

Curriculum Vitae

Bo Li

Address

Center for RNA Systems Biology
748 Evans Hall
University of California at Berkeley
Berkeley, CA 94720

Phone: (608) 609-3735
Email: bli25@berkeley.edu
Web: <https://math.berkeley.edu/~bli>

Academic Employment

Aug. 2013 — present	University of California at Berkeley Postdoctoral researcher Supervisor: Lior Pachter
---------------------	--

Education

Sept. 2008 — Jul. 2013	University of Wisconsin–Madison Ph.D. in Computer Sciences Advisor: Colin Dewey
Sept. 2008 — May 2010	University of Wisconsin–Madison M.S. in Computer Sciences GPA: 4.0/4.0
Sept. 2004 — Jul. 2008	Shanghai Jiao Tong University B.E. in Computer Science and Engineering (ACM Honor Class) GPA: 91/100 Rank: 1/19

Publications

Li B*, Fillmore N*, Bai Y, Collins M, Thomson JA, Stewart R and Dewey CN. Evaluation of *de novo* transcriptome assemblies from RNA-Seq data. *Genome Biology*, 15(12):553, 2014. (* Equal contribution)

Publications (continued)

Haas B, Papanicolaou A, Yassour M, Grabherr M, Blood PD, Bowden J, Couger MB, Eccles D, **Li B**, Lieber M, MacManes MD, Ott M, Orvis J, Pochet N, Strozzi F, Weeks N, Westerman R, William T, Dewey CN, Henschel R, LeDuc RD, Friedman N and Regev A. *De novo* transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. *Nature Protocols*, 8(8):1494–1512, 2013.

Li B and Dewey CN. RSEM: Accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics*, 12:323, 2011. (Highly accessed)

Chung D, Kuan PF, **Li B**, Sanalkumar R, Liang K, Bresnick EH, Dewey C and Keleş S. Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of ChIP-Seq data. *PLoS Computational Biology*, 7(7):e1002111, 2011.

Li B, Ruotti V, Stewart RM, Thomson JA and Dewey CN. RNA-Seq gene expression estimation with read mapping uncertainty. *Bioinformatics*, 26(4):493–500, 2010.

Posters

Li B and Pachter L. An RNA-Seq transcript quantification method that is robust to sequencing biases. *International Conference on Intelligence Systems for Molecular Biology (ISMB)*, 2014.

Li B, Fillmore N and Dewey CN. RSEM-EVAL: A Probabilistic Transcriptome Assembly Evaluator. *International Conference on Intelligence Systems for Molecular Biology (ISMB)*, 2012.

Honors and Awards

2013	Finalist, Lane Fellows in Computational Biology, Carnegie Mellon University
2010 — 2012	Morgridge Institute for Research support for senior graduate students in Computation and Informatics in Biology and Medicine
2008	Alumni Scholarship, Computer Sciences Department, University of Wisconsin–Madison
2007	State Scholarship, The Ministry of Education, China
2006	OOCL Scholarship, Orient Overseas Container Line Corporation, China
2006	Thirteenth Place, Google Code Jam China, Beijing, China
2005	Second Place, The 2005 ACM-ICPC Asia Programming Contest — Beijing Site (with Xiaorui Sun and Tao Xin), Beijing, China
2005	Fifth Place, The 2005 ACM-ICPC Asia Programming Contest — Taipei Site (with Xiaorui Sun and Tao Xin), Taipei, China

Honors and Awards (continued)

- 2005 OOCL Scholarship, Orient Overseas Container Line Corporation, China
- 2004 First Place, The 2004 ACM-ICPC Asia Programming Contest — Beijing Site
(with Yifan Chen and Xiaorui Sun), Beijing, China

Research

- Aug. 2013 — present **Postdoctoral Researcher**
Prof. Lior Pachter, Ph.D. (supervisor)
Department of Mathematics
University of California at Berkeley
- Develop novel computational methods to make sense of next generation sequencing data, projects include:
- a) Infer transcript co-expression networks from RNA-Seq data
 - b) Investigate the bioinformatics challenges in analyzing single-cell RNA-Seq data sets
 - c) Build models to extract RNA secondary structure information from sequencing data
- Jun. 2012 — Aug. 2012 **Intern**
Prof. Aviv Regev, Ph.D. (supervisor)
The Broad Institute of MIT and Harvard
Investigated the relationship between nucleosome organization and aging in mammal cells
- Sept. 2008 — Jul. 2013 **Research Assistant**
Prof. Colin Dewey, Ph.D. (advisor)
Department of Biostatistics and Medical Informatics
University of Wisconsin–Madison
- Dissertation: Computational analysis of RNA-Seq data in the absence of a known genome
- As a graduate student, I developed:
- a) RSEM, a widely used transcript abundance quantification tool for RNA-Seq data
 - b) CSEM, a multi-read allocator for ChIP-Seq data
 - c) RSEM-EVAL, a reference-free *de novo* transcriptome assembly evaluator for RNA-Seq data
- Oct. 2007 — Jul. 2008 **Research Assistant, B.E. Thesis Work**
Laboratory of Biocomputing & Bioinformatics
Prof. Bo Yuan, Ph.D. (advisor)
Department of Computer Science and Engineering

Research (continued)

Shanghai Jiao Tong University

Thesis title: The comparative study of cancer based on gene co-expression networks

Teaching

Fall 2008	Teaching Assistant, BMI/CS 576, Introduction to Bioinformatics, University of Wisconsin–Madison
Spring 2007	Teaching Assistant, CS 370, Project Workshop of Compiler, Shanghai Jiao Tong University
Fall 2006	Teaching Assistant, CS 479, Programming Practice of Computer Algorithms, Shanghai Jiao Tong University

Programming Skills

C/C++, Python, Perl, R, Java, Matlab