



Analysis of NextGen RNA-Seq data for expression profiling and protein-binding RNAs

METHOD COURSE

10.-14.10.2016 | Regensburg

The course aims to provide an introduction to the current state of RNA sequencing data analyses. Methods and applications will be presented by internationally renowned guest speakers in the mornings and hands-on training on the latest computational approaches will follow in the afternoons.

SPEAKERS | Simon Anders | [FIMM Helsinki](#)
 Markus Hafner | [NIAMS/NIH, Bethesda, USA](#)
 Steve Hoffmann | [Universität Leipzig](#)
 Stefan Kirsch | [Fraunhofer ITEM](#)
 Jan Medenbach | [Universität Regensburg](#)
 Charlotte Soneson | [University of Zurich](#)
 Rainer Spang | [Universität Regensburg](#)
 Nicholas Strieder | [Universität Regensburg](#)
 Grischa Toedt | [EMBL Heidelberg](#)

TOPICS | The R/Bioconductor environment for statistical data analyses and graphics
 Short read sequence alignment
 Quality control
 Normalization and data reformatting
 Basic Statistics
 Selecting differentially regulated genes
 Selecting alternative splicing events
 Identification of protein-bound RNAs
 Biological interpretation and visualization

MAIN ORGANISER | Jan Medenbach | Julia Engelmann | [Graduate Research Academy RNA Biology](#)