

Workshop "Biometrische Aspekte der Genomanalyse"

2015 in Heidelberg, Germany, March 5th-6th

(Formerly Rauschholzhausen workshop)

Topics:

Linkage analysis in the era of WGS- and WES studies

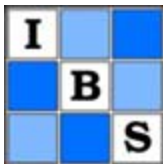
Microbiome data analysis

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Organisation team: A Scherag, C Hemmelmann (AK Humangenetik),

A Rudolph, P Ahnert (AG Genetische Epidemiologie),

J Lorenzo Bermejo, A Grosshennig and S Szymczak (AG Populationsgenetik und Genomanalyse)



Program

Thursday, March 5th 2015

13:30 - 14:00 *Welcome, Coffee Break*

14:00 - 15:30 **Tutorial:**
Linkage analysis in the era of WGS- and WES studies
Christine Fischer, Silke Szymczak
Chair: André Scherag

15:30 - 16:00 *Coffee Break*

Session 1: Rare Variant Analyses
Chair: Silke Szymczak

16:30 - 16:50 **Inferring variants contributing to synthetic association**
André Lacour

16:50 - 17:10 **Rare Variant Collapsing Test with Variable Binning**
Dmitriy Drichel, André Lacour, Christine Herold, Vitalia Schueller, Tatsiana Vaitsiakhovich, Tim Becker

17:10 - 17:30 **Association tests based on allele counts for DNA sequence data** Rosa González Silos, Özge Karadag, Barbara Peil, Christine Fischer, Maria Kabisch, Carine Legrand, Justo Lorenzo Bermejo

17:30 - 18:00 *Working group meetings*

18:00 - 18:30 *Dinner, afterwards Get-Together (Bar of the Youth hostel)*

Friday, March 6th 2015

Session 2: Microbiome data analysis
Chair: Justo Lorenzo Bermejo

09:00 - 10:00 **Invited Talk:**
Analysis of the human intestinal microbiota diversity
Mirjana Rajilić-Stojanović

10:00 - 10:20 **Enterotype based determination of statistical power in a study to link the microbiome to colon cancer**
Luc Bijnens, Karoline Faust, Bie Verbist, Jeroen Raes

10:20 - 10:50 *Coffee Break*

Session 3: Population genetics and Genetic Epidemiology

Chair: Tim Becker

10:50 - 11:10

Mutations causing complex disease may under certain circumstances be protective in an epidemiological sense

Sabine Siegert, Andreas Wolf, David N. Cooper, Michael Nothnagel, Michael Krawczak

11:10 - 11:30

Genetic ancestry and mortality in Chile

Justo Lorenzo Bermejo, Rosa González Silos, Barbara Peil, Katherine Marcelain, Macarena Fuentes, Francisco Rothhammer

11:30 - 11:50

Impact of population stratification on the validity of case-only studies of genome-wide gene-environment interactions

Pankaj Yadav, Sandra Freitag-Wolf, Michael Krawczak

11:50 - 12:10

Genomic analysis to detect selection signatures and trait associated SNPs in a segregating pig population

Patrick Stratz, Robin Wellmann, Jörn Bennewitz

12:10 - 12:30

Recessive inheritance and inbreeding in thyroid cancer

Hauke Thomsen

12:30 - 13:30

Lunch

Session 4: Data Integration and Applied Genetic Epidemiology I

Chair: Anika Grosshennig

13:30 - 13:50

A joint statistical model integrating multi-level biological data for genetic association analysis Stefan Konigorski, Yildiz E Yilmaz, Tobias Pischon

13:50 - 14:10

Testing integrated solutions for RNA-Seq analysis Alicia Poplawski, Federico Marini, Moritz Hess, Johanna Mazur, Harald Binder

14:10 - 14:30

Host genomics of sepsis fatality: A genome-wide association study for 28-day fatality

Franziska Schönebeck, Evelyn Kuhnt, Markus Scholz, Frank Martin Brunkhorst for the SepNet Study Group, André Scherag

14:30 - 15:00

Coffee Break

Session 5: Applied Genetic Epidemiology II

Chair: Christine Fischer

15:00 - 15:20

Linkage and association analyses of carotid intima media thickness for common genomic variants: results from the Bonn IMT Family Study and the Heinz Nixdorf Recall Study

Marie Henrike Geisel, Nicole Heßler, Stefan Coassin, Susanna Moskau-Hartmann, Gudrun Nürnberg, Frauke Hennig, Marcus Bauer, Stefan Möhlenkamp, Amir-Abbas Mahabadi, Susanne Moebus, Raimund Erbel, Karl-Heinz Jöckel, Barbara Hoffmann, Peter Nürnberg, Thomas Klockgether, Florian Kronenberg, André Scherag, Andreas Ziegler on behalf of the Heinz Nixdorf Recall Study Investigative Group

15:20 - 15:40	Comprehensive Gene-Gene Interaction Meta-Analysis of IGAP GWA studies Christine Herold, Sven J van der Lee, Qiong Yang, Alfredo Ramirez, Cornelia van Duijn, Sudha Seshadri, The International Genomics of Alzheimer's Project (IGAP), Tim Becker
15:40 - 16:00	Association between genetic variants in epigenetic pathways and risk of multiple cancers Dominique Scherer, Reka Toth, Linda Kelemen, Angela Risch, Aditi Hazra, Jean Pierre Issa, Simon Gayther, Victor Moreno, Rosalind A. Eeles John Quackenbush, Shuji Ogino, Ellen L. Goode, Rayjean Hung, Cornelia M. Ulrich
16:00 - 16:15	<i>Closing Remarks</i>
