INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Newsletter – *December 2023*

Contents

Letter from the President
John Witte

Dear Members of the IGES Community,

As 2023 and my IGES Presidency comes to an end, I want to thank you for your ongoing participation in our society. Your active involvement and contributions are what make IGES a vibrant and impactful society. I will remain very much involved with IGES as Past-President, working closely with our local host and IGES Board member **Stephanie Santorico** and the 2024 Scientific Program Committee chaired by **Linda Kachuri** to organize next year's meeting. I am also working with the 2024 Education Committee chaired by **Chunyu Liu** and **Luke Grosvenor** to organize a joint workshop with ASHG following our meeting. The meeting will be held in Denver on November 3-5th 2024, just before ASHG (which is also in Denver).

A special thank you to **David Balding**, who has completed his 3-year term as IGES President-elect, President, and Past-president. He provided outstanding service to the Society, including hosting our 2022 meeting in Paris and coordinating our 2023 meeting in Nashville. **Liz Gillanders** is taking over as President for 2024, so we are in good hands. The election for a new President-elect and three members of the Board of Director is now underway. We have excellent candidates. **Hae Kyung ("Haky") Im** is our candidate for President-elect. Board candidates are **Chloé Sarnowski**, **David Conti**, **Emmanuelle Génin**, **Lisa Strug**, and **Thomas Winkler**. Short biographies of our candidates are given in this newsletter. Please vote!

Congratulations again to **Heather Cordell** on receiving the IGES Leadership Award! This is the highest honor of the society and recognizes the awardee's contributions to both IGES and the field. Heather has provided extraordinary service to IGES, including as a member of the IGES Board of Directors (2006-2012), Secretary for two terms (July 2016-June 2022), and President (2010). She is a world-renowned leader in statistical genetics and genetic epidemiology. Heather has developed numerous novel methods, including for linkage analysis, maternal and imprinting effects, and causal models using multi-omics data. She has also collaborated on many applied projects. Heather is a dedicated educator who has mentored many students and provided extensive classroom and short-course teaching. This is a well-deserved honor recognizing Heather's leadership in IGES and the field.

Thanks to the 232 people who attended our 2023 IGES annual meeting. The society is largely organized and run by us, requiring substantial contributions by many people. Extra thanks to all the people who helped with the meeting, including:

- **Denise Daley**, chair of the Scientific Program Committee, which organized important oral and poster presentations;
- **Sarah Buxbaum** and **Chunyu Liu**, co-chairs of Education Committee, which put on the excellent IGES workshop on Single cell RNAseq and Multiomics Analysis;
- **Chloé Sarnowski**, chair of the Young Investigators Committee, which organized social events and a mentoring lunch, and judged the poster prizes;
- **Liz Gillanders**, chair of the Publications Committee, which selected the Robert C. Elston Award for Best Paper published in Genetic Epidemiology in 2022; and
- **Vanessa Olmo** and **Zenaida Mendoza** who helped organize and run the meeting.

Congratulations to the winners of the 2023 meeting awards:

Tianyuan Lu won the James V. Neel Young Investigator Award for the best IGES presentation by a young scientist;

Quan Sun won the Roger Williams Memorial Award for the best presentation by a student;

- **Charleston Chiang**, **Hannah Seagle**, and **Eric Sanders** were 1st, 2nd, and 3rd place winners, respectively, for the Best Poster Award; and
- **James Fryett**, **Andrew Morris**, and **Heather Cordell** won the Robert C. Elston Award for Best Paper.

Our annual general business meeting at the end of IGES was well attended, and participants made many important and helpful suggestions about the society and future meetings. Slides from the business meeting are located here: http://tinyurl.com/2efbevbt. The meeting ran a small deficit in part due to our room commitments to the conference hotel. For future meetings, if possible, please book the IGES conference hotel since the society is committed to a minimum number of rooms. Several important points were noted during the meeting and in the post-conference survey. The presentation on polygenic risk scores and embryo selection raised concerns regarding the presentation of and response to this controversial topic. IGES leadership and Committees have been discussing how to productively address potentially controversial topics in future meetings, including an opportunity for formal counterpoints and moderated discussion.

Please continue to give me or other Board members suggestions to improve IGES, including ideas for IGES 2024 in Denver. Don't forget to vote for the President-Elect and Board members.

Wishing you happy holidays and a nice start to 2024.

