INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Newsletter – Pre-Conference May 2015

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Letter from the President
France Gagnon

Dear IGES Community,

Five months into 2015 and a lot has moved forward already!

First, I would like to officially welcome Josée Dupuis as the incoming IGES President-Elect, as well as Celia Greenwood and Andrew Paterson, as new members on the IGES Board of Directors. I would also like to thank the outgoing Past President Andreas Ziegler and Board members Andrew Morris and Josée Dupuis for their generous contribution of time, effort, and ideas during the past year to make IGES a society our members are proud of. I take this opportunity to welcome new committee members and sincerely thank those who have already contributed so much in the past year!

I offer a special thankyou to Alec Wilson, as he moves from the position of President to Past President, for his strong leadership and pivotal contribution in reshaping IGES finances. Alec's highly collaborative personality contributed to this success, building on the momentum created by Past President Andreas Ziegler, rigorous work by Treasurer Mariza de Andrade, as well as the dedicated work by Secretary Heike Bickeböller, Editor-in-Chief of Genetic Epidemiology Sanjay Shete, and the Board members. The team, under Alec's leadership, has successfully led IGES out of a difficult period.

I believe IGES is now poised to reach new heights. Building on the culture of innovation in study designs and methodological approaches in complex traits research, and genomics being an

archetype of Big Data, IGES members are in an enviable position to capture new emerging and exciting opportunities from the general enthusiasm brought by data science in many fields, and the clear appreciation for interdisciplinary quantitative expertise. We, as a community, should lead in this area; IGES should play a key role in promoting its members' skills, know-how, and creativity in data science and health research.

My goal for the coming year is twofold: first, to continue the efforts of ensuring the long-term financial stability and institutional memory of IGES. Second, to work on innovative ways to further promote IGES and its members as key players in the area of data science and health. I recognize that you all have many options in selecting societies to which you wish to belong and I sincerely thank you for choosing IGES! I strongly encourage you to be active members of IGES and contribute to the growth of our society by sharing your experience and creativity toward IGES's success in achieving this goal. Please share your ideas with me (france.gagnon@utoronto.ca) or officers and board members (http://www.geneticepi.org/).

Finally, I enthusiastically invite you to submit an abstract to IGES 2015 to be held in Baltimore October 4-6. The meeting will feature seven inspiring scientific sessions framed by keynotes (see the IGES 2015 webpage "Invited Speakers and Topics" for details). In addition, there will be an exciting debate on the topic of "missing heritability", a session jointly organized by the IGES Education Committee and the American Society of Human Genetics meeting: "Prospecting for Hidden Heritability: Undiscovered Nuggets or Fool's Gold?" Make sure you do not miss all the fun and join us in Baltimore!

I look forward to a very productive year!

France Gagnon, PhD
2015 IGES President

Treasurer's Corner
Mariza de Andrade

The last year was challenging for IGES, and I am pleased as Treasurer to share with the IGES membership that we now are in good financial standing, though not totally off the hook. We are still careful in our negotiations and management of resources to maintain this good standing, and I would like to thank our two former Presidents, Alec Wilson and Andreas Ziegler, for their leadership, fiscal prudence, and for Alex's skilful negotiations with ASHG in support of the 2015 IGES meeting to be held in Baltimore, Maryland, US. The IGES membership and meeting registration for 2015 is open.

As a reminder for this year, 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!

Mariza de Andrade
Treasurer

Editor's Corner Genetic Epidemiology
Sanjay Shete

Dear IGES Members,

As the official journal for our Society, Genetic Epidemiology invites you to submit your work in the fields of statistical, epidemiological, and population genetics. Genetic Epidemiology is interested in both methodological and applied papers. Examples include: gene and environment interactions, risk prediction models, DNA methylation, and RNA seq data analysis. Other novel work is welcome!

