INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Newsletter – *November 2018 Pre-Election Edition*

Contents

Letter from the President
Inke König

Dear IGES community,

It was a great pleasure to see so many of you at our annual meeting in San Diego. Many thanks for attending and making the meeting so successful and enjoyable!

Special thanks certainly go to the local organization team chaired by our past president Andrew Morris and co-chaired by Julia Bailey for their hard work. Again, they were supported by Vanessa Olmo and her team (Tamiko Kinkade and Zenaida Mendoza), who made sure that everything went smoothly.

The scientific program committee (chaired by Guillaume Paré) did a wonderful job in putting together an extremely interesting scientific program including invited and contributed talks and posters. A brilliant novum were the flash presentations for the best-rated posters. On a more personal note, we remembered Newton Morton both at our IGES banquet and through a dedicated tribute session at the ASHG, with several IGES members standing up to share their memories of him.

Over the past years, the educational workshops by the Education Committee have become a great tradition. This time, the timely topic was "Translational Research in Medicine", and we thank Stephanie Santorico and Todd Edwards for organizing this. Finally, our meeting was concluded with a joint symposium with the ASHG and ISCB on "Working with Big Data in the Cloud".

I am happy to congratulate our award winners from this year: The Neel and Williams awards were granted to Ekaterina Yonova-Doing and Rachel Moore (thanks to Wiley for sponsoring), and the Young Investigators Committee selected Sisi Li, Sheethal Jose and Chubing Zeng for the poster awards (thanks to CIHR STAGE for sponsoring). Timothy Mak presented the best paper in Genetic Epidemiology from 2017 (doi: 10.1002/gepi.22050). Finally, the IGES leadership award was granted to John Witte. Congratulations to you all!

Looking forward, we were lucky to convince a number of outstanding members to run as **candidates for president-elect and the board of directors**. Please have a look at the information they have provided for you and remember to vote!

Also, I would like to remember you to **renew your membership of IGES**. The website is already open, and doing it now will get you a discount! As you are aware, being a member gives you reduced fees for attending our next annual meeting and online access to our journal Genetic Epidemiology.

Finally, “nach dem Spiel ist vor dem Spiel” (former German national soccer coach Sepp Herberger, meaning “after the game is before the game”), so please do mark your calendars for our **28th IGES annual meeting**! This will take place in Houston on October 12-14, 2019, and I am looking forward to seeing you all there!

Inke König

2018 IGES President

Treasurer's Corner
Mariza de Andrade

I am pleased as Treasurer to share with IGES members that we are now in good financial standing, and that we will continue to be vigilant in our negotiations and management of resources to maintain this good standing. The 2018 IGES meeting in San Diego was excellent, and the board members' skillful negotiations with several organizations in Canada, USA and UK provided robust sponsorship for the meeting, and enabled IGES to once again distribute travel and best poster awards to attendees.

I would like to remind IGES members that the 2019 IGES membership is open; an email reminder with details was sent to the members. You can also go to www.geneticepi.org for information. Please encourage your colleagues to join as well!

As a reminder for this year, IGES is a charitable and educational organization, and any contribution other than membership and meeting registration fee is tax-deductable. This can be done along with your membership renewal process. Your continuous support of IGES is appreciated!

We are looking forward to seeing you all in IGES 2019 in Houston, TX, USA. The IGES meeting will be before the ASHG that will also take place in Houston.

Mariza de Andrade

Treasurer

Editor's Corner, Genetic Epidemiology
Sanjay Shete

Dear IGES members, as an official journal for our society, **with a new improved impact factor of 2.544**, Genetic Epidemiology 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!

The October 2018 issue can be found here:

https://onlinelibrary.wiley.com/toc/10982272/2018/42/7

Benefits of Publishing in Genetic Epidemiology: There is no publishing cost for authors (e.g. page charges, black-white figures). In addition, every year, journal selects 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 where 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

IGES 2019 Membership Drive

Dear IGES members,

It is now time to renew your membership for 2019.

