INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Newsletter - Pre-Election 2015 October

Contents

Letter from the President
France Gagnon

Dear IGES Community,

What a scientifically stimulating and energizing meeting we had in Baltimore!

A warm thank you to all of you who attended the meeting! I would like to offer a special thank you to the local organizing committee, Alec Wilson, Priya Duggal, Alison Klein and Lynn Carrasco, and to the scientific program committee who worked intensely under the leadership of André Scherag to offer one of our best programs. Well done!

Heartfelt congratulations to our 2015 awardees: Andreas Ziegler (Leadership Award), Helen R. Warren (Neel Award), Shuai Li (Williams Award), and to the Robert Elston Best Paper Award team led by Hae Kyung Im.

I am deeply grateful to our officers and board members, committee and community members, who have contributed so many fantastic suggestions about ways to improve the annual meeting and the Society – so that IGES moves forward surpassing its best years so far! Our community is composed of dynamic and scientifically innovative members; let's apply some of this energy and creativity to improve the Society! Let's make IGES the place to go for anyone interested in sharing ideas and collaborating with like-minded colleagues passionate about finding solutions to the challenges faced toward improving population health through genetic epidemiologic and statistical research.
In the next few months, I will be working closely with officers, board members and committee chairs to implement suggestions made at our business meeting. I will report back about some of our progress in the next bulletin.

In closing, let me take this opportunity to remind you that the candidates in our upcoming election are presented in this IGES Newsletter issue. Please let us know who you wish to represent you and vote!

Again, a warm thank you to all!

France

Treasurer's Corner
Mariza de Andrade

The 24th Annual IGES Conference in Baltimore was successful on many fronts, including this year's opportunity to participate in a shared mini-symposium with ASHG, and a vigorous meeting program offered to participants. I would like to express appreciation to the Program Committee Chair André Scherag and the Program Committee for organizing this expansive and excellent program for this year's IGES conference.

I would also like to thank IGES' current Past-President, Alec Wilson, for his leadership, skilful negotiations, and fiscal prudence, along with meeting organizers Priya Duggal and Allison Klein for their diligence, commitment, and hard work to make the IGES meeting a success. The hotel and conference site worked well for the IGES conference and the National Aquarium was a fabulous place to have our banquet!

From a Treasury viewpoint, shared resources and the concurrent session with ASHG worked fiscally well for our Society and meeting attendees alike. Due to careful negotiations and management of resources, IGES was able to make a profit on the meeting. Profitability ensures that we can continue to keep both membership and registration rates reasonable in order to encourage student participation, as well as remain able to build a dynamic program of invited speakers.

IGES Membership registration for 2016 will open in November 2015 and at the same rates as for 2015 for early-bird registrants (if paid by January 1, 2016; a late fee of $25 for regular membership is incurred if you pay on January 2, 2016 or after). Membership is valid from January to December on a calendar year basis, and includes free online access to our journal "Genetic Epidemiology", which is otherwise unavailable to individuals, but only on institutional level for over $4K annually. Other benefits of membership are reduced registration rates for the annual meeting, as well as the opportunity for members to have information and job openings posted on our website at no charge.

As a reminder, please allow me to mention that IGES is a charitable and educational organization, and any contribution provided by its members is tax-deductible as allowable by law. This can be done along with your membership renewal process. Your continuous support of IGES is appreciated!

I am looking forward to seeing you all next year in Toronto.

Mariza de Andrade
Treasurer

IGES 2016 Membership Drive

Dear IGES members,

It is now time to renew your membership for 2016. Membership registration will be open by November 1, 2015 at the very latest. The membership fee is due by January 1, 2016.
Please observe the fact that membership registration and annual meeting registration have been separate since 2014. Therefore you are NOT automatically registered as a member just with meeting attendance. A separate registration for Society membership is necessary.

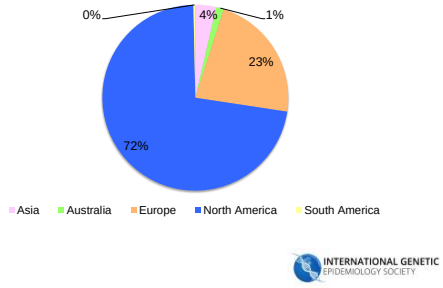
If you already renewed your membership for 2016 at the Baltimore meeting, your receipt (for professional members) will specify "Professional 2015 IGES Member Registration-(fee includes entrance to banquet)" and "2016 IGES Professional Membership" separately. If it ONLY specifies "Professional 2015 IGES Member Registration-(fee includes entrance to banquet)", then you registered only for the 2015 annual meeting. We will try to change the meeting receipt for 2016 in order to avoid any confusion in the future with respect to membership registration being separate.
These are the rates for 2016 membership:

