Meeting on Advances and Challenges of RNA-Seq Analysis

June 20-22, 2012, Halle/Saale

Wednesday, June 20

14.00 - 14.05 Welcome Host: Ivo Grosse
14.05 - 14.10 Welcome Dean of Faculty of Natural Sciences III of Martin Luther University Halle-Wittenberg: Peter Wycisk
14.15 - 15.15 Keynote lecture: Hidden Treasures in RNA-seq Data Sets, Peter Stadler, Leipzig University, Germany

15.15 - 15.45 Coffee break
15.45 - 16.45 Session 1:
   Jörg Hackermüller: Transcriptomics using Tiling arrays and RNASeq
   Arunkumar Srinivasan: A pipeline to detect alternative splicing (AS) in tomato using RNA-Seq data
   José M. Jimenez-Gomez: SNP calling pipeline for RNA-seq datasets
16.45 - 17.15 Coffee break
17:15 - 18:15 Tutorial: The art of mapping, Steve Hoffmann, Leipzig University, Germany

19.30 Welcome Reception in Rockery, Von-Seckendorff-Platz 1, 06120 Halle/ Saale

Thursday, June 21:

9.00 - 10.00 Keynote lecture: Computational Methods for Accurate Transcriptome Reconstruction, Gunnar Rätsch, Memorial Sloan Kettering Cancer Center, New York, United States of America

10.00 - 10.30 Coffee break
10.30 - 11.30 Session 2:
   Christina Ander: MeTrans – Software platform for the analysis of metatranscriptomes
   Rolf Hilker: VAMP: Visualization and Analysis of Mapped Sequences
   Andreas Teufel: RNA-Seq-Atlas – A reference database for gene expression profiling in normal tissue by next generation sequencing

11.30 - 12.00 Coffee break
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12.00 - 13.00  Tutorial: *Oqtans: Quantitative transcriptome analysis in the cloud I*, Sebastian Schultheiss, Computomics, Tuebingen, Germany & Geraldine Jean, University Nantes, France

13.00 - 14.15  Lunch

14.15 - 15.15  Demo Session

15.15 - 17.15  Poster Session & Coffee

17.15 - 18.15  Tutorial: *DARIO - analysis of small RNAs sequencing data*, David Langenberger, Leipzig University, Germany

19:30  Conference Dinner in Restaurant PalaisS, Ankerstrasse 3c, 06108 Halle/Saale

Friday, June 22

9.00 - 10.00  Keynote lecture: *An International Consortium sequencing the transcriptomes of 1000 phylogenetically diverse plant species from angiosperms to algae*, Gane Ka-Shu Wong, Alberta, Canada

10.00 - 10.30  Coffee break

10.30 - 11.30  Session 3:

François Buscot:  TrophínOak: a controlled system with oak microcuttings to study gene expression by RNA-Seq and resource allocation in multitrophic interactions

Artem Kasianov:  De novo sequencing, assembly and characterization of transcriptome in the tetraploid plant *Capsella bursa-pastoris*

Ivan Paponov:  Auxin transcriptional signature of Arabidopsis

11.30 - 12.00  Coffee break

12.00 - 13.00  Tutorial: *Oqtans: Quantitative transcriptome analysis in the cloud II*, Sebastian Schultheiss, Computomics, Tuebingen, Germany & Geraldine Jean, University Nantes, France

13.00 - 13.15  Closing Remarks Host: Ivo Grosse

13.15 - 14.15  Lunch

Meeting Venue: Martin-Luther University Halle-Wittenberg, Institute of Computer Science, Von-Seckendorff-Platz 1, D-06120 Halle/Saale
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14:15 - 16:00  Time for individual discussions

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Von-Seckendorff-Platz 1, D-06120 Halle/Saale