INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

# Newsletter - Pre-Election 2014 October

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## Letter from the President
**Alexander F. Wilson**

Dear Members,

As we enter the last quarter of 2014, my term as President of IGES is rapidly drawing to a close. It has been a pleasure serving as your President and I would like to offer special thanks to the other Officers and Members of the Board of Directors for their support during a very challenging period. As I noted in my closing remarks at the annual meeting in Vienna, I can't remember working with a more dedicated and selfless group of people who, to a person, always put the well-being of the Society ahead of other interests. I have greatly appreciated the opportunity to know my colleagues on a more personal level, and to have the opportunity to make some new friends in the process.

My goals for the year were to ensure the long-term financial stability of IGES, to improve the institutional memory of IGES, to broaden the membership base, to strengthen the international reputation of the Society and, most importantly, to showcase the best that the field has to offer at our annual meeting. I believe that we have made substantial progress in all these areas. The meeting in Vienna was both a scientific and financial success and the Society is once again on a stable financial footing. Membership is once again on the rise, particularly in the European Union. Although there is still much to be done, I am confident that Dr. France Gagnon will do an outstanding job as next year's President, and that the Society will be in good hands. Finally, I would like to thank all the existing and new members of IGES for their support during the past year. Without your support a highly focused and specialized international academic society like IGES would not be possible.

In closing, let me take this opportunity to remind you that the IGES meeting next year will be held in Baltimore, Maryland (October 4 – 6, 2015), just before the American Society of Human Genetics Meeting. We hope to see you there!

Alec Wilson

## IGES needs YOU!
## Volunteer Recruitment Drive

We should all remember that service to the International Genetic Epidemiology Society (IGES) is voluntary and that although many of us are over-committed, the time and effort of our Officers, Board, and Committee members is necessary for IGES to continue as a successful society, both academically and financially.

The Board of Directors of IGES is issuing a call to the membership for individuals interested in volunteering for next year's Education Committee; Ethical, Legal, and Social Issues Committee; Membership Committee, and Young Investigators Committee. A limited number of openings are available. The length of service is generally three years.

Individuals interested in being considered should send their c.v. and brief statement expressing their interest to Dr. Alexander F. Wilson (afwilsonphd@gmail.com) by November 1, 2014.

## Treasurer's Corner
## Mariza de Andrade

The 23rd annual IGES conference in Vienna was successful on many fronts, including this year's opportunity to participate in a shared mini-symposium with ISCB, and a vigorous meeting program offered to participants. I would like to express our appreciation to P-Star for the sponsorship of the IGES Pharmacogenomics Workshop.

From a Treasury viewpoint, IGES was successful in the management of meeting expenses. Due to careful negotiations and management of resources, we were able to make a profit on the meeting for the first time in four years. Specifically, I would like to thank the site meeting organizer, Andreas Ziegler, and his group, for their support and commitment to make the IGES meeting a success, and also to the current IGES president, Alex Wilson, for his leadership, fiscal prudence, and for his skilful negotiations with ASHG in support of the 2015 IGES meeting to be held in Baltimore, Maryland, USA next October.

The IGES Membership drive for 2015 will open in November 2014 and at the same rates as for 2014. Please note that membership is valid from January to December on a calendar year basis. Annual membership includes free online access to the journal "Genetic Epidemiology", which is otherwise not available to individuals, but only on the institutional level for over $4K annually. Other benefits of membership are reduced registration rates for the annual meeting, and the opportunity to have information and job openings posted on our website at no charge.

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

Mariza de Andrade
Treasurer

**2015 IGES Elections**
**(Please vote – List of Candidates)**

**Election Period November 1 – December 15, 2014**

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 2016:

**Josée Dupuis**

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

- **Celia Greenwood**
- **Marylyn Ritchie**
- **Andrew Paterson**
- **Xiaofeng Zhu**

**2015 Elections**
**Candidate for IGES President – Josée Dupuis**

***Josée Dupuis*** is Professor and Associate Chair of the Department of Biostatistics at Boston University School of Public Health. After obtaining her PhD in Statistics from Stanford University, she joined the faculty at Northwestern University, and subsequently took a senior statistical geneticist position at Genome Therapeutics Corporation, a small biotech company. She joined Boston University Faculty in 2003. She has extensive experience in the development and application of methods for mapping complex traits, with emphasis on approaches for large extended families and methods to incorporate gene by environment interactions.

