# Chun "Jimmie" Ye

7 Cambridge Center #6029
Cambridge, MA 02142
℘ (619) 316-7177
☎ (617) 714-7758
✉ yechun@broadinstitute.org
🖥 www.broadinstitute.org/˜yechun

## Affiliation

Postdoctoral Associate, Broad Institute

## Research Areas

Expression Quantitative Trait Loci (eQTL) Mapping, Quantitative Genetics, Gene-environment Interactions, Next-generation DNA/RNA Sequencing

## Education

| | |
|---|---|
| 2003–2009 | **Ph.D.**, *Bioinformatics and Systems Biology*, University of California, San Diego, California. |
| 1998–2002 | **B.S.**, *Computer Science*, University of California, Berkeley, California. |
| 1998–2002 | **B.S.**, *Bioengineering*, University of California, Berkeley, California. |

## Experience

### Academic Research Positions

| | |
|---|---|
| 2010–Present | **Postdoctoral Associate**, *Cell Circuits Program*, Broad Institute, Cambridge, Massachusetts.<br>Principal Investigator: Aviv Regev, Ph.D. |
| 2009–2010 | **Staff Research Associate**, *Department of Computer Science*, University of California, Los Angeles, California.<br>Principal Investigator: Eleazar Eskin, Ph.D. |
| 2003–2009 | **Graduate Student Researcher**, *Department of Computer Science*, University of California, Los Angeles, California.<br>Advisor: Eleazar Eskin, Ph.D. |
| 2005 | **NSF East Asia and Pacific Summer Institute (EAPSI) Fellow**, *Institute of Biophysics*, Chinese Academy of Sciences, Beijing, China.<br>Advisor: Runsheng Chen, Ph.D. |
| 2003 | **Graduate Student Rotation Researcher**, *Department of Computer Science*, University of California, San Diego, California.<br>Advisor: Vineet Bafna, Ph.D. |

### Teaching Positions

| | |
|---|---|
| Summer, 2013 | **Mentor**, Broad Institute, Cambridge, MA.<br>Research Science Institute |
| Winter, 2008 | **Teaching Assistant**, University of California, Los Angeles, California.<br>Current Topics in Bioinformatics (Instructor: Eleazar Eskin, Ph.D.) |
| Spring, 2007 | **Teaching Assistant**, University of California, Los Angeles, California.<br>Computational Genetics (Instructor: Eleazar Eskin, Ph.D.) |
| Summer, 2004 | **Graduate Student Coordinator**, University of California, San Diego, California.<br>Summer Training Academy for Research in the Sciences (STARS) |

## Industry Positions

2006–2009 **Discovery Biology Intern**, *Amylin Pharmaceuticals, Inc.*, San Diego, California.
Principal Investigator: Doug Fenger, Ph.D.

2003 **Engineering Scientist**, *Apple Computer, Inc.*, Cupertino, California.
Supervisor: Gary Feierbach

2001 and **Summer Intern**, *Apple Computer, Inc.*, Cupertino, California.
2002 Supervisor: Gary Feierbach

2000 **Summer Intern**, *Genentech, Inc.*, South San Francisco, California.
Principal Investigators: Lisa Bernstein, Ph.D. and Nick van Bruggen, Ph.D.

## Honors & Awards

2011-2014 Extramural NIH Loan Repayment Program Award in Clinical Research

2013 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist

2009 March of Dimes General Scholarship

2005 National Science Foundation East Asia and Pacific Summer Institutes Scholarship (EAPSI)

2003-2005 NIH NIGMS Training Grant

## Publications

### In Process

[1] Alexandria-Chloe Villani*, **Chun Ye***, Raktima Raychowdhury, Weibo Li, Aviv Regev, and Nir Hacohen. Integrative genomic and transcriptomic analysis of 775 human cancer cell lines reveal novel immune drivers and regulatory programs. **(In Preparation)**, 2014.

[2] **Chun Ye**, Ting Feng, Ho keun Kwon, Towfique Raj, Michael Wilson, Kristin McCabe, Michelle H. Lee, Irene Wood, Philip L. De Jager, Aviv Regev, and Christophe O. Benoist. Genetic analysis of the transcriptional response of primary human T cells identifies a common genetic variant associated with the transactivation of IL2RA by YY1. **(In Preparation)**, 2014.

