

## Quantitative Genetics & Genomics

### *Gordon Research Conference*

#### Exploiting Context and Increasing Predictive Value in Complex Trait Genetics

##### Dates

February 26 - March 3, 2017

##### Location

Hotel Galvez  
Galveston, TX

##### Organizers

Chair:

**Ann E. Stapleton**

Vice Chair:

**Mike Goddard**

#### Application Deadline

Applications for this meeting must be submitted by **January 29, 2017**. Please apply early, as some meetings become oversubscribed (full) before this deadline. If the meeting is oversubscribed, it will be stated here. *Note:* Applications for oversubscribed meetings will only be considered by the Conference Chair if more seats become available due to cancellations.

#### Meeting Description

Quantitative genetics is the body of knowledge fundamental to the application of genomic and environmental information to feed our growing global population and deliver on the promise of genomics for improved health of people and their associated natural systems. This meeting will bring outstanding new science and scientists into a strong existing community of quantitative genetics researchers. The 16th conference on Quantitative Genetics and Genomics will bring together leaders in quite different fields to discuss areas of shared interest and cutting edge developments with the potential to affect all researchers within the broad field of quantitative genetics. The meeting will integrate theory and experimental approaches to fully leverage large-scale data and expanded capacity for computationally intense data analyses. Increased quality and quantity of collaborations and development of new directions in research are also key goals for this meeting.

A broad perspective on quantitative genetics and genomics will be especially valuable in early 2017. Genomic selection has revolutionized animal and plant breeding and these methodologies are likely to have a major impact in human medicine as well – yet scientists already face what appear to be potential limitations of the technology. How to overcome these limitations, via a deeper understanding of the interactions between environmental context and the genetic architecture of complex traits, will be one of the major discussion points of the 2017 GRC. Sequencing and precise editing technologies are advancing at an accelerating pace and this is bound to profoundly impact agricultural and medical practices. How best to capitalize on these emerging technologies will also be a focus of discussion.

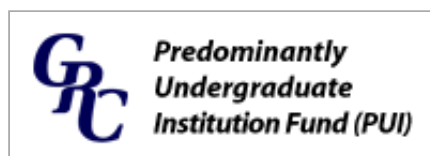
#### Related Meeting



This GRC will be held in conjunction with the "**Quantitative Genetics & Genomics**" Gordon Research Seminar (GRS). Those interested in attending both meetings must submit an application for the GRS in addition to an application for the GRC. Refer to the [associated GRS program page](#) for more information.

## Contributors

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## Meeting Program

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### Sunday

- 4:00 pm - 8:00 pm Arrival and Check-in
- 6:00 pm Dinner
- 7:30 pm - 7:40 pm Welcome / Introductory Comments by GRC Site Staff
- 7:40 pm - 9:30 pm **Statistical Predictions and Models: Causality, Scale and Experimental Connections**
- Discussion Leader: **Chris-Carolin Schoen** (Technical University of Munich, Germany)
- 7:40 pm - 7:55 pm Introduction by Discussion Leader
- 7:55 pm - 8:25 pm **Silvia Richardson** (MRC Biostatistics Unit, University of Cambridge, United Kingdom)  
"Statistical Modelling and Analysis of Complex Phenotypes in Genomics"
- 8:25 pm - 8:45 pm Discussion
- 8:45 pm - 9:15 pm **Eric Green** (National Human Genome Research Institute, NIH, USA)  
"From the Human Genome Project to Precision Medicine: A Journey to Advance Human Health"
- 9:15 pm - 9:30 pm Discussion

### Monday

- 7:30 am - 8:30 am Breakfast
- 8:30 am Group Photo
- 9:00 am - 12:30 pm **Genetics of Risk and Prediction – Applications**
- Discussion Leader: **Rebecca Doerge** (Carnegie Mellon University, USA)
- 9:00 am - 9:20 am Introduction by Discussion Leader

