

IGES 2014

Location: Pirouette, Imperial Riding School Renaissance Hotel
Ungargasse 60, 1030 Vienna, Austria

Saturday, August 30 (Morning)

8:30-9:30	Session 5: Sequencing: methods and applications
Chairs: Jeanine Houwing-Duistermaat and Mariza de Andrade	
8:30-8:45	C11 Suzanne M Leal: Why NGS studies may fail: challenges and solutions for gene identification in the presence of familial locus heterogeneity
8:45-9:00	C12 Elizabeth E Blue: Variation in estimates of kinship observed between whole-genome and exome sequence data
9:00-9:15	C13 Arthur L Gilly: Robust genotype calling from very low depth whole genome sequencing data
9:15-9:30	C14 Graham RS Ritchie: Insights into the genetic architecture of anthropometric traits using whole genome sequence data
9:30-10:00	Coffee break
10:00-11:30	Session 6: Coalescent theory and population genetics
Chairs: Andrew Paterson and Justo Lorenzo Bermejo	
10:00-10:30	I4 Invited speaker Sebastian Zöllner <i>Fine mapping of complex trait loci with coalescent methods in large case-control studies</i>
10:30-10:45	C15 Maria Kabisch: Standard imputation versus generalizations of the basic coalescent to estimate genotypes
10:45-11:00	C16 Barbara Peil: Improvement of genotype imputation accuracy through integration of sequence data from a subset of the study population
11:0-11:15	C17 Hua Tang: Learning genetic architecture of complex traits across populations
11:15-11:30	C18 Daniel Shriener: Genome-wide genotype and sequence-based reconstruction of the 140,000 year history of modern human ancestry
11:30-12:30	Lunch
Committee Meetings	
11:30-12:30	GE Editorial Board Meeting (Location: Levade) Membership Committee (Location: Piaffe) Publication Committee (Location: Courbette)
12:30-13:15	IGES Business Meeting

Saturday, August 30 (Afternoon)

13:15-14:45	POSTER SESSION/Coffee Break - (P83-P164 Abstracts Present)
14:45-16:30	Session 7: Microbiomics and data integration methods
Chairs: Heike Bickeböllner and Nathan Tintle	
14:45-15:00	Presentation of best paper in Genetic Epidemiology
15:00-15:30	I5 Invited speaker Knut Rudi <i>The interface hypothesis in explaining host-bacterial interactions in the human gut</i>
15:30-15:45	C19 Wei Xu: Model comparison and selection for count data with excess zeros in microbiome studies
15:45-16:00	C20 Lizhen Xu: Bayesian latent variable models for hierarchical clustered taxa counts in microbiome family studies with repeated measures
16:00-16:15	C21 Brunilda B Balliu: A retrospective likelihood approach for efficient integration of multiple omics and non-omics factors in case-control studies
16:15-16:30	C22 Claus T Ekstrøm: Inference for high-dimensional feature selection in genetic studies
16:30-16:40	Adjourn

Invited speakers are sponsored by:

Population Genetics and Genome Analysis of the German Region of the International Biometric Society (DR-IBS)

Genetic Epidemiology of the German Society for Epidemiology (DGEpi)

Human Genetics of the German Society of Medical Informatics, Biometry, and Epidemiology (gmids)

IGES 2014 23RD ANNUAL CONFERENCE August 28-30, 2014

Imperial Riding School Renaissance Hotel
Ungargasse 60
1030 Vienna, Austria



MEETING PROGRAM



**INTERNATIONAL GENETIC
EPIDEMIOLOGY SOCIETY**

www.geneticpi.org/iges-2014

**Human
Heredit**

 **Springer**

 **WILEY-VCH**

Mini-Symposium

Location: Auditorium 21, University of Vienna
Universitätsring 1, 1010 Vienna

Thursday, August 28 (Morning)

9:00-9:45	Martin Filipits	Clinical background
9:45-10:30	Joan Bailey-Wilson	Risk prediction models in families
11:00-11:45	Bertram Müller-Myhsok	QC in omics studies
11:45-12:30	Andreas Ziegler	Study designs for predictive biomarkers
12:45	Closure	

Educational Workshop – Pharmacogenomics: When Drug Response Gets Personal

Location: Große Reitschule, Imperial Riding School Renaissance Hotel
Ungargasse 60, 1030 Vienna, Austria

Thursday, August 28 (Afternoon)