Please observe the fact that membership registration and annual meeting registration have been separate since 2014. Therefore you are NOT automatically registered as an IGES member just with meeting attendance. A separate registration for IGES Society membership is necessary:

http://www.geneticepi.org/membership/

The early-bird membership fee is available before April 1, 2019.

Rates for 2019 IGES membership:

- Regular member **US$130**, if paid by April 1, 2019 (early-bird)
- Regular member **US$155** if paid on or after April 2, 2019
- Student and Post-Doctoral* member with online access to Journal **US$68**, rate continues all year but please aim to pay by April 1, 2019
- Student and Post-Doctoral* member **without** online access to Journal **US$25**, rate continues all year but please aim to pay by April 1, 2019
- Low- or lower-middle- income country* member with online access to Journal **US$68**; without online access to Journal **US$25.**

* For eligibility see IGES website

Benefits of IGES membership:

- Receive complimentary on-line access to **Genetic Epidemiology** (the offical IGES journal)
- Post announcements and job adverts on the IGES website at ***no cost***
- Attend annual IGES scientific meetings at ***reduced cost***
- Interact with **scientific peers** worldwide
- Learn about the **latest methodological developments**, **software**, and **research findings** in genetic epidemiology
- Help the society **promote** the field of **genetic epidemiology** internationally

- Continuous regular membership of IGES for 5 years or more makes you eligible for the title of "**Fellow Member of IGES**". See http://www.geneticepi.org/membership/iges-fellow-members/

Your IGES dues help to support…

- **Travel expenses** to the annual IGES meeting for worthy students in financial need
- **Continuing education** and outreach to the scientific community about the discipline, analytical methods, and software used in genetic epidemiology through workshops and classes
- Subsidies for **student subscriptions** to the journal *Genetic Epidemiology*

IGES 2019 Elections
List of candidates - Please vote!

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 separately from this newsletter. This newsletter contains the biosketches of all candidates.

Candidate for the position of President-Elect to serve as President in 2020:

- **Peter Kraft**

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

- Elizabeth Blue

- Brooke Fridley

- Jaya Satagopan

- Eleftheria Zeggini

[The ballot paper for these elections will be sent out by SurveyMonkey. Note that all members may opt-out of emails from IGES sent via sources such as MemberClicks, Cvent and SurveyMonkey. However, please note that by opting out, you will no longer receive ANY mail at all from IGES, including important election announcements and ballot links, as well as the newsletters and our annual meeting announcements].

2019 IGES Elections
Candidate for IGES President – Peter Kraft

Peter Kraft is Professor of Epidemiology and Biostatistics and Director of the Program in Genetic Epidemiology and Statistical Genetics at the Harvard T.H. Chan School of Public Health. He received his Ph.D. in Biostatistics from the Keck School of Medicine at the University of Southern California under the supervision of Dr. Duncan Thomas. His research concentrates on the design and analysis of genetic association studies, with particular emphasis on the genetic epidemiology of cancer. He has participated in many international consortia studying genetics and environmental exposures in relation to cancer risk over the last fifteen years, including the Breast and Prostate Cancer Cohort Consortium (BPC3); the NCI's PanScan and Cancer Genetic Markers of Susceptibility (CGEMS) projects; the NCI's "post-GWAS" GAME-ON consortium; the Breast Cancer Association Consortium (BCAC); and the Cancer Risk Estimates Related to Susceptibility Genes (CARRIERS) consortium, which is sequencing cancer predisposition genes in a large population-based breast cancer case-control sample. His methodological work has focused on efficient and interpretable "gene x environment interaction" analyses; building and evaluating risk prediction models incorporating high dimensional genetic data; and integrative analyses combining genetic and environmental risk factors with intermediate biomarkers (gene expression, metabolomics). He has taught introductory and advanced courses in genetic epidemiology and statistical learning at the Harvard Chan School since 2004 and co-chaired the American Association for Cancer Research's Integrative Molecular Epidemiology workshop since it started in 2013. Dr. Kraft has been an IGES member since 1997, serving on the board of directors, program committee and publications committee between 2008 and 2015.

