



Icahn
School of
Medicine at
Mount
Sinai

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	<i>Registration & Continental Breakfast</i>
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	<i>Break</i>
11:00 – 11:30a	"Speeding Up the DNA Pipeline in Practice," Paolo Narvaez, PhD, Intel Corp.
11:30 – 12:00p	"G-Make, a 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	<i>Lunch</i>
1:30 – 2:00p	"Accelerated GATK Best-Practices Variant Calling Pipeline," Mauricio Carneiro, PhD, Broad Institute
2:00 – 2:30p	<i>Parallelizing and Optimizing Genomic Codes,"</i> 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 – <i>cancelled</i>
3:30 – 4:00p	Closing Remarks & Discussion, Michael Linderman
4:00p	Workshop Ends