



Integrating layers of next generation genomic data to capture alternative epigenetic processes shaping responses to environment or disease



The acquisition of large amounts of data spurred by the sequencing of genomes, exomes and transcriptomes allows researchers to assess how mutations combined with regulatory control elements are associated with simple and complex traits or disease. Researchers are recognizing that the value of this "Big Data", and the opportunities for discovery, fall within the ability to integrate and interrogate multiple, complementary datasets simultaneously. By integrating such data captured from a deeply characterized longitudinal cohort of 40,000 individuals – the CARTaGENE program, we identified novel post-transcriptional modifications and determined their underlying genetic control. We showed how of these epigenomic changes are associated with important clinical endophenotypes and environmental response.

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Host: Dr. Howard Lipshitz

Date: Monday May 4th, 2015 Time: 2PM Place: 1 King's College Circle, Medical Sciences Building, Room 4171