

## Saturday, October 3

17:30-19:30 Early registration at the Hotel Lobby  
18:00-21:00 IGES Board meeting and dinner  
(Hyatt Hotel); Pratt(Calvert)

**Locations:** **Baltimore Convention Center (BCC)**  
One West Pratt Street &  
**Hyatt Regency Baltimore (Hyatt Hotel)**  
300 Light Street  
Baltimore, Maryland, USA, 21202

## IGES 2015

### Sunday, October 4, 2015 (Morning; BCC)

*IDs from the (first author) alphabetically ordered abstract book*

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| 7:30-5:15   | Registration   |
| 8:30-10:15  | <b>Session 1: Big health data opportunities and challenges: statistical and computational solutions</b><br>Chairs: <b>J Dupuis</b> (Boston; US)<br>& <b>F Gagnon</b> (Toronto; CANADA) |
| 8:30-9:00   | <b>F Gagnon:</b> Welcome and Presidential Address  |
| 9:00-9:30   | <b>91 Invited speaker: JT Leek (Baltimore; US):</b><br>Statistical analysis of RNA-seq data at scale   |
| 9:30-9:45   | <b>81 M Kaakinen</b> (London; UK): MARV: A novel method and software tool for genome-wide multi-phenotype analysis of rare variants  |
| 9:45-10:00  | <b>115 PJ Newcombe</b> (Cambridge; UK): A new and scaleable Bayesian framework for joint re-analysis of marginal SNP effects   |
| 10:00-10:15 | <b>29 A Cichonska</b> (Espoo; FINLAND): metaCCA: Summary statistics-based multivariate meta-analysis of genome-wide association studies using canonical correlation analysis           |
| 10:15-10:45 | Coffee Break   |
| 10:45-12:15 | <b>Session 2: Old methods, new twists: Admixture, heritability, linkage and more!</b><br>Chairs: <b>J Lorenzo Bermejo</b> (Heidelberg; GERMANY)<br>& <b>A Chu</b> (Framingham; US)     |
| 10:45-11:15 | <b>153 Invited speaker: TA Thornton (Seattle; US):</b><br>Mixed Model Association Mapping in Admixed Populations   |
| 11:15-11:30 | <b>158 DR Velez Edwards</b> (Nashville; US): Evolving ancestry: The shift in individual ancestry composition over time   |
| 11:30-11:45 | <b>69 JE Hicks</b> (St. Louis; US): Incorporating between-pedigree co-ancestry in variance-components  |

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| 11:45-12:00 | <b>138 CL Simpson</b> (NIH; US): The Renaissance of Linkage Analysis and Effects of Extreme High Density Genotype Data on Linkage Algorithms  |
| 12:00-12:15 | <b>93 S Li</b> (Melbourne; AUSTRALIA): The variation of DNA methylation at vast the majority of CpG sites are due to individual factors but not genetic or shared environment factors |
| 12:15-13:30 | Lunch (on your own)   |

### Committee meetings Part 1 at Hyatt Hotel

- Communications & Membership Committees (Chesapeake A)
- Education Committee (Chesapeake B)
- Publications Committee meeting (Pratt)
- Genetic Epidemiology Editorial Board meeting (Calvert)
- Young Investigators Committee meeting (Camden/Lombard)

### Sunday, October 4, 2015 (Afternoon; BCC)

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| 13:30-15:00 | <b>Session 3: Translational genetic epidemiology &amp; population health genomics</b><br>Chairs: <b>E Bouzigon</b> (Paris; FRANCE)<br>& <b>H Bickeböller</b> (Göttingen; GERMANY)          |
| 13:30-14:00 | <b>61 Invited speaker: KA Goddard (Portland; US):</b><br>Targeted genomic screening in the general adult population  |
| 14:00-14:15 | <b>30 DV Conti</b> (Los Angeles; US): Estimating clinical outcomes and classifying CFTR variants of unknown significance in children with a positive newborn screening for Cystic Fibrosis |
| 14:15-14:30 | <b>84 D Klebaner</b> (Atlanta; US): X chromosome-wide analysis identifies DNA methylation sites influenced by cigarette smoking  |
| 14:30-14:45 | <b>13 C Benner</b> (Helsinki; FINLAND): Mixed models for time-to-event outcomes with large-scale population cohorts and genome-wide data   |
| 14:45-15:00 | <b>34 R Darlay</b> (Newcastle; UK): Immunochip analysis identifies amino acid residues in five separate HLA genes driving the association between the MHC and primary biliary cirrhosis    |
| 15:00-15:30 | Coffee Break   |
| 15:30-17:15 | <b>Session 4: Neel and Williams awards and best paper</b><br>Chairs: <b>S Shete</b> (Houston; US)<br>& <b>A Paterson</b> (Toronto; CANADA)   |
| 15:30-15:45 | <b>Presentation of Best Paper in Genetic Epidemiology</b>  |

