BIOGRAPHICAL SKETCH

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NAME: Gabdank, Idan

eRA COMMONS USER NAME (credential, e.g., agency login): GABDANK

POSITION TITLE: Senior Biocuration Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Ben Gurion University of the Negev, Beer Sheva	BS	06/2004	Bioinformatics
Ben Gurion University of the Negev, Beer Sheva	MS	06/2007	Bioinformatics
Ben Gurion University of the Negev, Beer Sheva	PHD	06/2011	Bioinformatics
Stanford School of Medicine, department of Pathology, Stanford, California	Postdoctoral Fellow	06/2015	Bioinformatics
Stanford University Manager Academy, Stanford, California	Other training	present	Management
Project Management Institute, California	Other training	present	PMP

A. Personal Statement

As a seasoned leader in program management and computational biology with over 15 years of experience, I bring a unique combination of technical expertise and strategic leadership to genomics research initiatives. My career has spanned from computational algorithm development to directing large-scale research portfolios, giving me comprehensive insight into both the technical and administrative aspects of complex genomic projects. Currently, I contribute to the CZI-funded Billion Cell Project at Stanford as a Senior Biocuration Scientist, where I support data curation for single cell and CRISPR experiments. My recent experience as Program Director at NHGRI involved managing a substantial research portfolio spanning numerous grants while developing data-driven frameworks for portfolio assessment and strategic planning. As Director of Data Science for the IGVF Consortium at Stanford (2021-2024), I provided strategic oversight for a major international research consortium comprising dozens of laboratories across multiple institutions. My technical expertise encompasses developing and implementing computational pipelines for diverse NGS data analyses, architecting complex data models for genomic experiments, and establishing scalable cloud-based infrastructures. Throughout my career, I have focused on improving operational efficiency through systematic process improvements, enhanced team retention strategies, and streamlined issue resolution workflows. My leadership philosophy centers on data-driven decision-making, cross-functional collaboration, and fostering professional development within teams. I am particularly skilled at bridging the gap between computational methods and biological insights, making me well-positioned to advance genomics research initiatives and contribute to the broader scientific community.

1. Yao D, Tycko J, Oh JW, Bounds LR, Gosai SJ, Lataniotis L, Mackay-Smith A, Doughty BR, Gabdank I, Schmidt H, Guerrero-Altamirano T, Siklenka K, Guo K, White AD, Youngworth I, Andreeva K, Ren X, Barrera A, Luo Y, Yardımcı GG, Tewhey R, Kundaje A, Greenleaf WJ, Sabeti PC, Leslie C, Pritykin Y, Moore JE, Beer MA, Gersbach CA, Reddy TE, Shen Y, Engreitz JM, Bassik MC, Reilly SK. Multicenter integrated analysis of noncoding CRISPRi screens. Nat Methods. 2024 Apr;21(4):723-734. PubMed Central PMCID: PMC11009116.
2. Moore JE, Purcaro MJ, Pratt HE, Epstein CB, Shoresh N, Adrian J, Kawli T, Davis CA, Dobin A, Kaul R, Halow J, Van Nostrand EL, Freese P, Gorkin DU, Shen Y, He Y, Mackiewicz M, Pauli-Behn F, Williams BA, Mortazavi A, Keller CA, Zhang XO, Elhajjajy SI, Huey J, Dickel DE, Snetkova V, Wei X, Wang X, Rivera-Mulia JC, Rozowsky J, Zhang J, Chhetri SB, Zhang J, Victorsen A, White KP, Visel A, Yeo GW, Burge CB, Lécuyer E, Gilbert DM, Dekker J, Rinn J, Mendenhall EM, Ecker JR, Kellis M, Klein RJ, Noble WS, Kundaje A, Guigó R, Farnham PJ, Cherry JM, Myers RM, Ren B, Graveley BR, Gerstein MB, Pennacchio LA, Snyder MP, Bernstein BE, Wold B, Hardison RC, Gingeras TR,

Stamatoyannopoulos JA, Weng Z. Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature. 2020 Jul;583(7818):699-710. PubMed Central PMCID: PMC7410828.

3. Gabdank I, Chan ET, Davidson JM, Hilton JA, Davis CA, Baymuradov UK, Narayanan A, Onate KC, Graham K, Miyasato SR, Dreszer TR, Strattan JS, Jolanki O, Tanaka FY, Hitz BC, Sloan CA, Cherry JM. Prevention of data duplication for high throughput sequencing repositories. Database (Oxford). 2018 Jan 1;2018 PubMed Central PMCID: PMC5829560.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2025 -	Senior Biocuration Scientist, Department of Biomedical Data Science, Stanford University School of Medicine, Palo Alto, CA
2024 - 2025	Program Director, Division of Genome Sciences, National Human Genome Research Institute, NIH, Bethesda, MD
2021 - 2024	Director of Data Science, IGVF Data Administrative Coordination Center, Department of Genetics, Stanford University School of Medicine, Palo Alto, CA
2020 - 2022	Computational Pipelines Team Lead & ENCODE Data Wranglers Team Lead, Department of Genetics, Stanford University School of Medicine, Palo Alto, CA
2018 - 2020	ENCODE Data Wranglers Team Lead, Department of Genetics, Stanford University School of Medicine, Palo Alto, CA
2015 - 2018	Senior Data Wrangler, Department of Genetics, Stanford University School of Medicine, Palo Alto, CA

