

Dear colleagues,

we warmly welcome you to the 5th Workshop of Genetic Epidemiology in the Hotel St. Georg, Bad Aibling (see below).

We are looking forward to compelling talks and discussions.

With best regards,

Iris & Michael

This workshop is organized by the Department of Genetic Epidemiology of the University of Regensburg (Iris Heid, Sylvia Pfreintner) and the Pädiatrische Pneumologie und Allergologie, Krankenhaus der Barmherzigen Brüder, Regensburg (Michael Kabesch), supported by the Helmholtz Center Munich (Herbert Heilmaier).

Juggling -Omics data

The GRAINAU Meeting at
Bad Aibling

5th Workshop
of Genetic Epidemiology

March 25 - 27, 2015,
Hotel St. Georg, Bad Aibling



HelmholtzZentrum münchen
German Research Center for Environmental Health

We appreciate the support of the following
sponsors (TO BE CONTINUED):



Wednesday, March 25

13:00 Opening: Iris Heid & Michael Kabesch

Session I: Genomics goes rare variants 13:10 – 14:40

Session Chairs: Norman Klopp, Iris Heid
13:10-13:55 **Keynote:** Zoltan Kutalik, Lausanne, CH: Challenges and some solutions of genomic data analysis (30+15 min)
13:55-14:10 Matthias Olden, Regensburg: Insights into rare variation on the example of age-related macula degeneration (10+5)
14:10-14:25 Martina Müller-Nurasyid, Neuherberg: Experiences exploring the exome chip (10+5)
14:25-14:40 Carsten Böger, Regensburg: Extending GWAS on kidney function to larger and denser data (10+5)

Coffee Break – 20 min.

Session II: Next generation sequencing, RNA 15:00 – 16:45

Session Chairs: Konstantin Strauch, Thomas Meitinger
15:00-15:45 **Keynote speaker:** Roland Eils, Heidelberg: Massive genome and epigenome sequencing for dissecting pathomechanisms in cancer and environmentally induced diseases (30+15 min)
15:45-16:00 Tobias Haack, Neuherberg: Large-scale analysis of clinical exomes (10+5)
16:00-16:15 Steffen Sass, Neuherberg: Bioinformatic challenges of Next Generation Sequencing technology (10+5)
16:15-16:30 Thomas Wieland, Neuherberg: Exome sequencing based association studies (10+5)
16:30-16:45 Tim Kacprowki, Greifswald: Association Studies for Plasma Micro-RNAs (10+5)

Short break – 15 min.

Session III: Epigenomics and GxE 17:00 – 18:30

Session Chairs: Annette Peters, Rui Wang-Sattler
17:00-17:45 **Keynote speaker:** Steven Horvat, Los Angeles, USA: The epigenomic clock (30+15 min)
17:45-18:00 Tavin Ward-Taviness, Neuherberg, Epigenetics and incident myocardial infarction (10+5)
18:00-18:15 Thomas Panini, Affiliation: Ambient air pollution and genome-wide methylation (10+5)
18:15-18:30 Claudia Lamina, Innsbruck: Epigenome analysis on Lipoprotein a

19:00 Dinner

Thursday, March 26

Session IV: mtDNA – 1000 Genomes per cell 09:00 – 10:30

Session Chairs: Florian Kronenberg, Holger Prokisch
09:00-09:45 **Keynote:** Robert Taylor, Newcastle, UK: Title to be announced (30+15 min)
09:45-10:00 Antonia Flaquer, Neuherberg: Mitochondrial GWAS in several complex diseases using the KORA population (10+5)
10:00-10:15 Sebastian Schönherr, Innsbruck: highly distributed analysis pipeline for mtDNA next-generation sequencing (10+5)
10:15-10:30 Hansi Weißensteiner, Innsbruck: Pitfalls and perspectives of mtDNA heteroplasmy in NGS studies (10+5)

Coffee Break – 30 min.

Session V: Microbiome 11:00 – 12:30

Session Chairs: Stefan Weidinger, Jakob Linseisen
11:00-11:30 **Main talk:** André Gessner, Regensburg: Microbiome shapes host genome (function) (20+10 min)
11:30-12:00 **Main talk:** Andre Franke, Kiel: Gut microbiome and Crohn's disease (20+10)
12:00-12:30 **Main talk:** Dirk Haller, München: Microbiome and Host – Function beyond Sequencing (20+10)

12:30-13:30 Lunch

Discussion of New Projects in Genetic and Molecular Epidemiology
13:30 – 17:30

19:00 Dinner & Surprise

Friday, March 27

Session VI: Proteomics and Metabolomics 09:00 – 10:45

Session Chairs: Georg Homuth, Gabi Kastenmüller
09:00-09:30 **Main Talk:** Uwe Volker, Greifswald: New developments in proteomics (20+10 min)
09:30-09:45 Helmut Laumen, Freising: From GWAS to functional variants: an application of proteomics (10+5)
09:45-10:00 Maik Pietzner, Greifswald: What's beyond classical thyroid hormones: associations between serum 3,5-T2 and the metabolome (10+5)
10:00-10:15 Kieu Trinh Do, Neuherberg: Intra- and interfluid metabolite associations in human blood, urine and saliva (10+5)
10:15-10:30 Simone Wahl, Neuherberg: Metabolic consequences of body weight change in the general population – a multi-omic approach (10+5)

Coffee Break – 30 min.

Session VII: Integration of Omics data 11:00 – 12:30

Session Chairs: Christian Gieger, Fabian Theis
11:00-11:15 Liliane Pfeiffer, Neuherberg: DNA Methylation of Lipid-Related Genes Affects Blood Lipid Levels (10+5min)
11:15-11:30 Stefan Brandmaier, Neuherberg: Prioritization of Genetic Drug Targets within the CarTarDis Project (10+5)
11:30-11:45 Johannes Raffler, Neuherberg: SNIIPA: an interactive, genetic variant-centered annotation browser (10+5)
11:45-12:00 Gabi Kastenmüller, Neuherberg: Integrative analysis of metabolome wide association studies (10+5)
12:00-12:15 Jan Krumisek, Neuherberg: Systems metabolomics (10+5)
12:15-12:30 Nikola Müller, Neuherberg: Integration strategies for multi-level high dimensional data (10+5)

12:30-12:45 Closing remarks: Michael Kabesch & Iris Heid

12:45-13:45 Lunch