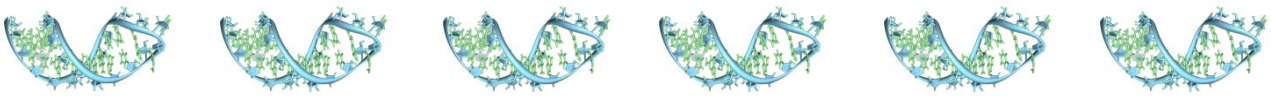
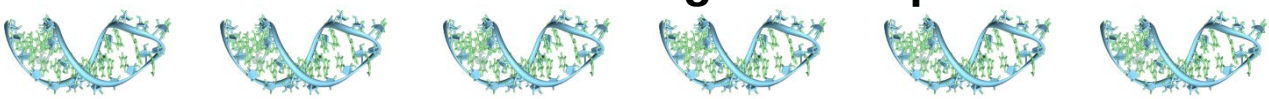
3rd RNA-seq Workshop 2015

RWTH Aachen 25th to 27th of March



Read Mapping
Statistical Evaluation
Enrichment Analyses
Clustering Tools
Biological Interpretation



HandsOn in ComputerLab

Basics Unix, Perl and R basics for complete beginners
Read mapping formatting reads, different mapping programs, parsing and testing results
statistical evaluation open source software to test for differential expression
enrichment analyses data preparation, Fishers exact test, multiple hypothesis testing correction
clustering tools principle component analyses, hierarchical clustering
biological interpretation of data

Lectures (planned)

Mapping of mutants
Genome Assembly
RNA-seq of non-models

Q&A session

Opportunity to discuss your own projects

The workshop fee is 50 Euro which is waived for those currently involved in a Plant Biotechnology (PLANT2030) or tri-national KBBE project through the Plant Biotechnology Primary database. To participate, send a letter of motivation of no more than 2000 characters stating how you (plan to) use NGS in your work and which sponsoring consortium you are a member of no later than 01.03.2015 to m.bolger@fz-juelich.de

Important Dates

01.03.15 Application Deadline
06.03.15 Notification of Participation
25.03.15 13:00 Start of Workshop
27.03.15 15:00 End of Workshop

More information can be obtained by writing to
m.bolger@fz-juelich.de or
andrea.braeutigam@hhu.de

CLC bio
SPP 1529 ADAPTOMICS
iGRADplant International Graduate Program for Plant Science
PlabiPD Plant Biotechnology Primary Database

Usadel Lab, RWTH Aachen & Weber Lab, Heinrich Heine University Düsseldorf