Five selected publications:

1. Michailidou K, Lindstrom S, Dennis J, Beesley J, Hui S, Kar S, …, Simard J, Kraft P, Easton D. Association analysis identifies 65 new breast cancer risk loci. Nature 2017 551(7678):92-94.
2. Aschard H, Vilhjálmsson BJ, Joshi AD, Price AL, Kraft P. Adjusting for heritable covariates can bias effect estimates in genome-wide association studies. Am J Hum Genet 2016 98(2):394-5.
3. Kraft P, Wacholder S, Cornelis MC, Hu FB, Hayes RB, Thomas G, Hoover R, Hunter DJ, Chanock S. Beyond odds ratios--communicating disease risk based on genetic profiles. Nat Rev Genet 2009 10(4):264-9
4. Monsees GM, Tamimi RM, Kraft P. Genome-wide association scans for secondary traits using case-control samples. Genet Epidemiol 2009 33(8):717-28.
5. Kraft P, Yen YC, Stram DO, Morrison J, and Gauderman WJ. Exploiting gene-environment interaction to detect genetic associations. Hum Hered 2007 63(2):111-9.

Keywords: Enthusiastic, collaborative, educator, mentor, inclusive.

2019 IGES Elections
Candidates for Board of Directors – Elizabeth Blue

Elizabeth (Liz) Blue is an Assistant Professor in the Division of Medical Genetics, member of the Institute for Public Health Genomics and Statistical Genetics Program faculty, and affiliate member of the Alzheimer's Disease Research Center at the University of Washington. She is also the Assistant Director of the Washington State Twin Registry. She earned a PhD from the University of Utah in the Department of Anthropology, focused on human population genetics, and trained in Statistical Genetics at the University of Washington during her postdoctoral fellowship.

Liz's research goals are to identify variants influencing disease within and between human populations, and predict and evaluate their functions. In particular, she is interested in the biology differentiating the genetic underpinnings of Mendelian disorders (single gene, high penetrance) from complex traits influenced by many genetic and environmental factors (ex., cardiovascular disease), and how genetic modifiers fit within that spectrum. She is a collaborative researcher, participating in several large-scale sequencing studies including the Alzheimer's Disease Sequencing Project, a genetic modifier study with the Cystic Fibrosis Foundation, the University of Washington Center for Mendelian Genomics, and soon the Pacific Northwest Undiagnosed Disease Network. Through these and other collaborations, she is investigating the functional consequences of pathogenic genetic variants associated with disease.

At IGES, Liz has served as chair of the Young Investigators Committee where she introduced the student-mentor lunch, job fair, and other programs. She continues to serve on the Communications Committee, where she maintains the society's Facebook pages.

Five selected publications:

1. **Blue E.E.**, Yu C-E., Thornton T.A., Chapman N.H., Kernfeld E., Jiang N., Shively K.M., Buckingham K.M., Marvin C.T., Bamshad M.J., Bird T.D., Wijsman E.M. (2018) Variants regulating *ZBTB4* are associated with age-at-onset of Alzheimer's disease. *Genes, Brain and Behavior* 17:e12429. https://www.ncbi.nlm.nih.gov/pubmed/29045054
2. **Blue E.E.**, Louie T.L., Chong J.X., Hebbring S.J., Barnes K.C., Rafaels N.M., Knowles M.R., NHLBI GO Exome Sequencing Project, LungGO, Gibson R.L., Bamshad M.J., Emond M.J. (2018) Variation in Cilia Protein Genes and Progression of Lung Disease in Cystic Fibrosis. *Annals of the American Thoracic Society* 15(4):440-448. https://www.ncbi.nlm.nih.gov/pubmed/29323929
3. Cox L.L, Cox T.C., Uribe L.M.M., Zhu Y., Richter C.T., Nidey N., Standley J., Deng M., **Blue E.**, Chong J., Yang Y… Roscioli T. (2018) Mutations in the Epithelial Cadherin-p120-Catenin Complex Cause Mendelian Non-Syndromic Cleft Lip with or without Cleft Palate. *American Journal of Human Genetics* 106(6): 1143-1157. https://www.ncbi.nlm.nih.gov/pubmed/29805042
4. Butkiewicz M., **Blue E.**, Leung F., Jian X., Marcora E., Renton A., Kuzma A., Wang L-S., Koboldt D., Haines J.L., Bush W.S. (in press) Functional Annotation of genomic variants in studies of Late-Onset Alzheimer's Disease. *Bioinformatics*. https://www.ncbi.nlm.nih.gov/pubmed/29590295
5. Witherspoon D.J., Wooding S., Rogers A.R., **Marchani E.E.**, Watkins W.S., Batzer M.A., Jorde L.B. (2007) Genetic Similarities Within and Between Human Populations. *Genetics* 176(1): 351-359. https://www.ncbi.nlm.nih.gov/pubmed/17339205

