continued	Group task continued	11:00
11:30						11:30
12:00			RNA-Seq Galaxy David			12:00
12:30		Lunch	Lunch	Lunch Lunch task: Get groups for Group task	prepare presentations	12:30
13:00	Lunch				Lunch	13:00
13:30						13:30
14:00	DIFFERENT ROOM Seminar series Introduction to Bioinformatics Thomas	Introduction to R Thomas	RNA-Seq II Clustering and integrative analysis C. diffical dataset R, heatmaps, GO, String, KEGG John Cole	Day to day Bioinformatics: Handling of data and downloading of data set The HPCC job submission Thomas	DIFFERENT ROOM Group presentations	14:00
14:30				Discussion		14:30
15:00	Introduction to sequencing technologies & genomic application Thomas				Final wrap up- Survey	15:00
15:30	Tea/Coffee				Finish	15:30
16:00	Transcriptomics (RNA-Seq / ChipSeq) John			Group task informal meeting		16:00
16:30						16:30
17:00						17:00
17:30						17:30

First steps

We are going to work most of the time on the University of Glasgow's high performance computer cluster (HPCC). You will have access to this after the course, enabling you to apply what you have learnt in the same environment. Galaxy is a web-based service for NGS analysis which will be explained fully during the course. You will also retain access to this service after the course.

Modules

A week before the start of the course, you should find all the pdfs of the different modules here. A printed manual will not be provided.

Monday morning: Introduction to [Linux](#)

Monday afternoon Introductions talks: Bioinformatics, NGS, genomics and Transcriptomic.

Tuesday Morning: [A short intro to the best genomic viewer](#). If you are running artemis locally, the files are also [here!](#)

Tuesday Morning: [Introduction to mapping and variant calling on the example of drug resistance](#).

Tuesday Afternoon: [R](#). The required files if you want to run it from your computer are [here](#).

Wednesday is going to be all about RNA-Seq

[Transcriptional shift due to the knock out of gene in Plasmodium berghei](#).

Galaxy

[Integrated analysis of C. diffical RNA-Seq data from different stress conditions](#).

Chip-Seq

Thursday afternoon: [A session with exercises how to apply what you learnt \(getting things from EB\) and also time for catch up questions](#).

To come, surprise, surprise - [Draft ideas for Group task on Friday](#).

The team

Instructors: (full time)

Kathryn Crouch - WCMP

Thomas Otto - Centre of Immunobiology

David Meltzer - Polyomics
Francesca Young - CVR
Ben Stamp - CVR

Experts for some sessions
John Cole - Centre of Immunobiology
Katarzyna Modrzynska - WCMP
Joseph - CVR

WCMP - Wellcome Center of Molecular Parasitology
CVR - Centre for Virus Research

Organization [Kathryn Crouch](#) and [Thomas D. Otto](#)