Stanford

Russ B. Altman

Kenneth Fong Professor and Professor of Bioengineering, of Genetics, of Medicine, of Biomedical Data Science, Senior Fellow at the Stanford Institute for Human-Centered AI and Professor, by courtesy, of Computer Science

NIH Biosketch available Online   Curriculum Vitae available Online

CONTACT INFORMATION

- **Alternate Contact**

  Tiffany Murray - Administrative Associate

  Email tiffany.murray@stanford.edu

  Tel 650-725-0659

Bio

BIO

Russ Biagio Altman is the Kenneth Fong Professor of Bioengineering, Genetics, Medicine, Biomedical Data Science and (by courtesy) Computer Science) and past chairman of the Bioengineering Department at Stanford University. His primary research interests are in the application of computing (AI, data science and informatics) to problems relevant to medicine. He is particularly interested in methods for understanding drug action at molecular, cellular, organism and population levels. His lab studies how human genetic variation impacts drug response (e.g., http://www.pharmgkb.org/). Other work focuses on the analysis of biological molecules to understand the actions, interactions and adverse events of drugs (e.g., http://helix.stanford.edu/). He helps lead an FDA-supported Center of Excellence in Regulatory Science & Innovation.

Dr. Altman holds an AB from Harvard College, and an MD from Stanford Medical School, and a PhD in Medical Information Sciences from Stanford. He received the U.S. Presidential Early Career Award for Scientists and Engineers and a National Science Foundation CAREER Award. He is a fellow of the American College of Physicians (ACP), the American College of Medical Informatics (ACMI), the American Institute of Medical and Biological Engineering (AIMBE), and the American Association for the Advancement of Science (AAAS). He is a member of the National Academy of Medicine. He is a past-president, founding board member, and a fellow of the International Society for Computational Biology (ISCB), and a past-president of the American Society for Clinical Pharmacology & Therapeutics (ASCPT). He has chaired the Science Board advising the FDA commissioner, and has served on the NIH Director’s Advisory Committee, and as cochair of the IOM Drug Forum. He is an organizer of the annual Pacific Symposium on Biocomputing, and a founder of Personalis (NASDAQ: PSNL). Dr. Altman is board certified in Internal Medicine and in Clinical Informatics. He received the Stanford Medical School graduate teaching award in 2000 and 2020, and the mentorship award in 2014. He is the founding editor of the Annual Reviews of Biomedical Data Science, and hosts a podcast entitled “The Future of Everything.”

ACADEMIC APPOINTMENTS

- Professor, Bioengineering
- Professor, Genetics
- Professor, Computational Medicine
- Professor, Department of Biomedical Data Science

- Senior Fellow, Institute for Human-Centered Artificial Intelligence (HAI)
- Professor (By courtesy), Computer Science
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Faculty Director, SPADA (Stanford Predictives & Diagnostics Accelerator), (2016- present)
- Faculty Director, 100 Year Study of Artificial Intelligence, (2015- present)
- Associate Director, Human-Centered Artificial Intelligence Institute, (2018- present)
- Member, Biomedical Library and Informatics Research Commitee Study Section (NIH), (2002-2005)
- President, International Society for Computational Biology, (2000-2001)
- President, American Society for Clinical Pharmacology and Therapeutics, (2013-2014)
- Director, Biomedical Informatics Training Program, (2000-2018)
- Chairman, Department of Bioengineering, (2007-2012)
- Chair, FDA Science Board, (2013-2014)
- Member, Advisory Committee to the Director (ACD), NIH, (2013-2016)