She is a Framingham Heart Study investigator, collaborating on projects to identify genes influencing pulmonary function and type 2 diabetes. Some of her recent work has focused on meta-analysis approaches because of her involvement in multiple large international consortiums. She is an associate editor for the *Annals of Applied Statistics* and *Biostatistics*. In 2013, she was elected Fellow of the American Statistical Association for outstanding contributions to the development and application of statistical methods for genetics data; for excellence of collaborative research in mapping human complex disease genes; and for significant service to the profession, particularly at the interface of statistics with genetic epidemiology and medicine. She joined the IGES Board of Directors in 2012.

***Five selected publications:***


- Liu C, **Dupuis J**, Larson MG, Levy D. Association Testing of the Mitochondrial Genome Using Pedigree Data. Genet Epidemiol. 2013; 37(3):239-47.

- Lu C, Latourelle J, O'Connor GT, **Dupuis J***, Kolaczyk ED*. Network-guided sparse regression modeling for detection of gene-by-gene interactions. Bioinformatics. 2013; 29(10):1241-9.
- Chen H, Meigs JB, **Dupuis J**. Sequence kernel association test for quantitative traits in family samples. Genet Epidemiol. 2013 Feb;37(2):196-204.
- Manning AK, LaValley M, Liu CT, Rice K, An P, Liu Y, Miljkovic I, Rasmussen-Torvik L, Harris TB, Province MA, Borecki IB, Florez JC, Meigs JB, Cupples LA, **Dupuis J**. Meta-Analysis of Gene-Environment Interaction: Joint Estimation of SNP and SNP x Environment Regression Coefficients. Genet Epidemiol 2011, 35(1):11-8.
- **Dupuis J***, Langenberg C*, Prokopenko I*, Saxena R*, Soranzo N*, et al. New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nat Genet 2010, 42:105-16.


## 2015 Elections
## Candidates for the Board of Directors

***Celia Greenwood*** has been Senior Investigator at the Lady Davis Institute of the Jewish General Hospital in Montreal, and an associate professor at McGill University, Montreal, Canada, since 2010. Prior to this, she was associate scientist at the Hospital for Sick Children and associate professor at the University of Toronto. In Canada, she is on the board of the newly formed Canadian Genetics and Genomics Society, on the committee ensuring appropriate access to data from CARTaGENE, a population-based biobank of 20,000 individuals from Quebec, and a director of the new Ludmer Centre for Neuroinformatics and Mental Health.

Within IGES, she served on the Program Committee (2012-2014) and was the Chair of this committee in 2013; she also sat on the IGES ELSI committee from 2010-2014. She feels that a major strength of the society is its focus on interdisciplinary and methodologically sound research in multiple aspects of genetics and genomics and that links with researchers in these domains should be strengthened and encouraged.

Her research interests lie in developing and applying appropriate methods for the analysis of genetic and genomic associations with complex diseases, including cancer and behavioural traits. In the last few years, in collaboration with researchers from the UK10K project, she has worked extensively on analysis methods for studies of association between quantitative traits and rare genetic variation, including how to set significance thresholds for region-based tests of association, the development of test statistics, and comparisons of methods. Currently, she is working actively on analysis of epigenetic data as well as integration of data from different sources.

***Five selected publications:***


- **CMT Greenwood**, AD Paterson, L Linton, IL Andrulis, C Apicella, A Dimitromanolakis, V Kriukov, LJ Martin, A Salleh, E Samiltchuk, RV Parekh, MC Southey, EM John, JL Hopper, NF Boyd, JM Rommens (2011). A genome-wide linkage study of mammographic density, a risk factor for breast cancer. Breast Cancer Research. 13(6):R132.
- K Klein Oros, SL Arcand, JA Squire, A-M Mes-Masson, PN Tonin, **CMT Greenwood** (2013). Analysis of genomic abnormalities in tumours: a review of available methods for Illumina two-color SNP genotyping and evaluation of performance. Cancer Genetics 206(4):103-15.