- Regular member **130 USD**, if paid by January 1, 2016 (early-bird)
- Regular member **155 USD** if paid on or after January 2, 2016 (approved at the Baltimore Business Meeting)
- Student member with online access to Journal **68 USD**, please pay by January 1, 2016
- Student member without online access to Journal **25USD**, please pay by January 1, 2016

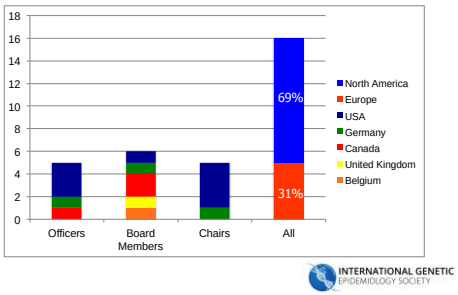
IGES Demographics
Distribution by continent and gender

Currently, 72% of IGES' members reside in the continental region of North America. This correlates well with the number of official positions (69%) in the Society occupied by North American resident members. However, the Board is not representative of the continental regional membership distribution as it stands currently. These data were presented during the recent 2015 IGES business meeting in Baltimore, just prior to the IGES Meeting.

Membership by continent

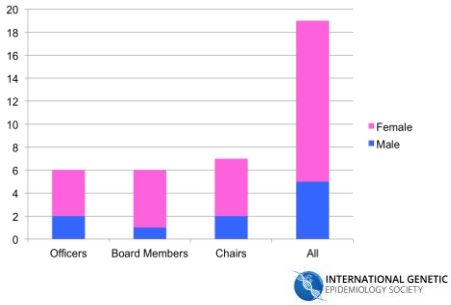


2015 IGES leadership by country



It is interesting to note that nearly all the members have made no information available to the IGES membership database with respect to their gender. IGES only has this information for the official positions, which is displayed here.

2015 IGES leadership by gender



2016 IGES Elections
(Please vote – List of Candidates)

Election Period November 1 – December 15, 2015

All current IGES members are eligible to vote in the upcoming election of members to the Board of Directors. You will receive your ballot paper electronically and separate from this newsletter. This newsletter contains the biosketches of all candidates.

Candidate for the position of President-Elect to serve as President in 2017:

Andrew Morris

Candidates to serve as members on the Board of Directors (you will be requested to select only 2 candidates):

- **Julia Bailey**
- **Xihong Lin**
- **Marylyn D. Ritchie**
- **Nathan Tintle**

2016 Elections
Candidate for IGES President – Andrew Morris

Keywords: Motivated, dedicated, creative, focused, and approachable

Andrew Morris is Professor of Statistical Genetics and Wellcome Trust Senior Research Fellow at the University of Liverpool, UK, and has visiting appointments at the University of Oxford, UK, and the University of Tartu, Estonia. His research focusses on the development and evaluation of novel statistical methodology for the analysis of the "next-generation" of genome-wide association and re-sequencing studies of complex human traits. Current themes of his research include: (i) discovery of novel loci through improved modelling of traits, including multivariate methodologies for correlated intermediate phenotypes, trans-ethnic meta-analysis across the allele frequency spectrum, and survival analysis of "time to event" outcomes; and (ii) fine-mapping of loci through aggregation of genetic studies from multiple ethnic groups, and integration with genomic annotation in relevant tissues to allow inference of the causal variants and transcripts, and the mechanisms through which they impact association signals. Andrew co-leads analytical groups in several international consortia investigating the genetic contribution to type 2 diabetes, glycemic traits, anthropometric measures, birth weight, blood pressure, endometriosis, and kidney function. In 2010, he and his co-authors won the award for "Best Paper in *Genetic Epidemiology*". He has previously contributed to ground-breaking studies of human genetic variation and its impact on common diseases including the International HapMap Consortium and the Wellcome Trust Case Control Consortium. He has co-edited books on "Statistics for Geneticists: Analysis of complex disease association studies" and "Assessing Rare Variation in Complex Traits: Design and Analysis of Genetic Studies". Andrew has served as a member of the IGES Board of Directors (2012-2014) and is currently an IGES Program Committee member (2015-present), as well as serving as a member of the Editorial Board of *Genetic Epidemiology*.

Five selected publications (as first or senior author):

- Horikoshi M, *et al*. (2015). Discovery and fine-mapping of glycaemic and obesity-related trait loci using high-density imputation. *PLoS Genet* 11: e1005230.
- Shungin D, *et al*. (2015). New genetic loci link adipose and insulin biology to body fat distribution. *Nature* 518: 187-96.
- Mahajan A, *et al*. (2014). Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nat Genet* 46: 234-44.
- Franceschini N, *et al.* (2012). Discovery and fine mapping of serum protein loci through transethnic meta-analysis. *Am J Hum Genet* 91: 744-53.
- Morris AP, *et a*l. (2012). Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat Genet* 44: 981-90.

