DAVID N.P. KOPPSTEIN

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Education

Massachusetts Institute of Technology	CAMBRIDGE, MA
Ph.D, Biology	*2015*
Yale University	NEW HAVEN, CT
B.S., Molecular Biophysics and Biochemistry	*2008*

Experience

Nikolaus Rajewsky Lab, Max Delbrück Center for Molecular Medicine   BERLIN, GERMANY
Postdoctoral Researcher   *June '18 – present*
Investigating the function of alternative polyadenylation during differentiation of neural lineages in single cells.

Viral Immunology Systems Program, Kirby Institute, UNSW   SYDNEY, AUSTRALIA
Postdoctoral Researcher   *Apr '17 – April '18*
Developed computational methods for analyzing single-cell transcriptomics data of immune cells. Mentored two Ph.D students, a Master's student, and an Honor's student.

Juno Therapeutics   SEATTLE, WA
Data Scientist   *Jan '16 – Mar '17*
Analyzed and communicated immunosequencing analyses for internal projects and external academic collaborators. Conducted analyses for internal RNA-seq and vector integration profiling projects. Served as interim manager of the data science team.

AbVitro   BOSTON, MA
Data Scientist   *Mar '15 – Dec '15*
Designed bioinformatics pipeline for single-cell immunosequencing. Mined receptor sequences from tumor-infiltrating lymphocytes and nominated candidates for screening. *(Acquired by Juno Therapeutics).*

David Bartel Lab, MIT   BOSTON, MA
Graduate Student   *May '10 – Mar '15*
Designed, implemented, and analyzed high-throughput sequencing experiments using the Illumina platform to investigate influenza's cap-snatching repertoire. Utilized 3P-seq to precisely examine alternative cleavage and polyadenylation in diverse genetic backgrounds and model organisms.

Joan Steitz Lab, Yale   NEW HAVEN, CT
Undergraduate Student   *May '06 – Apr '08*
Investigated the function of Herpesvirus saimiri Small U RNAs (HSURs).

Publications and Preprints

Singh M, Jackson KJL, Wang JJ, Schofield P, **Koppstein D**, Field M, Peters T, Nevoltris D, Burnett DL, Masle-Farquhar E, Faulks M, Jackson J, Chataway T, Collela, Blackburn J, Mercer T, Jefferis R, Christ D, Brink R, Rischmueller M, Luciani F, Gordon TP, Goodnow CC, Reed JH. Evolution of pathogenic autoantibody by lymphoma mutations in rogue clones. *Submitted, Nature.*

Rizzetto S, **Koppstein D**, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. B-cell receptor reconstruction from single-cell RNA-seq with VDJPuzzle. 2018. *Bioinformatics. doi:10.1093/bioinformatics/bty203.*

Grüning B, Dale R, Sjödin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Koster J, **The Bioconda Team**. Bioconda: sustainable and comprehensive software distribution for the life sciences. 2018. *Nature Methods 15, 475-76.*

Grigaityte K, Carter JA, Goldfless SJ, Jefferey EW, Hause RJ, Jiang Y, **Koppstein D**, Briggs AW, Church GM, Vigneault F, Atwal GS. Single-cell sequencing reveals $\alpha\beta$ chain pairing shapes the T cell repertoire. 2017. *bioRxiv.*

Briggs AW, Goldfless SJ, Timberlake S, Belmont BJ, Clouser CR, **Koppstein D**, Sok D, Vander Heiden JA, Tamminen MV, Kleinstein SH, Burton DR, Church GM, Vigneault F. 2017. Tumor-infiltrating immune repertoires captured by single-cell barcoding in emulsion. *bioRxiv.*

Koppstein D, Ashour J, and Bartel DP. Sequencing the cap-snatching repertoire of H1N1 influenza provides insight into the mechanism of viral transcription initiation. 2015. *Nucleic Acids Research 43(10), 5052-5064.*

Hezroni H, **Koppstein D**, Schwartz M, Tabin CJ, Bartel DP, and Ulitsky I. 2015. Principles of long noncoding RNA

evolution derived from direct comparison of transcriptomes in 14 vertebrates. *Cell Reports 11(7), 1110-1122.*

Nam J-W, Rissland OS, **Koppstein D**, Abreu-Goodger C, Jan CH, Agarwal V, Yildirim, Rodriguez A, and Bartel DP. 2014. Global Analyses of the Effect of Different Cellular Contexts on MicroRNA Targeting. *Molecular Cell. 53, 1031-1043.*

Ulitsky I, Shkumatava A, Jan C, Subtelny AO, **Koppstein D**, Bell G, Sive H, and Bartel DP. 2012. Extensive alternative polyadenylation during zebrafish development. *Genome Research. 22(10):2054-66.*

Agarwal A*, **Koppstein D***, Rozowsky J, Sboner A, Habegger L, Hillier LW, Sasidharan R, Reinke V, Waterston RH, and Gerstein M. 2010. Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. *BMC Genomics. 11:383.*

Mukhopadhyay J, Das K, Ismail S, **Koppstein D**, Jang M, Hudson B, Sarafianos S, Tuske S, Patel J, Jansen R, Irschik H, Arnold E, and Ebright RH. 2008. Myxopyronin, Corallopyronin, and Ripostatin Inhibit Transcription by Binding to the RNA Polymerase Switch Region. *Cell. 135:295-307.*

Presentations and Posters

Koppstein D, Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJPuzzle: A computational method for BCR and TCR reconstruction from single-cell sequencing data. Australian Bioinformatics And Computational Biology Society. Oral presentation delivered in Adelaide, Australia, November 2017.

Koppstein D Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJPuzzle: A computational method for BCR and TCR reconstruction from single-cell sequencing data. Australian Cellular Panomics Consortium. Poster presentation delivered in Melbourne, Australia, November 2017.

Koppstein D, Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJPuzzle: A computational method for BCR and TCR reconstruction from single-cell sequencing data. Australian Society for Immunology. Oral presentation delivered in Bowral, Australia, November 2017.

Koppstein D, Ashour J, Bartel D. Quantitative assessment of influenza's cap-snatching repertoire by RNA sequencing. RNA Society. Poster presentation delivered in Quebec City, Canada, June 2014.

Skills

Wet lab
> Extensive experience with Illumina library preparation and custom design: 3P-Seq, SMART-seq, and standard RNA-seq. Experience running single-cell 10X Chromium. Experience with molecular cloning, tissue culture, Northern/Western blots, protein purification, PCR, and yeast genetics.

Dry lab
> Fluent in Python and R. Expertise with modern bioinformatics tools including samtools, STAR, feature-Counts, edgeR, Picard, etc. Experience with analysing single-cell sequencing data using scater, Seurat, etc. Experience writing scalable computational pipelines using Snakemake. Experience with statistical methods and machine learning techniques. Experience administering Amazon EC2 clusters using CFNCluster and Ansible. Experience managing a team of computational biologists using agile methods.

Fellowships and Awards

- Juno CEO Discretionary Award for Outstanding Performance, 2016

- NSF Graduate Research Fellowship Program, Honorable Mention, 2011

- Yale STARS II Research Fellowship, 2007-8

Extracurricular

- Urban Cycling Skills and Safety Clinic Organizer, 2013-4

- Whitehead Partner for High School Science Teacher Outreach, 2012

- MIT Cycling Team Officer, 2012-2014

References

References are available upon request.

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*Authors contributed equally to this publication.