
**[CISfacV] CIS Distinguished Speaker Series 2015-2016: Thursday, April 7:
Terry Gaasterland, UC San Diego**

1 message

Christopher Rasmussen <ras@udel.edu>

Fri, Mar 25, 2016 at 3:26 PM

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CIS Distinguished Speaker Series



Terry Gaasterland, Ph.D.

Professor of Computational Biology and Genomics
Director, Scripps Genome Center
University of California, San Diego

Thursday, April 7, 2016

Time: 2:00 pm - 3:15 pm

Place: [Willard Hall 007](#)

Please contact Prof. Christopher Rasmussen cer@cis.udel.edu if you are interested in meeting with Prof. Gaasterland during her visit.

Tying Genome Variation in Regulatory Regions to Neurodegenerative Phenotypes

Abstract: The use of exome sequencing (genome-wide sequencing enriched to cover exons) to identify disease-causing genomic changes has focused to date on the interpretation of variants within protein coding regions. We have developed computational and statistical methods to use exome data to examine introns, promoters and untranslated regions (UTRs) in the context of

disease cohorts compared with general populations including the 1000 Genomes (1000G), Exome Sequencing Project (ESP), and the Exome Aggregation Consortium (ExAC) and control populations in the Alzheimer's Disease Sequencing Project. These methods were applied to 333 patients of European descent and 12 patients of African descent with progressive optic nerve degeneration due to primary open angle glaucoma (POAG), 13 patients of Taiwanese descent with migraine, and 32 patients of mixed descent born with congenital glaucoma. All patients analyzed have first-degree relatives with disease, thus increasing the likelihood of finding genetic explanations for disease. Relationships between sequenced individuals, if any, are known. The genetics of POAG, migraine, and congenital glaucoma are complex; to date, no single causative genomic variant has been established as causing any of these diseases. Our analysis of regulatory regions provides new insights for further functional study through targeted experiments.

In the case of POAG, genome-wide sequencing of exons from protein coding and non-coding genes in 285 patients revealed ~50 associated SNP sites within ~30 genes. Of these, two-thirds were located in introns or untranslated regions (UTR). To rank and prioritize genes and generate hypotheses about molecular mechanisms disrupted by associated variant sites, mRNA and small RNA (microRNA) were sequenced from ocular tissues relevant to the disease. Intronic SNPs were assessed for impact on alternative splice isoforms, and UTR SNPs were assessed for impact on microRNA binding. An additional cohort of associated SNPs appear between genes and in follow-up analysis may implicate enhancers or promoters in disease processes.

Analysis protocols and techniques for integrated data interpretation to construct putative regulatory networks underlying disease will be discussed. The data collection and analysis methods are generally applicable beyond glaucoma to other chronic, progressive diseases associated with aging.

Biography: Dr. Terry Gaasterland is a computational molecular biologist trained as a computer scientist. She earned her undergraduate degree in Computer Science and Russian with a minor in Chemistry from Duke University as an A.B. Duke Scholar, and her Ph.D. in Computer Science from University of Maryland. As an Enrico Fermi Fellow at the Department of Energy's Argonne National Laboratory and then as an Assistant Professor of Computer Science at the University of Chicago, she applied techniques from her work in "cooperative answering", natural language processing, and deductive database research to the interpretation of the first three DOE-funded microbial genomes and a fourth Canadian-funded archaeal genome. During seven years as a Head of Lab at Rockefeller University, Dr. Gaasterland focused on the integration of gene expression data and genome sequence data analysis in human and model eukaryotic organisms.

Ten years ago, Dr. Gaasterland moved her Laboratory of Computational Genomics to UCSD to establish the Scripps Genome Center, a UCSD resource based at the Scripps Institution of Oceanography in the Marine Biology Division, with bioinformatics hardware and software housed at the San Diego Supercomputer Center. At UCSD, she is now Professor of Computational Biology and Genomics at SIO and a faculty member in UCSD's Institute for Genomic Medicine. Since receiving the Presidential Early Career Award in Science and Engineering (PECASE) in 2000, she has been continuously funded by the National Science Foundation and the National Institutes of Health to develop and use methods in computational genomics. Her accomplishments in computational molecular biology as well as her early career work in

deductive databases is reflected in over 90 refereed publications, with over 80 indexed in PubMed. A member of the NEIGHBOR Consortium to study primary open angle glaucoma (POAG) and the NHGRI Medical Sequencing program, Dr. Gaasterland is sequencing and analyzing variation in transcribed exons genome-wide for 400 primary open angle glaucoma cases and controls. Her work aims to address the general question of how regulation of transcription and translation modulate and affect cell state changes.