2016 Elections
Candidates for the Board of Directors

Julia Bailey is the Director of the Statistical Genetics Core at the Epilepsy Genetics/Genomics Laboratory, West LA VA and an Adjunct Associate Professor in the Department of Epidemiology at UCLA where she teaches genetic epidemiology and serves on the curriculum and admissions committees. Her research involves genetic epidemiology of epilepsy and post traumatic stress disorder. Focus of her research is on gene localization through family-based linkage and association methods as well as next generation deep sequencing technology.She is co-PI of an international GENESS Consortium with members from the USA, Mexico, Honduras, El Salvador, Peru, Brazil, Spain, Japan and Canada. Within their consortium they ascertain large, multigenerational families, as well as cases and controls for genetic and clinical analyses. To date they have identified several genes including EFHC1 for juvenile myoclonic epilepsy, which they found the old fashioned way – linkage then mutation analyses then in vitro and in vivo functional analyses. They have many more genes in the pipeline thanks to next gen sequencing and advice Drs. Robert Elston and Ken Lange gave their neurologist/biochemist co-PI before she was even in grad school to 'collect large families'.

She was on the IGES membership committee 2000-2009, IGES Ambassador to Latin America 2000-present, on the educational committee 2009-2013 (Chair 2013), and her IGES claim to fame is that she is the student who asked for a student rate policy at the first IGES meeting. Julia has been an active participant at the Genetic Analyses Workshop (GAW) since 1992 and is currently a member of the GAW Advisory Committee.

Keywords: Innovative, organized, open-minded, inclusive, fun

Five selected publications:

- **Bailey JN**, Almasy L (1995): A brute force dichotomization approach to quantitative trait linkage analyses. *Genetic Epidemiology* 12:719-722.
- Suzuki T, Delgado-Escueta AV, Aguan K, Alonso ME, Shi J, Hara Y, Nishida M, Numata T, Medina MT, Takeuchi T, Morita R, Bai D, Ganesh S, Sugimoto Y, Inazawa J**, Bailey JN,** Ochoa A, Jara-Prado A, Rasmussen A, Ramos-Peek J, Cordova S, Rubio-Donnadieu F, Inoue Y, Osawa M, Kaneko S, Oguni H, Yamakawa K (2004): Mutations in EFHC1 cause juvenile myoclonic epilepsy. *Nature Genetics* 36(8):842-849.
- **Bailey JN**, Breidenthal SE, Jorgensen JM, McCracken JT, Fairbanks LA (2007). The association of DRD4 and novelty seeking is found in a nonhuman primate model. *Psychiatric Genetics* 17(1):23-7.
- Goenjian A, Walling DP, Noble EP, Ritchie T, Goenjian HA, **Bailey JN** (2008). Heritabilities of symptoms of posttraumatic stress disorder, anxiety, and depression in earthquake exposed Armenian families. *Psychiatric Genetics* 18(6):261-6.
- Goenjian AK, Noble EP, Steinberg AM, Walling DP, Stepanyan ST, Dandekar S**, Bailey JN**. Association of COMT and TPH-2 genes with DSM-5 based PTSD symptoms. J Affect Disord. 2014 Oct 22;172C:472-478. doi: 10.1016/j.jad.2014.10.034. PMID: 25451452

Xihong Lin is Henry Pickering Walcott Professor and Chair of the Department of Biostatistics as well as Coordinating Director of the Program of Quantitative Genomics at the Harvard T. H. Chan School of Public Health. Dr. Lin's research interests lie in the development and application of statistical and computational methods for analysis of massive genetic and genomic, epidemiological, environmental, and clinical data. Dr Lin's specific areas of expertise include statistical methods for genome-wide association studies and next generation sequencing association studies, genes and environment, analysis of integrated data, and statistical learning methods for massive data. She received the 2006 Presidents' Award for outstanding statistician from the Committee of the Presidents of Statistical Societies (COPSS), and the 2002 Mortimer Spiegelman Award for outstanding biostatistician from the American Public Health Association. She is an elected fellow of the American Statistical Association, Institute of Mathematical Statistics, and International Statistical Institute. Dr. Lin was the Chair of the Committee of the Presidents of the Statistical Societies (COPSS) between 2010 and 2012. She is a former member of the Committee of Applied and Theoretical Statistics of the US National Academy of Science. Dr. Lin is a recipient of both the MERIT award (2007-2015) and the Outstanding Investigator Award (2015-2022) from the National Cancer Institute, which provides long-term research grant support. She is the contacting PI of the Program Project on Statistical Informatics in Cancer Research, and the T32 training grant on interdisciplinary training in statistical genetics and computational biology. She has served on numerous editorial boards of statistical journals. She was the former Coordinating Editor of *Biometrics*, and the co-editor of *Statistics in Biosciences, and* the Associate Editor of the *Journal of the American Statistical Association* and *American Journal of Human Genetics*. She was the permanent member of the NIH study section of Biostatistical Methods and Study Designs (BMRD), and has served on a large number of other study sections at NIH and NSF.