John Witte

2024 IGES Elections
Candidate for IGES President – Hae Kyung Im

Hae Kyung Im is an Associate Professor in the Section of Genetic Medicine and the Department of Human Genetics at the University of Chicago. She trained in Physics at the Instituto Balseiro, a center of excellence in Argentina, and later earned her PhD in Statistics from the University of Chicago. After exploring research in manufacturing and consulting in information security and finance, she found her calling in statistical genetics research.

She develops statistical methods to make sense of large amounts of genomic and other high-dimensional data to make discoveries that can be translated into improving human health.

To translate GWAS findings into actionable target genes, she developed and implemented an approach that uses genotype data to predict gene expression levels. The resulting system, a first-in-class gene-based association method called PrediXcan, expanded the test unit from genetic variants to more biologically meaningful units such as genes. Her publication of PrediXcan inspired similar approaches, creating a new class of methods now known as TWAS.

She was an active member of the GTEx consortium, a decade-long collaborative effort that collected RNA-sequencing and whole-genome sequencing data from 54 tissues across hundreds of individuals - in total, over 17,000 samples. This resource offers unprecedented opportunities to advance our understanding of transcriptomic effects on biological processes and human diseases. She co-supervised the analysis of the final GTEx flagship paper and co-wrote the manuscript along with four other members of the writing group. As the chair of the GWAS working group, she examined the downstream consequences of gene regulatory effects on human traits.

She has a strong track record of developing and sharing impactful methods with the community. Many research groups in academia, pharmaceutical companies, and biotech start-ups use her tools to interpret GWAS results and identify actionable disease targets. Committed to open science, she releases preprints of manuscripts and makes tools publicly available early on.

At IGES, her work has been recognized with the Robert C. Elston Best Paper Award in 2015. She has been a member of the IGES communications committee from 2015 to 2022 and has been instrumental in creating and managing the IGES intranet and Slack channels. She has been an IGES Board member since the beginning of 2023.

Five Selected papers

Gamazon, E., Wheeler, H., Shah, K. et al. A gene-based association method for mapping traits using reference transcriptome data. Nat Genet 47, 1091–1098 (2015). https://doi.org/10.1038/ng.3367

Milton Pividori , Padma S. Rajagopal, Alvaro Barbeira, Yanyu Liang, Owen Melia, Lisa Bastarache, YoSon Park, GTEx Consortium, Xiaoquan Wen, and Hae Kyung Im*. 2020. “PhenomeXcan: Mapping the Genome to the Phenome through the Transcriptome.” Science Advances 6 (37). 2020.

Yanyu Liang, François Aguet, Alvaro N. Barbeira, Kristin Ardlie, and Hae Kyung Im*. 2021. “A Scalable Unified Framework of Total and Allele-Specific Counts for Cis-QTL, Fine-Mapping, and Prediction.” Nature Communications 12 (1): 1424.

The GTEx Consortium. Atlas of genetic regulatory effects across human tissues. Science. 10-Sep-2020 DOI: 10.1126/science.aaz1776

Milton D Pividori, Nathan Schoettler, Dan L Nicolae, Carole Ober, and Hae Kyung Im*. Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. The Lancet Respiratory Medicine, 2019.

2024 IGES Elections
Candidate for Board of Directors – Chloé Sarnowski

Dr. Chloé Sarnowski is an Assistant Professor in the Department of Epidemiology at the University of Texas Health Science Center at Houston, School of Public Health. Before joining UTHealth, she completed her PhD in France in Dr. Florence Demenais' research unit, and a postdoctoral training in the Department of Biostatistics at Boston University, School of Public Health under Dr. Josée Dupuis' supervision.

Dr. Sarnowski research interests include the characterization of 1) the biological mechanisms underlying complex traits through multi-omics data integration, and 2) the genetic architecture of complex traits in diverse populations. Her research spans multiple disease areas applying statistical genetics to neurological disorders (Alzheimer's disease) and related endophenotypes and biomarkers, type 2 diabetes and glycemic traits, and aging-related traits.

Dr. Sarnowski has been a Framingham Heart Study (FHS) investigator since 2016 and an Atherosclerosis Risk in Communities (ARIC) Study investigator since 2021. She is involved in collaborative and applied research in large-scale international consortia such as the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium, the Trans-Omics for Precision Medicine (TOPMed) Program, and the Alzheimer's Disease Sequencing Project (ADSP), as well as in methodological work applied to omics data. She is the co-convener of three TOPMed working groups (Neurocognitive, Reproductive Health, and Longevity and Healthy Aging), and is active in international genetic societies such as the American Society of Human Genetics (ASHG) and the International Genetic Epidemiology Society (IGES).

