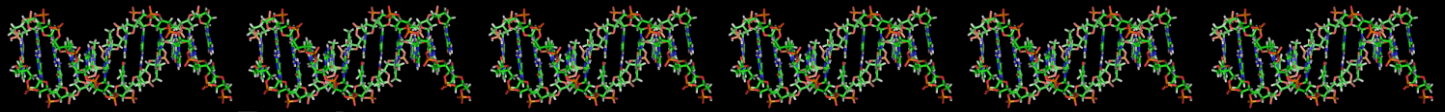


RNA-seq Workshop Düsseldorf 2012

23rd to 25th of May
in the framework of SPP1529



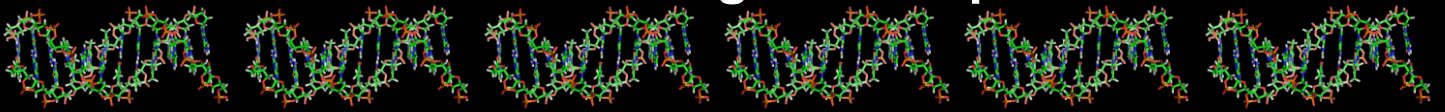
Basics

Experimental Design

Assembly

Gene expression

Biological Interpretation



HandsOn in ComputerLab

Basics Unix, Perl and R basics for complete beginners

Experimental Design

Assembly formatting reads, de novo assembly for model and non-model species, annotation, assembly quality controls, interpretation

gene expression read mapping, SNP calling, differential splicing, re-sequencing, statistical evaluation of results

Biological interpretation of data Unix, command line tools, JAVA based tools, using KEGG, using GO, using publicly available information

Lectures

Eric Schranz: Genome assembly

Udo Gowik: RNA-seq in plants

Wolfgang Kaisers: R bases analysis

Alice McHardy: Metagenomics

Björn Usadel: The robin platform

CLC: A commercial analysis platform

Korbinian Schneeberger: Mapping

mutations by sequencing

Jens Georg: RNA-seq in cyanobacteria

Visit of HHU Genomics Facilities (SOLiD, Ion Torrent, Illumina, Roche machines available on site)

The workshop is **free of charge**. To participate, send (i) a letter of motivation of no more than 2000 characters stating how you (plan to) use NGS in your work and (ii) a recommendation by the head of the lab no later than 31.03.12 to RNA-seq@hhu.de.

36 participants will be chosen from the letters and notified until 15.04.12.

Important Dates

31.03.12 Application Deadline

15.04.12 Notification of Participation

23.05.12 9am Start of Workshop

25.05.12 1pm End of Workshop

More information can be found at

RNA-seq.hhu.de

RNA-seq@hhu.de



Roche?

BASF?

Weber Lab, Heinrich Heine University Düsseldorf, www.plant-biochemistry.hhu.de