Keywords: collaborative, interdisciplinary, detail-oriented, helpful, creative

2019 IGES Elections
Candidates for Board of Directors – Brooke Fridley

Brooke Fridley is a Professor, Senior Member and Chair of the Department of Biostatistics and Bioinformatics at Moffitt Cancer Center. In July 2018, she also became the Scientific Director for Moffitt Cancer Center's Biostatistics and Bioinformatics Shared Resource. Prior to joining Moffitt Cancer Center, Dr. Fridley was at the University of Kansas Medical Center and the Mayo Clinic. At the University of Kansas, she was Director of the Biostatistics and Informatics Shared Resource for the NCI designated University of Kansas Cancer Center and Site Director for the Kansas-INBRE Bioinformatics Core. Brooke received her MS and PhD in statistics from Iowa State University. Her research focus is in the areas of statistical genomics, molecular epidemiology of cancer, cancer genomics, and pharmacogenomics. She has extensive experience as a collaborating statistician, particularly in the design and analysis of studies involving multiple types of 'omic data. Recently, she has been particularly involved in molecular epidemiology studies of ovarian cancer, pediatric pharmacogenomic collaborations examining the ontogeny-related metabolomic and transcriptomic changes, and the development of integrative 'omic analysis methods. Brooke has been an active member in IGES since 2006 and served on and chaired the Program Committee in 2012.

Five selected publications:

1. Fridley BL, de Andrade M. Missing phenotype data imputation in pedigree data analysis. Genet Epidemiol. 2008;32(1):52-60. doi: 10.1002/gepi.20261. PubMed PMID: 17685457
2. Fridley BL, Biernacka JM. Gene set analysis of SNP data: benefits, challenges, and future directions. Eur J Hum Genet. 2011;19(8):837-43. PubMed PMID: 21487444; PMCID: 3172936.
3. Larson NB, Jenkins GD, Larson MC, Vierkant RA, Sellers TA, Phelan CM, Schildkraut JM, Sutphen R, Pharoah PP, Gayther SA, Wentzensen N, Ovarian Cancer Association C, Goode EL, Fridley BL. Kernel canonical correlation analysis for assessing gene-gene interactions and application to ovarian cancer. Eur J Hum Genet. 2014;22(1):126-31. PubMed PMID: 23591404; PMCID: 3865403.
4. Usset JL, Raghavan R, … Goode EL, Fridley BL, Ovarian Cancer Association C, the Australian Cancer S. Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiol Biomarkers Prev. 2016;25(5):780-90. PubMed PMID: 26976855; PMCID: PMC4873330.
5. Chalise P, Fridley BL. Integrative clustering of multi-level 'omic data based on non-negative matrix factorization algorithm. PLoS One. 2017;12(5):e0176278. PubMed PMID: 28459819; PMCID: PMC5411077.