Dr. Sarnowski has been a member of IGES since 2011 and has attended 11 meetings. She was a finalist of the Robert C. Elston Best Paper Award (IGES 2022, Paris) and a finalist of the James V. Neel Award (IGES 2017, Cambridge). She is the present Chair of the IGES Young Investigators Committee (YIC) and helps coordinate multiple activities during the annual conference.

Five selected publications:

1. **Sarnowski C***, Leong A*, Raffield LM, Wu P, de Vries PS, DiCorpo D, Guo X, Xu H, Liu Y, Zheng X, Hu Y, Brody JA, Goodarzi MO, Hidalgo BA, Highland HM, Jain D, Liu CT, Naik RP, O'Connell JR, Perry JA, Porneala BC, Selvin E, Wessel J, Psaty BM, Curran JE, Peralta JM, Blangero J, Kooperberg C, Mathias R, Johnson AD, Reiner AP, Mitchell BD, Cupples LA, Vasan RS, Correa A, Morrison AC, Boerwinkle E, Rotter JI, Rich SS, Manning AK, Dupuis J, Meigs JB. Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. ***Am J Hum Genet***. 2019 Oct 3;105(4):706-718. PubMed PMID: 31564435; PubMed Central PMCID: PMC6817529.
2. **Sarnowski C**, Huan T, Jain D, Liu C, Yao C, Joehanes R, Levy D, Dupuis J. JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. ***Genet Epidemiol***. 2021 Apr;45(3):280-292. PubMed PMID: 33038041; PubMed Central PMCID: PMC8005415.
3. Zhang Y, Meigs JB, Liu CT, Dupuis J, **Sarnowski C**. Leveraging family history in genetic association analyses of binary traits. ***BMC Genomics***. 2022 Oct 1;23(1):678. PubMed PMID: 36182916; PubMed Central PMCID: PMC9526325.

4. **Sarnowski C**, Conomos MP, Vasan RS, Meigs JB, Dupuis J, Liu CT, Leong A. Genetic Effect on Body Mass Index and Cardiovascular Disease Across Generations. ***Circ Genom Precis Med***. 2023 Feb;16(1):e003858. PubMed PMID: 36598822; PubMed Central PMCID: PMC9974769.

5. Bouzid H, Belk JA, Jan M, Qi Y, **Sarnowski C**, Wirth S, Ma L, Chrostek MR, Ahmad H, Nachun D, Yao W, Beiser A, Bick AG, Bis JC, Fornage M, Longstreth WT Jr, Lopez OL, Natarajan P, Psaty BM, Satizabal CL, Weinstock J, Larson EB, Crane PK, Keene CD, Seshadri S, Satpathy AT, Montine TJ, Jaiswal S. Clonal hematopoiesis is associated with protection from Alzheimer's disease. ***Nat Med***. 2023 Jul;29(7):1662-1670. PubMed PMID: 37322115; PubMed Central PMCID: PMC10353941.

Keywords: Genetic Epidemiology, Complex Traits, Multi-Omics, Data Integration

2024 IGES Elections
Candidate for Board of Directors – David Conti

David Conti, Ph.D.

After receiving his B.S. and M.S. in Earth Systems at Stanford University, David was trained in Genetic Epidemiology at Case Western Reserve University under the guidance of John Witte and Robert Elston. In 2001, David received the Roger Williams award from the International Genetic Epidemiology Society (IGES). Since 2002, he has been at the University of Southern California in the Division of Biostatistics, Department of Population and Public Health Sciences. He is currently Professor, Associate Director for Data Science Integration for the Norris Comprehensive Cancer Center at USC, and the Kenneth T. Norris, Jr. Chair in Cancer Prevention. David's research covers applied genetic epidemiology, environmental epidemiology, and statistical methods development. His methodological research focuses on statistical approaches to epidemiologic studies with specific interest in the integration of omic data and biological knowledge in modeling. This methodological work is part of the current cycle of a P01 project for Statistical Methods for Integrative Genomics in Cancer and includes an approach for integrating multiomic data by estimating latent subgroups within a mediation-type framework. He also has a R01-level project as part of the PRIMED consortium to develop methods to construct polygenic risk scores that are effective across ancestral populations and evaluate them in diverse prospective cohorts, most notably the Multiethnic Cohort. Central to his approach is the translation and incorporation of the underlying biological and social contexts, which necessitates strong, collaborative interdisciplinary efforts for success. Reflective of this, he is also Director of the Data Science Core for a P01 project investigating aggressive prostate cancer in African American men integrating the built environment, germline and somatic genetic profiles, gene expression, and tumor microenvironment data.

