

# Schedule of Events

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## 2010

# Schedule of Events

## Sunday, October 10

Time	Event	Location
10:30 –6:00	Registration Open	Courtyard Reception
1:00-5:00	<b>WORKSHOP:</b>  Moderator: Susan Santangelo	Thomas Paine  Overflow in William Dawes
	<b><u>Next Generation Sequencing in Genetic Epidemiological Studies</u></b>	
1:00-1:40	Scott Williams, PhD Center for Human Genetics Research “Evolutionary Origins of Human Genetic Variation”	
1:40-2:00	Trena Cormier, PhD Affymetrix “Validation of Next Generation Sequencing SNP Calls on the Affymetrix Axiom™ Genotyping Platform”	
2:00 -2:40	Robi Mitra, PhD Center for Genome Sciences and Systems Biology Washington University School of Medicine “NextGen Sequencing Methods and Applications”	
2:40-3:00	David Dailey, PhD Illumina “Emerging Applications of Next Generation Sequencing”	
3:00-3:15	Break	

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- 3:15-4:00** **Suzanne Leal, PhD**  
**Department of Molecular and Human Genetics**  
**Baylor College of Medicine**
- “Statistical Methods for Genomic Analysis”
- 4:00-4:20** **Christophe Lambert , Ph.D.**  
**Golden Helix**  
“ Combining Next-Gen Sequencing and SNP  
Microarray Data Using Imputation”
- 4:20 – 4:40** **Mr. Timo Kanninen, Founder and Technical  
Director**  
**BC Platforms:**  
“Imputing Low Coverage Sequence Data in Cloud”
- 4:40-5:00** Q&A Discussion with all speakers
- 6:00 – 7:30** **Welcome Reception** **Courtyard**  
**(If rain – reception will begin at 7:00pm)** **(rain Ballroom CD)**
- 7:00-9:00**
- ▶ **IGES Board of Director’s Meeting** **Cambridge Rm - 2<sup>nd</sup>  
floor**
- 8:00-10:00** **Poster Room Open for Posting abstracts** **Riverside Pavilion**
- \*\*PLEASE NOTE: ALL POSTER SPACE MAY NOT BE  
AVAILABLE DUE TO PRIOR SCHEDULED EVENT AND LATE  
SETUP. ROOM WILL BE AVAILABLE AT 6:30AM MONDAY  
MORNING FOR POSTING ABSTRACTS**
- Molly Pitcher**  
**Thomas Paine**  
**Haym Saloman**

# Schedule of Events

## Monday, October 11

Time	Event	Abstract Number	Location
6:30-8:30	Poster Room Open for Posting abstracts		Riverside Pavilion
7:30 – 5:00	Registration Open		Courtyard Reception
7:00 – 8:30	Breakfast [provided]		Prefunction ABCD
	<b>Session 1: Presidential Address / Looking to the Future: Prediction, New Approaches, Training</b>		Ballroom ABC
	Session Chairs: Heather Cordell, Michael Province		
8:30 – 9:00	<b>Welcome/Presidential Address:</b> Heather Cordell		Ballroom ABC
9:00 – 9:15	<b>Genetic signatures of exceptional longevity</b>  P. Sebastiani, N. Solovieff, A. Puca, S.W. Hartley, E. Melista, S. Andersen, D.A. Dworkis, J. Wilks, R.H. Myers, M.H. Steinberg, M. Montano, C.T. Baldwin, T.T. Perls	1	“
9:15 – 9:30	<b>Fishing for disease genes in the random forest of GWAS SNPs</b>  W.W. Yang, C.C. Gu	2	“
9:30 – 9:45	<b>Exploiting homozygosity tracts to search for rare recessive variants involved in complex traits</b>  S. Gazal, M. Babron, J. Lambert, D. Champion, C. Berr, C. Tzourio, D. Hannequin, F. Pasquier, O. Hanon, J. Epelbaum, J. Dartigues, M. Lathrop, P. Amouyel, E. Génin, A. Leutenegger	3	“

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Time	Event	Abstract Number	Location
9:45 – 10:00	<b>A characterization of the training needs in genetic epidemiology</b>  M. Krishnan, NIH Working Group on Statistical Genetics Training Needs, A.F. Wilson	4	“
10:00 -10:30	<b>Break</b>		Prefunction ABCD
10:30-12:00	<b>Session 2: Neel and Williams Award Finalists</b>  Session Chairs: Inke Koenig, David Conti		Ballroom ABC
	<b>Neel Award – Young Investigators</b>		“
10:30 –10:45	<b>On optimal pooling designs to identify rare variants through massive resequencing</b>  Joon Sang Lee, Murim Choi, Xiting Yan, Richard P Lifton, Hongyu Zhao	5	“
10:45 –11:00	<b>Comprehensive Approach to Analyzing Rare Genetic Variants</b>  T.J. Hoffmann, N.J. Marini, J.S. Witte	6	“
11:00 –11:15	<b>Genome wide Meta-analysis of Joint Tests for Genetic and Gene-environment Interaction Effects</b>  H. Aschard, D.B. Hancock, S,J. London, P. Kraft	7	“
	<b>Williams Award – Doctoral Students</b>		“
11:15 -11:30	<b>In Silico Genotype Imputation on Large Pedigrees</b>  C.Y.K Cheung, E.A. Thompson, E.M Wijsman	8	“

