

Preliminary Program

Workshop Biometrische Aspekte der Genomanalyse 2017

May 4th-5th, 2017 in Heidelberg, Germany

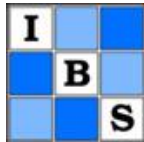
Topics:

Ancient DNA Mendelian Randomization Integration of Biological Knowledge into Genomic Prediction

Financially supported by GMDS, DGepi and IBS-DR

Organisation team:

D Drichel (AK Humangenetik, GMDS)
A Rudolph, P Ahnert (AG Genetische Epidemiologie, DGepi),
J Lorenzo Bermejo, S Szymczak (AG Populationsgenetik und
Genomanalyse, IBS-DR)



Thursday, May 4th 2017

13:30-14:00	Registration, welcome reception
14:00-15:30	Session 1: Ancient DNA (invited) Chair: Silke Szymczak Amke Caliebe & Ben Krause-Kyora
15:30-16:00	Coffee break
16:00-17:30	Session 2: Contributed Chair: Dmitriy Drichel Lucas Vicuña Genome-wide detection of positive selection in Chileans, an admixed population Felix Boekstegers Subtypes of Native American Ancestry and Leading Causes of Death: Mapuche Ancestry-Specific Associations with Gallbladder Cancer Risk in Chile Karen Garcia Mesa Hereditary breast cancer in Colombia Maren Vens Population structure and cardiovascular diseases in resettlers and the autochthone German population Torsten Pook Creation of haplotype blocks in DH-lines in maize Regina Brinster Optimal Selection of Polymorphisms for Adjustment of Population Stratification in European Association Studies
17:30-18:30	Working group meeting: AG Genetische Epidemiologie DGepi AK Humangenetik der GMDS AG Populationsgenetik und Genomanalyse der IBS-DR
19:00	Dinner (historic city center)

Friday, May 5th 2017

09:00-10:30	Session 3: Mendelian Randomization (invited)	Chair: Anja Rudolph
	Stephen Burgess	
10:30-11:00	Coffee break	
11:00-12:30	Session 4: Contributed	Chair: Maren Vens
	Sonja Neumeyer	Mendelian randomization analysis of colorectal cancer risk in association with age at menarche and age at menopause
	Janne Pott	Genetic regulation of PCSK9 plasma levels and its impact on cardio-vascular disease
	Rosa González Silos	Are Allele Counts from NGS-Data a Better Alternative than Called Genotypes for Testing Phenotype-Genotype Associations?
	Miriam Kesselmeier	Robust logistic regression in genetic association studies: Assessment of the standard technique and a robust counterpart with different observation weighting functions
	Hauke Thomsen	Meta-analysis of Correlated Traits via Summary Statistics from Genome-wide Association Studies
	Stephan Seifert	Simulation of omics data for machine learning
12:30-13:30	Lunch	
13:30-14:30	Session 5: Integration of Biological Knowledge into Genomic Prediction (invited)	Chair: TBA
	Johannes Martini	
14:30-15:00	Coffee break	
15:00-16:00	Session 6: Contributed	Chair: TBA
	Iman Meziane	Depicting AL amyloidosis through data-integration in the post-GWAS era
	Susanne Jäger	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes

	Maria Maushammer	Gut Microbial and genomic prediction of complex traits in pigs
	Kristina Schlicht	Genetic characterization of growth and production traits in turbot (<i>Scophthalmus maximus</i>)
16:00	Closing	