David feels that IGES offers a unique and more intimate opportunity for people in this field to interact and discuss current methods, applications, and the implications of our research. His past involvement in IGES includes serving as a member on the Ethical, Legal, and Social Issues Committee (2003-2007), the Program Committee (2009-2011), and the Publication Committee (2012-2015).

Five Selected Publications:

1. Peng, C., Wang, J., Asante, I., Louie, S., Jin, R., Chatzi, L., Casey, G., Thomas, D.C., and **Conti, D.V.** (2019). A Latent Unknown Clustering Integrating Multi-Omics Data (LUCID) with Phenotypic Traits. Bioinformatics. Feb 1;36(3):842-850.
2. Jiang, L., Xu, S., Mancuso, N., Newcombe, P.J., and **Conti, D.V.** (2021). A Hierarchical Approach Using Marginal Summary Statistics for Multiple Intermediates in a Mendelian Randomization or Transcriptome Analysis. Am J Epidemiol Jun 1;190(6):1148-1158.
3. **Conti, D.V.,** Darst, B.F., Moss, L.C., Saunders, E.J., Sheng, X., Chou, A., Schumacher, F.R., Olama, A.A.A., Benlloch, S., Dadaev, T., et al. (2021). Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nat Genet 53, 65-75.

4. Stratakis, N., **Conti, D.V.,** Jin, R., Margetaki, K., Valvi, D., Siskos, A.P., Maitre, L., Garcia, E., Varo, N., Zhao, Y., et al. (2020). Prenatal Exposure to Perfluoroalkyl Substances Associated with Increased Susceptibility to Liver Injury in Children. Hepatology. 2020 NIEHS Paper of the Year.
5. Colicino E, Margetaki K, Valvi D, Pedretti NF, Stratakis N, Vafeiadi M, Roumeliotaki T, Kyrtopoulos SA, Kiviranta H, Stephanou EG, Kogevinas M, McConnell R, Berhane KT, Chatzi L, **Conti DV.** Prenatal exposure to multiple organochlorine compounds and childhood body mass index. Environ Epidemiol. 2022 Apr 22;6(3):e201. PMID: 35702503.

Keywords: genetic epidemiology, environmental epidemiology, prostate cancer, multiomics, and exposome

2024 IGES Elections
Candidate for Board of Directors – Emmanuelle Génin

Emmanuelle Génin

My first research experience was in 1993 in the laboratory of Dr. Josué Feingold, under the supervision of Dr. Françoise Clerget-Darpoux, where I conducted a project for my master's degree on linkage analysis and evaluated, through a bayesian approach, the probability that a recently reported linkage in an extended Alzheimer disease family was wrong. I discovered the field of statistical genetics at the interface between genetics and mathematics and decided to continue in this field for my PhD research where I extended different methods used to map genes involved in human diseases to account for inbreeding. During this PhD work, I found out that the genetic structure of the population where patients are sampled was a major driver of the power to detect genes involved in disease. After my PhD, in 1997, I decided to join Glenys Thomson lab's in the department of Integrative Biology at UC Berkeley for a post-doctoral experience in population genetics. Then, in 1997, I moved to Cambridge (UK) to work with Hexagen, a start-up company where I was responsible for the statistical analyses of genetic data.

In 1999, I move back to France to join Françoise Clerget's laboratory in Paris and continued working on the statistical analysis of human genetic data with a particular focus on multifactorial diseases and some applications on auto-immune diseases such as multiple sclerosis. I was particularly interested on the HLA component of these diseases and modeling its role in disease susceptibility but also kept a strong interest in population genetics. In 2008, I joined Florence Demenais' lab at CEPH and worked on the impact of population stratification. In 2010, I obtained a grant from the French embassy in London and the Churchill College in Cambridge to spend a year as oversea fellow in the College and work with David Clayton and Matthew Hurles at the Sanger Institute.