Keywords: Curious, Hard-Working, Approachable, Collaborative, Fun-loving

2019 IGES Elections
Candidates for Board of Directors – Jaya Satagopan

Jaya Satagopan is an Attending Biostatistician in the Department of Epidemiology and Biostatistics at Memorial Sloan Kettering Cancer Center (MSKCC). Jaya received her undergraduate degree in Mathematics from the University of Madras in India (1988), a master's degree in Statistics from the Indian Statistical Institute (1990), and a PhD in Statistics from the University of Wisconsin – Madison, USA (1995). Her NIH-funded research program is at the intersection of statistics and genetic epidemiology of cancer. Jaya develops optimal study designs and novel analysis methods to detect risk factors for cancer and cancer-related traits, to estimate cancer risk and to investigate cancer biomarkers. She applies these methods to various molecular epidemiology studies in collaboration with colleagues at MSKCC and elsewhere to examine genetic and environmental determinants of the etiology and progression of cancer.

Jaya served on the IGES Education Committee from 2014 to 2016. She is currently a member of the IGES Program Committee, and served as the Program Chair for the 2017 conference. Jaya is also a member of the Editorial Board of *Genetic Epidemiology*.

Jaya is passionate about science communication and public engagement with data. To this end, she has mentored and given talks to school students about the use of foundational statistical concepts from high school curriculum in cancer research. Jaya helped establish and co-directs a NIH-funded training program at MSKCC to introduce young researchers to cancer-related quantitative sciences and to inspire them to pursue biostatistics-related careers. She also helped establish and co-chaired two successful NIH-funded symposia on statistical methods in genetic epidemiology, which brought together leading and emerging junior and minority statistical methods researchers, clinical oncologists and cancer epidemiologists to discuss contemporary issues in cancer molecular epidemiology, exchange ideas and stimulate collaborations.

In her spare time, Jaya enjoys music, gardening, baking and reading.

Five Selected Publications:

1. Satagopan JM, Zhou Q, Oliveria SA, Dusza SW, Weinstock MA, Berwick M, Halpern AC (2011). Properties of preliminary test estimators and shrinkage estimators for evaluating multiple risk factors – Application to questionnaire data from the SONIC study. Journal of the Royal Statistical Society Series C (Applied Statistics), 60: 619 – 632.

2. Satagopan JM, Elston RC (2013). Evaluation of removable statistical interaction for binary traits. Statistics in Medicine, 32: 1164-1190.

3. Satagopan JM, Sen A, Zhou Q, Lan Q, Rothman N, Langseth H, Engel LS (2015). Bayes and empirical Bayes methods for reduced rank regression models in matched case-control studies. Biometrics, 72: 584 - 595.

4. Iasonos A, Chapman PB, Satagopan JM (2016). Quantifying treatment benefit in molecular subgroups to assess a predictive biomarker. Clinical Cancer Research, 22: 2114-2120.

5. Satagopan JM, Iasonos A (2017). Measuring differential treatment benefit across marker specific subgroups: the choice of outcome scale. Contemporary Clinical Trials, doi: 10.1016/j.cct.2017.02.007.

Keywords: Communication, Enthusiasm, Innovation, Cancer.

2019 IGES Elections
Candidates for Board of Directors – Eleftheria Zeggini

Eleftheria Zeggini, Director of the Institute of Translational Genomics, Helmholtz Centre Munich, Germany.

I left my native Greece when I was 18 to pursue my love of genomic science in the UK. I studied for a BSc in Biochemistry at UMIST, and then completed a PhD on the Immunogenetics of juvenile arthritis, at the arc Epidemiology Unit, School of Medicine, University of Manchester. I spent the first half of my PhD in the lab and quickly realized that my true calling was in data analysis. Following a statistical genetics post doc at the Centre for Intergated Genomic and Medical Research in Manchester, I moved to the Wellcome Trust Centre for Human Genetics in Oxford to undertake a post doc in type 2 diabetes genetics, where I became centrally involved in the Wellcome Trust Case Control Consortium study. While in Oxford, I was awarded a Wellcome Research Career Development Fellowship to work on design, analysis and interpretation issues in large-scale association studies. I joined the Wellcome Sanger Institute's faculty 10 years ago, where I built a programme of work on the analytical genomics of complex traits. I have recently moved to the Helmholtz Centre in Munich, Germany, where I direct the newly-established Institute of Translational Genomics. We leverage big data in genomics for medically important human traits, aiming to shorten the path to translation and to empower precision medicine.

