



INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Newsletter – *November 2019 Pre-Election Edition*

Contents

[Letter from the President](#)

[Treasurer's Corner](#)

[Editor's Corner](#)

[2020 Membership Drive](#)

[IGES Fellow Members](#)

[Secretary Election Results](#)

[2020 IGES Elections: Candidates](#)

[Houston 2019: Award Winners and Thanks](#)

[Seoul 2020: Plan to attend!](#)

[Highlighted papers by IGES members](#)

[Listing of IGES Officials](#)

Letter from the President Celia Greenwood

It was a great pleasure to see many IGES members in Houston last month. The meeting was right downtown, and the venue was very comfortable with our presentations and our posters side by side. I think all the talks were excellent and well appreciated. Our keynote speakers (Dr. Genevera Allen, Dr. Kari North, Dr. Toby Johnson, Dr. Hongyu Zhao, and the winner of the Robert C. Elston prize for the 2018 best paper in Genetic Epidemiology: Sai Chen [Jingjing Yang, Sai Chen, Gonçalo Abecasis, and IAMDGC; “Improved score statistics for meta-analysis in single-variant and gene-level association studies”]) all gave excellent presentations.



The hands-on format of the Educational workshop on Mendelian randomization was well attended, clearly presented, and strongly appreciated. The poster sessions and the well-attended mentoring lunch provided ample opportunities for formal and informal discussions. This year, we instituted a series of coloured dots on nametags to indicate first-time attendees versus seasoned IGES attendees happy to be approached for questions. Hopefully, many of you were able to benefit from this simple meet-and-greet mechanism.

Congratulations to the winner of the 2019 Neel award: Carl Melbourne (Genome-wide gene-smoking interaction analysis of lung function in UK Biobank) and to the 2019 Williams award

winner: Austin Wang (Allele-specific QTL fine-mapping with PLASMA). Congratulations also to the winners of the prizes for best posters: 1st prize: Natalia Zemlianskaia (High-dimensional regularized regression for identifying gene-environment interactions incorporating external information); 2nd prize: Brandon Coombes (A principal component approach to polygenic risk scores to avoid over and underfitting); and 3rd prize: Arjun Bhattacharya (A framework for transcriptome-wide association studies in breast cancer in diverse study populations). Thanks to the Program Committee, Chaired by Dr. Eleanor Wheeler, for the variety and excellence of the presentations, to the Educational Committee co-chairs Todd Edwards and Stephanie Santorico, and a warm thanks to Vanessa Olmo, Tamiko Kinkade, & Zenaida Mendoza of Business Endeavours and to Past President Inke König for the planning.

This year's IGES leadership award went to Dr. Josée Dupuis of the Boston University School of Public Health. Josée was President of IGES in 2016 (term 2015 – 2017), was a member of the Board of Directors from 2012-2014, attends almost every IGES meeting and is an enthusiastic supporter of the society. She organized our 2017 IGES meeting in Cambridge, UK; a beautiful location and a superb meeting, held in conjunction with the Genomics of Common Diseases meeting at the Wellcome Trust Sanger Centre nearby. Congratulations Josée!

As we move forward to 2020, I would like to warmly thank our Past President, Inke König (University of Lübeck, Germany), who has done an excellent job shepherding the society in the last three years and who is now leaving the IGES Board, and to welcome Dr. Peter Kraft (Harvard T.H. Chan School of Public Health) who is looking forward to being your 2020 President. Dr. Heike Bickeböller (University of Göttingen, Germany) is nominated for President Elect, and we have four excellent candidates who are up for election for Board of Directors Members at Large: Frank Dudbridge (University of Leicester, UK), Jinko Graham (Simon Fraser University, Canada), Wei Pan (University of Minnesota, USA) and Chih-Chieh Wu (National Cheng Kung University, Taiwan). Short biographies of our candidates are given in this newsletter, and I hope you will take the time to vote later this month.