Last year, the US National Cancer Institute sponsored a workshop that highlighted important challenges including the simulation of whole genome sequence data, providing standards and improved documentation for simulation software, and encouraging the simulation community to work together. As a result of this meeting, we recently published a special issue on "***Genetic Simulation Tools for post-GWA Studies of Complex Diseases***" Volume 39, Issue 1, 2015, Guest Editor: Jason Moore (http://onlinelibrary.wiley.com/doi/10.1002/gepi.2015.39.issue-1/issuetoc)

There is no publishing cost for authors (e.g. page charges, black-white figures). In addition, the journal selects a few papers every year for "open access" (unrestricted online access) publication 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.

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

IGES NEEDS YOU!
Volunteer Recruitment Drive 2015

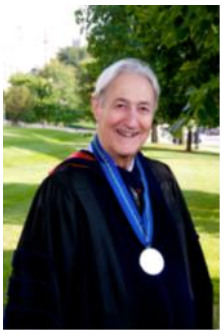
Are you interested in taking a more active role in IGES?

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 the coming years' ELSI and Young Investigators Committee. A limited number of openings are available. The length of service is generally three years.

Interested members should send their CV and a statement of interest to France Gagnon (france.gagnon@utoronto.ca).

Robert C. Elston Symposium
Alexander Wilson



On April 7, 2015, "The Robert C. Elston Symposium: The Evolution of Genetic Epidemiology" was held in the Tinkham Veale University Center, Case Western Reserve University, in honor of the distinguished career of Robert C. Elston, Ph.D. Dr. Elston has published over 650 scientific papers and mentored more than 50 graduate and 50 post-doctoral students, served as both the Treasurer and President of IGES, and has taught courses on S.A.G.E. software to over 1000 researchers around the world. His career spans over 50 years and 3 universities. The Symposium, moderated by Dr. Chris Amos, was attended by about 100 of Dr. Elston's former students, faculty, friends, and family. Invited spearkers included Drs. Nancy Mendell, Margaret Pericak-Vance, Hemant Tiwari, Thomas Sellers, Courtney Montgomery, Joan Bailey-Wilson, Alexander Wilson, Varghese George, and Jonathon Haines, focusing mostly on his accomplishments in the field of genetics and his interactions as a mentor and friend. His other accomplishments in genetics (with of course his wife, Pam) are children Jennifer, Bridget, Timothy, and Gillian, who were on hand to provide a unique perspective on the Elston household! An updated pedigree plot of his trainees and their subsequent trainees covered nearly the entire length of one of the walls of the conference center. The end of the symposium was magical, literally, with Dr. Elston entertaining the audience with some magic tricks.

IGES 2015
Baltimore, MD, USA – October 4-6 2015

General Information

This years' IGES meeting will be held October 4-6, 2015, at the Hyatt Regency Baltimore on the Inner Harbor Hotel, Maryland, USA. For October 4 and 5, the Baltimore Hyatt will be the site of the poster sessions and break-out meetings and the Baltimore Convention Center will be the site of the IGES main scientific sessions. The meeting will feature seven inspiring scientific sessions over two days framed by keynotes from invited top experts (see Invited Speakers and Topics). In addition, on October 6, there will be an exciting joint session with the **American Society of Human Genetics** entitled "Prospecting for Hidden Heritability: Undiscovered Nuggets or Fool's Gold?" moderated by Alexander Wilson (IGES) and Carole Ober (ASHG). The National Aquarium will be the site of our annual event on the evening of Monday October 5, 2015. We strongly encourage members to book their hotel reservations early at the Baltimore Hyatt Regency on the Inner Harbor where we have negotiated a very favorable room rate for the IGES meeting. We look forward to seeing you there!

IMPORTANT DATES

Abstract submission is now possible. Please visit http://www.geneticepi.org/abstract-submission-guidelines/ for details and submission.

June 18, 2015: general abstract submission deadline (extension **not possible**)

July 6, 2015: general abstract acceptance notification

Participants requiring an official abstract notice of acceptance for visa or grant purposes will be provided with early notification on demand. The final decision on the type of presentation, be it platform or poster, will be made and communicated at a later stage.