- Oualkacha, K., Dastani, Z., Li, R., Cingolani, P. E., Spector, T. D., Hammond, C. J., Richards, J. B., Ciampi, A. and **Greenwood, C. M**. **T.** (2013) Adjusted Sequence Kernel Association Test for Rare Variants Controlling for Cryptic and Family Relatedness. Genetic Epidemiology 37:366–376.
- Changjiang Xu, Ioanna Tachmazidou, UK10K Consortium, Antonio Ciampi, Eleftheria Zeggini, **Celia MT Greenwood**. (2014). Estimating genome-wide significance for whole genome sequencing studies**.** Genetic Epidemiology 38:281-90.
- Kelly M. Burkett, Brad McNeney, Jinko Graham, **Celia MT Greenwood** (2014). Using gene genealogies to detect rare variants associated with complex traits. Human Heredity 78:117-130.

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***Marylyn Ritchie*** is a professor in the Department of Biochemistry and Molecular Biology and Director for the Center for Systems Genomics at Pennsylvania State University. Prior to this, she was an associate professor at Vanderbilt University Medical Center from 2004-2011. 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, particularly in the area of pharmacogenomics. Some of her methods include Multifactor Dimensionality Reduction (MDR), the Analysis Tool for Heritable and Environmental Network Associations (ATHENA), and the biosoftware suite for annotating/filtering variants and genomic regions as well as building models of biological relevance for gene-gene interactions and rare-variant burden/dispersion tests. Dr. Ritchie is the Principal Investigator of the Pharmacogenomics Research Network (PGRN) Statistical Analysis Resource (P-STAR) as well as the lead of the Genomics Data Coordination for the Electronic Health Records and Genomics (eMERGE) Network. She is the managing editor for BioData Mining and recently edited a special topic for Frontiers in 'Genetics Research in Electronic Health Records Linked to DNA Biobanks'. 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, and a KAVLI Frontiers of Science fellow by the National Academy of Science for each of the past four consecutive years. She was a member on the Education Committee of IGES from 2009-2013, officially, but also participated in 2014 during which she organized the education session on pharmacogenomics. Dr. Ritchie has extensive experience in all aspects of genetic epidemiology and bioinformatics as it relates to human genomics, including study design, statistical analysis, and interpretation of results. 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.

***Five selected publications:***

1. **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

2. Schwartz UI, **Ritchie MD**, Bradford Y, Dudek S, Frye-Anderson A, Kim RB, Roden DM, Stein CM. Genetic determinants of response to warfarin during initial anticoagulation. NEJM, 358(10):999-1008 (2008). PM 18322281, PMC 2367541
3. 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
4. **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). PM 20362271, PMC2850440
5. Pendergrass SA, Brown-Gentry K, Dudek SM, Torstenson ES, Ambite JL, Avery CL, Buyske S, Cai C, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Jackson RD, Kooperberg C, Le Marchand L, Lin Y, Matise TC, Moreland L, Monroe K, Reiner AP, Wallace R, Wilkens LR, Crawford DC, **Ritchie MD**. The Use of Phenotype-Wide association study (PheWAS) for exploration of novel genotype-phenotype relationships and pleiotropy discovery. Genetic Epidemiology, 35: 410-22 (2011) PMC 3116446.

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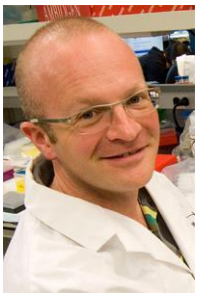

***Andrew Paterson*** (MB ChB) is a senior scientist in the Genetics and Genome Biology Program at the Hospital for Sick Children Research Institute, Toronto, Canada, as well as Professor of Epidemiology and Biostatistics at the Dalla Lana School of Public Health at the University of Toronto. Since 2001, he has been Director and now Co-Director of the Statistical Analysis Facility at The Centre for Applied Genomics, a genome centre based at Sickkids. Andrew works on the genetics of rare and common disease, as well as quantitative traits, with a particular focus on the genetics of both risk factors and outcomes of long-term complications of diabetes. He was on the IGES Publications Committee from 2009-2013, and since 2013 has been on the Program Committee. He is also a member of the Advisory Committee for Genetic Analysis Workshop (GAW). He has published over 180 peer-reviewed articles, and dreams of using genetic information to improve public health.