I am sure you are all aware that Hong Kong has been experiencing political unrest during the last few months. In consequence, at the 2019 Business Meeting in Houston, members voted to move our 2020 meeting from Hong Kong to Seoul, South Korea. First, I would like to express my heartfelt sympathy for the citizens of Hong Kong who are or may be caught in the middle, and my hope that the situation calms down quickly and happily. This was a difficult decision, and I would like to thank all the members who expressed their thoughts and opinions. Furthermore, on behalf of IGES, I would like to express a large vote of thanks for the immense time and effort spent by Dr. Maggie Wang and Dr. Pak Sham in organizing the plans for the Hong Kong location. IGES 2020, therefore, will be held at Seoul National University (Seoul, South Korea; July 1-3 with an educational workshop on July 4th), within the Engineering complex on the campus. Some accommodation has been reserved on campus at Hoam Faculty House; additional accommodation will be reserved shortly at a hotel in the Gangnam district, near the main convention centre (where the International Biometric Society 2020 meeting will be held immediately following IGES 2020). Keep checking the IGES website over the next weeks to find

out about the upcoming Scientific Program and topics for the Educational Workshop; early abstract submission will open at the beginning of December.

We are a small and very interdisciplinary society, which I hope makes us welcoming, friendly and provides good opportunities for informal mentoring. For those who are recent members, feel free to reach out for advice if needed. For long-time members, consider becoming an IGES Fellow Member, and promote the benefits to your colleagues. I hope you all remember to renew your memberships for 2020 and I hope to see many of you in July, 2020 in Seoul. Please come and chat with me!

Celia Greenwood

2019 IGES President

Treasurer's Corner
Mariza de Andrade



I am pleased as Treasurer to share with IGES members that we remain in good financial standing, and that we will continue to be vigilant in our negotiations and management of resources to maintain this good standing.

I would like to remind IGES members that the 2020 IGES membership is open – please go to <https://www.geneticepi.org/membership-fees-2020> for details. Please encourage your colleagues and collaborators to join as well! Don't forget that IGES continues to offer additional categories of registration for members from low- or lower-middle- income countries.

As a reminder, IGES is a charitable and educational organization, and any contribution other than membership and meeting registration fee is tax-deductible. 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 an official journal for our society, **with an impact factor of 2.5**, 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 December 2019 issue can be found here:

<https://onlinelibrary.wiley.com/toc/10982272/2019/43/8>

- Best paper published in Genetic Epidemiology award was given to:

Improved score statistics for meta-analysis in single-variant and gene-level association studies

Authors: Jingjing Yang, Sai Chen, [Gonçalo Abecasis](#), IAMDGC

Free online access to the paper can be found here:

<https://onlinelibrary.wiley.com/doi/10.1002/gepi.22123>

- Top-cited Genetic Epidemiology articles can be found here:

[https://onlinelibrary.wiley.com/doi/toc/10.1002/\(ISSN\)1098-2272.GEPI-top-cited](https://onlinelibrary.wiley.com/doi/toc/10.1002/(ISSN)1098-2272.GEPI-top-cited)

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 2020 Membership Drive

Dear IGES members,

It is now time to renew your membership for 2020. Registration/renewal opened on November 1st 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:

<https://www.geneticepi.org>

The early-bird membership fee is available until January 31, 2020.

Rates for 2020 IGES membership:

- Regular member **US\$130**, if paid by January 31, 2020 (early-bird)
- Regular member **US\$155** if paid on or after February 1, 2020
- Student and Post-Doctoral* member with online access to Journal **US\$68**, rate continues all year but please aim to pay by January 31, 2020
- Student and Post-Doctoral* member **without** online access to Journal **US\$25**, rate continues all year but please aim to pay by January 31, 2020
- 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 official 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 <https://www.geneticepi.org/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 Fellow Members

A reminder that, as a new initiative since 2018, IGES confers the title of “Fellow Member of IGES” to long-term regular members of the society. Through this title, IGES rewards these consistent members and encourages others to maintain membership.

