DAVID N.P. KOPPSTEIN

david.koppstein@gmail.com • +61 2 9385 0466 • Skype: david.koppstein

Education

Massachusetts Institute of Technology — CAMBRIDGE, MA
Ph.D, Biology — *2015*

Yale University — NEW HAVEN, CT
B.S., Molecular Biophysics and Biochemistry — *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 an 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, Corallopyronin, 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.