Please broadly advertise the IGES annual meeting at your institution
Download the IGES 2015 flyer here…

IGES 2015 Time frame

Saturday October 3, 2015: Travel day

17:30 – 19:30: Registration in the ***hotel lobby***

Sunday October 4, 2015

07:30: Registration opens in the ***Baltimore Convention Center***
08:30 – 19:30: Conference Day One

Monday October 5, 2015

07:30: Registration opens in the ***Baltimore Convention Center***
08:30 – 16:30: Conference Day Two
18:30 – 22:00: Conference event
A Fishing Expedition: National Aquarium, Baltimore, Maryland

Tuesday October 6, 2015

13:00 – 16:00: Joint ASHG/IGES Symposium
"Prospecting for Hidden Heritability: Undiscovered Nuggets or Fool's Gold?"

IGES 2015
Joint ASHG/IGES Symposium on October 6, 2015, 1 to 4 pm

Prospecting for Hidden Heritability: Undiscovered Nuggets or Fool's Gold?

Registration Fee: $25 (registration through either the IGES or ASHG websites)

In this joint symposium, speakers will present new data and analyses of "hidden heritability," and in a panel discussion format, will debate approaches to identify causative variants through study designs and analytic strategies. The symposium will be co-moderated by **Alexander Wilson**, NIH/NHGRI and **Carol Ober**, University of Chicago.

Is there such a thing as "hidden heritability"? Methods to estimate the proportion of the variation in human traits that are attributable to genetic effects are well established, but the genetic effects identified thus far do not account for much of the expected trait heritability. Although many explanations for this "hidden heritability" have been put forth, their relative importance is currently under debate. Some would even argue that "hidden heritability" does not exist. The importance of understanding the sources of currently unexplained genetic effects lies in the next challenge ahead of us: interpreting how the wealth of functional and regulatory variants to be identified by next generation sequencing play a role in human development and health. Audience participation is encouraged. A list of panelists will be available in May.

To attend this event, a separate ticket must be purchased during the meeting registration process. Limited tickets are available and sell out early. Tickets will not be available for sale on site.

IGES 2015 Invited Speakers

Big health data opportunities and challenges: statistical and computational solutions

Jeff Leek, PhD, is an Associate Professor of Biostatistics and Oncology at the Johns Hopkins Bloomberg School of Public Health. His research focuses on the intersection of high dimensional data analysis, genomics, and public health. He has developed widely-used methods and software for the analysis of RNA-seq data and for turning genomics data into clinically useful signatures. He is the co-editor of the Simply Statistics Blog and co-director of the Johns Hopkins Data Science Lab.

Title: Statistical analysis of RNA-seq data at scale

Abstract: RNA-seq is now the primary technology used to measure transcriptional abundance. The analysis of RNA-seq data can be done at multiple levels (genes, regions, or transcripts) and at multiple scales (small experiments or large population cohorts). I will discuss statistical challenges in developing and applying software for the analysis of RNA-seq data at multiple scales including reproducibility, statistical power, trust in genomic annotations, and detection and removal of artifacts. These issues are critical in the analysis of data from genomic experiments in general, but are particularly acute in the analysis of dynamic data from transcriptomes.

Cross-Consortia and Mega-Cohorts: Ongoing and future directions

Ruth Loos, PhD, is Director of the Genetics of Obesity and Related Metabolic Traits Program, in The Charles Bronfman Institute of Personalized Medicine of the Icahn School of Medicine at Mount Sinai.

Her primary research interests focuses on the identification of genes and genetic loci contributing to the risk of obesity and related metabolic traits. She has been involved in gene-discovery since 2005, when 'genome-wide association' was introduced and has since actively contributed to many consortia that use this approach to identify genetic loci for a large number of metabolic traits. Increasingly, her gene-discovery work also focuses on the identification of low-frequency variants through the implementation exome-chip genotyping and sequencing projects, not only in individuals of white European descent, but also in those of African and Hispanic descent.