Then in 2012, I moved to Brest and joined Claude Férec's laboratory to work on the characterization of the genetic diversity of the French population in order to better design association studies to find genes involved in complex diseases or modifier genes involved in monogenic diseases. I got involved in the French Genomic Medicine Plan and I am now responsible for one of the four pilot projects of this plan. This pilot project aims at providing population references to help interpret sequence data. In 2017, I became head of the UMR1078 research unit and, last year, I was appointed director of the Inserm Genetics, Genomics and Bioinformatics Thematic Institute that makes a link between the different labs working in the field at the national level. I discovered IGES in 1994 during my PhD and really enjoyed the society and the annual meetings. I got involved in the organization of two annual meetings, the first one in 2004 in Nöördwijkerhout (NL) and the second one in 2022 in Paris. I will be honored to be offered again the possibility to serve IGES and promote the field of genetic epidemiology.

Five selected references

1. Génin E, Martinez M, Clerget-Darpoux F. (1995). Posterior probability of linkage and maximal lod score. Annals of Human Genetics, 59, 123-132
2. Genin E, Hannequin D, Wallon D et al. (2011) APOE and Alzheimer disease: a major gene with semi-dominant inheritance. Mol Psychiatry, 2011. 16(9): p. 903-7
3. Genin E (2020) Missing heritability of complex diseases: case solved? Hum Genet 139 (1): 103-113. doi: 10.1007/s00439-019-02034-4
4. Saint Pierre A, Giemza J, Alves I, Karakachoff M, Gaudin M, Amouyel P, Dartigues JF, Tzourio C, Monteil M, Galan P, Hercberg S, Mathieson I, Redon R, Génin E*, Dina C* (2020) The genetic history of France. Eur J Hum Genet. Published online Feb 2020. doi: 10.1038/s41431-020-0584-1

5. Bocher O, Ludwig TE, Oglobinsky MS, Marenne G, Deleuze JF, Suryakant S., Odeberg J, Morange PE, Trégouët DA, Perdry H, Génin E (2022) Testing for association with rare variants in the coding and non-coding genome: RAVA-FIRST, a new approach based on CADD deleteriousness score. PLOS Genetics 18(9): e1009923. https://doi.org/10.1371/journal.pgen.1009923

2024 IGES Elections
Candidate for Board of Directors – Lisa Strug

Dr. Strug is Professor in the Departments of Statistical Sciences and Computer Science and cross-appointed in Biostatistics at the University of Toronto, and is a Senior Scientist in the Program in Genetics and Genome Biology at the Hospital for Sick Children. Dr. Strug is the inaugural Academic Director of the University of Toronto's Data Sciences Institute (DSI), a tri-campus, multi-divisional, multi-institutional, multi-disciplinary hub for data science activity at the University and affiliated Research Institutes. Dr. Strug holds other leadership positions in statistical science and genomics in Canada including the Director of the Canadian Statistical Sciences Institute Ontario Region (CANSSI Ontario), and Associate Director of the Centre for Applied Genomics, one of three nationally funded genome centers that provide sequencing infrastructure and analysis for the Canadian research community.

Dr. Strug leads the Canadian Cystic Fibrosis Gene Modifier Consortium and the Biology of Juvenile Myoclonic Epilepsy International Consortium, where her research focuses on the development of novel statistical methodology to identify modifier genes of disease variability. Her research focuses on the development of novel statistical approaches to analyze and integrate multi-omics data to identify alternative therapeutic targets, build predictive models of disease severity and therapeutic response, and understand the impact of modifier genes in complex human traits. She has received several honours including the Tier 1 Canada Research Chair in Genome Data Science and the Cystic Fibrosis Canada 2023 Senior Scientist Research Award for a continued track record of significant research accomplishments in the field of cystic fibrosis.

Dr. Strug has been an active member of IGES since 2007 and would be honoured to serve the society as an elected member of the IGES Board of Directors.

Five Selected Publications:

1) Wang, F, Panjwani, N, Wang, C, Sun, L, and **Strug, LJ.** (2022) A flexible summary-based colocalization method with application to the mucin Cystic Fibrosis lung disease modifier locus. *The American Journal of Human Genetics*. 109(1):1-17.

2) Panjwani, N, Wang, F, Mastromatteo, S, Bao, A, Wang, C, He, G, Gong, J, Rommens, JM, Sun, L, **Strug, LJ.** (2020) LocusFocus: Web-based colocalization for the annotation and functional follow-up of GWAS. *PLOS Computational Biology*. 16(1): e1008336.