- 9:20 am - 9:50 am **Natalia De Leon** (University of Wisconsin-Madison, USA)  
"The Effect of Artificial Selection on Phenotypic Plasticity in Maize"
- 9:50 am - 10:15 am Discussion
- 10:15 am - 10:45 am Coffee Break
- 10:45 am - 11:15 am **Iona MacLeod** (University of Melbourne, Australia)  
"Exploiting Prior Biological Knowledge for Genomic Prediction and Mapping of Causal Variants"
- 11:15 am - 11:40 am Discussion
- 11:40 am - 12:10 pm **David Heckerman** (Microsoft Research, USA)  
"Surprises in the Statistical Analysis of Associations"
- 12:10 pm - 12:30 pm Discussion
- 12:30 pm Lunch
- 1:30 pm - 4:00 pm Free Time
- 3:00 pm - 4:00 pm Power Hour
- The GRC Power Hour is an optional informal gathering open to all meeting participants. It is designed to help address the challenges women face in science and support the professional growth of women in our communities by providing an open forum for discussion and mentoring.*
- Organizer: **Susan Lamont** (Iowa State University, USA)

4:00 pm - 6:00 pm

Poster Session

6:00 pm

Dinner

7:30 pm - 9:30 pm

**Evolutionary Contexts for Prediction and Selection**Discussion Leader: **Josephine Pemberton** (University of Edinburgh, United Kingdom)

7:30 pm - 7:50 pm

Introduction by Discussion Leader

7:50 pm - 8:20 pm

**John Novembre** (University of Chicago, USA)  
"Evaluating Polygenic Signatures of Selection in Ancient DNA"

8:20 pm - 8:40 pm

Discussion

8:40 pm - 9:10 pm

**Nicholas Barton** (Institute of Science and Technology Austria, Austria)  
"Epistasis and the Limits to Selection"

9:10 pm - 9:30 pm

Discussion

**Tuesday**

7:30 am - 8:30 am

Breakfast

9:00 am - 12:30 pm

**Genetic Context – Making Sense of Multivariate Phenotypes**Discussion Leader: **Lauren McIntyre** (University of Florida, USA)

9:00 am - 9:20 am

Introduction by Discussion Leader

9:20 am - 9:50 am

**Barbara Engelhardt** (Princeton University, USA)  
"Heritability, Effect Sizes, and Pleiotropy in Expression QTLs Across Tissues"

9:50 am - 10:15 am

Discussion

10:15 am - 10:45 am

Coffee Break

10:45 am - 11:15 am

**Eleazar Eskin** (University of California, Los Angeles, USA)  
"Fine Mapping and Allelic Heterogeneity"

11:15 am - 11:40 am

Discussion

11:40 am - 12:10 pm **Bin Yu** (University of California, Berkeley, USA)  
"Spatial Gene Expression Patterns in *Drosophila*: Mapping a Cell's Destiny"

12:10 pm - 12:30 pm Discussion

12:30 pm Lunch

1:30 pm - 4:00 pm Free Time

4:00 pm - 6:00 pm Poster Session

6:00 pm Dinner

7:30 pm - 9:30 pm **Modeling of Context – Interaction Terms and Beyond**

Discussion Leader: **Bruce Walsh** (University of Arizona, USA)

7:30 pm - 7:50 pm Introduction by Discussion Leader

7:50 pm - 8:20 pm **Ian Ehrenreich** (Translational Imaging Center, University of Southern California, USA)  
"Genetic Architectures of a Complex Trait Across Backgrounds and Environments"

8:20 pm - 8:40 pm Discussion

8:40 pm - 9:10 pm **Paul Magwene** (Duke University, USA)  
"Exploring Pleiotropy and Epistasis Using a Novel Yeast Mapping Panel"

9:10 pm - 9:30 pm Discussion

### Wednesday

7:30 am - 8:30 am Breakfast

9:00 am - 12:30 pm **Late-Breaking Topics**

Discussion Leader: **Peter Visscher** (University of Queensland, Australia)

9:00 am - 9:20 am Introduction by Discussion Leader

9:20 am - 9:50 am **Gustavo Stolovitsky** (Translational Systems Biology and Nanobiotechnology Group, IBM, USA)  
"Crowdsourcing Biological Network Inference, Drug Synergy Prediction and Beyond: The DREAM Challenges"

