

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
2008

Experience

German Cancer Research Center (DKFZ)

DÜSSELDORF, GERMANY

Junior Group Leader, Cancer Bioinformatics and Multiomics

June '23 – present

Spearheading multiple projects relating to transcriptomic diversity in cancers and detection of fusion genes with single-cell and long read sequencing. Successfully applied for two grants for lineage tracing of childhood ALL preleukemic cells and detection of fusion genes (BMBF) and determinants of gastric cancer metastasis through single-cell CRISPR screening (DFG). Supervising 3 Ph.D students and a postdoc.

Bioinformatics Core, MPI for Immunobiology and Epigenetics

FREIBURG, GERMANY

Staff Bioinformatician

August '22 – April '23

Developed pipelines for demultiplexing and processing high-throughput sequencing data for end users. Spearheaded projects on transcriptome isoform annotation and chromosomal conformation capture using long reads and virus detection in single-cells.

Nikolaus Rajewsky Lab, Max Delbrück Center for Molecular Medicine

BERLIN, GERMANY

Postdoctoral Researcher

June '18 – June '22

Conceived and executed a Chan-Zuckerberg Initiative Neurodegeneration Grant to use 10X Visium spatial and Nanopore long read sequencing to analyze aberrant RNA isoforms in neuromuscular organoids models of Amyotrophic Lateral Sclerosis. Wrote a grant for the Berlin Institute of Health to research the effects of COVID-19 patient serum the endothelial transcriptome. Wrote and executed a grant from the Bundesministerium für Bildung und Forschung to explore the role of vault RNAs in SARS-CoV-2 infection. Trained one Masters student.

Viral Immunology Systems Program, Kirby Institute, UNSW

SYDNEY, AUSTRALIA

Postdoctoral Researcher

Apr '17 – April '18

Developed VDJ Puzzle, a computational method for analyzing single-cell transcriptomics data of immune cells. Used this data and other methods to analyze single-cell transcriptomes of rogue B cells in Sjögren's disease. Performed single-cell RNA-seq using 10X Chromium and downstream bioinformatic analysis. Mentored two Ph.D students, a Masters student, and an Honors student.

Juno Therapeutics

SEATTLE, WA, USA

Data Scientist

Jan '16 – Mar '17

Principal architect of the immunosequencing bioinformatics pipeline. Scaled pipeline to the AWS cloud using CfnCluster and Snakemake. Codiscovered effective TCR binders for HPV E6 and E7, resulting in a patent. 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 during the acquisition.

AbViro

BOSTON, MA, USA

Data Scientist

Mar '15 – Dec '15

Principal architect of the immunosequencing pipeline for single-cell immunosequencing. Mined receptor sequences from tumor-infiltrating lymphocytes and developed automated data visualization strategies to nominate candidates for screening. Communicated with external academic and industry collaborators. (*Acquired by Juno Therapeutics*).

David Bartel Lab, MIT

BOSTON, MA, USA

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, discovering that small nuclear RNAs are the primary targets of this process. Utilized 3P-seq to precisely examine alternative cleavage and polyadenylation in diverse genetic backgrounds and model organisms in order to update annotations and improve microRNA targeting models.

Skills

Wet lab

Extensive experience with NGS library preparation and custom design: 3P-Seq, SMART-seq, high-throughput 5' RACE, and standard RNA-seq. Experience running single-cell 10X Chromium, 10X Visium spatial sequencing, and Nanopore long-read sequencing. Experience with molecular cloning, tissue culture, Northern/Western blots, protein purification, PCR/qPCR, microscopy, cryotome sectioning, and yeast genetics.

Dry lab

Fluent in Python and R. Expertise with modern bioinformatics tools including samtools, STAR, featureCounts, edgeR, Picard, GSEA, etc. Experience with analysing single-cell and spatial sequencing data using scater, Seurat, napari, etc. Experience writing scalable computational pipelines using Snakemake and scaling to the cloud using AWS. Experience with statistical methods and machine learning techniques. Experience managing teams of computational biologists using agile methods.

Fellowships and Awards

- Juno CEO Award for Outstanding Performance, 2016
- NSF Graduate Research Fellowship Program, Honorable Mention, 2011
- Yale STARS II Research Fellowship, 2007-8

Grants

David Koppstein, Jovan Mircetic, Daniel Stange. Determinants of gastric cancer metastases by single-cell CRISPR screening. Deutsche Forschungsgemeinschaft (DFG).