Fellow Members of IGES

- are listed on the IGES website
- are announced at the annual IGES meeting, and
- receive a certificate stating their special status

Eligibility

To be eligible, the applicant must have continuous regular membership of IGES for 5 years or more. Breaks in membership due to, for example, maternity/paternity leave or illness, have to be justified in the application.

Application

To apply, please fill in the Application Form available from the website:

<https://www.geneticepi.org/iges-fellow-members>

and email it to the IGES secretary at iges@geneticepi.org. Please include information on your years of IGES membership and, if applicable, justify any breaks in your continuous membership. Eligibility will be confirmed by the IGES Board of Directors.

Current listing of Fellow Members:

Joan Bailey-Wilson	Stephen Rich
Jenny Barrett	Stephanie Santorico
Alexandre Bureau	Jaya Satagopan
Heather Cordell	Daniel Schaid
Denise Daley	Ricardo Segurado
Mariza de Andrade	Sanjay Shete
Celia Greenwood	Daniel Shriner
Inke Koenig	Ellen Wijsman
Jurg Ott	

Election of IGES Secretary July 2019 - June 2022

Elected candidate: Heather Cordell

All IGES members were eligible to cast their vote in the election (held between May and June 2019) of a new IGES Secretary for the period of office of three years from July 2019 to June 2022, in accordance with the IGES Bylaws.

The ballot paper for these elections was sent out by SurveyMonkey. The elected candidate, obtaining 93 out of a total of 93 votes was:

Heather Cordell



Heather is looking forward to serving a second term (i.e. for a further 3 years) as IGES secretary.

[The ballot paper for these elections was 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].

IGES 2020 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 2021:

- **Heike Bickeböller**

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

- **Frank Dudbridge**

- **Jinko Graham**

- **Wei Pan**

- **Chih-Chieh Wu**

[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].

2020 IGES Elections
Candidate for IGES President – Heike Bickeböllner



Heike Bickeböllner is chair of the Department of Genetic Epidemiology at the University of Göttingen, Germany, in 2001 the first dedicated chair to this field in Germany. She has a long standing record as a genetic epidemiologist and statistical geneticist with a clear dedication to IGES, for which she received the IGES leadership award in 2011. For IGES she has served as a member of the board and in several other functions. She hosted the 2001 IGES meeting in Garmisch, Germany, as chair of both the program and organizing committee, in 2007 she initiated the ambassador programme as head of the membership committee and in 2011 she initiated the statement of several German societies on American regulations for Human Research Protection as an answer to a discussion of the IGES ELSI committee. From 2013-2016 she was the IGES secretary. She also was a member of the advisory board for the biannual Genetic

Analysis Workshops (GAW) and editor of the GAW18 proceedings. Her research focuses both on methodological developments as well as genetic epidemiological studies. These cover linkage and association approaches for candidate genes as well as for genomewide and –omics searches. In this respect she is a member of different consortia, e.g. the TRICL Lung Cancer Consortium Methodological developments currently focus on pathway integration, gene-environment interaction and longitudinal approaches on a genomic scale. Regarding teaching she wrote an introductory textbook for statisticians and molecular biologists in German (Springer).

Five selected publications:

1. Ji X, Bossé Y, ...Bickeböllner H, ..., Brennan P, Amos CI (2018) Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. *NAT COMMUN* 9(1): 3221, doi: 10.1038/s41467-018-05074-y PMID: 30104567
2. Rosenberger A, Hung RJ, ...,Bickeböllner H, Gomolka M (2018) Genetic modifiers of radon-induced lung cancer risk: a genome-wide interaction study in former uranium miners. *INT ARCH OCC ENV HEA* 91(8): 937-950 doi: 10.1007/s00420-018-1334-3 PMID: 29971594
3. McKay JD, Hung RJ, ..., Bickeböllner H, ..., Brennan P, Landi MT, Amos CI (2017) Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. *NAT GENET* 49(7): 1126-1132, doi: 10.1038/ng.3892 PMID: 28604730
4. Friedrichs S, Manitz J, Burger P, Amos CI, Risch A, Chang-Claude J, Wichmann HE, Kneib T, Bickeböllner H, Hofner B (2017) Pathway-Based Kernel Boosting for the Analysis of Genome-Wide Association Studies. *COMPUT MATH METHOD M* 2017: 6742763, doi: 10.1155/2017/6742763 PMID: 28785300
5. Rosenberger A, Friedrichs S, Amos CI, Brennan P, Fehring G, Heinrich J, Hung RJ, Muley T, Müller-Nurasyid M, Risch A, Bickeböllner H (2015) META-GSA: Combining Findings from Gene-Set Analyses across Several Genome-Wide Association Studies. *PLOS ONE* 10(10): e0140179, doi: 10.1371/journal.pone.0140179 PMID: 26501144

Keywords: Encouraging, Supportive, Collaborative, Inclusive, Approachable.

2020 IGES Elections
Candidates for Board of Directors – Frank Dudbridge



Frank Dudbridge is Professor of Statistical Genetics at the University of Leicester. He received his PhD on fractal image compression from Imperial College London and held a postdoctoral fellowship at the University of California, San Diego before moving into genetic epidemiology via a training fellowship at the University of Cambridge. Following a brief flirtation with industry he held academic appointments at the MRC Biostatistics Unit and the London School of Hygiene and Tropical Medicine before coming to Leicester in 2016.

His interests are in statistical methods for genetic epidemiology, in which he has made highly cited contributions to haplotype analysis [1], genome-wide association studies [2], genetic risk prediction [3] and Mendelian randomisation [4]. These papers resulted directly from collaborations with applied researchers and consortia in numerous areas including cardiovascular, respiratory, cancer and psychiatric genetics. These collaborations have also spurred methodological developments for DNA methylation, tumour phylogenetics and capture Hi-C data [5].

Frank has been an IGES member since 2000 and served on the program committee from 2006-8. He is an associate editor of *Human Heredity* and has previously served for *Bioinformatics*, *JRSS series C* and *BMC Bioinformatics*. He is an enthusiastic mentor of early career researchers, having organised networking events and travel bursary schemes, acted as a departmental tutor and is co-director of a Wellcome Trust doctoral training programme. He is an amateur pianist and distance runner.

Five selected publications:

1. Dudbridge F (2003) Pedigree disequilibrium tests for multilocus haplotypes. *Genet Epidemiol* 25:115-21
2. Dudbridge F, Gusnanto A (2008) Estimation of significance thresholds for genomewide association scans. *Genet Epidemiol* 32:227-34
3. Dudbridge F (2013) Power and predictive accuracy of polygenic risk scores. *PLoS Genet* 9:e1003348
4. Holmes MV, Dale CE, ... , Dudbridge F, Casas JP (2014) Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ* 349:g4164
5. Baxter JS, Leavy OC, Dryden NH, ... , Dudbridge F, Haider S, Fletcher O (2018) Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. *Nat Commun* 9:1028

Keywords: Multiplicity, causality, frequentist, twins, pizza

2020 IGES Elections
Candidates for Board of Directors – Jinko Graham



Jinko Graham

I am a Professor and Graduate Chair in the Department of Statistics and Actuarial Science at Simon Fraser University. I obtained an MSc in Statistics from University of British Columbia and a PhD in Biostatistics from the University of Washington. After a postdoctoral fellowship at North Carolina State University and the US National Institute of Statistical Sciences, I joined Simon Fraser University and have been there ever since. My research focus is on statistical genetics with particular interest in how variation in the DNA sequences of individuals reflects their underlying genealogical relationships. These relationships can tell us about our ancestry and origins. They can also tell us about individual predisposition to inherited traits, and so are of use in mapping the genomic location of DNA variants that contribute to disease traits.