Keywords: Partnership with statistical societies; Boosting membership; Increasing visibility of IGES; Engagement of members; Improving society finance

Five selected publications:

- Wu, M.C., Lee, S., Cai, T., Li, Y., Boehnke, M., **Lin, X** (2011) Rare variant association testing for sequencing data using the Sequence Kernel Association Test (SKAT). Am J Hum Genet, 89(1):82-93.
- Lin, X., Li, L., Christiani, D.C., **Lin, X**. (2013) Test for interactions between a genetic marker set and environment in generalized linear models. Biostatistics, 14(4): 667-681.
- Lee, S., Abecasis, G., Boehnke, M., **Lin, X**. (2014) Rare-variant association analysis: Study designs and statistical tests. Am J Human Genetics, 95(1):5-23.
- Wang, C., Zhan, X., Bragg-Gresham, J., Kang, H.M., Stambolian, D., Chew, E.Y., Branham, K., Heckenlively, J., The FUSION Study, Fulton, R., Wilson, R.K., Mardis, E.R., **Lin, X**., Swaroop, A., Zollner, S., Abecasis, G.R. (2014). Estimating individual ancestry using next generation sequencing. Nature Genetics, 46(4):409-415.
- Huang, Y., Liang, L, Moffatt, M., Cookson, W., and **Lin, X**. (2015). iGWAS: Integrative Genome-Wide Association Studies of Genetic and Genomic Data for Disease Susceptibility Using Mediation Analysis. Genetic Epidemiology, 39. 347-359.

Marylyn D. Ritchie is a Professor in the Department of Biochemistry and Molecular Biology and director for the Center for Systems Genomics at The Pennsylvania State University. She is also the founding Director of Biomedical and Translational Informatics at Geisinger Health System. Dr. Ritchie is a statistical and computational geneticist with a focus on understanding genetic architecture of complex human disease. She has expertise in developing novel bioinformatics tools for complex analysis of big data in genetics, genomics, and clinical databases, in particular in the area of Pharmacogenomics. Dr. Ritchie has received several awards and honors including selection as a Genome Technology, Rising Young Investigator in 2006, an Alfred P. Sloan Research Fellow in 2010, a KAVLI Frontiers of Science fellow by the National Academy of Science for each of the past four consecutive years (2011-2014), and she was named one of the most highly cited researchers in her field by Thomas Reuters in 2014. Dr. Ritchie has extensive experience in all aspects of genetic epidemiology and translational bioinformatics as it relates to human genomics. She also has extensive expertise in dealing with big data and complex analysis including GWAS, next-generation sequencing, CNVs, data integration of meta-dimensional omics data, Phenome-wide Association Studies (PheWAS), and development of data visualization approaches.

Keywords: bioinformatics, innovative, systems genomics, precision medicine, leader

Five selected publications:

- ***Ritchie MD***, Hahn LW, Roodi N, Bailey LR, Dupont WD, Plummer WD, Parl FF, Moore JH. Multifactor dimensionality reduction reveals high-order interactions among estrogen metabolism genes in sporadic Breast Cancer. American Journal of Human Genetics, 69:138-147 (2001). PM 11404819, PMC 1226028
- ***Ritchie MD***, Denny JC, Crawford DC, Havens A, Weiner J, Pulley JM, Basford M, Balser JR, Masys DR, Haines JL, Roden DM. Robust replication of genotype-phenotype associations across multiple diseases in an electronic medical record. American Journal of Human Genetics, 86(4):560-72 (2010). doi: 10.1016/j.ajhg.2010.03.003. PM 20362271, PMC2850440
- ***Ritchie MD***, Holzinger ER, Li R, Pendergrass SA, Kim D. Methods of integrating data to uncover genotype-phenotype interactions. Nat Rev Genet. 2015 Feb; 16(2):85-97. doi: 10.1038/nrg3868. Epub 2015 Jan 13. Review. PM 25582081
- S.A. Pendergrass, K. Brown-Gentry, S. Dudek, E.S. Torstenson, R.Goodloe, J.L. Ambite, C.L. Avery, S. Buyske, P. Bůžková, C. Cai, E. Deelman, M.D. Fesinmeyer,C. Haiman G. Heiss, L.A. Hindorff, C.-N. Hsu; R. D. Jackson; C. Kooperberg,L. LeMarchand, Y. Lin, T. C. Matise, K.R. Monroe, L. Moreland, A. Reiner, R. Wallace, L. R. Wilkens, D.C. Crawford, ***M.D. Ritchie***. Phenome-Wide Association Study (PheWAS) for Detection of Pleiotropy within the Population Architecture Using Genomics and Epidemiology (PAGE) Network. PLoS Genetics, 2013 January; 9(1): e1003087. PM 23382687, PMC 3561060
- Moore CB, Wallace JR, Wolfe DJ, Frase AT, Pendergrass SA, Weiss KM, ***Ritchie MD***. Low frequency variants, collapsed based on biological knowledge, uncover complexity of population stratification in 1000 genomes project data. PLoS Genet. 2013 Dec; 9(12):e1003959. doi: 10.1371/journal.pgen.1003959. Epub 2013 Dec 26. PM 24385916, PMC 3873241

