

Basic statistics with R

Objective

To familiarize participants with the foundations of practical biostatistics.

Description

The course addresses the following topics:

- Sampling theory: Obtaining information about a population via sampling. Sample characteristics (location, dispersion, skewness), estimation of the mean, standard error of the mean
- Discrete and continuous probability distributions: Central limit theorem
- Hypothesis testing: Basic principles, one- and two-sided testing, types of errors, power calculations
- "Cookbook of tests": Location testing, normality, variance comparisons, counting statistics, contingency tables, regression tests

Methodology

Instructor-led lectures plus hands-on exercises using the R programming language (accessed via a dedicated web server).

Conditions

Basic familiarity with the R programming language is required. In particular the following skills are necessary:

- Using the R interpreter, either the command-line program or in R Studio <https://rstudio.com/>
- How to invoke R functions, pass optional/named parameters
- Some familiarity with simple plotting commands

Trainer



Dr. András Aszódi

VBCF BioComp, Vienna

- He has extensive computational biology experience - both in academia and industry
- He is currently working at the Bioinformatics and Scientific Computing Core Facility at the Vienna Bio-center Campus
- His main tasks are the development of short courses on biostatistics and scientific programming

Organizational Information

Language	English
Target group	Doctoral Candidates at all stages and Postdocs from from all faculties
Date	Tuesday-Wednesday, 20-21 October 2020, 9:00 – 13:00
Registration	For registration click here