Together with our collaborators, we have led on the discovery of hundreds of genetic changes associated with the pathogenesis of complex diseases of high public health importance. Further, we have addressed statistical challenges by developing novel methods, specifically in the areas of rare variant burden testing, functional annotation of the non-coding genome, accounting for relatedness and sample overlap in association meta-analyses, and pleiotropy. Going forward, we will continue to dissect the role of sequence variation across the entire frequency spectrum in medically important traits by coupling high-throughput sequencing technologies with the study of diverse populations and strategies linking electronic health records to genomics. Our activities will continue to be underpinned by method development to empower the integration of multi-omics (genetics, gene expression, epigenetics and proteomics) data, and by developing statistical genetics approaches for next generation sequencing studies.

I am committed to developing early career researchers. My team has hosted over 40 visiting scientists training in statistical genetics. We have organised three dedicated statistical genetics workshops and an annual summer school on complex trait genetics (in my hometown, Volos, Greece). I am delighted to engage in informal mentoring arrangements, and have served on formal mentorship panels e.g. for IGES, ASHG and EMBO. I am interested in diversity and inclusion; in 2011, I founded the Wellcome Genome Campus Sex in Science programme and have led the Sanger Institute's Equality, Diversity and Inclusion work. I also have a strong interest in capacity building and cultivating scientific talent in regions with limited access to resources and expertise.

In my spare time I enjoy travelling with my family (mostly to sunny destinations), playing with my two young sons, and reading.

Five Selected Publications:

1. Zengini E, Hatzikotoulas K, Tachmazidou I, Steinberg J, Hartwig FP, Southam L, Hackinger S, Boer CG, Styrkarsdottir U, Suveges D, Kilian B, Gilly A, Ingvarsson T, Jonsson H, Babis GC, McCaskie A, Uitterlinden AG, van Meurs JBJ, Thorsteinsdottir U, Stefansson K, Davey Smith G, Wilkinson JM, **Zeggini E**. The genetic architecture of osteoarthritis: insights from UK Biobank. *Nat Genet* 2018;50:549-558. PMID: 29559693.

2. **Zeggini E**, Panoutsopoulou K, Southam L, Rayner NW, Day-Williams AG, Lopes MC, Boraska V, Esko T, Evangelou E, Hofman A, Houwing-Duistermaat JJ, Ingvarsson T, Jonsdottir I, Jonsson H, Kerkhof HJM, Kloppenburg M, Bos S, Mangino M, Metrustry S, Slagboom PE, Thorleifsson G, Raine EVA, Ratnayake M, Ricketts M, Beazley C, Blackburn H, Bumpstead S, Elliott KS, Hunt SE, Potter SC, Shin SY, Yadav VK, Zhai G, Sherburn K, Dixon K, Arden E, Aslam N, Battley PK, Carluke I, Doherty S, Gordon A, Joseph J, Keen R, Koller NC, Mitchell S, O'Neill F, Paling E, Reed MR, Rivadeneira F, Swift D, Walker K, Watkins B, Wheeler M, Birrell F, Ioannidis JPA, Meulenbelt I, Metspalu A, Rai A, Salter D, Stefansson K, Styrkarsdottir U, Uitterlinden AG, van Meurs JBJ, arcOGEN Consortium, Chapman K, Deloukas P, Ollier WER, Wallis GA, Arden N, Carr A, Doherty M, McCaskie A, Wilkinson JM, Ralston SH, Valdes AM, Spector TD, Loughlin J. Identification of new susceptibility loci for osteoarthritis -the arcOGEN study. *Lancet* 2012;380:815-23. PMID: 22763110.

3. Morris A, **Zeggini E**. An evaluation of statistical approaches to rare variant analysis in genetic association studies. *Genet Epidemiol* 2010; 34(2):188-93. PMID: 19810025.