HONORS AND AWARDS

- The Arthur Kornberg and Paul Berg Lifetime Achievement Award in Biomedical Sciences, Stanford Medical School (2023)
- Teaching Honor Roll, Tau Beta Pi (2020)
- Excellence in Graduate Teaching Award, Stanford Biosciences (2020)
- Fellow, American Association for the Advancement of Science (2014)
- Stanford Medical School Mentorship Award, Stanford Medical School (2014)
- Fellow, International Society for Computational Biology (2010)
- Member, Institute of Medicine of the National Academies (2009)
- Fellow, American Institute for Medical and Biological Engineering (2007)
- Award for Excellence in Graduate Teaching, Stanford Medical School (2000)
- Fellow, American College of Medical Informatics (1998)
- Fellow, American College of Physicians (1998)
- U.S. Presidential Early Career Award for Scientists & Engineers, NIH (1997)
- Post-Doctoral Fellowship, Howard Hughes Medical Institute (1991)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Global Health Faculty#Fellow, Center for Innovation in Global Health (CIGH) (2024 - present)
- Co-Founder, Personalis.com (2013 - present)
- Editor-in-Chief, Annual Reviews of Biomedical Data Science (2016 - present)
- Board of Directors, YouScript.com (2018 - present)

- Advisor, Vanderbilt University Medical School (2014 - present)
- Advisor, NIH Advisory Committee to the Director (ACD) (2013 - 2017)
- Member, FDA Commissioner Science Board (2011 - 2014)
- Co-Organizer, Pacific Symposium on Biocomputing (psb.stanford.edu) (1995 - present)

PROGRAM AFFILIATIONS

- Symbolic Systems Program

PROFESSIONAL EDUCATION

- AB (summa cum laude), Harvard College , Biochemistry and Molecular Biology (1983)
- PhD, Stanford University , Medical Information Sciences (1989)
- MD, Stanford University , Medicine (1990)

COMMUNITY AND INTERNATIONAL WORK

- Host, "The Future of Everything with Russ Altman" Podcast, https://engineering.stanford.edu/magazine/collection/future-everything
- Physician, Pharmacogenomics Consult Service, Stanford Clinics, CA

PATENTS

- Nicholas Tatonetti, Russ B. Altman, Guy Haskin Fernald. "United States Patent 9305267 Signal detection algorithms to identify drug effects and drug interactions", The Board of Trustees of the Leland Stanford Junior University, Apr 5, 2016
- Kathleen A. Thompson, Russ B. Altman, Oliver M. Duschka. "United States Patent 6178416 Method and apparatus for knowledgebase searching", Jan 23, 2001
- Ramon M. Felciano, Russ B. Altman. "United States Patent 6052730 Method for monitoring and/or modifying web browsing sessions", The Board of Trustees of the Leland Stanford Junior University, Apr 18, 2000

LINKS

- Helix Group Website: http://helix.stanford.edu
- Personal home page: https://rbaltman.people.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

I am interested in the application of computational technologies to problems in molecular biology of relevance to medicine. In particular, my laboratory focuses on drug response at the molecular level, working in three areas. First, we are building a comprehensive pharmacogenomics knowledge base (http://www.pharmgkb.org/) that provides access to information relating genotype to phenotype (in particular, how variation in genetics leads to variation in response to drugs). We are interested in collaboratively discovering and applying new pharmacogenomics knowledge. Second, we are interested in the analysis of three dimensional biological structures. We have methods for analyzing protein structures to recognize and annotate active sites and binding sites, particularly in the context of interactions with small molecule drugs. We are also interested in physics-based simulation of biological structures to understand how their dynamics impact their function (http://simbios.stanford.edu/). Finally, we are interested in computational methods for analyzing functional genomics information. We use natural language processing techniques for extracting and summarizing information in the literature, chemoinformatics methods for understanding small molecule function, and machine learning & data mining techniques to understand the molecular responses to drugs.