I have a general interest in enabling researchers working in isolated groups or regions to connect with peers and fertilize ideas. From 2004-2012, I served on the organizing committee of the Canadian Institutes of Health Research, Institute of Genetics, for its annual meeting in statistical and human genetics. More recently, I have served on the Student Travel Grants Committee of the Statistical Society of Canada, in the last two years as the chair. I am the regional representative to the Statistical Society of Canada for the Alberta, British Columbia and the Yukon region. I have enjoyed the IGES Meetings since my days as a graduate student and would welcome the chance to connect with international colleagues and support the work of the Society.

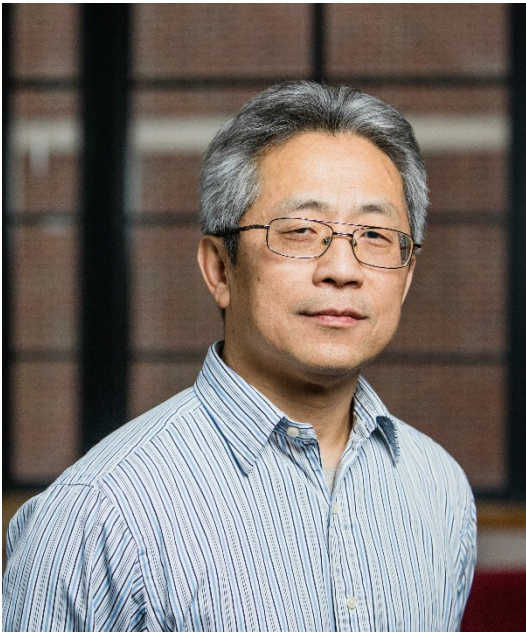
In my spare time, I enjoy spending time with my family, getting out into nature, music and reading..

Five selected publications:

1. Choi JC, Lu D, Beg F, Graham J and McNeney B. The Contribution Plot: Decomposition and Graphical Display of the RV Coefficient, with Application to Genetic and Brain Imaging Biomarkers of Alzheimer's Disease. *Human Heredity*, DOI:10.1159/000501334, August 2019.
2. C Nieuwoudt, SJ Jones, A Brooks-Wilson, J Graham. Simulating pedigrees ascertained for multiple disease-affected relatives. *Source Code for Biology and Medicine*, 2018 13:2. <https://doi.org/10.1186/s13029-018-0069-6>
3. Charith B Karunaratna and Jinko Graham. Using gene genealogies to localize rare variants associated with complex traits in diploid populations. *Human Heredity*, 2017-18;83:30–39. DOI <https://doi.org/10.1159/000486854>. Published online May 15, 2018.
4. Elena Szefer, Donghuan Lu, Farouk Nathoo, Mirza Faisal Beg, Jinko Graham for the Alzheimer's Disease Neuroimaging Initiative. Multivariate association between single-nucleotide polymorphisms in Alzgene linkage regions and structural changes in the brain: discovery, refinement and validation. *Statistical Applications in Genetics and Molecular Biology*. 16: 349-366. DOI: <https://doi.org/10.1515/sagmb-2016-0077>
5. Burkett KM, McNeney B, Graham J. sampletrees and Rsampletrees: Sampling gene genealogies conditional on SNP genotype data. *Bioinformatics* 2016; doi: 10.1093/bioinformatics/btv763. Published online Jan 20, 2016.