Nathan Tintle has been involved in genetic epidemiology research for the past 15 years, with a primary focus on the statistical design and analysis of association studies. His main areas of interest include considering the downstream effects of genotype uncertainty, the mathematical structure of association tests and post-hoc approaches to gene-based and pathway-based testing strategies. More recently, his research interests have expanded to include applied research in metabolomics/genetics of fatty acids, and is currently participating in multiple consortia and meta-analyses related to this topic. He has published over 50 peer-reviewed articles, most of which are in statistical genetics and many of which have involved undergraduate student collaborators. He has been PI or co-PI for numerous research grants, most of which explore novel methods of analyzing genetic data, with an emphasis on doing cutting edge science with undergraduate student trainees---novel work that has earned him numerous teaching, training and research awards. Nathan has worked with over 70 undergraduate students on statistical genetics research over the last 10 years, with most students going on to pursue graduate degrees in statistical genetics and biostatistics. He has been an active member of IGES for many years, currently serves on the Scientific Program Board (2014-16), and will be the program chair of IGES 2016 (Toronto). Nathan Tintle is Associate Professor of Statistics at Dordt College, Iowa, United States, where he also serves as the Director for Research and Scholarship and Chair of the Department of Mathematics, Statistics and Computer Science.

Keywords: Passionate, Focused, Dedicated, Hard-working, Service-oriented

Five Selected Publications:

- Liu K, Luedtke A, ***Tintle NL*** (2013) “Optimal methods for using posterior probabilities in association testing” Human Heredity. 75(1): 2-11.
- S, Zawistowski M, ***Tintle NL*** (2013) “A geometric framework for the evaluation of rare variant tests of association” Genetic Epidemiology. 37(4): 345-357.
- ***Tintle NL***, Pottala JV, Lacey S, Ramachandran V, Westra J, Rogers A, Clark J, Olthoff B, Larson M, Harris W, Shearer G. “A genome wide association study of fourteen red blood cell fatty acids in the Framingham Heart Study” (2015) Prostoglandins, Leukotrienes and Essential Fatty Acids. 94:65-72.
- ***Tintle NL***, Newman JW, Shearer GC. (2015) “Optimal fatty-acid profiles and metabotypes for prevention of acute coronary syndrome using biomarkers of fatty-acid elongase and desaturase” Metabolomics. 11(5):1327-1337.
- Greco B, Hainline A, Arbet J, Grinde K, Benitez A and ***Tintle NL***. (2015) “A general approach for combining diverse rare variant association tests provides improved robustness across a wider range of genetic architecture” European Journal of Human Genetics. Accepted. May 2015. To appear.

NCI Up for a Challenge (U4C)
Competition reminder

Reminder: Submissions Due for NCI Up For A Challenge (U4C) – January 15, 2016

By now, we hope that the IGES community has heard about the NCI's Division of Cancer Control and Population Sciences (DCCPS) prize competition. The competition, "Up For a Challenge (U4C): Stimulating Innovation in Breast Cancer Genetic Epidemiology," aims to leverage a tremendous amount of existing germline DNA data from breast cancer genome-wide association studies to stimulate innovation and ultimately facilitate new scientific discoveries that will impact the genomic basis of breast cancer.

It's not too late to participate!

The U4C shifts the focus away from individual genetic variants to pathways (e.g., combinations of genes, genetic variants, or sets of genomic features) and emphasizes the development of new analytical methods to maximize the utilization of existing data and enable researchers to pursue new directions of research.

U4C participants are encouraged to leverage at least one of seven existing datasets from breast cancer genome-wide association studies, along with other relevant publicly accessible datasets. There are approximately 13,000 breast cancer cases and controls from ethnically diverse populations in the seven U4C datasets.

Additionally, participants are encouraged to incorporate additional relevant, publicly available data sets (e.g., the International Cancer Genome Consortium, The Cancer Genome Atlas, the Encyclopedia of DNA Elements, and the Genotype-Tissue Expression program) to complement the U4C data.

For more information about the challenge—including eligibility rules, prizes, and frequently asked questions—visit the U4C website (https://www.synapse.org/upforachallenge). Video and slides from the July 23, U4C Introductory Webinar and the October 27 "Details on the Submission Process for U4C" can be found on the News and Updates page.

