

Melissa A. Gymrek

CONTACT INFORMATION

Harvard-MIT Health Sciences and Technology
Bioinformatics and Integrative Genomics
Whitehead Institute for Biomedical Research

9 Cambridge Center
Cambridge, MA 02141
E-mail: mgymrek@mit.edu

EDUCATION

- **Harvard-MIT** Division of Health Sciences and Technology. PhD Program in Bioinformatics and Integrative Genomics. 2011-Present
 - **Thesis Advisors:** Dr. Yaniv Erlich and Professor David Altshuler
 - **Academic Advisor:** Professor Leonid Mirny
- **Massachusetts Institute of Technology** B.S. in Computer Science and Mathematics. 2007-2011.
- **Andean High School** Valedictorian. 2003-2007.

AWARDS

- 2013 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - finalist
- 2012 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist
- MIT Senior Academic Award from the Association of MIT Alumnae (AMITA) (2011)
- MIT Experimental Study Group teaching award (2011)
- Randolph G. Wei undergraduate research award (2010)
- MIT Experimental Study Group community service award (2009)
- National Merit Scholar (2007)

FELLOWSHIPS

- National Defense Science and Engineering Graduate Fellowship (2011)
- National Science Foundation Graduate Fellowship (declined in order to accept NDSEG) (2011)
- Hertz Foundation Fellowship finalist (2011)

TEACHING EXPERIENCE

(By MIT course number)

- **Teaching Assistant: 6.047/6.878 - Computational Biology: Genomes, Networks, Evolution** (Fall 2011): I prepared weekly recitation presentations, wrote and graded problem sets and exams, held weekly office hours, and helped guide students in completing significant final projects in a wide range of computational biology topics. Reference: Manolis Kellis (manoli@mit.edu)

- **Instructor: SP.268 - The Mathematics of Toys and Games** (Spring 2009, Spring 2010, Spring 2011): I co-taught this undergraduate seminar with classmate Jing Li. We covered algorithms and mathematical strategies applied to popular games. We developed the material and organized the curriculum. Reference: Erik Demaine (edemaine@mit.edu)
- **Teaching Assistant: 18.02 - Multivariable Calculus, Experimental Study Group** (Fall 2008): I led weekly problem solving sessions and held office hours and review sessions. Reference: Gabrielle Stoy (gstoy@mit.edu)
- **Lab Assistant: 6.01 - Introduction to Electrical Engineering and Computer Science** (Fall 2008): I helped students complete weekly software and design projects. Reference: Tomas Lozano-Perez (tlp@mit.edu), Leslie Pack Kaelbling (lpk@mit.edu)

WORK EXPERIENCE

- Software Engineer Intern, Google (Summer 2011)
 - Improved and tested algorithms with the Google Books Team
 - Gained experience in C++/Python programming and the MapReduce framework

PUBLICATIONS

- Michal Breker, Melissa Gymrek, Ofer Moldavski, & Maya Schuldiner. “LoQAtE—Localization and Quantitation ATlas of the yeast proteomE. A new tool for multiparametric dissection of single-protein behavior in response to biological perturbations in yeast.” *Nucleic Acids Res.* October 2013.
- Melissa Gymrek & Yaniv Erlich. “Profiling short tandem repeats from short reads.” Book chapter in *Deep Sequencing Data Analysis by Methods Mol Biol.* 2013.
- Melissa Gymrek, Amy L. McGuire, David Golan, Eran Halperin, & Yaniv Erlich. “Identifying personal genomes by surname inference.” *Science.* January 2013.
- Dina Zielinski, Melissa Gymrek, & Yaniv Erlich. “Back to the family: a renewed approach to rare variant studies.” *Genome Med.* December 2012.
- Carlos Sebastian, Bernadette M.M. Zwaans, Dafne M. Silberman, Melissa Gymrek, Alon Goren, Lei Zhong, Oren Ram, Jessica Truelove, Alexander R. Guimaraes, Debra Toiber, Claudia Cosentino, Joel K. Greenson, Alasdair I. MacDonald, Liane McGlynn, Fraser Maxwell, Joanne Edwards, Sofia Giacosa, Ernesto Guccione, Ralph Weissleder, Bradley E. Bernstein, Aviv Regev, Paul G. Shiels, David. B. Lombard, & Raul Mostoslavsky. “The histone deacetylase SIRT6 is a tumor suppressor that controls cancer metabolism.” *Cell.* December 2012.
- Michal Nadler-Holly, Michal Breker, Ranit Bruber, Ariel Azia, Melissa Gymrek, Miriam Eisenstein, Keith R. Willison, Maya Schuldiner, Amnon Horovitz. “Interactions of subunit CCT3 in the yeast chaperonin CCT/TRiC with Q/N-rich proteins revealed by high-throughput microscopy analysis.” *PNAS.* November 2012.
- Melissa Gymrek, David Golan, Saharon Rosset, Yaniv Erlich. “lobSTR: a short tandem repeat profiler for personal genomes.” *Genome Research.* April 2012.

- Oren Ram*, Alon Goren*, Ido Amit, Noam Shores, Nir Yosef, Jason Ernst, Manolis Kellis, Melissa Gymrek, Robbyn Issner, Michael Coyne, Timothy Durham, Xiaolan Zhang, Julie Donaghey, Chuck Epstein, Aviv Regev, & Bradley Bernstein. (* = equal contributors) "Combinatorial patterning of chromatin regulators uncovered by genome-wide location analysis in human cells." *Cell*. December 2011.
- Melissa Gymrek, Yaniv Erlich. "Using DNA sequencers as stethoscopes." *Genome Medicine*. November 2011.
- Naegle, Kristen M,* Melissa Gymrek*, Brian A. Joughin, Joel P. Wagner, Roy E. Welsch, Michael B. Yaffe, Douglas A. Lauffenburger, and Forest M. White. (* = equal contributors) "PTMScout: A web resource for analysis of high-throughput post-translational proteomic studies." *MCP*. November 2010.
- Ozsolak, Fatih*, Alon Goren*, Melissa Gymrek*, Mitchell Guttman, Bradley Bernstein, and Patrice Milo. (* = equal contributors) "Digital transcriptome profiling from attomole-level RNA Samples." *Genome Research*. April 2010.
- Goren, A., Fatih Ozsolak, Noam Shores, Manching Ku, Mazhar Adli, Chris Hart, Melissa Gymrek, Or Zuk, Aviv Regev, Patric M Milos, & Bradley E Bernstein. "Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA." *Nat Meth*. Published online: 29 November 2009.

CONFERENCES

- **Genome Informatics 2013** Presentation: "Short tandem repeat polymorphisms create an abundant source of expression variability."
- **American Society of Human Genetics 2013** Platform presentation: "Short tandem repeat polymorphisms create an abundant source of expression variability."
- **Arvados Summit 2013** Presentation: "Profiling short tandem repeats from large genomics datasets."
- **American Society of Human Genetics 2012** Platform presentation: "Charting the population-scale landscape of short tandem repeat variation in humans."
- **RECOMB 2012** Presentation: "lobSTR: A Novel Pipeline for Short Tandem Repeats Profiling in Personal Genomes."
- **Personal Genomes 2011** Poster: "lobSTR: A Novel Pipeline for Short Tandem Repeats Profiling in Personal Genomes."