4. **Zeggini E**, Scott LJ, Saxena R, Voight BF, the DIAGRAM Consortium. Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nat Genet* 2008; 40:638-45. PMID: 18372903.

5. **Zeggini E**, Weedon MN, Lindgren CM, Frayling TM, Elliott KS, Lango H, Timpson NJ, Perry JB, Rayner NW, Freathy RM, Barrett JC, Shields B, Morris AP, Ellard S, Groves CJ, Harries LW, Marchini JM, Owen KR, Knight B, Cardon LR, Walker M, Hitman GA, Morris AD, Doney ASF, the Wellcome Trust Case Control Consortium, McCarthy MI, Hattersley AT. Replication of genome-wide association signals in U.K. samples reveals risk loci for type 2 diabetes. *Science* 2007;316(5829):1336-41. PMID: 17463249.

Keywords: Proactive, inclusive, innovative, open, collaborative.

Announcement
NIH Seeks Public Comment on Proposed Provisions for a Future Draft Data Management and Sharing Policy

See announcement from NIH below.

The ELSI Committee previously drafted a response on behalf of the Society to the NIH Genomic Data Sharing Policy back in 2013:

http://www.geneticepi.org/wp-content/uploads/2013/11/IGES_Response_to_GDS_Policy_2013.pdf

and is considering preparing an updated response to the proposed key provisions to serve as the foundation for future NIH policy.

October 11, 2018

NIH Seeks Public Comment on Proposed Provisions for a Future Draft Data Management and Sharing Policy

On October 10, 2018, the National Institutes of Health (NIH) issued a Request for Information (RFI) in the *NIH Guide to Grants and Contracts* to solicit public input on proposed key provisions that could serve as the foundation for a future NIH policy for data management and sharing. The feedback we obtain will help to inform the development of a draft NIH policy for data management and sharing, which is expected to be released for an additional public comment period upon its development.

Comments on the proposed key provisions will be accepted through **December 10, 2018**, and can be made electronically by visiting here.

For a perspective on the importance of obtaining robust stakeholder feedback on this topic, please see the latest *Under the Poliscope* by Dr. Carrie D. Wolinetz.

- A Data Sharing Renaissance: Music to My Ears!

Questions about the proposed provisions may be sent to the NIH Office of Science Policy at SciencePolicy@od.nih.gov

IGES 2019 in Houston, USA
Save the date!

IGES 28th Annual Meeting

12-14 October 2019

Houston, TX, USA

Hilton of the Americas

(before ASHG Meeting)

IGES 2018 San Diego
Award Winners

The IGES's most prestigious award, the ***leadership award,*** for 2018 was presented to John Witte:

John Witte, PhD
Professor of Epidemiology and Biostatistics, and Urology;
Head of the Division of Genetic and Cancer Epidemiology;
Associate Director of the Institute for Human Genetics;
Co-Leader of the Cancer Genetics Program;
University of California, San Francisco

The ***James V. Neel Young Investigator Award*** for the best IGES presentation by a **young scientist** was awarded to **Ekaterina Yonova-Doing**.

The ***Roger Williams Award*** for the best IGES presentation by a **student** was awarded to **Rachel Moore**.

The winners of the ***Robert C. Elston Award for Best Paper*** published in *Genetic Epidemiology* in 2017 were Timothy Shin Heng Mak, Robert Milan Porsch, Shing Wan Choi, Xueya Zhou, and Pak Chung Sham for their paper "*Polygenic scores via penalized regression on summary statistics"* (https://doi.org/10.1002/gepi.22050).