Teaching

COURSES

2025-26

- Computational Applications of High-Throughput Protein Data for Machine Learning: BIOS 442 (Spr)
- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Informatics Research Methodology: BIOE 212, BMDS 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BMDS 224, GENE 224 (Aut, Spr)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BMDS 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BMDS 216 (Aut)

2024-25

- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Informatics Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BIOMEDIN 224, GENE 224 (Aut, Spr)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BIOMEDIN 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BIOMEDIN 216 (Aut)

2023-24

- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Data Science Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BIOMEDIN 224, GENE 224 (Aut, Spr)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BIOMEDIN 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BIOMEDIN 216 (Aut)

2022-23

- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Data Science Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BIOMEDIN 224, GENE 224 (Aut, Win, Spr, Sum)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BIOMEDIN 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BIOMEDIN 216 (Aut)

STANFORD ADVISEES

Med Scholar Project Advisor

Christine Lee, Johnny Powell, Helen Xu

Doctoral Dissertation Reader (AC)

Ibtihal Elfaki, Hannah Field, EJ Fine, Jessica Kain, Jessica Karaguesian, Aviv Korman, Haim Krupkin, Louise Gabrielle Lima, Tianyu Lu, Holly McCann, Shuyu Shi, Elana Simon, Courtney Smith, Yixin Wang

Doctoral Dissertation Advisor (AC)

Vidal Arroyo, Stephanie Arteaga, Susie Avagyan, Gowri Nayar, Kae Nurge, Issah Samori, Betty Xiong

Doctoral Dissertation Co-Advisor (AC)

Jeonghyeon Kim, Mohini Misra

Master's Program Advisor

Emily Liu, Sam Moghaddam, Asmani Yamin, Bowen Zheng

Doctoral (Program)

Sarah Arnold, Yasa Baig, Aviv Korman, Kara Liu, Janella Schwab Lizárraga, Emily Yemington

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Bioengineering (Phd Program)
- Biomedical Data Science (Masters Program)
- Biomedical Data Science (Phd Program)
- Biophysics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **TikTok is a valuable data source for tracking the opioid crisis.** *NPJ digital medicine*
  Samori, I. A., Carpenter, K. A., Smith, D. A., Humphreys, K., Lembke, A., Eichstaedt, J. C., Altman, R. B.
  2026

- **Interpreting PLMs for cancer discovery: High attention hotspots predict pathogenic mutation positions and novel drug binding sites**
  Pribus, S. J., Nayar, G., Altman, R.
  AMER ASSOC CANCER RESEARCH.2026

- **GATSBI: Improving context-aware protein embeddings through biologically motivated data splits.** *bioRxiv : the preprint server for biology*
  Nayar, G., Altman, R. B.
  2026

- **The Human Omnibus of Targetable Pockets.** *Journal of cheminformatics*
  Carpenter, K. A., Altman, R. B.
  2025; 17 (1): 180

- **Identifying DNA methylation sites affecting drug response using electronic health record-derived GWAS summary statistics.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Smith, D. A., Arteaga, S. A., Sadler, M. C., Altman, R. B.
  2025; 30: 457-472

- **Detecting clinician implicit biases in diagnoses using proximal causal inference.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Liu, K., Altman, R., Syrgkanis, V.
  2025; 30: 330-345

- **Paying attention to attention: High attention sites as indicators of protein family and function in language models.** *PLoS computational biology*
  Nayar, G., Tartici, A., Altman, R. B.
  2025; 21 (9): e1013424

- **Protein functional site annotation using local structure embeddings.** *Proceedings of the National Academy of Sciences of the United States of America*
  Derry, A., Tartici, A., Altman, R. B.
  2025; 122 (34): e2513219122

- **CRISPR-GPT for agentic automation of gene-editing experiments.** *Nature biomedical engineering*
  Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H. C., Johnson, W. A., Wang, X., Shah, M., Altman, R. B., Zhou, D., Wang, et al
  2025

