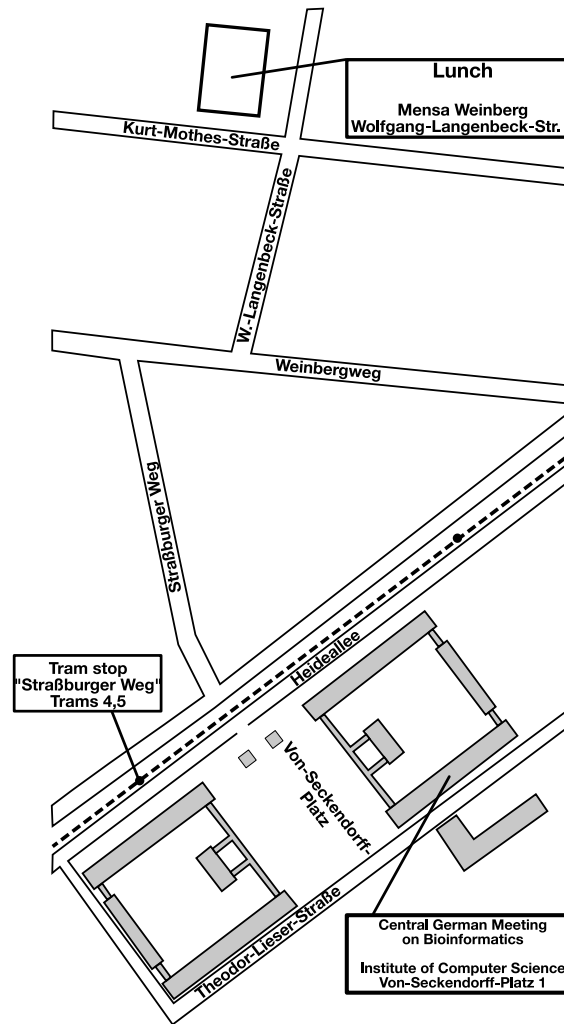## Posters (continued)

P23 Semi-automatic interpretation of local secondary structure motifs in lncRNAs

P24 UAP - Reproducible and Monitored Next-Generation Sequencing Data Analysis

P25 Searching with tandem mass spectra in molecular structure databases

P26 Combined Metabolome and Transcriptome Analysis of the Circadian Rhythm in the Cyanobacterium Synechocystis sp. Strain PCC 6803

P27 AnnoTALE - Identification, Annotation and Classification of Transcription Activator-Like Effectors

P28 Temperature sensitive RNAalifold - effects of using varyings temperatures on consensus structure prediction.

P29 Simulation of cell and tissue dynamics using a deformable cell model

P30 Polar Plots Visualizing the Effects of Different Treatments on Gene Regulation

P31 Normoxic accumulation of HIF1α is associated with glutaminolysis

P32 Modelling slime mould electrical properties by a fractional order system in the frequency domain

Supporting organizations & Sponsors

Venue & Lunch

Lunch

Mensa Weinberg
Wolfgang-Langenbeck-Str. 3

Kurt-Mothes-Straße

W.-Langenbeck-Straße

Weinbergweg

Straßburger Weg

Heideallee

Tram stop "Straßburger Weg" Trams 4,5

Von-Seckendorff-Platz

Theodor-Lieser-Straße

Central German Meeting on Bioinformatics

Institute of Computer Science Von-Seckendorff-Platz 1

Central German Meeting on Bioinformatics 2015

August 26/27, 2015

Martin Luther University Halle–Wittenberg

MARTIN-LUTHER-UNIVERSITÄT HALLE-WITTENBERG

U.Z.I   Universitätszentrum Informatik - Halle

IPB   Leibniz Institute of Plant Biochemistry

iDiv   German Centre for Integrative Biodiversity Research

IPK   GATERSLEBEN

Program

Wednesday, August 26, 2015

10:00 Opening
Welcome address: Prof. Dr. Olaf Christen,
Dean of the Faculty of Natural Sciences III, MLU

10:15 Francois Buscot
Keynote: New perspectives and challenges in plant-soil ecology research at the age of next generation sequencing