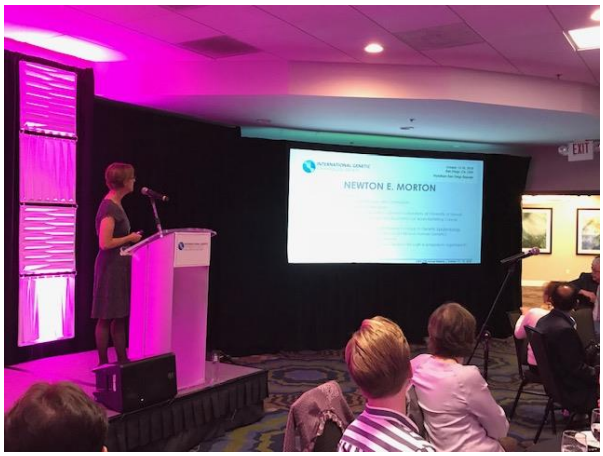
The 1st, 2nd and 3rd CIHR STAGE ***best poster*** awards prize winners were:

1st place: **Sisi Li**, University of Southern California, Los Angeles, USA

2nd place: **Sheethal Jose**, National Institutes of Health Bethesda, USA

3rd place: **Chubing Zeng**, University of Southern California, Los Angeles, USA

More IGES 2018 Photos
Remembering Newton Morton



To upload your own photos from IGES 2018, the steps are:

- login into your MemberClicks account at https://iges.memberclicks.net/login
- click on “Membership”
- click on “My Profile”

To upload photos, people should click on “Upload Photos” under “My Status”.
They can create albums here as well, or just upload a single photo.

To view all photos from anyone who has shared photos, they need to click on "My Community”, which shows a newsfeed / wall.

Committee reports
Latest news from IGES Committees

This section contains current news and announcements from the IGES Committees. Here we report on some recent and upcoming changes to Committee memberships.

[We often have vacancies to fill on IGES committees. If you are interested in joining an IGES Committee, please contact the relevant Committee Chair listed on the IGES website, or email iges@geneticepi.org]

Program Committee

Rotating off in 2019: Guillaume Paré and Jaya Satagopan. Many thanks for your outstanding service to, and chairmanship of, the Program committee!

Publications Committee

Rotating off in 2019: Lei Sun and Xiaofeng Zhu. Many thanks for your outstanding service to the Publications committee!

ELSI Committee

Rotating off in 2019: Robert Igo and Diptasri Mandal. Many thanks for your outstanding service to the ELSI committee!

Communications Committee

Rotating off in 2019: Sahir Bhatnagar, Todd Edwards, David Fardo, Claire Simpson. Many thanks for your outstanding service to the Communications committee!

Young Investigators Committee

Rotating off in 2019: Han Chen, Sarah Gagliano, Audrey Hendricks. Many thanks for your outstanding service to the YI committee!

Education Committee

Rotating off in 2019: Mark Seielstad. Many thanks for your outstanding service to the Education committee!

2018 IGES Officials

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

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

Current **officers** are: President: Inke König; Past President: Andrew Morris; President-Elect: Celia Greenwood; Treasurer: Mariza de Andrade; Secretary: Heather Cordell; Editor-in-Chief, Genetic Epidemiology: Sanjay Shete.

Board members comprise the officers and the following 6 people: Julia Bailey, Xihong Lin, David Balding, Jeanine Houwing-Duistermaat, Liz Gillanders and Pak Sham.

The **Education Committee** is co-chaired by Stephanie Santorico and Todd Edwards.

The **ELSI Committee** is chaired by Daniel Shriner.

This year's **Publications Committee** is chaired by Celia Greenwood (ex-officio).

The **Scientific Program Committee** for 2018 is chaired by Guillaume Paré.

The **Young Investigators' Committee** is chaired by James Cook.

The **Communications Committee** is chaired by Heather Cordell (ex-officio).

Please refer to the above website for the current respective committee members.

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

The **IGES webmaster** is Sarah Gagliano. The **IGES Facebook contact** is Elizabeth Blue, the **Twitter contact** is Priya Duggal and the **LinkedIn contact** is Han Chen.

Membership and conference administration is organized by Vanessa Olmo.

IGES Web Site: http://www.geneticepi.org/
IGES Facebook page: https://www.facebook.com/geneticepi?ref=hl
IGES Twitter page: https://twitter.com/genepisociety
IGES LinkedIn page: https://www.linkedin.com/groups/12061041/

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

The November 2018 Pre-Election Newsletter was edited, proofread, and formatted by Heather Cordell