Deadline: Submissions are due January 15, 2016.

Annual Meeting 2016
Toronto – save the date!

The 25th IGES Annual Meeting will be held in the city of ***Toronto, Canada***, from ***October 24 until October 26, 2016***. Save the date in your diaries for the Meeting and celebrations!

Committees

Current news and announcements from the IGES Committees

Publication Committee
Chair: Josée Dupuis

Congratulations go to

Heather Wheeler

Heather E. Wheeler, Keston Aquino-Michaels, Eric R. Gamazon, Vassily V. Trubetskoy, M. Eileen Dolan, R. Stephanie Huang, Nancy J. Cox, and Hae Kyung Im

whose paper, published in *Genetic Epidemiology* in 2014 (Genet. Epidemiol., 38: 402–415. doi: 10.1002/gepi.21808),

Poly-Omic Prediction of Complex Traits: OmicKriging

was selected as winner of the

Robert C. Elston Award for Best Paper

Abstract:
High-confidence prediction of complex traits such as disease risk or drug response is an ultimate goal of personalized medicine. Although genome-wide association studies have discovered thousands of well-replicated polymorphisms associated with a broad spectrum of complex traits, the combined predictive power of these associations for any given trait is generally too low to be of clinical relevance. We propose a novel systems approach to complex trait prediction, which leverages and integrates similarity in genetic, transcriptomic, or other omics-level data. We translate the omic similarity into phenotypic similarity using a method called Kriging, commonly used in geostatistics and machine learning. Our method called OmicKriging emphasizes the use of a wide variety of systems-level data, such as those increasingly made available by comprehensive surveys of the genome, transcriptome, and epigenome, for complex trait prediction. Furthermore, our OmicKriging framework allows easy integration of prior information on the function of subsets of omics-level data from heterogeneous sources without the sometimes heavy computational burden of Bayesian approaches. Using seven disease datasets from the Wellcome Trust Case Control Consortium (WTCCC), we show that OmicKriging allows simple integration of sparse and highly polygenic components yielding comparable performance at a fraction of the computing time of a recently published Bayesian sparse linear mixed model method. Using a cellular growth phenotype, we show that integrating mRNA and microRNA expression data substantially increases performance over either dataset alone. Using clinical statin response, we show improved prediction over existing methods. We provide an R package to implement OmicKriging (http://www.scandb.org/newinterface/tools/OmicKriging.html)

Hae Kyung Im accepted the award on behalf of the authors at the IGES Annual Meeting in Baltimore

Program Committee
Chair: André Scherag

Congratulations to **Helen R. Warren** of the William Harvey Research Institute at Queen Mary University London, who was selected as the winner of the

2015 James V. Neel Young Investigator Award

for the best presentation by a young scientist at the 2015 Annual Meeting in Baltimore. The winning presentation was titled:

"Investigating the Association of Rare Genetic Variants with Blood Pressure Traits"

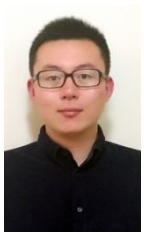
Following a BSc in mathematics and then a PhD in statistics, her first postdoc position in genetic epidemiology was at The London School of Hygiene and Tropical Medicine, working on statistical methodology for genetic risk prediction. Helen is currently a postdoctoral statistical geneticist at the William Harvey Research Institute, Barts and The London School of Medicine, Queen Mary University of London, working with Prof Mark Caulfield and Prof Patricia Munroe in cardiovascular genetics. As the analyst for the ASCOT and BRIGHT studies, her focus is on the genetic discovery of blood pressure, heart rate and ECG traits, and pharmacogenetics of anti-hypertensives and statins, as well as contributing to many other consortia projects.

Our congratulations also go out to **Shuai Li** from the University of Melbourne on winning the

2015 Roger Williams Award

for the best presentation by a student at the 24th Annual IGES Meeting in Baltimore for his presentation titled:

"The variation of DNA methylation at vast the majority of CpG sites are due to individual factors but not genetic or shared environment factors".



After completing his bachelor of medicine and bachelor of surgery (BMBS) in preventive medicine at Peking University, Beijing, China, Shuai went on to complete his MSc in epidemiology, also in Beijing, on a family study of polygenic risk score and ischemic stroke.
He is currently a PhD student at the University of Melbourne working on a family study of DNA methylation and breast cancer risk factors.

Editor's Corner of Genetic Epidemiology
Editor-in-Chief: Sanjay Shete

Dear IGES members, Genetic Epidemiology as the official journal for our Society invites you to submit your work in the fields of statistical, epidemiological, and population genetics. Genetic Epidemiology is interested in both the methodological and applied papers. Examples include: applied genetic epidemiology papers (e.g. meta-analyses of GWAS, Secondary analyses of GWAS data), gene and environment interactions, risk prediction models, DNA methylation and RNA seq data analysis. Other novel work is welcome!