3) Strug, LJ. (2018) The evidential statistical paradigm in genetics. *Genetic Epidemiology.* 42 (7) 590-607.

4) Soave, D, Corvol, H, Panjwani, N, Gong, J, Li, W, Boelle, PY, Durie, P, Paterson, AD, Rommens, JM, **Strug, LJ,** Sun, L. (2015) A joint location-scale test improves power to detect associated SNPs, gene-sets and pathways. *The American Journal of Human Genetics.* 97(1): 125-38.

5) Sun, L, Rommens, JM, Corvol, H, Li, W, Li, X, Chiang, T, Lin, F, Dorfman, R, Busson, P, Parekh, R, Zelenika, D, Blackman, S, Corey, M, Doshi, V, Henderson, L, Naughton, K, O'Neal, WK, Pace, RG, Stonebraker, JR, Wood, SD, Wright, FA,Zielenski, J, Clement, A, Drumm, ML, Boelle, PY, Cutting, GR, Knowles, MR, Durie, PR, **Strug, LJ**. (2012) Multiple apical plasma membrane constituents are associated with Meconium Ileus in Cystic Fibrosis. *Nature Genetics.* 44(5): 562-9.

2024 IGES Elections
Candidate for Board of Directors – Thomas Winkler

Thomas Winkler is a Genetic Epidemiology researcher at the University of Regensburg in Germany. His educational background encompasses a Degree in Mathematics (equivalent to a Master's degree) and a Ph.D. in Biomedical Sciences. He has worked as a Research Assistant, PhD Student, Post-Doc, and currently as senior researcher at the Department of Genetic Epidemiology of the University of Regensburg, chair Prof. Iris Heid. Additionally, he has undertaken a research visit to the Charles Bronfman Institute for Personalized Medicine at Mount Sinai School of Medicine, New York, collaborating with Prof. Ruth Loos.

He is specializing in the development and application of statistical methods and bioinformatical tools for the analysis of Genome-Wide Association Studies (GWAS). His primary focus includes meta-analysis and gene-environment interaction studies. Actively contributing to large GWAS consortia, he is an integral part of initiatives related to obesity (GIANT), kidney function (CKDGen), age-related macular degeneration (AMD), and gene-lifestyle interactions (CHARGE-GLI). He is well-regarded for his role as the developer of the "Easy R packages", including EasyQC (for quality control of GWAS) and EasyStrata (for analysis and graphical presentation of stratified GWAS summary statistics).

His dedication to the IGES is evident through his outgoing role as a member of the Scientific Program Committee (SPC), and through having delivered three talks and presented five posters since 2011. His leadership as chair of the SPC in 2022, along with then past president Heike Bickeboeller, resulted in a comprehensive guide outlining tasks and responsibilities for future SPC members and chairs. Funded by NIH and DFG, he remains committed to advancing genetic epidemiology and contributing to cutting-edge research within IGES. He would be honored to serve on the IGES Board of Directors.

Five selected publications:

1. **Winkler TW**, Rasheed H, Teumer A, … Köttgen A, Pattaro C, Heid IM. Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Commun Biol. 2022 Jun 13;5(1):580.
2. Stanzick KJ, Li Y, Schlosser P, … Heid IM, **Winkler TW**. Discovery and prioritization of variants and genes for kidney function in >1.2 million individuals. Nat Commun. 2021 Jul 16;12(1):4350.
3. **Winkler TW**, … Kutalik Z, Heid IM. A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. Nat Commun. 2018 May 16;9(1):1946.
4. **Winkler TW**, Kutalik Z, Gorski M, Lottaz C, Kronenberg F, Heid IM. EasyStrata: evaluation and visualization of stratified genome-wide association meta-analysis data. Bioinformatics. 2015 Jan 15;31(2):259-61.
5. **Winkler TW**, Day FR, Croteau-Chonka DC, Wood AR, Locke AE, Mägi R, Ferreira T, Fall T, Graff M, Justice AE, Luan J, Gustafsson S, Randall JC, Vedantam S, Workalemahu T, Kilpeläinen TO, Scherag A, Esko T, Kutalik Z, Heid IM, Loos RJ; Genetic Investigation of Anthropometric Traits (GIANT) Consortium. Quality control and conduct of genome-wide association meta-analyses. Nat Protoc. 2014 May;9(5):1192-212.

This December 2023: IGES Pre-Election Newsletter was edited, proofread, and formatted by Andrew Paterson