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PhD Program Biomedicine (BioMed)

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Course advertisement

Bioinformatics and Next Generation Sequencing 2026

Within this course you will learn important bioinformatic concepts and tools and in particular focus on the analysis of Next Generation Sequencing datasets with many examples and exercises.

The course is open to all PhD students. Students of the PhD Program Biomedicine (BioMed) have priority.

Date	Topic	Time
Tue 3rd Nov 2026	Introduction to Statistics	09:30-17:00 GMT
Tue 10th Nov 2026	Introduction to R	09:30-17:00 GMT
Tue 17th Nov 2026	Introduction to Unix and Sequencing QC	09:30-17:00 GMT
Tue 24th Nov 2026	RNA Seq Data Analysis	09:30-17:00 GMT
Tue 1st Dec 2026	10X single cell RNA Seq Data Analysis	09:30-17:00 GMT
Tue 8th Dec2026	Extracting Biological Information from Gene Lists	09:30-17:00 GMT

Room	via Zoom, details to follow
Type	Interactive Course with many hands-on exercises
Requirement	Basic bioinformatics knowledge is recommended
Recommendation	PhD students who will work with NGS datasets
Maximum participants	**10**
Further information	BioMed Coordinating Office (andrea.schmitz-derron@uzh.ch) and here https://www.bioinformatics.babraham.ac.uk/training.html
Credit points	3 ECTS (exercises within the course)
Registration and Fee	By e-mail to andrea.schmitz-derron@uzh.ch until **31 May 2026**. The course fee is **500 CHF** for each participants. **The course fee has to be transferred until 20 June 2026.** **If the course isn't fully booked and/or the fee isn't received until 20 June 2026, we have to cancel the course (based on the contract we have with Babraham Institute).** If the number of applications exceeds the maximum number of possible participants, priority will be given to BioMed students.

Course Program 2026

Introduction to Statistics

This course will cover a short introduction to statistics, introducing key terms and concepts to get you started thinking about how to use and interpret different statistical outputs. Topics covered will include why we use statistical tests; statistical power and experimental design; what statistical terms mean (e.g. what a p-value of <0.05 tells us); and descriptive statistics (e.g. the difference between standard deviation, standard error of the mean, and confidence intervals), as well as exploring some key statistical analyses and data types.

Introduction to R

R is a specialised programming language whose main purpose is the manipulation, visualisation and analysis of datasets. It is one of the core tools used in many numerical disciplines and is very popular in the field of bioinformatics.
This course provides a ground-up introduction to the core R language, and uses the modern tidyverse framework to show how to easily import, transform and plot datasets.
This course is an invaluable foundation for anyone wanting to use R in their work.

Introduction to Unix/Bash and Sequencing QC

The processing of many modern datasets requires the use of a unix or linux environment, and many people use this as their preferred operating system. In this course we look at how you can use the unix command line to control the running of individual programs, to manage your data and to perform some basic automation to make large scale processing easier.

In NGS sequencing you want to be able to identify problems in your data as early as possible to save wasted effort and to allow you to apply corrections. This course looks at the ways you can assess the quality of NGS data, the different types of failure you can have, and the options for ways to correct any issues you identify. It covers both the theory of how Illumina sequencing works, and the practical early stage analysis of this data.

RNA Seq data analysis,

RNA-Seq is a very common high throughput sequencing technique used to measure the transcriptome of a biological sample. This course goes through the whole process of RNA-Seq data processing, visualisation and analysis, from raw fastq data to a validated and annotated set of hits.
We look at the way RNA-Seq libraries are constructed and the effect this has on downstream steps in the analysis. For each part of the pipeline we look at what can go wrong, how to assess that things are working, and remedial steps you can take to correct or explore problems.
After this course you should have the confidence to be able to process and analyse your own data for a simple RNA-Seq experimental design.

10X scRNA Seq data analysis

The ability to look at samples at the level of single cells has transformed the way we can look at complex samples. 10X is the most frequently used platform for the creation of high throughput single cell RNA-Seq data. In this course we look at the processing, exploration and analysis of this data using both desktop tools such as the Loupe Browser, and R packages such as Seurat. As well as standard analyses we also look at the types of artefacts and problems which affect this data and how to identify and remedy them.

Extracting Biological information from Gene Lists

The end point of many different high throughput experiments is a list of interesting genes, often accompanied by metrics such as p-values or fold changes. Making biological sense of these lists can be challenging but is crucial if we are to target the most relevant aspects of biology.

In this course we look at the data sources and analysis techniques which allow us to find the interesting biology behind a set of genes. We look at functional gene set enrichment analysis from both lists of gene names and quantitative data. We consider the choices we get in these techniques, the artefacts and biases which can mislead us, and the options for how to present the results we get.

We run the analyses initially in a web browser, but then also show how to do this in R