Keywords: open, collaborative, inclusive, curious

2020 IGES Elections
Candidates for Board of Directors – Wei Pan



Wei Pan

After obtaining his Ph.D. in Statistics at the University of Wisconsin-Madison in 1997, Wei immediately joined the Division of Biostatistics, School of Public Health, University of Minnesota (at Twin Cities) as an assistant professor, promoted to associate professor in 2003 and full professor in 2007. His recent research interests are in statistical genetics and genomics, and statistical learning and data mining, though he previously worked on correlated data analysis and survival analysis. His recent work includes gene network- and pathway-based hypothesis testing, network-based penalized regression and classification for high-dimensional genomic data. In particular, in the last 10 years, along with his collaborators he has been working on analysis of GWAS data and next-generation sequencing data, mainly developing new and powerful statistical tests

for complex traits-common or rare variant associations. He has expanded his research into analysis of neuroimaging data, including genetic association analysis of multiple neuroimaging phenotypes, and estimation and inference of brain functional connectivity based on resting-state fMRI data. Most recently, Wei and his group have been working on integrating GWAS and DNA-sequencing summary data with omic and imaging data, such as in transcriptome-wide association studies (TWAS) and image-wide association studies (IWAS), for causal inference. He enjoys most working with and mentoring students and junior researchers.

Wei has enjoyed attending the IGES annual meetings in the last few years, and is a frequent (co-)author and reviewer for the IGES journal, *Genetic Epidemiology*.

Five Selected Publications:

1. Pan, W. (2009). Asymptotic tests of association with multiple SNPs in linkage disequilibrium. *Genetic Epidemiology*, 33: 497-507.
2. Pan W, Kwak I-Y, Wei P (2015). A powerful pathway-based adaptive test for genetic association with common or rare variants. *American Journal of Human Genetics*, 97: 86-98.
3. Xu Z, Wu C, Pan W; Alzheimer's Disease Neuroimaging Initiative (2017). Imaging-wide association study: Integrating imaging endophenotypes in GWAS. *NeuroImage*, 159: 159-169.
4. Xu Z, Wu C, Wei P, Pan W (2017). A Powerful Framework for Integrating eQTL and GWAS Summary Data. *Genetics*, 207: 893-902.
5. Xiao M, Shen X, Pan W (2019). Application of deep convolutional neural networks in classification of protein subcellular localization with microscopy images. *Genetic Epidemiology*, 43: 330-341.

Keywords: Collaboration, Computing, Data, Sports, Traveling.

2020 IGES Elections
Candidates for Board of Directors – Chih-Chieh Wu



Chih-Chieh Wu is Associate Professor in the Environmental and Occupational Health Department and Statistics Department, National Cheng Kung University in Tainan, Taiwan. Prior to the current position, he was Assistant Professor of Epidemiology at MD Anderson Cancer Center in Houston, Texas, with research focus on Statistical Genetics. Chih-Chieh completed a PhD in Applied Mathematics and Statistics from the Stony Brook University, New York. He received US National Institutes of Health (NIH)/National Cancer Institute (NCI)-funded grant awards as principal investigator to develop and implement statistical methods for modeling the measured susceptibility genotypes for the proband and relatives in a family, and for identifying copy number variations associated with complex disease in a whole genome scale. In IGES, Chih-Chieh has served as a member of the Scientific Program Committee since 2017.

His research interests are focused on developing and implementing methods for quantitatively estimating cancer risks attributable to measured genetic and non-genetic variants in family studies, identifying copy number variations associated with complex diseases, and detecting gene-gene and gene-environment interactions. Chih-Chieh applied these methods to study various diseases, including cancer families of Li-Fraumeni syndrome, rheumatoid arthritis, and head and neck cancer. In addition to human genetic analyses, he has also developed models for temporal and spatial statistics to identify temporal and geographical variation and anomalies of disease incidence, and applied to data of disease incidence on adolescent suicide, childhood Langerhans cell histiocytosis, and dengue.