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Time	Event	Abstract Number	Location
11:30 - 11:45	<p><b>A Flexible Likelihood Framework for Dissecting Gene Pleiotropy Combining Non-randomly Ascertained Samples: Application to Sequence Data</b></p> <p>D.J. Liu, S.M. Leal</p>	9	“
11:45 - 12:00	<p><b>A Bayesian partitioning model for detection of multilocus interaction in case-control studies</b></p> <p>X. Li, S. Basu</p>	10	“
12:00 - 1:30	<b>Lunch [provided]</b>		Ballroom D
12:00 - 1:30	<b><u>Committee Meeting/lunches</u></b>		
	▶ <b>Membership Committee Meeting</b>		Paul Revere
	▶ <b>ELSI</b>		William Dawes A
	▶ <b>Genetic Epidemiology Editorial Board Meeting</b>		William Dawes B
	▶ <b>Program Committee</b>		Chrispus Attucks
	▶ <b>Training Session: Workshop on Scientific Publishing</b> Orli Bahcall – Senior Editor <i>Nature Genetics</i> For students, post-docs, and junior scientists interested in how scientific publishing works. Review how editorial assessment of manuscripts and peer review are conducted and a tutorial for authors and referees		Charles View Ballroom 16 <sup>th</sup> floor
	<b>Session 3: Resequencing and Rare Variants I: Design and Application</b>		Ballroom ABC
	Session Chairs: John Witte, Florence Demenais		

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<b>Time</b>	<b>Event</b>	<b>Abstract Number</b>	<b>Location</b>
1:30 – 2:00	<b>Invited Speaker #1 : Shaun Purcell:</b>  <b>The Genetics of Neuropsychiatric Disease: Results From GWAS and Whole-exome sequencing Studies</b>		“
2:00– 2:15	<b>Realities and Limitations of Coverage in Current Whole-exome Sequencing Capture Approaches</b>  K.B. Jacobs, M. Yeager, M.G. Cullen, X. Zhang, J. Boland, J. Baciorek, V. Lonsberry, C. Matthews, D. Roberson, Q. Chen, L. Burdett, I. Menashe, X.R. Yang, L.R. Goldin, M.L. McMaster, N.E. Caporaso, P.R. Taylor, M.T. Landi, J. Sampson, N. Chatterjee, M.L. Nickerson, K. McGee, M.C. Dean, J. Khan, M.A. Tucker, S.J. Chanock, A.M. Goldstein	<b>11</b>	<b>Ballroom ABC</b>
2:15 – 2:30	<b>Replication Strategies and Rare Variants Discoveries in Genetic Studies of Complex Traits using Next Generation Sequencing Technologies</b>  S.M. Leal, D.J. Liu	<b>12</b>	“
2:30 – 2:45	<b>Enriching Targeted Sequencing Experiments for Rare Disease Alleles</b>  T.L. Edwards, Z. Song, C. Li	<b>13</b>	
2:45 – 3:30	<b>IGES Business Meeting</b>		<b>Ballroom ABC</b>
3:30 – 5:15	<b>Poster Session - ODD-NUMBER ABSTRACTS PRESENTED (refreshments served)</b>		<b>Riverside Pavilion</b>
5:30-6:30	<b>Charter Buses transport to Boston Harbor</b>  (Buses will leave every 15 minutes beginning at 5:30 and ending at 6:30pm)		<b>Courtyard Reception</b>
5:45 – 6:30	<b>Cocktail Reception on board The Odyssey Dinner Cruise Ship</b>		<b>Dinner Cruise Boat Boston Harbor</b>

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<b>Time</b>	<b>Event</b>	<b>Abstract Number</b>	<b>Location</b>
6:45 – 9:45	<b>Banquet – DINNER CRUISE ON BOSTON HARBOR</b> (**all attendees must have a cruise ticket to board the boat)		<b>Dinner Cruise Boat Boston Harbor</b>
9:45-10:30	<b>Charter Buses return to hotel</b>  (Buses will leave every 15 minutes until 10:30pm in front of the Boston Harbor Hotel)		