***Five Selected Publications:***

1. **Paterson AD**, Lopes-Virella MF, Waggott D, Boright AP, Hosseini SM, Carter RE, Shen E, Mirea L, Bharaj B, Sun L, Bull SB, and The Diabetes Control and Complications Trial/Epidemiology of Diabetes Interventions and Complications Research Group (2009) Genome-wide association identifies the ABO Blood Group as a Major Locus Associated with Serum Levels of Soluble E-Selectin. Atherosclerosis, Thrombosis, and Vascular Biology 29:1958-67. PMID: 19729612
2. **Paterson AD**, Waggott D, Boright AP, Hosseini SM, Shen E, Sylvestre MP, Wong I, Bharaj B, Cleary PA, Lachin JM, MAGIC, Below JE, Nicolae D, Cox NJ**,** Canty AJ, Sun L, Bull SB, and The Diabetes Control and Complications Trial/Epidemiology of Diabetes Interventions and Complications Research Group (2010) A genome-wide association study identifies a novel

major locus for glycemic control in type 1 diabetes, as measured by both A1C and glucose. Diabetes 59: 539-549. PMID: 19875614
3. **Paterson AD**, Rommens JM, Bharaj B, Blavignac J, Wong I, Diamandis M, Waye JS, Rivard GE, Hayward CPM (2010) Persons with Quebec platelet disorder have a tandem duplication of PLAU, the urokinase plasminogen activator gene. Blood 115: 1264-6. PMID: 20007542
4. Liu XQ, Georgiades S, Duku E, Thompson A, Devlin B, Cook EH, Wijsman EM, **Paterson AD**, Szatmari P, The Autism Genome Project (2011) Identification of genetic loci underlying the phenotypic constructs of autism spectrum disorders. Journal of the American Academy of Child and Adolescent Psychiatry 50: 687-696. PMID: 21703496
5. Eny KM, Lutgers HL, Maynard J, Klein BEK, Lee KE, Atzmon G, Monnier VM, van Vliet–Ostaptchouk JV, Graaff R, van der Harst P, Snieder H, van der Klauw MM, Sell DR, Hosseini SM, Cleary PA, Braffett BH, Orchard TJ, Lyons TJ, Howard K, Klein R, Crandall JP, Barzilai N, Milman S, Ben-Avraham D, LifeLines Cohort Study Group, DCCT/EDIC Research Group, Wolffenbuttel BHR, **Paterson AD** (2014) GWAS identifies an *NAT2* acetylator status tag single nucleotide polymorphism to be a major locus for skin fluorescence. Diabetologia **57**:1623-34. PMID: 24934506

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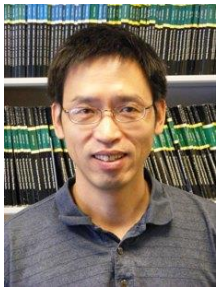


***Xiaofeng Zhu***, Ph.D. is currently a professor in the Department of Epidemiology and Biostatistics, School of Medicine, Case Western Reserve University. He received a Bachelor of Science degree in mathematics in 1986 and Master of Science degree in 1989 from Beijing University, China. He received a Doctor of Philosophy degree in Statistical Genetics in 1999 from Case Western Reserve University. Xiaofeng's interest in genetic epidemiology includes the mapping of genes underlying hypertension and obesity using the genome wide association and next generation sequencing studies. He is especially interested in genetic studies in African-American and African populations. He is constantly interested in developing statistical methods for association analysis, including controlling population structure, admixture mapping, rare-variant association methods using family data, as well as unrelated population data and cross-phenotype association analysis. He is interested in mentoring pre- and post-doctoral fellows and is enjoying teaching. He is currently on the editorial board of Genetic Epidemiology.

