

# Bo Li

## Address

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## Education

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|------------------------|---|
| Aug. 2013 — present    | <b>University of California at Berkeley</b><br>Postdoctoral researcher in Computational Biology<br>Supervisor: Lior Pachter |
| Sept. 2008 — Jul. 2013 | <b>University of Wisconsin–Madison</b><br>Ph.D. in Computer Sciences<br>Advisor: Colin Dewey                                |
| Sept. 2004 — Jul. 2008 | <b>Shanghai Jiao Tong University</b><br>B.E. in Computer Science and Engineering (ACM Honor Class)                          |

## Representative Publications

1. **Li B**, Tambe A, Aviran S and Pachter L. PROBer: A general toolkit for analyzing sequencing-based ‘toeprinting’ assays. *Submitted*, 2016. <http://biorxiv.org/content/early/2016/07/12/063107>

*This paper describes PROBer – the first unified probabilistic framework for the analysis of a diverse set of sequencing-based ‘toeprinting’ assays. These assays are used to probe RNA secondary structures (DMS/SHAPE-Seq), detect epitranscriptomic marks (Pseudo-Seq), or identify RNA-protein interactions (iCLIP/eCLIP), which are important to understanding post-transcriptional gene regulation from all aspects.*

2. **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. Highly accessed. (\* Equal contribution)

*This paper describes the first principled method for evaluating de novo transcriptome assemblies without ground truth.*

3. **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. (Citation: **1,584**)

*This paper describes the RSEM software – a widely-used RNA-Seq transcript quantification tool that is actively serving in nationwide projects such as ENCODE (The Encyclopedia of DNA Elements) and TCGA (The Cancer Genome Atlas).*

4. **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. (Citation: **386**)

*This paper describes the RSEM algorithm.*

## Other Publications

1. Choudhary K, Shih NP, Deng F, Ledda M, **Li B** and S. Aviran. Metrics for rapid quality control in RNA structure probing experiments. *Bioinformatics*, advance online access, 2016.
2. Zeng X, **Li B**, Welch R, Rojo C, Zheng Y, Dewey CN and Keleş 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.
3. 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. (Citation: **847**)

*This paper describes the widely-used Trinity de novo transcriptome assembly pipeline. RSEM contributes to the pipeline as its transcript quantification tool.*

4. 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.

*This paper describes CSEM, one of the first ChIP-Seq multi-mapping read allocators. This work was highlighted in Nature Reviews Genetics.*

## Invited Talks

The Center for RNA System Biology (CRSB) 4th Annual & Advisory Meeting with Poster Session, Berkeley, CA, USA. *PROBer: A General Toolkit for Analyzing Sequencing-based ‘Toeprinting’ Assays*. (10/2016)

RNA 2016: The 21st Annual Meeting of the RNA Society, Kyoto, Japan. *PROBer: A General Toolkit for Analyzing Sequencing-based ‘Toeprinting’ Assays*. (06/2016)

NGS Data Analysis and Informatics Conference, San Diego, CA, USA. *Quantifying RNA Information from Transcriptome-wide Chemical Probing Experiments*. (02/2016)

Core Skills in Computational Biology, Center for Computational Biology, UC Berkeley, Berkeley, CA, USA. *RNA-Seq Transcript Quantification with RSEM: A Detailed Tutorial with Common Use Cases*. (11/2015)

## Teaching

### University of Wisconsin–Madison

Department of Biostatistics & Medical Informatics

Fall 2008      **Teaching Assistant**, Introduction to Bioinformatics  
Introducing classic computational biology algorithms for undergraduates. Responsible for office hour, homework & exam grading, and test case design for programming assignments.

### Shanghai Jiao Tong University

Department of Computer Science and Engineering

Spring 2007      **Teaching Assistant**, Design and Implementation of Modern Compilers  
Helping computer science majors to implement a compiler from scratch for the Tiger language. Responsible for lecturing and final project grading.

Fall 2006      **Instructor**, Programming Bootcamp: Data Structures and Algorithms  
Helping computer science majors to learn data structures and algorithms by solving programming challenges. Responsible for course design, lecturing, and assignment & exam grading.

## 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

## Professional Service

Reviewer: BMC Bioinformatics, Bioinformatics, and Nucleic Acids Research

Program Committee: RECOMB-Seq 2016, IJCAI 2016