Honors

2011 - 2015	Human Frontiers Science Program Postdoctoral Long-Term Cross-Disciplinary Fellowship, Human Frontiers Science Program
2006 - 2010	Pratt Ph.D. Fellowship, Ben Gurion University of the Negev
2010	Research Excellence Prize and Teaching Excellence Award, Ben Gurion University of the Negev
2009	Research Excellence Prize, Ben Gurion University of the Negev

C. Contribution to Science

1. My work has been instrumental in establishing data standards and computational infrastructure for major genomics initiatives. As Director of Data Science for IGVF Consortium Data Administrative Coordination Center and previously for ENCODE Consortium Data Coordination Center, I led the development of comprehensive data models that capture experimental artifacts and enable reproducible research across hundreds of laboratories. My team's work on the ENCODE data portal serves over 20K users monthly and has become a critical resource for the genomics community. I also spearheaded the modernization of our application development and deployment processes, implementing CI/CD pipelines with infrastructure as code using AWS CDK, which significantly improved our deployment reliability and reduced time to production. Additionally, I contributed to international standardization efforts through GA4GH and IHEC, ensuring interoperability across global genomics resources.
    a. Luo Y, Hitz BC, Gabdank I, Hilton JA, Kagda MS, Lam B, Myers Z, Sud P, Jou J, Lin K, Baymuradov UK, Graham K, Litton C, Miyasato SR, Strattan JS, Jolanki O, Lee JW, Tanaka FY, Adenekan P, O'Neill E, Cherry JM. New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. Nucleic Acids Res. 2020 Jan 8;48(D1):D882-D889. PubMed Central PMCID: PMC7061942.
    b. Davis CA, Hitz BC, Sloan CA, Chan ET, Davidson JM, Gabdank I, Hilton JA, Jain K, Baymuradov UK, Narayanan AK, Onate KC, Graham K, Miyasato SR, Dreszer TR, Strattan JS, Jolanki O, Tanaka FY, Cherry JM. The Encyclopedia of DNA elements (ENCODE): data portal update. Nucleic Acids Res. 2018 Jan 4;46(D1):D794-D801. PubMed Central PMCID: PMC5753278.
    c. Gabdank I, Chan ET, Davidson JM, Hilton JA, Davis CA, Baymuradov UK, Narayanan A, Onate KC, Graham K, Miyasato SR, Dreszer TR, Strattan JS, Jolanki O, Tanaka FY, Hitz BC, Sloan CA, Cherry

JM. Prevention of data duplication for high throughput sequencing repositories. Database (Oxford). 2018 Jan 1;2018 PubMed Central PMCID: PMC5829560.

   d. Sloan CA, Chan ET, Davidson JM, Malladi VS, Strattan JS, Hitz BC, Gabdank I, Narayanan AK, Ho M, Lee BT, Rowe LD, Dreszer TR, Roe G, Podduturi NR, Tanaka F, Hong EL, Cherry JM. ENCODE data at the ENCODE portal. Nucleic Acids Res. 2016 Jan 4;44(D1):D726-32. PubMed Central PMCID: PMC4702836.

