

Curriculum Vitae

Bo Li

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Academic Employment

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

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| 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

Zeng X, **Li B**, Welch R, Rojo C, Zheng Y, Dewey CN, Keles S. Perm-seq: Mapping protein-DNA interactions in segmental duplication and highly repetitive regions of genomes with prior-enhanced read mapping. *PLoS Computational Biology*, 11(10):e1004491, 2015.

Publications (continued)

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)

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

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| 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 |

Honors and Awards (continued)

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| 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 |
| 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

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| 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 |

Research (continued)

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
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