Data collection is ubiquitous in all fields of biology. Especially with the development of new techniques to analyze biological systems, large data sets of many interacting variables become available. It is not obvious how this data should be handled, processed and analyzed. The aim of this course is to provide a computational framework for handling biological data. This will be achieved in two ways. First, through lectures that cover statistical and data analysis methods, and second, through processing this data in one of the commonly used computational platforms, Matlab. This includes the very first steps of loading the data, plotting the data, and understanding the data. The course is aimed at biology students who collect data in their everyday work (bachelor, Master and PhD students). We will cover the following topics:

- Basic use of Matlab, including variables, functions
- Plotting (bar plots, scatter plots, histograms, cumulative histograms)
- Statistical inference
- Comparing distributions and means (e.g. t-test)
- ANOVA (Analysis of Variance)
- Fitting functions to data
- Detecting correlations in your data

Optional topics (time permitting):
- Fourier analysis
- Convolution and filtering
- Dimensionality reduction (including principal component analysis, or PCA)

No preliminary knowledge is necessary for this course, but a strong motivation to learn! Progress in the course will be evaluated through daily exercises, and there will be a final project and a presentation for the examination.

This course is offered as a block course. The course will take place on 14-16 and 19-21 February 2018 in the computer room DGL01. We will start the morning (9:00-12:30) with a lecture of the mathematical and statistical concepts, and then proceed to more hands-on work with Matlab in the afternoon (13:30-17:00). You can register for the course on TUMonline.

This course is offered for the second year and it has 3 ETCS.

If you have any questions, please get in touch: gjorgjieva@tum.de
Happy Matlab-ing!