Besides gene-discovery, Ruth uses epidemiological methods to follow-up on established loci with the aim to elucidate the pathways through which they increase risk of metabolic disease. Furthermore, her work also assesses the public health implications of the established loci by examining their predictive value and their interaction with lifestyle factors such as diet and physical activity.

Title: The Genetics of Obesity – Going beyond common variation and common traits

Abstract: Large-scale genome-wide association studies (GWAS) have identified >150 loci associated with adiposity traits, predominantly in European, but also in Asian and African ancestry populations. While the explained variance remains small, each of the loci may harbor

genes that are involved in pathways relevant to obesity. However, for most loci the causal gene(s) or variant(s) remain to be determined. Pinpointing the causal gene/variant, however, is a critical, yet challenging, step towards translation of GWAS-discoveries into functional follow-up experiments, which are needed to elucidate the mechanisms that regulate body weight and energy homeostasis. The reasons why translation of GWAS-identified loci has been challenging are, at least in part, because phenotypes most often studied are heterogeneous and genotypes are common.

So far, most large-scale GWAS meta-analyses have focused on body mass index (BMI), as a proxy of overall obesity, and waist-to-hip ratio (WHR), as a proxy for abdominal obesity. However, both BMI and WHR are heterogeneous phenotypes; for example, body fat percentage can differ widely across individuals with the same BMI. In addition, these GWAS have so far focused on common variants and BMI/WHR-associated loci are typically predicted to be non-functional, as they often lie in non-coding regions of genes or even in-between genes. Thus, while large-scale GWAS meta-analyses for BMI and WHR have been extremely successful in identifying new loci, heterogeneous outcomes and non-functional variants have hampered the translation of these GWAS discoveries.

I will review how studying more homogenous adiposity outcomes and/or functional variants might facilitate translation. For example, in a recent GWAS for body fat percentage, a more accurate estimate of adiposity, we integrated association data of a wide range of cardiometabolic traits, revealing fascinating association patterns with estimates of growth and maturation, and also (paradoxically) with favorable lipid and glycemic profiles. The identified loci for body fat percentage only partially overlapped with those for BMI, and their cross-phenotype association signature provided informative insights that point towards the potential candidate genes in the loci. A GWAS of circulating leptin levels, a biomarker of adiposity, revealed six loci, one of which near LEP. To locate the causal gene in the other five loci, we developed a knockdown transplant strategy in adipose tissue of mice, revealing potential new genes that regulate circulating leptin levels.

Most recently, the GIANT (Genetic Investigation of ANthropometric Traits) consortium has started the meta-analyses of data from >400,000 individuals genotyped using the ExomeChip, which contains around 240,000, predominantly low-frequency and rare, coding variants. Preliminary analyses confirmed mutations in the well-known MC4R gene, and have identified functional variants in genes involved in thyroid disease and food metabolism.

Taken together, while GWAS of common outcomes have been successful in identifying many loci, translation of these observations has been difficult. Studying more accurate measures of adiposity and potentially coding variants promises to result in loci that are easier to interpret. Such loci might provide the insights needed to carefully design experimental follow-up studies that will help elucidate the pathways involved.

Xihong Lin, PhD, is Henry Pickering Walcott Professor and Chair of Department of Biostatistics and 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 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 methods for massive data. She received the 2006 Presidents' Award for the outstanding statistician from the Committee of the Presidents of Statistical Societies (COPSS), and the 2002 Mortimer Spiegelman Award for the 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 currently a member of the Committee of Applied and Theoretical Statistics of the US National Academy of Science. Dr. Lin is a recipient of the MERIT (Method to Extend Research in Time) from the National Cancer Institute, which provides a 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 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.