9:50 am - 10:15 am Discussion

10:15 am - 10:45 am Coffee Break

10:45 am - 11:15 am **Matthew Webster** (Uppsala University, Sweden)  
"The Genomic Basis of Local Adaptation in Honeybees"

11:15 am - 11:40 am Discussion

11:40 am - 12:10 pm **Alexis Battle** (Johns Hopkins University, USA)  
"Predicting the Complex and Cascading Impact of Non-Coding Variation"

12:10 pm - 12:30 pm Discussion

12:30 pm Lunch

1:30 pm - 4:00 pm Free Time

4:00 pm - 6:00 pm Poster Session

6:00 pm Dinner

7:30 pm - 9:30 pm **Context – Drugs, Weather and the Systems to Integrate Genotypes and Environments**

Discussion Leader: **Ed Buckler** (Institute for Genomic Diversity, Cornell University, USA)

- 7:30 pm - 7:50 pm Introduction by Discussion Leader
- 7:50 pm - 8:20 pm **Mark Cooper** (DuPont Pioneer, USA)  
"Crop Modeling and Genomic Prediction"
- 8:20 pm - 8:40 pm Discussion
- 8:40 pm - 9:10 pm **Sally Aitken** (University of British Columbia, Canada)  
"Comparative Genomics Approach Reveals Convergent Adaptation to Climate in Conifers"
- 9:10 pm - 9:30 pm Discussion

## Thursday

- 7:30 am - 8:30 am Breakfast
- 8:30 am - 9:00 am Business Meeting  
*Nominations for the Next Vice Chair; Fill in Conference Evaluation Forms; Discuss Future Site and Scheduling Preferences; Election of the Next Vice Chair*
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- 9:00 am - 12:30 pm **Quantitative Perspectives on Gene Editing – Why to Edit What**  
Discussion Leader: **Ann Stapleton** (University of North Carolina at Wilmington, USA)
- 9:00 am - 9:20 am Introduction by Discussion Leader
- 9:20 am - 9:50 am **Kevin Esvelt** (Massachusetts Institute of Technology, USA)  
"Daisy Drives for Grassroots Ecological Engineering"
- 9:50 am - 10:10 am Discussion
- 10:10 am - 10:40 am Coffee Break
- 10:40 am - 11:10 am **Mattheos Koffas** (Rensselaer Polytechnic Institute, USA)  
"Rewiring Cellular Metabolism Using Metabolic Flux Analysis Models for Chemical Production"
- 11:10 am - 11:30 am Discussion
- 11:30 am - 11:45 am Short Talk Selected from Poster Abstracts
- 11:45 am - 11:50 am Discussion
- 11:50 am - 12:05 pm Short Talk Selected from Poster Abstracts
- 12:05 pm - 12:10 pm Discussion
- 12:10 pm - 12:25 pm Short Talk Selected from Poster Abstracts
- 12:25 pm - 12:30 pm Discussion
- 12:30 pm Lunch
- 1:30 pm - 4:00 pm Free Time
- 4:00 pm - 6:00 pm Poster Session
- 6:00 pm Dinner
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- 7:30 pm - 9:30 pm **Next Generation Quantitative Genetics and Genomics**  
Discussion Leader: **Mike Goddard** (University of Melbourne, Australia)
- 7:30 pm - 7:50 pm Introduction by Discussion Leader
- 7:50 pm - 8:20 pm **Christine Queitsch** (University of Washington, USA)  
"Hyper-Variable Genetic Elements in Complex Trait Genetics"
- 8:20 pm - 8:40 pm Discussion
- 8:40 pm - 9:10 pm **Jeff Leek** (Johns Hopkins Bloomberg School of Public Health, USA)  
"What Can We Learn from Analyzing Every Human RNA-Seq Sample Ever Collected"

Together?"

9:10 pm - 9:30 pm Discussion

Friday

7:30 am - 8:30 am Breakfast

9:00 am Departure

Funding for this conference was made possible (in part) by 1R13 HG009449-01 from the National Human Genome Research Institute (NHGRI). The views expressed in written conference materials or publications and by speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services; nor does mention of trade names, commercial practices, or organizations imply endorsement by the U.S. Government.