[3] Towfique Raj, Katie Rothamel, Sara Mostafavi, **Chun Ye**, Mark Lee, Joseph M Replogle, Alina Von Korff, Selina Imboya, Cristin McCabe, Yukinori Okada, Nikolaos Patsapolous, Michelle Lee, Irene Wood, Diane Mathis, David Hafler, Daphne Koller, Aviv Regev, Nir Hacohen, Christophe Benoist, Barbara E. Stranger, and Philip L. De Jager. Primary immune cells uncover polarization in the effects of neurodegenerative and inflammatory disease variants. **(Under revision)**, February 2014.

### Journals

[4] Mark Lee*, **Chun Ye***, Alexandria-Chloe Villani, Towfique Raj, Weibo Li, Thomas M. Eisenhaure, Selina H. Imboywa, Portia I. Chipendo, F. Ann Ran, Kamil Slowikowski, Lucas D. Ward, Khadir Raddassi, Cristin McCabe, Michelle H. Lee, Irene Wood, Manolis Kellis, Soumya Raychaudhuri, Feng Zhang, Barbara E. Stranger, Christophe O. Benoist, Philip L. De Jager, Aviv Regev, and Nir Hacohen. Common genetic variants that modulate pathogen-sensing in human dendritic cells. ***Science***, March 2014. **(Platform Talk and Semi-finalist Award at ASHG 2013)**.

[5] Jae Hoon Sul*, Buhm Han*, **Chun Ye***, Ted Choi, and Eleazar Eskin. Effectively identifying eQTLs from multiple tissues combining mixed model and meta-analytic approaches. ***PLoS Genetics***, Jun 2013.

[6] Andrew Kirby, Andreas Gnirke, David B Jaffe, ..., **Chun Ye** (7/43), ..., and Mark J Daly. Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. ***Nature Genetics***, Feb 2013.

[7] Ryan S. Friese, **Chun Ye**, Caroline M. Nievergelt, ..., and Daniel T. O'Connor. Integrated computational and experimental analysis of the neuroendorcine transcriptome in genetic hypertension identifies novel control points for the cardio-metabolic syndrome. ***Circulation Cardiovascular Genetics***, 5(4):430–440, Aug 2012.

[8] Nicholas A. Furlotte, Hyun Min Kang, **Chun Ye**, and Eleazar Eskin. Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. ***Bioinformatics***, 27(13):i288–i294, Jul 2011.

[9] Eun Yong Kang, **Chun Ye**, Ilya Shpitser, and Eleazar Eskin. Detecting the presence and absence of causal relationships between expression of yeast genes with very few samples. ***J Comput Biol***, 17(3):533–46, Mar 2010.

[10] **Chun Ye**, Simon J Galbraith, James C Liao, and Eleazar Eskin. Using network component analysis to dissect regulatory networks mediated by transcription factors in yeast. ***PLoS Comput Biol***, 5(3):e1000311, Mar 2009.

[11] Hyun Min Kang*, **Chun Ye\***, and Eleazar Eskin (* indicates equal contribution). Accurate discovery of expression quantitative trait loci under confounding from spurious and genuine regulatory hotspots. ***Genetics***, 180(4):1909–25, Dec 2008.

[12] **Chun Ye** and Eleazar Eskin. Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. ***Bioinformatics***, 23(2):e84–90, Jan 2007.

[13] Ali Bashir, **Chun Ye**, Alkes L Price, and Vineet Bafna. Orthologous repeats and mammalian phylogenetic inference. ***Genome Res***, 15(7):998–1006, Jul 2005.

[14] Martin Tompa, Nan Li, Timothy L Bailey, ..., **Chun Ye** (24/25), and Zhou Zhu. Assessing computational tools for the discovery of transcription factor binding sites. ***Nat Biotechnol***, 23(1):137–44, Jan 2005.

## Ph.D. Thesis

| | |
|---|---|
| Title | *Statistical Methods for the Integrated Analysis of Expression Quantitative Traits* |
| Advisor | Eleazar Eskin, Ph.D. |
| Committee | Nicholas Schork, Ph.D., Vineet Bafna, Ph.D., Amy Pasquinelli, Ph.D. and Bing Reng, Ph.D. |

# Peer Reviewing

## Journals

| | |
|---|---|
| 2014 | Genome Research |
| 2012 | IEEE/ACM Transactions on Computational Biology |
| 2012 | Nature Communications |
| 2009 | Bioinformatics |

## Conferences

| | |
|---|---|
| 2014 | 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014) |
| 2009 | 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2009) |
| 2008 | 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009) |
| 2007 | 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2008) |
| 2004 | The Ninth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005) |