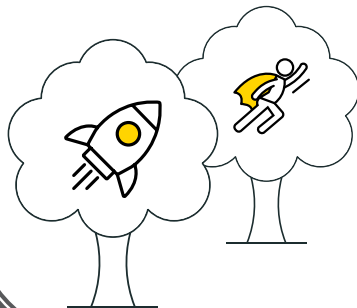


Bioinformatics courses

for PhD candidates of the GSLS



Utrecht
Bioinformatics
Center



Data is the new gold.

It's heavy, it is valuable, and it shimmers. And everyone wants it!

But if you really want to make your data shine, you need to learn how to polish, clean, analyse, manage, code & visualise it.

Welcome to our world of data.

Join our new courses!

We offer courses where you learn the basics of a **programming language** in order to handle and analyse big datasets. We give you an introduction in **managing your research data**. And we want you to **bring your own data** (BYOD) and learn how to analyse and/or visualise your dataset.



Utrecht University



GRADUATE SCHOOL
OF LIFE SCIENCES



UMC Utrecht



“
Come and join us!
Turn your data to gold.
Check the code for more
information.”

Introduction to R for Life Sciences

Would you like to learn how to analyse large datasets in an appropriate way? R is widely used for statistical computing and provides a wide variety of libraries for data manipulation, modelling and visualisation.

Introduction to Python for Life Sciences

Is your dataset too large or too complicated to load and process in Microsoft Excel? Get an introduction in Python and learn some basic functions and scripts.

Introduction to the Command Line

Linux is a popular operating system among bioinformaticians. Once familiar with the *command line* (the text-based interface) you will find it to be very efficient and powerful to use for your analyses.

Introduction to Research Data Management

Proper management of research data is a requirement by the university but also by funding agencies and publishers. Learn how to efficiently store and reuse data and the available techniques, to make these tasks easier.

Bring Your Own Data: Create figures in R using *ggplot2*

Learn how to make figures for your publications using the R package *ggplot2*. The trainer can assist you in choosing the correct statistics to apply to your data.

Bring Your Own Data: Create figures in Python

Learn how to make figures for your publications using Python and let the trainer help you in choosing the correct statistics to apply to your data.

Bring Your Own Data: R-coding for analysing RNA-seq data

You will learn the steps needed to analyse your processed RNA-seq data (count tables) using R. In addition, you will create figures to visualise your data using *ggplot2*.

Bring Your Own Data: Analysing Metagenomics

Explore your own metagenomics data step-by-step. The trainer will guide you through the available statistical methods and visualisation options.