We are also planning to have a special issue on Cancer Genetic Epidemiology (details forthcoming). If you have interesting work related to this topic, please contact the editor or editorial board members (John Witte, Jaya Satagopan, Daniel Schaid, or Alisa Goldstein).

Benefits of Publishing in Genetic Epidemiology: There is no publishing cost for authors (e.g. page charges, black-white figures). In addition, every year, the journal selects a few papers for "open access" (unrestricted online access) publishing at no cost to the authors. Please register on Wiley online library to receive email alerts for new content and saved searches. The website for registration is http://onlinelibrary.wiley.com/user-registration.

AUTHOR SERVICES: Wiley has an updated list of services it offers our authors. For more information, please visit http://authorservices.wiley.com

We now offer Kudos (https://www.growkudos.com/), a social media service that provides authors with a free set of tools to explain and share their published work for greater usage and impact. Authors also receive access to a publication dashboard via which they can view downloads, citations, and altmetrics for their articles.

This is your journal: make it reflect your work by submitting your papers to Genetic Epidemiology!

Thanks and I look forward to your active participation in the journal.

Sanjay Shete
Editor-in-Chief
sshete@mdanderson.org

Education Committee
Chair: Elizabeth Gillanders

The IGES Education Committee works on a variety of educational and training initiatives each year. These activities can be 1) internally focused, targeting the IGES membership or 2) externally focused, targeting the membership or education committees of other societies or groups. Ideally we would coordinate one of each type of activity per year.

This year our activities focused externally on the ASHG/IGES Joint Symposium: Prospecting for Hidden Heritability: Undiscovered Nuggets or Fool's Gold?, which was co-moderated by Alexander Wilson, NIH/NHGRI and Carole Ober, University of Chicago. The joint symposium was very well attended. Speakers presented new data and analyses of "hidden heritability" and, in a panel discussion format, (heatedly) debated approaches to identify causative variants through study designs and analytic strategies. Thanks to all who helped contribute to the session's success.

In the upcoming year we, plan to continue our activities related to education sessions as well as 1) investigate the use of the new IGES intranet for education resource sharing and 2) investigate developing a "genetic epidemiology" 101 course, which could help develop the IGES brand.

We welcome a number of new members this year. All members are listed below:

Current Members:
Sarah Buxbaum
Todd Edwards
Elizabeth Gillanders
Ellen Goode
Heather Ochs-Balcom
George Papanicolaou
Marylyn Ritchie
Tae-Hwi Schwantes-An "Linus"
Mark Seielstad
Stephanie Santorico
Silke Szymczak

Communications Committee
Chair: Heike Bickeböller

Thank you for your enthusiasm with our plans proposed for 2015-2016.

At the IGES meeting in Baltimore, a special call for expertise and service was made for the communications committee. We are very glad that members were excited among others about the plan to implement an intranet for the Society and are willing to support us and that several very qualified and dynamic colleagues have come forward to offer their time to support these activities.

The following members will join the Communications Committee:
Sahir Rai Bhatnagar, Elizabeth Blue (Facebook), Todd L. Edwards, Priya Dugal (Twitter), David Fardo
Hae Kyung Im

Current and ongoing members are:
Heike Bickeböller (Chair), Jessica Dennis (web master), Claire Simpson, Kristel van Steen

Our appreciation goes to Saonli Basu and Jin Zhou for their service, as they will both be rotating off the committee at the end of year after 3 years of participation. We are already giving these thanks, as it should be mentioned now that Jin Zhou will stay our Facebook and Twitter master until the end of the year.

Young Investigators Committee
Chair: Elizabeth Blue

Student-mentor lunch: The mentoring session was a success! Over 60 young investigators and 8 mentors met for an hour and participated in lively discussion. Given the numbers presented at the business meeting, this suggests nearly every trainee attending IGES attended this session. Many thanks to our fantastic mentors for their participation; we could not have done it without you. Contact us if you would like to participate as a mentor in such an event next year.

Job fair: We had a great turn out at the first IGES job fair. At the peak time, ~50 people were discussing job opportunities, and a dozen remained after nearly two hours. We are continuing the fair on Facebook, search for "International Genetic Epidemiology Society (IGES) Next Generation" to see the job postings from the fair. Contact us to add your advertisement to the site.

Areas for growth: We are looking for new arenas to assist the Society and its junior members. Current discussions include a trainee-organized session at IGES, a social event on the night before IGES 2016, facilitating room-sharing and child care at IGES 2016, educational outreach, and attracting new members to the Society. Contact us with any comments or ideas for what you would like from the Committee.

Committee members:
Stella Aslibekyan
Liz Blue (chair; em27@uw.edu)
Han Chen
Sarah Gagliano
Audrey Hendricks
Lara Sucheston-Campbell
Nora Zwingerman

2015 Leadership Award

The International Genetic Epidemiology Society presents the 2015 IGES Leadership Award to

Andreas Ziegler

in recognition of his outstanding leadership through research, teaching, and service to the Society.