***Five selected publications:***

1. **Zhu X**, Zhang S, Zhao H, Cooper RS. Association mapping using a mixture model for complex traits. Genetic Epidemiol 2002; 23: 181-196. PMID: 12214310
2. **Zhu X**, Luke A, Cooper RS, Quertermous T, Hanis C, Mosley TH, Gu C, Risch N, Rao DC, Weder A. Admixture mapping for hypertension loci with genome scan markers. Nature Genetics 2005; 37, 177-181. PMID: 15665825
3. **Zhu X**, Feng T, Li Y, Lu Q, Elston RC. Detecting rare variants for complex traits using family and unrelated data. Genet Epidemiol. 2010 ;34(2):171-87. PMID: 19847924; PMCID: PMC2811752
4. Franceschini N, Fox E, Zhang Z, … Levy D, Keating BJ, **Zhu X**. Genome-wide association analysis of blood pressure traits in nearly 30,000 African ancestry individuals reveals a

common set of associated genes in African and non-African populations. 2013. Am J Hum Genet. 2013. 93:545-54. PMID: 23972371

5. Wang Y, Tayo BO, Bandyopadhyay A, Wang H, Feng T, Franceschini N, Tang H, Gao J, Sung Y, the COGENT BP consortium, Elston RC, Williams SM, Cooper RS, Mu T, **Zhu X**. The Association of the Vanin-1 N131S Variant with Blood Pressure is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. PLoS Genet. 2014. 10(9):e1004641. PMID: 25233454

## Annual Meeting 2015

The 24th Annual Meeting of the International Genetic Epidemiology Society (IGES) will be held in

***Baltimore, Maryland, on October 4 – 6, 2015***

just prior to the American Society of Human Genetics (ASHG) Meeting. The meeting will be held at the Hyatt Regency Baltimore on the Inner Harbor Hotel, and at the Baltimore Convention Center, about a one minute walk from the Hyatt Regency. The IGES meeting will be followed by an education session on Tuesday morning, October 6, 2015, with a Joint IGES/ASHG session on "Best Practices in Genetic Epidemiology" to be held on Tuesday afternoon (October 6, 2015).

The National Aquarium will be the site of our annual event, to be held on Monday, October 5, 2015 from about 7 to 10 pm.

We request that you visit the IGES website regularly for updates and information on the Annual Meeting.

We look forward to you joining us in Baltimore!

## Publication Committee
## Chair: France Gagnon

With great pleasure we would like to congratulate

**Clement Ma and his co-authors**

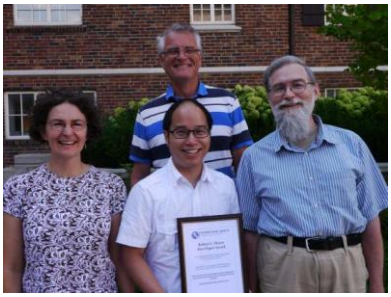
for their paper titled ***"Recommended joint and meta-analysis strategies for case-control association testing of single low count variants"***, which was selected as the winner of the

***Robert C. Elston Award for Best Paper***

published in "Genetic Epidemiology" in 2013. (Genet Epidemiol 37(6): 539-550).

Clement Ma will graduate shortly with his Ph.D. in Biostatistics from the University of Michigan. He received his Bachelor of Applied Science in Biomedical Engineering and Master of Science in Biostatistics from the University of Toronto. His research focuses on developing and evaluating statistical methods for association analysis of DNA sequencing data, including single marker

association tests, methods to combine data across multiple studies, and aggregation tests for rare genetic variants. He is an active member of the DIAGRAM and GoT2D genetics consortia and helped to coordinate an international team of analysts to identify novel type 2 diabetes susceptibility genes. From his prior experience at the Princess Margaret Cancer Center in Toronto, he was the lead biostatistician for more than 30 published clinical research projects in oncology, radiology, surgery, and palliative care.