Five Selected Publications:

1. Wu CC, Shete S, Amos CI, Strong LC. Joint effects of germ-line p53 mutation and sex on cancer risk in Li-Fraumeni syndrome. *Cancer Research* 66(16):8287-92, 2006.
2. Wu CC, Shete S, Chen WV, Peng B, Lee AT, Ma J, Gregersen PK, Amos CI. Detection of disease-associated deletions in case-control studies using SNP genotypes with application to rheumatoid arthritis. *Human Genetics* 126(2):303-15, 2009.
3. Wu CC, Shete S, Jo EJ, Xu Y, Lu EY, Chen WV, Amos CI. Whole-Genome Detection of Disease-Associated Deletions or Excess Homozygosity in a Case-Control Study of Rheumatoid Arthritis. *Human Molecular Genetics* 22(6):1249-1261, 2013.
4. Wu CC, Grimson RC, Amos CI, Shete S. Statistical methods for anomalous discrete time series based on minimum cell count. *Biometrical Journal* 50(1):86-96, 2008.
5. Lai WT, Chen CH, Hung H, Chen RB, Shete S, Wu CC. Recognizing Spatial and Temporal Clustering Patterns of Dengue Outbreaks in Taiwan. *BMC Infectious Diseases* 18:256, 2018.

Keywords: Enthusiastic, Creative, Interdisciplinary, Collaborative.

**IGES 2019 Houston
Award Winners and Thanks**

The IGES's most prestigious award, the *leadership award*, for 2019 was presented to **Josée Dupuis**, for her substantial contributions to the field and for her service to the society (including as 2016 President).



The winners of the *Robert C. Elston Award for Best Paper* published in *Genetic Epidemiology* in 2018 were Jingjing Yang, Sai Chen, Gonçalo Abecasis, and IAMDGC for their paper “*Improved score statistics for meta-analysis in single-variant and gene-level association studies*” (<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22123>).





The **James V. Neel Young Investigator Award** for the best IGES presentation by a **young scientist** was awarded to **Carl Melbourne** for his presentation “Genome-wide gene-smoking interaction analysis of lung function in UK Biobank”.

The **Roger Williams Award** for the best IGES presentation by a **student** was awarded to **Austin Wang** for his presentation “Allele-specific QTL fine-mapping with PLASMA”.



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



1st place: **Natalia Zemlianskaia**

“High-dimensional regularized regression for identifying gene-environment interactions incorporating external information”

2nd place: **Brandon Coombes**

“A principal component approach to polygenic risk scores to avoid over and underfitting”

3rd place: **Arjun Bhattacharya**

“A framework for transcriptome-wide association studies in breast cancer in diverse study populations”

Thanks to outgoing committee members/chairs **David Balding**, **Eleanor Wheeler**, **James Cook** and **Alisa Manning**, and also to our past-president **Inke König**.



IGES 2020 in Seoul, South Korea
Please publicise and plan to attend!



The poster for the International Genetic Epidemiology Society (IGES) Annual Meeting 2020 features a blue DNA double helix logo on a globe. The main text reads: "INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY Annual meeting 2020 July 1-3, 2020, Seoul, South Korea". Below this, there are three distinct sections: 1) A green box with yellow text: "Also, on July 4th: an Educational Symposium with leaders in the discipline", accompanied by a photograph of a rocky mountain peak overlooking a city. 2) A photograph of a modern glass skyscraper with a green box overlay containing white text: "At the Global Education Center for Engineers Convention, Seoul National University." and yellow text: "For more information: www.geneficepi.org/iges-2020". 3) A green box with white text: "Combine your IGES trip with the International Biometric Society meeting, July 5-10 ibc2020.org IGES is sponsoring an invited session on polygenic scores", accompanied by a photograph of a city skyline at sunset.

Although we are disappointed to have had to change the venue of IGES 2020 (originally planned for Hong Kong), we are excited to now be holding the 2020 IGES meeting in Seoul, South Korea. This will be the first time that an IGES meeting has been held in Asia (and only the second IGES meeting outside North America or Europe).

We need the help of **all IGES members** to actively publicise this meeting, especially to your networks across Asia (China, Singapore, Japan etc.) and beyond, in order to make it a success.

Highlighted papers by IGES members
As selected by the IGES Communications Committee

This year the IGES Communications Committee has continued its initiative of highlighting selected published papers by IGES members via Facebook and Twitter. Here is a listing of this year's papers:

General Journal Highlights:

September 2018: **Priya Duggal** was senior author of "Case-Control Study of Cryptosporidium Transmission in Bangladeshi Households" published in *Clin Infect Dis*.