Title: Statistical Analysis of Massive Genetic and Genomic Data in Genetic Epidemiology

Abstract: The human genome project in conjunction with the rapid advance of high throughput technology has transformed the landscape of health science research. The genetic and genomic era provides an unprecedented promise of understanding genetic underpinnings of complex diseases or traits, studying gene-environment interactions, predicting disease risk, and improving prevention and intervention, and advancing precision medicine. A large number of genome-wide association studies conducted in the last ten years have identified over 1,000 common genetic variants that are associated with many complex diseases and traits. Massive targeted, whole exome and whole genome sequencing data as well as different types of 'omics data have become rapidly available in the last few years. These massive genetic and genomic data present many exciting opportunities as well as challenges in data analysis and result interpretation. They also call for more interdisciplinary knowledge and research, e.g., in statistics, machine learning, data curation, molecular biology, genetic epidemiology and clinical science. In this talk, I will discuss analysis strategies for some of these challenges, including rare variant analysis of whole-genome sequencing association studies; analysis of multiple phenotypes (pleiotropy), and integrative analysis of different types of genetic and genomic data.

After 25 years in the USA, much of it at the University of Southern California, **Simon Tavaré**, PhD, moved to the University of Cambridge in 2003 as Professor of Cancer Research (Bioinformatics) in the Department of Oncology, a group leader in the Cambridge Research Institute from 2006, and a Professor in the Department of Applied Mathematics and Theoretical Physics, where he is currently Director of the Wellcome Trust PhD programme in Mathematical Genomics and Medicine.

In February 2013, he became Director of the (renamed) Cancer Research UK Cambridge Institute, a department of the University of Cambridge since January 2013. His research group focuses on statistical bioinformatics, particularly for DNA sequencing, and evolutionary approaches to cancer biology. In 2009 Simon was elected as a Fellow of the Academy of Medical Sciences and in 2011 as a Fellow of the Royal Society. He gave the American Mathematical Society's Einstein Public Lecture in Mathematics for 2015, and was an invited speaker at ICIAM2015 in Beijing. He is currently President-Designate of the London Mathematical Society.

Title: Data integration in cancer genomics

Abstract: I will describe some of the statistical data integration problems our group has addressed in the context of cancer `omics. Among the examples are methods for integrating genome-wide binding profiles of transcription factors with their responsive gene expression profiles (the Rcade package in Bioconductor), for interpreting copy number, expression and lineage tracing data to understand the evolutionary history of glioblastomas, and one from the world of ABC (Approximate Bayesian Computation) used to study cancer stem cells.

Timothy Thornton, PhD, is an Associate Professor in the Department of Biostatistics at the University of Washington (UW). He is also an Affiliate Investigator at the Fred Hutchinson Cancer Research Center in Seattle. The focus of his research is the development and application of statistical methods for the identification of genetic variants underpinning complex traits and diseases. He has developed statistical methods and software that are widely used for the analysis of large-scale SNP genotyping data in samples with pedigree and/or population structure. Prior to joining the faculty at the University of Washington, Dr. Thornton was a University of California President's Postdoctoral Fellow in the Department of Statistics at the University of California at Berkeley. He earned a B.S. degree in mathematics from Hampton University and a Ph.D. in statistics from the University of Chicago. Dr. Thornton is currently a principal investigator (PI) of a National Cancer Institute funded Career Development Award (K01) and co-PI of a Project Grant (P01) funded by the National Institute of General Medical Sciences. He is also a member of the UW Genetic Analysis Center for the Hispanic Community Healthy Study / Study of Latinos.

Title: Mixed Model Association Mapping in Admixed Populations

Abstract: Genetic association studies in recently admixed populations, such as African Americans and Hispanics, offer exciting opportunities for the identification of genetic variants that underlie phenotypic diversity. At the same time, heterogeneous genetic background and dependencies among sample individuals pose special challenges for complex trait mapping in admixed populations. Linear mixed models (LMMs) have garnered significant attention as a powerful approach for genetic association testing in the presence of sample structure, including population stratification, family structure and/or cryptic relatedness. Existing implementations of LMMs, however, may not appropriately account for the diverse genomes of admixed individuals. In this talk, we propose MMAAPS, a LMM method that appropriately accounts for sample structure in samples from admixed populations by (1) using individual-specific allele frequencies at SNPs that are calculated on the basis of ancestry derived from whole-genome analysis, and (2) partitioning recent and more distant genetic relatedness into two separate components. In simulation studies we demonstrate that MMAAPS provides improved type-I error rates and power over widely used LMM methods, such as EMMAX and GEMMA. The utility of MMAAPS is further demonstrated with applications to the Hispanic Community Health Study / Study of Latinos for genetic association mapping of hematology phenotypes.