14:00-14:45	Brooke Fridley	Pharmacogenetics: past, present and future
14:45-15:30	William S Bush	Extraction of pharmacogenomics traits from electronic health records
15:30-16:00	Break	
16:00-16:45	Hae Kyung Im	Clinical utility in pharmacogenomics: getting beyond individual variants
16:45-17:30	Chris Amos	Smoking behaviour and lung cancer risk related to nicotinic acetylcholine receptor variants and metabolic variants

Sponsored by the Pharmacogenomics Research Network (PGRN)
Statistical Analysis Resource (P-STAR)

IGES 2014 Welcome Reception

18:00-19:30 August, 28 Location: Imperial Riding School Renaissance Hotel, Garden or Restaurant Borromäus (depending on the weather conditions)

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Friday, August 29 (Morning)

8:30-10:15	Session 1: Genetic data and clinical trial design	
Chairs: Andreas Ziegler and France Gagnon		
8:30-8:35	Welcome and announcements	
8:35-9:00	Presidential address "Rare and common variants: From here to there and back again" and disclosure of the best paper in Genetic Epidemiology	
9:00-9:30	I1 Invited speaker Martin Posch <i>Enrichment designs for the development of personalized medicine</i>	
9:30-9:45	C1 Christian Müller: Identification of blood pressure candidate genes by population-based transcriptome analyses within the MetaXpress Consortium	
9:45-10:00	C2 Jacob B. Hall: Mixed-model analysis of common variation reveals pathways explaining variance in AMD risk	
10:00-10:15	C3 Anurag Verma: A phenome-wide association study of numerous laboratory phenotypes in AIDS clinical trials group protocols	
10:15-10:45	Coffee break	
10:45-12:15	Session 2: Causal inference and pleiotropy	
Chairs: Sanjay Shete and Inke R König		
10:45-11:15	I2 Invited speaker Krista Fischer <i>Causal association structures in -omics data: how far can we get with statistical modeling?</i>	
11:15-11:30	C4 Shefali S Verma: eMERGE phenome-wide association study identifies clinical associations and pleiotropy for functional variants	
11:30-11:45	C5 Quan Long: A novel G-BLUP-like phenotype predictor leveraging regional genetic similarity and its applications in predicting disease severity and drug response	
11:45-12:00	C6 Antonia A Flaquer: Mitochondrial GWA analysis in several complex diseases using the KORA population	
12:00-12:15	C7 Françoise Clerget-Darpoux: A dramatic resurgence of the garbage-in garbage-out syndrome in the 21st century	
12:15-13:00	Lunch	
Committee Meetings		
12:15-13:00	Program Committee (Location: Piaffe) Education Committee (Location: Levade)	

Friday, August 29 (Afternoon)

13:00-14:15	Session 3: Epigenetics and personalized medicine	
Chairs: Christine Fischer and Michael Nothnagel		
13:00-13:30	I3 Invited speaker Christoph Bock <i>The relevance of epigenomics for personalized medicine</i>	
13:30-13:45	C8 Hae Kyung Im: Large Scale Prediction and Dissection of Complex Traits	
13:45-14:00	C9 Jennifer H Barrett: Genetic predictors of longer telomeres are strongly associated with risk of melanoma	
14:00-14:15	C10 Silva Kasela: Detection of cis and trans eQTLs/mQTLs in purified primary immune cells	
14:15-15:45	POSTER SESSION/Coffee Break - (P1-P82 Abstracts Present)	
15:45-17:15	Session 4: Neel and Williams awards	
Chairs: Alexander F Wilson and Celia Greenwood		
Neel Candidates		
15:45-16:00	A1 Haley J Abel: A novel method using cross pedigree shared ancestry to map rare causal variants in the presence of locus heterogeneity	
16:00-16:15	A2 Mar Rodriguez Girondo: Survival analysis with delayed entry in selected families with application to human longevity	
16:15-16:30	A3 Mohamad Saad: Combining family- and population-based imputation data for association analysis of rare and common variants in large pedigrees	
Williams Candidates		
16:30-16:45	A4 Christian Benner: Mixed modeling for time-to-event outcomes with large-scale population cohorts and genome-wide data	
16:45-17:00	A5 Gao T Wang: The collapsed haplotype pattern method for linkage analysis of next-generation sequencing data	
17:00-17:15	A6 Shuai SW Wang: Meta-analysis approach for haplotype association tests: a general framework for family and unrelated samples	
17:15-17:30	Sanjay Shete: <i>On the anniversary of the first issue of Genetic Epidemiology</i>	
18:00-21:30	Conference evening in the MOYA	



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