

DAVID N.P. KOPPSTEIN

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Education

Massachusetts Institute of Technology

Ph.D, Biology

CAMBRIDGE, MA

2015

Yale University

B.S., Molecular Biophysics and Biochemistry

NEW HAVEN, CT

2001 – 2002

Experience

Kirby Institute, UNSW

SYDNEY, AUSTRALIA

Postdoctoral Fellow

Apr '17 – present

Developing computational methods for analyzing single cell transcriptomics data of immune cells in the context of viral infection. Fellow in the Viral Immunology Systems Program.

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

Implemented computational pipeline for a single-cell paired-chain immunosequencing technique at this biotech start-up (*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.

Mark Gerstein Lab, Yale

NEW HAVEN, CT

Bioinformatics Staff

Sept '08 – June '09

Used statistical methods to compare data quality of RNA-seq to tiling microarrays with matched samples.

Joan Steitz Lab, Yale

NEW HAVEN, CT

Undergraduate Student

May '06 – Apr '08

Investigated the function of Herpesvirus saimiri Small U RNAs (HSURs) by sequencing candidate targets and pulldowns.

Publications

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, Ploegh H, 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, Coralopyronin, and Ripostatin Inhibit Transcription by Binding to the RNA Polymerase Switch Region. *Cell*. 135:295-307.

* Authors contributed equally to this publication.

Skills

Wet lab

Extensive experience with Illumina library preparation and custom experiment design: Poly(A)-Position Profiling (3P-Seq), SMART-seq, vector integration sequencing (VIS-seq), and standard RNA-seq. Experience with molecular cloning, tissue culture maintenance and transfection, Northern/Western blots, protein purification, PCR, and yeast genetics.

Dry lab

Fluent in Python and R, including data analysis and visualization with IPython, pandas, and seaborn. Expertise with modern bioinformatics tools including samtools, bedtools, BWA, STAR, RSEM, Cufflinks, etc. Familiarity with immunosequencing-related toolkits including pRESTO and IGBLAST. Experience writing scalable computational pipelines for industrial next-generation sequencing assays 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 including Scrum and continuous integration (Jenkins).

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

- MIT 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.