- **Unsupervised learning reveals landscape of local structural motifs across protein classes.** *Bioinformatics (Oxford, England)*
  Derry, A., Krupkin, H., Tartici, A., Altman, R. B.
  2025
- **Pool PaRTI: A PageRank-Based Pooling Method for Identifying Critical Residues and Enhancing Protein Sequence Representations.** *Bioinformatics (Oxford, England)*
  Tartici, A., Nayar, G., Altman, R. B.
  2025
- **Monitoring the opioid epidemic via social media discussions.** *NPJ digital medicine*
  Smith, D. A., Lavertu, A., Salecha, A., Hamamsy, T., Humphreys, K., Lembke, A., Kiang, M. V., Altman, R. B., Eichstaedt, J. C.
  2025; 8 (1): 284
- **Leveraging large-scale biobank EHRs to enhance pharmacogenetics of cardiometabolic disease medications.** *Nature communications*
  Sadler, M. C., Apostolov, A., Cevallos, C., Auwerx, C., Ribeiro, D. M., Altman, R. B., Kutalik, Z.
  2025; 16 (1): 2913
- **Genetic association studies using disease liabilities from deep neural networks.** *American journal of human genetics*
  Yang, L., Sadler, M. C., Altman, R. B.
  2025
- **Conditional Generative Models for Synthetic Tabular Data: Applications for Precision Medicine and Diverse Representations.** *Annual review of biomedical data science*
  Liu, K., Altman, R. B.
  2025
- **Toward a framework for risk mitigation of potential misuse of artificial intelligence in biomedical research.** *Nature machine intelligence*
  Trotsyuk, A. A., Waeiss, Q., Bhatia, R. T., Aponte, B. J., Heffernan, I. M., Madgavkar, D., Felder, R. M., Lehmann, L. S., Palmer, M. J., Greely, H., Wald, R., Goetz, L., Trengove, et al
  2024; 6 (12): 1435-1442
- **COLLAPSE: A representation learning framework for identification and characterization of protein structural sites.** *Protein science : a publication of the Protein Society*
  Derry, A., Altman, R. B.
  2022: e4541
- **POPDx: an automated framework for patient phenotyping across 392 246 individuals in the UK Biobank study.** *Journal of the American Medical Informatics Association : JAMIA*
  Yang, L., Wang, S., Altman, R. B.
  2022
- **Construction of disease-specific cytokine profiles by associating disease genes with immune responses.** *PLoS computational biology*
  Liu, T., Wang, S., Wornow, M., Altman, R. B.
  2022; 18 (4): e1009497
- **Quantifying the Severity of Adverse Drug Reactions Using Social Media: Network Analysis.** *Journal of medical Internet research*
  Lavertu, A., Hamamsy, T., Altman, R. B.
  2021; 23 (10): e27714
- **Leveraging the Cell Ontology to classify unseen cell types.** *Nature communications*
  Wang, S., Pisco, A. O., McGeever, A., Brbic, M., Zitnik, M., Darmanis, S., Leskovec, J., Karkanias, J., Altman, R. B.
  2021; 12 (1): 5556
- **Drug Response Pharmacogenetics for 200,000 UK Biobank Participants.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  McInnes, G. n., Altman, R. B.
  2021; 26: 184–95
- **Analyzing the vast coronavirus literature with CoronaCentral.** *Proceedings of the National Academy of Sciences of the United States of America*
  Lever, J., Altman, R. B.

2021; 118 (23)