11:00 Daniel Arend
e!DAL - A new approach to publish your data

11:25 Sarah Berkemer
Remolding and Evolution of tRNA genes in Eukaryotes

11:50 Lunch break

13:20 Stefan Schuster (invited)
The Fibonacci code in lipidomics

13:45 Christoph Ruttkies
Classification of reliable MetFrag candidate identifications for tandem mass spectra from selected lipid samples

14:10 Jan Ewald
Dynamic optimization: a powerful approach to elucidate optimality principles within metabolism

14:35 Guillermo Restrepo
Green chemical fitness landscapes

15:00 Coffee break

15:30 Manja Marz (invited)
Challenges in virus genomics

15:55 Markus Fleischauer
Bad Character Deletion Supertrees

16:20 Konstantin Riege
Basal fungi phylogeny reconstructed by proteome, rRNA, RNome and mitochondrial genes

16:45 Martin Nettling
Improving phylogenetic footprinting by neglecting evolution

17:10 Poster session

19:00 Barbecue

Thursday, August 27, 2015

09:00 Nicole van Dam
Keynote: Managing multiple menaces: Transcriptomics and metabolomics analysis of multiple stress responses in plants

09:45 Christoph Schuster
Whole transcriptome analysis of rare, meristematic plant cell populations using laser capture microscopy followed by strand-specific total RNA-Seq

10:10 Time for discussions with coffee

11:05 Steve Hoffmann (invited)
Cancer Epigenomics - attempts to disentangle methylation, histone modification and transcription

11:30 Ivo Hedtke
Optimal Block-Based Trimming for Next Generation Sequencing

11:55 Christian Hoener zu Siederdissen
Generalized Algebraic Dynamic Programming

12:20 Lunch break

13:50 Peter Stadler (invited)
Orthology, Paralogy, and Cographs: How to use paralogs in phylogenomics

14:15 Sebastian Germerodt
Pervasive selection for cooperative cross-feeding in bacterial communities

14:40 Martin Porsch
De-Novo Transcriptome Analysis and Characterization of Juncus effusus with a Multi-Module Bioinformatics Pipeline

15:05 Coffee break

15:35 Frank Jühling
Fast and sensitive detection of differential DNA methylation

16:00 Rainer König
Keynote: Inferring sample specific regulators for the genes of interest using gene expression data and chromatin binding information

16:45 Closing remarks

17:00 End

Posters

P1 e!DAL - A new approach to publish your data

P2 Computer-Aided Design of Small Molecules Targeting Parasitic Histone Deacetylases

P3 Modelling for activity prediction of in silico mutants exemplified by trisporic acid synthesis

P4 Homology Modeling and Molecular Dynamics Simulations of Sirtuin 4

P5 Modeling the host-pathogen interactions of the human immune system and C. albicans using game theory and dynamic optimization

P6 Structure-based Development of Novel Inhibitors for the Epigenetic Target EZH2

P7 Machine learning in computer-aided drug design

P8 What sequence information can reveal: The evolution of arrestins in deuterostomes

P9 Phylogenetic analysis of components of the Tat (twin arginine translocation) protein transport machinery

P10 Modeling Evolutionary Shifts of Ecological Niches Based on Climatic Spaces

P11 Correcting mass shifts in mass spectrometry imaging data using lock-mass-free recalibration procedure

P12 Omics for non-model organisms: the case of amphipods from Lake Baikal

P13 Prediction of conserved long-range RNA-RNA interaction in full viral genomes using the example of HCV

P14 Preliminary comparison of differentially expressed ncRNAs in bat and human cells infected with Ebola Zaire virus

P15 Why Respirofermentation? Explaining the Warburg effect in tumour (and other) cells by a minimal model

P16 Phylogenetic distribution of plant snoRNAs

P17 The hidden world of non-canonical aliphatic amino acids

P18 Comparative visualization of sequence motifs with DiffLogo

P19 High-throughput plant phenotyping at IPK: facilities and methods for integrated image analysis

P20 Analysis of whole-genome sequencing data for elucidating floral transition and discovery of bolting resistance genes in Beta vulgaris

P21 Model-supported experimental improvement of a continuous algae production process: Minimizing medium supply via a light/dark cycle dependent dilution rate

P22 Detecting paralog-specific gene expression associated with floral induction in the allopolyploid Brassica napus