2. As team lead for computational pipelines at ENCODE Consortium Data Coordination Center, I established a comprehensive framework for developing and executing platform-independent, production-grade genomic data processing workflows. Our team pioneered the implementation of containerized pipelines using WDL (Workflow Description Language) and Docker, enabling reproducible analyses across local and cloud environments. These pipelines process diverse NGS data types including WGBS, Hi-C, DNase-seq, ATAC-seq, ChIP-seq, and RNA-seq at scale, with full provenance tracking and quality control metrics. By implementing CI/CD practices and automated testing, we ensured reliability for production use across the international consortium. Our framework has been adopted globally through Dockstore and DockerHub repositories, setting new standards for computational reproducibility in genomics.
   a. Hitz BC, Lee JW, Jolanki O, Kagda MS, Graham K, Sud P, Gabdank I, Strattan JS, Sloan CA, Dreszer T, Rowe LD, Podduturi NR, Malladi VS, Chan ET, Davidson JM, Ho M, Miyasato S, Simison M, Tanaka F, Luo Y, Whaling I, Hong EL, Lee BT, Sandstrom R, Rynes E, Nelson J, Nishida A, Ingersoll A, Buckley M, Frerker M, Kim DS, Boley N, Trout D, Dobin A, Rahmanian S, Wyman D, Balderrama-Gutierrez G, Reese F, Durand NC, Dudchenko O, Weisz D, Rao SSP, Blackburn A, Gkountaroulis D, Sadr M, Olshansky M, Eliaz Y, Nguyen D, Bochkov I, Shamim MS, Mahajan R, Aiden E, Gingeras T, Heath S, Hirst M, Kent WJ, Kundaje A, Mortazavi A, Wold B, Cherry JM. The ENCODE Uniform Analysis Pipelines. Res Sq. 2023 Jul 19; PubMed Central PMCID: PMC10371165.
   b. Moore JE, Purcaro MJ, Pratt HE, Epstein CB, Shoresh N, Adrian J, Kawli T, Davis CA, Dobin A, Kaul R, Halow J, Van Nostrand EL, Freese P, Gorkin DU, Shen Y, He Y, Mackiewicz M, Pauli-Behn F, Williams BA, Mortazavi A, Keller CA, Zhang XO, Elhajjajy SI, Huey J, Dickel DE, Snetkova V, Wei X, Wang X, Rivera-Mulia JC, Rozowsky J, Zhang J, Chhetri SB, Zhang J, Victorsen A, White KP, Visel A, Yeo GW, Burge CB, Lécuyer E, Gilbert DM, Dekker J, Rinn J, Mendenhall EM, Ecker JR, Kellis M, Klein RJ, Noble WS, Kundaje A, Guigó R, Farnham PJ, Cherry JM, Myers RM, Ren B, Graveley BR, Gerstein MB, Pennacchio LA, Snyder MP, Bernstein BE, Wold B, Hardison RC, Gingeras TR, Stamatoyannopoulos JA, Weng Z. Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature. 2020 Jul;583(7818):699-710. PubMed Central PMCID: PMC7410828.

3. During my postdoctoral fellowship, I combined classical genetics approaches with modern sequencing technologies to advance our understanding of the C. elegans genome. I developed chromatin structure analysis methods, including the Tethered Chromosome Conformation Capture (TCC) protocol, to study 3D genome organization in this model organism. My work on high-throughput sequencing data analysis directly contributed to the re-sequencing and improved assembly of the C. elegans reference genome, identifying previously missed sequences and correcting assembly errors. Additionally, I investigated classical genetic phenomena such as crossover interference patterns during meiosis, revealing gamete-specific differences in recombination frequencies.
   a. Yoshimura J, Ichikawa K, Shoura MJ, Artiles KL, Gabdank I, Wahba L, Smith CL, Edgley ML, Rougvie AE, Fire AZ, Morishita S, Schwarz EM. Recompleting the Caenorhabditis elegans genome. Genome Res. 2019 Jun;29(6):1009-1022. PubMed Central PMCID: PMC6581061.
   b. Shoura MJ, Gabdank I, Hansen L, Merker J, Gotlib J, Levene SD, Fire AZ. Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in Caenorhabditis elegans and Homo sapiens. G3 (Bethesda). 2017 Oct 5;7(10):3295-3303. PubMed Central PMCID: PMC5633380.
   c. Gabdank I, Ramakrishnan S, Villeneuve AM, Fire AZ. A streamlined tethered chromosome conformation capture protocol. BMC Genomics. 2016 Apr 1;17:274. PubMed Central PMCID: PMC4818521.
   d. Gabdank I, Fire AZ. Gamete-type dependent crossover interference levels in a defined region of Caenorhabditis elegans chromosome V. G3 (Bethesda). 2014 Jan 10;4(1):117-20. PubMed Central PMCID: PMC3887527.

4. The early part of my career involved experimental validation of RNA secondary structure alternations of in-silico designed thermo-switches and development of an accurate sequence-directed nucleosome

positioning prediction algorithm. I supervised the development of a web server implementation of the nucleosome positioning prediction method. In addition to that, I have developed Monte Carlo simulations verifying analytical results from a theoretical physical model studying the universal behavior of disordered lattices at low temperatures. I have served as an instructor in "Workshop in Software Engineering" and "Introduction to Programming" courses.

a. Gabdank I, Barash D, Trifonov EN. FineStr: a web server for single-base-resolution nucleosome positioning. Bioinformatics. 2010 Mar 15;26(6):845-6. PubMed PMID: 20106816.
b. Gabdank I, Barash D, Trifonov EN. Nucleosome DNA bendability matrix (C. elegans). J Biomol Struct Dyn. 2009 Feb;26(4):403-11. PubMed PMID: 19108579.
c. Avihoo A, Gabdank I, Shapira M, Barash D. In silico design of small RNA switches. IEEE Trans Nanobioscience. 2007 Mar;6(1):4-11. PubMed PMID: 17393844.