**Program Committee**
**Chair: Justo Lorenzo Bermejo**

Congratulations go to **Mohamad Saad,** who was selected as the the winner of the **2014 James V. Neel Young Investigator Award** for the best presentation by a young scientist at the 2014 annual meeting in Vienna for his presentation "Combining family- and population-based imputation data for association analysis of rare and common variants in large pedigrees".

**Mohamad Saad**, Ph.D. is a senior postdoctoral fellow in the Department of Biostatistics at the University of Washington, Seattle, USA in Professor Ellen Wijsman's lab. He is interested in developing statistical methods to study complex diseases. His work focuses on imputation, association, and linkage analysis in both population- and family-based designs, using GWAS and sequencing data. He has been working on neurodegenerative diseases, such as Parkinson's and Alzheimer's diseases. He obtained his Ph.D. in Statistical Genetics at the University of Paul Sabatier, France, after finishing his Bachelor's degree in Applied Mathematics at the Lebanese University, Lebanon.

Our congratulations go to **Christian Benner, the Roger Williams Award Winner** for the best presentation by a student at the 2014 annual meeting in Vienna for his presentation titled "Mixed modeling for time-to-event outcomes with large-scale population cohorts and genome-wide data".

**Christian Benner** is a Ph.D. student at the Institute for Molecular Medicine Finland and the University of Helsinki under supervision of Samuli Ripatti and Matti Pirinen. He has a background in mathematical statistics and a keen interest in computational statistical genetics and genetic epidemiology. His Ph.D. project is focused on genetic analyses of time-to-event outcomes using genome-wide data and population registries. He is particularly interested in developing computationally feasible implementations for mixed survival models that scale to millions of genetic markers and health events in tens of thousands of individuals. Motivation for this work comes from a large and unique collection of Finnish population cohorts for which both detailed genomic data and comprehensive health registry data (such as cardiovascular events or cancers) are available.

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

*Genetic Epidemiology* is celebrating 30 years of publication! Please visit the link below to read top downloaded articles for FREE online.

http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1098-2272

*Genetic Epidemiology* needs papers. We are running relatively low on papers submitted to the journal. I invite you to submit papers in all aspects of genetic epidemiology (applied and methodological) Examples include (but are not limited to) gene-gene, gene-environment interactions, risk prediction models, methods to analyze DNA methylation, RNA seq data.

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. Thanks and looking forward to your active participation in the journal.

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

## Young Investigators (YI) Committee
## Chair: Elizabeth Blue (formerly Marchani)

*From the Annual Meeting:*

- The 2014 IGES Lunch was attended by ~20 young investigators, and covered topics from job search strategies to current research. We plan on hosting a similar lunch at the 2015 meeting, focusing on job search strategies.
- The IGES YI Facebook pages served as a location to search for potential roommates during the annual meeting. After the meeting, we also shared job opportunities that were posted at IGES 2014 on the Facebook page to boost their audience.

*Additional opportunities:*

- The IGES Facebook page (https://www.facebook.com/geneticepi?ref=hl) and Twitter account (https://twitter.com/Iges2013) provide a great opportunity to ask questions regarding the meeting and resources available.
- The American Society of Human Genetics annual meeting will be held October 18-22 in San Diego, California, USA. This large conference offers the opportunity to meet with thousands of your peers, as well as multiple workshops for various analytical tools, networking, career resources, and professional development. For more information, see www.ashg.org/2014meeting/.
- Researchers are encouraged to explore the Pacific Symposium on Biocomputing, http://psb.stanford.edu/index.html. This annual meeting usually occurs in January in Hawaii, USA. Discussions at IGES and the Genetic Analysis Workshop highlighted this meeting as an opportunity to engage with our colleagues who focus on computer science and informatics. The workshops at PSB 2015 include topics on the analysis of big data, including the public in research, and human evolutionary genomics.

## Ethical, Legal and Social Issues (ELSI) Committee
## Chair: Claire Simpson

Dear Members,

The ELSI committee has been working with Cathy Stein (former ELSI committee chair) and Aaron Goldenberg (bioethics) at Case Western Reserve University to develop a survey to examine experiences and perspectives on identification and return of incidental findings specific to genetic epidemiologists. While other surveys on this topic have been circulating from different genetics groups, this survey uniquely focuses on issues relevant to IGES membership.