Andreas Ziegler is Professor and Head of the Institute of Medical Biometry and Statistics at the University of Lübeck, Germany. After studying statistics and mathematics at the University of Munich, Germany, he obtained his doctoral degree from the University of Dortmund, Germany, and his habilitation from the University of Marburg, Germany. He was President of the German Region of the International Biometric Society and has received numerous awards, including the Susanne-Dahms-Medal for outstanding service to the German Region of the International Biometric Society.

Over the past decades, Andreas Ziegler has contributed to the field of genetic epidemiology in a number of roles. He has left a remarkable footprint in research, in which he is oriented towards both methods and applications, visible in more than 400 co-authored papers. He is also a devoted teacher. Those who experience him in classes or tutorial talks are impressed by his profound knowledge, precision, and effort to reach everyone in the audience. Accordingly, his review papers are frequently cited and the textbook “A Statistical Approach to Genetic Epidemiology” has become well known and is used by other teachers in our field. The award especially honors his service to IGES, because, after having served on several committees, he led the Society as President in a time of severe fiscal austerity. Combining creative and visionary ideas with whole-hearted personal engagement and the spirit to enforce suitable measures, Andreas Ziegler ensured the financial survival and earned a place in the annals of IGES.

Roger M. Siervogel
Obituary

In remembrance of Roger M. Siervogel Ph.D., former Director of the Lifespan Health Research Center and Wright State University Boonshoft School of Medicine faculty member, who died on April 15, 2015 at the age of 70.

Dr. Siervogel served as the Secretary/Treasurer of the International Genetic Epidemiology Society from 1998 to 2000. He earned his Ph.D. in Genetics at the University of Oregon in 1971 and conducted postdoctoral research at the University of North Carolina, Chapel Hill under the direction of Dr. Robert C. Elston. He held faculty appointments in pediatrics and community health and had the honorary title of Fels Professor during his tenure at Wright State. Dr. Siervogel received many honors in his 36 years with the University: in 2002, he received the Wright State University Presidential Award for Faculty Excellence in Research and in 2006 he was named the Wright State Board of Trustees Brage Golding Distinguished Professor of Research.

2015 IGES Officials

The names of all the IGES officials are available on our **website:**

http://www.geneticepi.org/organization/

Current **officers are**: President: France Gagnon; Past President: Alexander F. Wilson; President-Elect: Josée Dupuis; Treasurer: Mariza de Andrade; Secretary: Heike Bickeböller; Editor-in-Chief, Genetic Epidemiology: Sanjay Shete.

Board members are the officers and the following 6 people: Jenny Barrett, L. Adrienne Cupples, Celia Greenwood, Inke König, Andrew Paterson, and Kristel Van Steen.

The **Education Committee** is chaired by Elizabeth Gillanders. The **ELSI Committee** is chaired by Claire Simpson. The **Membership Committee** in chaired by Yan Sun. Please refer to the website for the respective committee members.

This year's **Publications Committee** is chaired by Josée Dupuis. Standing member as Editor of Genetic Epidemiology is Sanjay Shete. Further members are Shelley Bull, Denise Daly, France Gagnon, Peter Kraft, Rasika Mathia, Bertram Müller-Myhsok, and Michael Nothnagel.

The **Program Committee** for 2015 is chaired by André Scherag. Further members are Justo Lorenzo Bermejo, Emmanuelle Bouzigon, Andrew Morris, Andrew Paterson, Nathan Tintle, Alec Wilson, France Gagnon and Josée Dupuis.

The **Young Investigators Committee** is chaired by Elizabeth Blue (formerly Marchani). Please refer to the website for the respective committee members.

The **Communication Committee** is chaired by Heike Bickeböller (ex officio). Members are Saonli Basu, Jessica Dennis, Claire Simpson, Kristel van Steen, and Jin Zhou.

The **Wiley/Genetic Epidemiology Liaison Committee** is chaired by Mike Province. Members are Sanjay Shete, Angelo Canty, and Alexander Wilson.

The **IGES webmaster** is Jessica Dennis. The **IGES Facebook and Twitter master** is Jin Zhou.

The **office** is thankfully organized by Lynn Carrasco.

IGES Web Site: http://www.geneticepi.org/
IGES Facebook page: https://www.facebook.com/geneticepi?ref=hl
IGES Twitter page: https://twitter.com/Iges2013

IGES Facebook page exclusively for Young Investigators:
https://www.facebook.com/pages/International-Genetic-Epidemiology-Society-Iges-Next-Generation/174416209303988?ref=hl

The October 2015 Pre-Election Newsletter was edited, proofread, and formatted by Andrew Entwistle.