# Schedule of Events

## Tuesday, October 12

Time	Event	Abstract Number	Location
7:30 – 5:00	Registration Open		Courtyard Reception
7:00 – 8:30	<b>Breakfast [provided]</b>		Prefunction ABCD
7:30-8:30	<u>Committee Meeting</u>		
	▶ Ambassadors Meeting		Chrispus Attucks
	<b>Session 4: Interactions, Environment and Pathways</b>		Ballroom ABC
	Session Chairs: Peter Kraft, Alexandre Alcais		
8:30 – 9:00	<b>Invited Speaker #2: Cornelia Ulrich</b>		“
	Inflammatory Pathways on the Intersection Between Genetics and Environment		
9:00 – 9:15	<b>An Efficient Test of Gene-Environment Interaction for Genomewide Association Studies</b>	14	“
	M.Sohns, J.P. Lewinger, H. Bickebölller, D.C. Thomas		
9:15 – 9:30	<b>Detecting Gene-Gene/Gene-Environment Interactions for Quantitative Traits with U-Statistics</b>	15	“
	M. Li, W. Fu, Q. Lu		
9:30 – 9:45	<b>Gene-environment Interactions in Genome-wide Association Studies: A Comparative Study of Tests Applied to Empirical Studies of Type 2 Diabetes</b>	16	“
	M.C. Cornelis, E.J. Tchetgen, L. Liming, L. Qi, N. Chatterjee, F.B. Hu, P. Kraft		

# Schedule of Events

Time	Event	Abstract Number	Location
9:45 – 10:00	<p><b>An integrative Genomic Strategy Combining Linkage and Association Analysis with Expression Profile Analysis for Localizing Genetic Variants Influencing Quantitative Traits: an Example From the San Antonio Family Heart Study</b></p> <p>E. Drigalenko, A.G. Comuzzie, J.E. Curran, M.P. Johnson, M.A. Carless, J.W. Kent Jr, J. Peralta, T.D. Dyer, S.A. Cole, L. Almasy, M.C. Mahaney, E.K. Moses, J. Blangero, H.H. Göring</p>	17	
10:00 - 10:30	<b>Break</b>		Prefunction ABC
10:30 – 12:00	<p><b>Session 5: Diverse populations; diverse phenotypes</b></p> <p>Session Chairs: Nancy Saccone, Glen Satten</p>		Ballroom ABC
10:30 – 11:00	<p><b>Invited Speaker #3: David Reich</b></p> <p><b>Taking Advantage of Human Diversity to Discover Disease Genes</b></p>		“
11:00 – 11:15	<p><b>Bayesian Meta-analysis of Trans-ethnic Genome-wide Association Studies: Application to Fine-Mapping</b></p> <p>A.P. Morris</p>	18	“
11:15 – 11:30	<p><b>Phenotype-Wide Association Study (PheWAS) for Exploration of Novel SNP and Phenotype Relationships within PAGE</b></p> <p>S.A. Pendergrass, K.D. Brown-Gentry, S. Dudek, J.L. Ambite, C.L. Avery, S. Buyske, C. Cai, G. Heiss, L. Hindorff, C. Kooperberg, Y. Lin, T.A. Manolio, T. Matise, L. Wilkens, M.D. Fesinmeyer, C. Hsu, D.C. Crawford, M.D. Ritchie</p>	19	“

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Time	Event	Abstract Number	Location
11:30 – 11:45	<b>Estimation of Odds Ratios of Genetic Variants for the Secondary Phenotypes Associated with Primary Diseases</b>  J. Wang, S. Shete	20	“
11:45 – 12:00	<b>A Powerful Multi-Phenotype Approach on Genome-Wide Association Studies (GWAS) to Identify Novel Pleiotropic Genes that Affected Multiple Quantitative Traits</b>  Y. Hsu, X. Chen, M. Gupta, D. Karasik, J. Meigs, L.A. Cupples, D.P. Kiel	21	“
12:00 - 1:30	<b>Lunch [provided]</b>		Ballroom D
12:00-1:30	<b><u>Committee Meeting/lunches</u></b>		
	▶ <b>Education Committee</b>		Chrispus Attucks
	▶ <b>Publication Committee</b>		Paul Revere A
1:30 – 3:15	<b>Poster Session - EVEN-NUMBER ABSTRACTS PRESENTED</b>		
3:15 – 3:30	<b>Break</b>		Prefunction ABC
	<b>Session 6: Resequencing and Rare Variants II: Methods</b>  Co-Chairs: Alisa Goldstein, Brooke Fridley		Ballroom ABC
3:30- 4:00	<b>Invited Speaker #4: Suzanne Leal</b>  Detecting Complex Trait Rare Variant Associations Using Next Generation Sequence Data		“

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<b>Time</b>	<b>Event</b>	<b>Abstract Number</b>	<b>Location</b>
4:00 –4:15	<b>Identifying Rare Haplotypes Associated with Common Diseases through Bayesian Lasso</b>  S. Biswas, S. Lin	<b>22</b>	“
4:15 –4:30	<b>A powerful approach for rare variants analysis in quantitative traits based association studies</b>  Dalin Li, David V. Conti	<b>23</b>	“
4:30 –4:45	<b>Methods for identifying rare variants with bidirectional effects on quantitative traits</b>  Qunyuan Zhang, Ingrid B Borecki, Michael A Province	<b>24</b>	“
4:45 - 5:00	<b>Final Announcements:</b> Please fill out the comments/suggestions form in the back of your program and drop in the box at the registration desk		“

**We hope to see you in**

**Heidelberg, Germany Next Year!**