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Academic Employment

May 2019 — present **Center for Immunology and Inflammatory Diseases, Massachusetts General Hospital**
Assistant Investigator
Director of the Bioinformatics and Computational Biology Program

May 2019 — present **Harvard Medical School**
Member of the Faculty

May 2019 — present **Broad Institute of MIT and Harvard**
Associated Scientist

Postdoctoral Training

Jul. 2017 — Apr. 2019 **Broad Institute of MIT and Harvard**
Postdoctoral Associate
Supervisor: Aviv Regev

Aug. 2013 — Jun. 2017 **University of California at Berkeley**
Postdoctoral Researcher
Supervisor: Lior Pachter

Education

Sept. 2008 — Jul. 2013 **University of Wisconsin–Madison**
Ph.D. in Computer Science
Thesis: Computational analysis of RNA-Seq data in the absence of a known genome
Advisor: Colin Dewey

Sept. 2004 — Jul. 2008 **Shanghai Jiao Tong University**
B.E. in Computer Science and Engineering (ACM Honor Class)

Representative Publications

1. Gaublomme JT*†, **Li B***, McCabe C, Knecht A, Yang Y, Drokhlyansky E, Van Wittenberghe N, Waldman J, Dionne D, Nguyen L, De Jager P, Yeung B, Zhao X, Habib N, Rozenblatt-Rosen O† and Regev A†. Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. *Nature Communications*, 10(1):2907, 2019. (* equal contribution, †corresponding author)

Representative Publications (continued)

This paper describes a novel experimental protocol to pool single nuclei from multiple samples and a novel algorithm, demuxEM, to demultiplex the pooled samples.

2. **Li B**, Tambe A, Aviran S and Pachter L. PROBer provides a general toolkit for analyzing sequencing-based toeprinting assays. *Cell Systems*, 4(5):568–574, 2017.

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 structure (DMS/SHAPE-Seq), detect epitranscriptomic mark (Pseudo-Seq), or identify RNA-protein interaction (iCLIP/eCLIP), which are important to understanding post-transcriptional gene regulation from all aspects.

3. **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, citation: **159**)

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

4. **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: **5,586**)

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 Altas).

5. **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: **693**)

This paper describes the RSEM algorithm.

Software

1. scCloud: cloud-based single-cell and single-nucleus RNA-Seq analysis. Git repo: https://github.com/klarman-cell-observatory/scCloud, https://github.com/klarman-cell-observatory/scCloudPy

2. PROBer: a principled and unified probabilistic framework for analyzing sequencing-based 'toeprinting' assays. Git repo: https://github.com/pachterlab/PROBer

3. DETONATE: a *de novo* transcriptome assembly evaluation package, consisting of RSEM-EVAL and REF-EVAL. Source codes: http://deweylab.biostat.wisc.edu/detonate

4. CSEM: as one of the first ChIP-Seq multi-mapping read allocators, CSEM allows multi-reads to be utilized by peak callers. Source codes: http://deweylab.biostat.wisc.edu/csem

5. RSEM: widely-used RNA-Seq transcript quantification tool, cited over 6,200 times. Git repo: https://github.com/deweylab/RSEM