The survey will only take 10 minutes or less to complete and upon completion, you may enter a free draw to win an Amazon gift card. The survey will be open until ***October 31, 2014***. We ask you to participate in the survey following this link:

https://cwru.az1.qualtrics.com/SE/?SID=SV_cuv2WW17C1imJ4V

This study was approved by the IRB at Case Western Reserve University. No identifying information will be collected; the draw for the gift card will be separate from the survey.

## 2014 Leadership Award
## Sanjay Shete

In recognition of his outstanding leadership through research, teaching, and service to the Society, the International Genetic Epidemiology Society presents the ***2014 IGES Leadership Award*** to

***Sanjay Shete***

The International Genetic Epidemiology Society honors Sanjay Shete, Ph.D., M.S., M.Ph. for his many contributions in the fields of genetic epidemiology and biostatistics and particularly for having served as the editor of Genetic Epidemiology since 2011. In that role, Dr. Shete has led an innovative reorganization of the journal by instituting a system that includes associate editors with specialized expertise in bioinformatics and statistical genetics. Additional innovations include interviews with leaders in the field of genetic epidemiology and a blog allowing commentary on editorials and major papers. Dr. Shete was trained in statistics, receiving his B.S., M.S., and M.Ph. degrees from Shivaji University in Kolhapur Maharastra India, between 1987 and 1990. Subsequently, he received his Ph.D. at the University of Georgia in Athens in 1998 and pursued further postdoctoral training under Dr. Elston from 1998-2000.

He then joined the Section of Computational and Genetic Epidemiology at the U.T. M.D. Anderson Cancer Center from 2000-2012, before becoming the head of the Section of Behavioral and Social Statistics. Dr. Shete plays a key role in mentorship by leading the newly renamed Program in Biostatistics, Bioinformatics, and Systems Biology at the University of Texas Graduate School for Biomedical Sciences. Dr. Shete also leads a training grant on statistical genetics of addiction with Dr. Shine Chang and heads additional research projects studying the genetics of head and neck cancer as well as the genetics of pain response related

to this disease. Dr. Shete is also well recognized for his contributions to statistics, as a fellow of the American Statistical Association and elected member of the International Statistic Institute.

Dr. Shete has brought together diverse areas of statistics, genetic epidemiology, and behavioral studies in important and novel ways to enhance the field of genetic epidemiology. We recognize him for his research excellence, mentorship, administrative assistance, and last but by no means least for his outstanding leadership and editorship of our journal.

## 2014 IGES Officials

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

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

Current **officers are**: President: Alexander F. Wilson; Past President: Andreas Ziegler; President-Elect: France Gagnon; 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, Josée Dupuis, Inke König, Andrew Morris, Kristel Van Steen

The **Education Committee** is led by Elizabeth Gillanders. The **ELSI Committee** is chaired by Claire Simpson. The **Membership Committee** in chaired by Yan Sun (chair). For members see our website.

This year's **Publication Committee** is chaired by France Gagnon. Standing member as Editor of Genetic Epidemiology is Sanjay Shete. Further members are Alexander Wilson, Nancy Saccone, David Conti, Peter Kraft, Bertram Müller-Myhsok, Rasika Mathias and Shelley Bull.

The **Program Committee** included Justo Lorenzo Bermejo (Chair), Celia Greenwood, Jeanine Houwing-Duistermaat, Andrew Paterson, André Scherag, Nathan Tintle, Alec Wilson (President) and France Gagnon (President-Elect). André Scherag will be the Chair for the 2015 meeting.

The **Young Investigators Committee** includes Elizabeth Blue (formerly Marchani) (Chair), Katie O'Brian, Melanie Quintana, Lara Sucheston, Amy Spencer.

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

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

The **office** is thankfully organized by Delaine Anderson.

**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 2014 Newsletter was edited, proofread, and formatted by Andrew Entwistle.