STRATEGIES FOR ACCELERATING THE GENOMIC SEQUENCING PIPELINE

Hosted by: **Patricia Kovatch, Associate Dean for Scientific Computing**
Michael Linderman, PhD, Assistant Professor, Genetics and Genomic
Sciences, Icahn School of Medicine at Mount Sinai

When: **Tuesday, December 10, 2013 from 8:30 AM - 4:00 PM**

Where: **Leon and Norma Hess Center for Science and Medicine**
1470 Madison Avenue, Seminar Room "B"
New York, NY

AGENDA

8:30 – 9:00a	*Registration & Continental Breakfast*
9:00 – 9:05a	Welcome, Patricia Kovatch, Mount Sinai
9:00 – 9:30a	Opening Remarks and "A *Pipeline 'for every purse and purpose': Building, Validating and Deploying Genome Pipeline(s) for Multiple Clinical and Research Applications,"* Michael Linderman, Mount Sinai
9:30 – 10:00a	*"Parallelizing the Sequence Analysis Pipeline: What are the Tradeoffs?"* Toby Bloom, PhD, New York Genome Center
10:00 – 10:30a	*"Integrating New and Existing Tools within a Sequencing Analysis Pipeline,"* Timothy Danford, PhD, Genome Bridge
10:30 – 11:00a	*Break*
11:00 – 11:30a	*"Speeding Up the DNA Pipeline in Practice,"* Paolo Narvaez, PhD, Intel Corp.
11:30 – 12:00p	"G-Make, *our Make-Based Infrastructure for Rapid Genome Characterization and the Genomes in a Bottle Consortium,"* Sheng Li, Weill Cornell Medical College of Cornell University
12:00 – 1:30p	*Lunch*
1:30 – 2:00p	*"Accelerated GATK Best-Practices Variant Calling Pipeline,"* Mauricio Carneiro, PhD, Broad Institute
2:00 – 2:30p	*Parallelizing and Optimizing Genomic Codes,"* Clay Breshears, PhD, Intel Corp.
2:30 – 3:00p	*"Community Based Approaches to Scaling Best-Practice Variant Calling Workflows,"* Brad Chapman, PhD, Harvard School of Public Health
3:00 – 3:30p	*"Fast Whole Genome Processing with ADAM,"* Matt Massie, University of California, Berkeley
3:30 – 4:00p	Closing Remarks & Discussion, Michael Linderman
4:00p	Workshop Ends