Advanced analysis of quantitative proteomics data using R

You will learn...

- how to use the popular statistical programming language R for your daily analyses
- about the theoretical background of the statistical methods applied to proteomics data

Topics

- Data preprocessing and quality control (e.g. normalization, principal component analysis)
- Advanced analysis of proteomics data (e.g. clustering, ROC-curves)

Date	Tuesday, 19th Nov 2019, 10:00 a.m. – 6:00 p.m.
Venue	Ruhr-University Bochum Universitätsstr 150, 44801 Bochum
Further Details	https://www.denbi.de/training
Requirements	Basic knowledge of R and differential analysis of proteomics data
Registration	https://forms.gle/3pkpVmWKdbShJwWz5
Fee	This course is for free!
Contact	bioinfoservice@rub.de