NEW YORK GENOME CENTER®

January 13, 2016 | 9:00 a.m. - 10:30 a.m.

FIVE POINTS

Kasper Lage, PhD

Massachusetts General Hospital

Functional interpretation of genomes using biological networks

101 Avenue of the Americas
Between Watts and Grand
New York, NY 10013

Named for an early Manhattan crossroads – remembered as a rowdy but cosmopolitan gathering place, and as a nexus for progress in public health – the Five Points Lectures bring outstanding scientists from near and far, to discuss their work in technical detail* with researchers and clinicians from institutions served by NYGC, in order to strengthen our grasp of key biological questions and methods. Speakers present fresh and intriguing findings, along with thoughtful views on their respective fields, in full scientific depth. Talks last roughly 45 minutes — often framing five or so key points, in a nod to the series' name — followed by 15 minutes of open Q&A, and 30 minutes of informal chat over refreshments. Speakers may then meet with one or several attending colleagues, for further discussion.

*The Five Points Lectures thus complement NYGC's monthly Evening Talks, which address listeners of more varied expertise, including layfolk.

To view all Five Points lectures, please visit us here.

BIOGRAPHY

Kasper Lage (Twitter: @kasper_lage, email: lage.kasper@mgh.harvard.edu) is the Director of Bioinformatics of the Massachusetts General Hospital (MGH) Department of Surgery where he leads a computational research group. He holds an academic appointment as Assistant Professor at Harvard Medical School and is an Associate Member and Group Leader at the Broad Institute of MIT and Harvard.

His research revolves around computational analyses of very large genomic datasets and the integration of these data with functional genomics networks. The aim of these analyses is to functionally interpret genomic data to gain high-resolution insight into the biological underpinnings of a variety of diseases. His group is also focused on using their approaches to enable clinical action based on genomic data. He has contributed to several technologies and algorithms that are widely used in the genetics and genomics communities and in the 1000 Genomes Project. Examples include InWeb (a human protein-protein interaction network), DAPPLE, and the Broad Institute Web Platform for Genome Networks – GeNets. His analyses and methods have led to the identification of specific genes involved in metabolic, reproductive and cardiovascular disorders.

Kasper serves on a number of boards and committees for example the Research Computation Oversight Committee of Partners HealthCare that defines the vision for research computing across the 13 hospitals that are part of the organization. He is also the Principal Investigator of the Functional Interpretation Group of Harvard University in the 1000 Genomes Project. He has been involved in several biotech startups in translational genetics and bioinformatics which together have raised > 24 MUSD in funding.

ABSTRACT

The recent explosion in genome-wide association studies, exome-sequencing projects, and epigenetic data sets, have revealed many genetic variants likely to be involved in disease processes, but the composition and function of the tissue-specific molecular systems they affect remain largely obscure. This limits our progress towards biological understanding and therapeutic intervention.

Computational analyses that systematically integrate biological networks (i.e., networks in which genes are connected if they are functionally associated in some experimental system) with genetic data have emerged as a powerful and scalable approach to functionally interpret very large genomic data sets by enabling the identification of de novo pathways perturbed in disease.

This talk will highlight approaches and methods we have developed in this area, and exemplify how different network-based methods have been used to analyze common and rare genetic variants to deduce the molecular networks perturbed by genetics in a wide range of diseases. Furthermore, as a general model for how in silico networks can be expanded, consolidated and validated, I will show how cardiac ion-channel networks involved in human arrhythmia were elucidated and validated by combining, GWAS, quantitative interaction proteomics, electrophysiology and model organisms through rigorous statistical frameworks.