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| 15:45-16:00 | <b>Williams Candidates</b><br><b>155 X Tong</b> (East Lansing; US): A non-parametric method for joint association analysis of sequencing and Imaging data         |
| 16:00-16:15 | <b>166 H Wang</b> (Cleveland; US): Genome-Wide Survey in African Americans Demonstrates Widespread Epistasis of Fitness in the Human Genome                       |
| 16:15-16:30 | <b>88 CA Lareau</b> (Oklahoma City; US): Computationally Efficient Solutions for Functionalizing Common Variants in Three-Dimensional Models                      |
| 16:30-16:45 | <b>Neel Candidates</b><br><b>32 LJ Corbin</b> (Bristol; UK): An exploration of known type 2 diabetes susceptibility variants: informative heterogeneity revisited |
| 16:45-17:00 | <b>73 YJ Hu</b> (Atlanta; US): Integrative analysis of sequencing and array genotype data for discovering disease associations with rare mutations                |
| 17:00-17:15 | <b>168 HR Warren</b> (London; UK): Investigating the Association of Rare Genetic Variants with Blood Pressure traits  |
| 17:30-19:30 | <b>POSTER SESSION 1 and WELCOME RECEPTION (Hyatt Hotel: Constellation CDEF)</b>   |

### Monday, October 5, 2015 (Morning; BCC)

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| 8:30-10:00 | <b>Session 5: New study designs, methods and applications in Genetic Epidemiology</b><br>Chairs: <b>N Tintle</b> (Sioux Center; US)<br>& <b>AP Klein</b> (Baltimore; US)          |
| 8:30-9:00  | <b>97 Invited speaker: X Lin (Boston; US):</b> Statistical Analysis of Massive Genetic and Genomic Data in Genetic Epidemiology   |
| 9:00-9:15  | <b>160 M Wang</b> (Columbus; US): A Near-Optimal Test of Association that Combines Case-Control and Affected Pedigree Designs   |
| 9:15-9:30  | <b>178 J Xu</b> (Toronto; CANADA): A Novel Multiple-SNP Approach for Fine-Mapping Studies   |
| 9:30-9:45  | <b>65 B Greco</b> (Austin; US): A general approach for combining diverse rare variant association tests provides improved robustness across a wider range of genetic architecture |
| 9:45-10:00 | <b>145 J Sun</b> (Montreal; CANADA): Multivariate association test for rare variants controlling for cryptic and family relatedness   |

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| 10:00-10:30 | Coffee Break  |
| 10:30-12:00 | <b>Session 6: Cross-Consortia and Mega-Cohorts: Ongoing and future directions</b><br>Chairs: <b>A Scherag</b> (Jena; GERMANY) & <b>AE Hendricks</b> (Denver; US)  |
| 10:30-11:00 | <b>100 Invited speaker: RJF Loos (New York; US):</b> The Genetics of Obesity - Going beyond common variation and common traits  |
| 11:00-11:15 | <b>121 LE Petty</b> (Houston; US): Impact of reference population relatedness on imputation quality   |
| 11:15-11:30 | <b>60 A Gilly</b> (Cambridge; UK): Meta-analysis of summary statistics from quantitative trait association studies with unknown sample overlap  |
| 11:30-11:45 | <b>172 TW Winkler</b> (Regensburg; GERMANY): A systematic evaluation of approaches for stratified genome-wide association meta-analyses to identify gene-strata interaction effects   |
| 11:45-12:00 | <b>147 YJ Sung</b> (St. Louis; US): An Empirical Comparison of Interaction and Stratified Models to GxE Interactions Analysis: Smoking and Systolic Blood Pressure in the CHARGE Gene-Lifestyle Interactions Working Group  |
| 12:00-13:15 | Lunch (on your own)<br><br><i>Committee meetings Part 2 and Student-Mentor lunch at Hyatt Hotel</i> <ul style="list-style-type: none"> <li>• Program Committee (Chesapeake AB)</li> <li>• ELSI Committee (Camden/Lombard)</li> <li>• Wiley Advisory Committee (Pratt\Calvert)</li> <li>• Student - Mentor Lunch (Piscis)</li> </ul> |
| 13:15-15:00 | <b>POSTER SESSION 2 (Hyatt Hotel: Constellation CDEF)</b>   |