October 2018: **Audrey Hendricks** was first author and **Josée Dupuis** was senior author of "ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls" published in *PloS Genet*.

November 2019: **Arthur Gilly** was first author and **Eleftheria Zeggini** was senior author of "Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits" published in *Nat Commun*.

December 2018: **Nick Shrine** was first author of "Moderate-to-severe asthma in individuals of European ancestry: a genome-wide association study" published in *Lancet Respir Med*.

January 2019: **Han Chen** was first author of "Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies" published in *Am J Hum Genet*.

February 2019: **Sarah Gagliano** was first author of "Relative impact of indels versus SNPs on complex disease" published in *Genet Epidemiol*.

March 2019: We had a special edition focused on Gene by Environment interaction! **Marie-Hélène Roy-Gagnon** was senior author of "Investigating Gene-Gene and Gene-Environment Interactions in the Association Between Overnutrition and Obesity-Related Phenotypes" published in *Front Genet*, and **Adrienne Cupples** was senior author of "Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids" published in *Nat Genet*.

April 2019: **Nathan Tintle** was senior author of "Leveraging summary statistics to make inferences about complex phenotypes in large biobanks" published in *Pac Symp Biocomput*.

May 2019: **Michael Boehnke** was senior author of "Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls" published in *Nature*.

June 2019: **Lei Sun** was senior author of "Fast and Accurate Shared Segment Detection and Relatedness Estimation in Un-phased Genetic Data via TRUFFLE" published in *Am J Hum Genet*.

July 2019: **Iuliana Ionita-Laza** was senior author of "A genome-wide scan statistic framework for whole-genome sequence data analysis" published in *Nat Commun*.

August 2019: **Christopher Wilson** was first author of "Multiple-kernel learning for genomic data mining and prediction" published in *BMC Bioinformatics*.

September 2019: **David Conti** was senior author of "A Latent Unknown Clustering Integrating Multi-Omics Data (LUCID) with Phenotypic Traits" published in *Bioinformatics*.

Genetic Epidemiology Journal Highlights:

September 2018: **Alexandre Bureau** was first author of “Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants”

<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22155>

October 2018: **Diptavo Dutta** was first author of “Multi-SKAT: General framework to test for rare-variant association with multiple phenotypes” <https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22156>

December 2018: **Robert Elston** was sole author of “Fisher's influence on me”

<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22165>

February 2019: **Kelsey Grinde** was first author of “Generalizing polygenic risk scores from Europeans to Hispanics/Latinos” <https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22166>

March 2019: **David Conti** was senior author of “Using Bayes model averaging to leverage both gene main effects and $G \times E$ interactions to identify genomic regions in genome-wide association studies”

<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22171>

April 2019: **Heather Wheeler** was first author and **Hae Kyung Im** was senior author of “Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways and complex traits” <https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22205>

June 2019: **Osvaldo Espin-Garcia** was first author of “A finite mixture model for X-chromosome association with an emphasis on microbiome data analysis”

<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22190>

July 2019: **Lei Sun** was senior author of “Analytical strategies to include the X-chromosome in variance heterogeneity analyses: Evidence for trait-specific polygenic variance structure”

<https://onlinelibrary.wiley.com/doi/full/10.1002/gepi.22247>

2019 IGES Officials

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

<https://www.geneticepi.org/organization>

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

Board members comprise the officers and the following 6 people: David Balding, Jeanine Houwing-Duistermaat, Liz Gillanders, Pak Sham, Ele Zeggini and Jaya Satagopan.

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 Peter Kraft (ex-officio).

The **Scientific Program Committee** for 2019 is chaired by Eleanor Wheeler.

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: <https://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>

This November 2019 Pre-Election Newsletter was edited, proofread, and formatted by Heather Cordell