Ute Fischer, Conny Eckert, Britta Meyer, Aleksandra Pandya, **David Koppstein**, Stefan Janssen. EDI-4-ALL: Early Detection and Interception for Childhood Acute Lymphoblastic Leukemia. Bundesministerium für Bildung und Forschung (BMBF).

Wolfgang Kübler, Holger Gerhardt, Philipp Mertins, Nikolaus Rajewsky, Martin Witzenth, **David Koppstein**, Laura Michalick, Anna Szymborska-Mell. The COVID-19 puzzle - The microvascular barrier as a missing piece between coagulation and organ failure. Berlin Institute for Health, Vascular Biomedicine Focus Area Grant.

Mina Gouti and Nikolaus Rajewsky. Spatial Analysis of aberrant RNA isoforms in ALS neuromuscular organoids. Neurodegeneration Challenge Network Collaborative Pair Pilot Project Award. (Written on behalf of Nikolaus Rajewsky)

Nikolaus Rajewsky, Marcel Müller, and Markus Landthaler. Molecular exploration of SARS-CoV-2 host-virus interactions with targeted knockouts and pulldowns. Bundesministerium für Bildung und Forschung, COVID-19 awards. (Written on behalf of Nikolaus Rajewsky).

Presentations and Posters

Koppstein D, Rizzetto S, Samir J, Singh M, Reed JH, Cai CH, Lloyd AR, Eltahla AA, Goodnow CC, Luciani F. VDJ Puzzle: 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. VDJ Puzzle: 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. VDJ Puzzle: 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.

Publications and Preprints

Jepsen V et al., ... **Koppstein D**, Koegler G, Remke M, Bhatia S, Heinaniemi M, Borkhardt A, Fischer U. H1-0 is a specific mediator of the repressive ETV6::RUNX1 transcriptional landscape in preleukemia and B cell acute lymphoblastic leukemia. 2025. Accepted, *Hemasphere*.

Purkait S, Praeger S, Felsberg J, Pauck D, Kaulich K, Wolter M, **Koppstein D**, Reifemberger G. Strong immunohistochemical positivity for HOXB13 is a reliable surrogate marker for DNA methylome profiling to distinguish myxopapillary ependymoma from spinal ependymoma. 2025. Accepted, *Acta Neuropathologica*.

Alfonso-Gonzalez C, Legnini I, Holec S, Arrigoni L, Ozbulut HC, Mateos F, **Koppstein D**, Rybak-Wolf A, Bönisch U, Rajewsky N, Hilgers V. Sites of transcription initiation drive mRNA isoform selection. 2023. *Cell*. doi: 10.1016/j.cell.2023.04.012.

Bujanic L, Shevchuk O, von Kügelgen N, Kalinina A, Ludwik K, **Koppstein D**, Zerna N, Sickmann A, Chekulaeva M. The key features of SARS-CoV-2 leader and NSP1 required for viral escape of NSP1-mediated repression. 2022. *RNA*. doi: 10.1261/rna.079086.121.

Wyler M, Mösbauer K, Franke F, Diag A, Gottula LT, Arsie R, Klironomos F, **Koppstein D**, ..., Rajewsky N, Drosten C, Landthaler M. Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. 2021. *iScience*. doi: 10.1016/j.isci.2021.102151.

Singh M, Jackson KJL, Wang JJ, Schofield P, Field MA, **Koppstein D**, ..., Luciani F, Gordon TP, Goodnow CC, Reed JH. Lymphoma driver mutations in the pathogenic evolution of an iconic human autoantibody. 2020. *Cell*. doi:10.1016/j.cell.2020.01.029.

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 VDJ-Puzzle. 2018. *Bioinformatics*. doi:10.1093/bioinformatics/bty203.

Grüning B, Dale R, Sjödin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Köster 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, Coralopyronin, and Ripostatin Inhibit Transcription by Binding to the RNA Polymerase Switch Region. *Cell*. 135:295-307.

*Authors contributed equally to this publication.

Teaching and Extracurricular

- Instructor for BIOME seminar, “Introduction to Snakemake”, 2024
 - Instructor for Max Planck Institute internal seminar, “Introduction to R and the tidyverse”, 2024
 - Instructor for NGSSchool seminar, “Introduction to Snakemake”, 2020
 - Science outreach with “Lange Nacht für Wissenschaft” (Long Night of Science), Berlin, 2019-2021
 - Urban Cycling Skills and Safety Clinic Organizer, 2013-4
 - Whitehead Partner for High School Science Teacher Outreach, 2012
 - MIT Cycling Team Officer, 2012-2014
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Languages

- English - native speaker
- German - B2 level