Katrina Goddard, PhD, is a genetic epidemiologist who focuses on public health genomics and the translation of genetic testing into practice. She joined the Kaiser Permanente Center for Health Research in 2007.

Dr. Goddard is the principal investigator of a study funded by the National Human Genome Research Institute (NHGRI) that is exploring how to use a new technology—whole genome sequencing—in everyday clinical practice. The study will test would-be parents before they conceive for genetic mutations that could cause rare but serious diseases in their children. The study will compare couples who get usual care to couples who get tested with whole genome sequencing, and will explore how to implement such testing in a health plan.

Dr. Goddard founded the NW Biobank, a repository of blood and tissue samples linked to health plan members' comprehensive electronic medical records. The biobank enables researchers to connect people's genetic information with their health care, including vital signs, diagnoses and treatments. This regional biobank has recently been assimilated into a national initiative called the Kaiser Permanente Research Bank.

Dr. Goddard directs the Knowledge Synthesis Team, and is co-chair of the Actionability Work Group for NHGRI's ClinGen Consortium. The Knowledge Synthesis Team provides detailed, systematic evidence summaries for each gene/phenotype topic being considered for clinical actionability. These summaries are used by the Actionability Work Group to produce semi-quantitative metric scoring for each topic. Dr. Goddard was formerly the co-principal investigator of the Knowledge Synthesis Center supporting the CDC's EGAPP Working Group, which developed and piloted the methodology that is used in ClinGen. Additional recent research efforts include a study on implementation of Lynch Syndrome tumor screening in a managed care setting, and a large comparative effectiveness research project in genomic and personalized medicine for colon cancer (CERGEN). Dr. Goddard completed a one-year fellowship in the National Office of Public Health Genomics in 2007, which was jointly sponsored by the Centers for Disease Control and the American Society of Human Genetics.

Prior to her appointment as a Senior Investigator, Dr. Goddard was on the faculty at Case Western Reserve University in the Division of Genetic & Molecular Epidemiology. At Case Western, she was involved in several large-scale gene-discovery projects, and was the associate director of the Human Genetic Analysis Resource, which produces the SAGE software package. She received her PhD in biostatistics from the University of Washington in 1999, and a BS in Molecular Biology from the University of Wisconsin-Madison.

Title: Targeted genomic screening in the general adult population

Abstract: The application of genome or exome technology in healthy adult populations has promise as a predictive tool to guide preventive medicine strategies, but the technology has not yet been rigorously assessed for this purpose. Debate about recent calls for widespread expansion of screening for individual genes in populations has highlighted the numerous knowledge gaps that remain. Several efforts are underway to explore emerging opportunities for this application of genomic medicine, but these efforts are also revealing the challenges that must be addressed and overcome. I will discuss early findings from these exploratory programs, and clarify the implications of population level screening with genomic approaches from a variety of stakeholder perspectives.

IGES 2015
Student-Mentor Lunch, October 5

The Young Investigators Committee is excited to announce a student-mentor lunch to be held at the annual meeting in Baltimore, MD on

October 5th at the Hyatt Hotel from 12:00-1:15pm.

Use this time to meet with other students, seek advice from established members of the Genetic Epidemiology community, and take a little time at the conference to think about your future plans.

Over the last quarter, we have advertised 8 postdoctoral positions, a short-course on Statistical Genetics, and a symposium on the genetic epidemiology of homogeneous populations. Follow us at "International Genetic Epidemiology Society (IGES) - Next Generation" on Facebook for more details.

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). Current members are Saskia Freytag, Katie O'Brien, Melanie Quintana, Amy Spencer, and Lara Sucheston.

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 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 May 2015 Pre-Conference Newsletter was edited, proofread, and formatted by Andrew Entwistle.