### Monday, October 5, 2015 (Afternoon; BCC)

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| 15:00-16:30 | <b>Session 7: Omics data integration</b><br>Chairs: <b>AP Morris</b> (Liverpool; UK) & <b>IR König</b> (Lübeck; GERMANY)            |
| 15:00-15:30 | <b>151 Invited speaker: S Tavaré</b> (Cambridge; UK): Data integration in cancer genomics: non-coding mutations                     |
| 15:30-15:45 | <b>5 H Aschard</b> (Boston; US): Playing musical chairs in multi-phenotype studies improves power and identifies novel associations |

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| 15:45-16:00 | <b>43 T Dudding</b> (Bristol; UK): Characterization of the metabolic impact of rare genetic variation within APOC3: Proton NMR based analysis of rare variant gene effects  |
| 16:00-16:15 | <b>41 R Do</b> (New York; US): Different Genomic Subsets and Cell Types Contribute to the Polygenicity and Heritability for Coronary Artery Disease                         |
| 16:15-16:30 | <b>171 SJ Winham</b> (Rochester; US): Integrating Genotype, RNA Sequencing, and DNA Methylation Data to Investigate the Role of X Chromosome Inactivation in Ovarian Cancer |
| 16:30-17:30 | <b>IGES Business meeting</b><br>Chairs: <b>F Gagnon</b> (Toronto; CANADA) and <b>AF Wilson</b> (Baltimore; US)  |
| 18:30-22:00 | <b>Banquet: A Fishing Expedition National Aquarium, Baltimore, Maryland</b>   |

### Tuesday, October 6, 2015 (Afternoon; BCC)

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|             | <b>Joint IGES/ASHG Symposium "Prospecting for hidden Heritability: Undiscovered Gems or Fool's Gold?"</b><br>Chairs: <b>C Ober</b> (Chicago; US) & <b>AF Wilson</b> (Baltimore; US) |
| 13:00-13:10 | Introduction  |
| 13:10-13:40 | <b>R Elston (Cleveland; US):</b> What is heritability and how is it estimated?  |
| 13:40-14:00 | <b>AG Clark (Ithaca; US):</b> The misguided search for missing heritability.  |
| 14:00-14:20 | <b>MD Ritchie (Pennsylvania; US):</b> A game of Clue - Which 'omics are guilty?   |
| 14:20-14:30 | Break   |
| 14:30-14:50 | <b>B Neale (Boston; US):</b> Leveraging genome-wide association data to gain insight into the structure of clinical phenotypes.   |
| 14:50-15:10 | <b>E Wijsman (Seattle; US):</b> How do you know you have it if you can't measure it?  |
| 15:10-15:30 | <b>N Cox (Chicago; US):</b> Harnessing genetic architecture to find genes.  |
| 13:00-16:00 | Panel discussion/Q&A  |

# IGES 2015

## 24<sup>th</sup> ANNUAL CONFERENCE

October 4 – 6, 2015

Hyatt Regency Baltimore  
On the Inner Harbor (Hyatt Hotel) &  
Baltimore Convention Center (BCC)  
Baltimore, Maryland, USA



## MEETING PROGRAM



INTERNATIONAL GENETIC  
EPIDEMIOLOGY SOCIETY

<http://www.geneticipi.org/iges-2015/>