- **Analyzing the vast coronavirus literature with CoronaCentral.** *bioRxiv : the preprint server for biology*
  Lever, J., Altman, R. B.
  2020
- **RedMed: Extending drug lexicons for social media applications.** *Journal of biomedical informatics*
  Lavertu, A., Altman, R. B.
  2019: 103307
- **High precision protein functional site detection using 3D convolutional neural networks.** *Bioinformatics (Oxford, England)*
  Torng, W., Altman, R. B.
  2019; 35 (9): 1503–12
- **Graph Convolutional Neural Networks for Predicting Drug-Target Interactions.** *Journal of chemical information and modeling*
  Torng, W. n., Altman, R. B.
  2019
- **Pocket similarity identifies selective estrogen receptor modulators as microtubule modulators at the taxane site.** *Nature communications*
  Lo, Y. C., Cormier, O. n., Liu, T. n., Nettles, K. W., Katzenellenbogen, J. A., Stearns, T. n., Altman, R. B.
  2019; 10 (1): 1033
- **A global network of biomedical relationships derived from text** *BIOINFORMATICS*
  Percha, B., Altman, R. B.
  2018; 34 (15): 2614–24
- **Data-Driven Prediction of Drug Effects and Interactions** *SCIENCE TRANSLATIONAL MEDICINE*
  Tatonetti, N. P., Ye, P. P., Daneshjou, R., Altman, R. B.
  2012; 4 (125)
- **Clinical assessment incorporating a personal genome** *LANCET*
  Ashley, E. A., Butte, A. J., Wheeler, M. T., Chen, R., Klein, T. E., Dewey, F. E., Dudley, J. T., Ormond, K. E., Pavlovic, A., Morgan, A. A., Pushkarev, D., Neff, N. F., Hudgins, et al
  2010; 375 (9725): 1525-1535
- **Optimizing Enterprise Referral Processing through Automated Fax Triage** *NEJM CATALYST INNOVATIONS IN CARE DELIVERY*
  Mui, D., Tran, J. L. A., Onofre, S., Ramirez, S., Singh, V., Lago, A., Ng-Thow-Hing, J., Lavertu, A., Kaushal, A., Altman, R., Pallas, J., Boosi, S., Gohil, et al
  2026; 7 (5)
- **Drug-Target Interaction Prediction with PIGLET.** *bioRxiv : the preprint server for biology*
  Carpenter, K. A., Altman, R. B.
  2026
- **Biological data governance in an age of AI.** *Science (New York, N.Y.)*
  Bloomfield, D., Black, J. R., Crook, O., Brandes, N., Hanke, M. S., Inglesby, T. V., Cicero, A., Pollack, R., Hernandez-Boussard, T., Imperiale, M. J., Altman, R. B., Pannu, J.
  2026; 391 (6785): 558-561
- **Publisher Correction: CRISPR-GPT for agentic automation of gene-editing experiments.** *Nature biomedical engineering*
  Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H. C., Johnson, W. A., Wang, X., Shah, M., Altman, R. B., Zhou, D., Wang, et al
  2025
- **Empirical Drug Dosage Validates Pharmacogenomic Associations in All of Us.** *Clinical and translational science*
  Matthias, J., Falaguera, M. J., Altman, R. B.
  2025; 18 (11): e70406
- **SubCell: Proteome-aware vision foundation models for microscopy capture single-cell biology.** *bioRxiv : the preprint server for biology*
  Gupta, A., Wefers, Z., Kahnert, K., Hansen, J. N., Misra, M. K., Leineweber, W., Cesnik, A., Lu, D., Axelsson, U., Ballllosera, F., Altman, R. B., Karaletsos, T., Lundberg, et al
  2025

- **Reframing Justice in Healthcare AI: An Ubuntu-Based Approach for Africa.** *Developing world bioethics*
  Ochasi, A., Mahamadou, A. J., Altman, R. B., Nkwocha, L. U.
  2025
- **Membrane-wide screening identifies potential tissue-specific determinants of SARS-CoV-2 tropism.** *PLoS pathogens*
  Dinesh, R. K., Wang, C., Qu, Y., Rustagi, A., Cousins, H., Zengel, J., Wang, X., Barnard, T. R., Johnson, W. A., Xu, G., Zhang, T., Magazine, N., Beck, et al
  2025; 21 (7): e1013157
- **A calcium-sensing receptor allelic series and underdiagnosis of genetically driven hypocalcemia.** *American journal of human genetics*
  Chang, J. B., Barnhill, C. P., Apostolov, A. M., Soliai, M. M., Hecker, J., Nierenberg, J. L., Stapleton Smith, L. M., Mathew, A. S., Zeng, X., Diao, J., Fernando, C. D., Chen, Q., Dulken, et al
  2025
- **Semi-supervised data-integrated feature importance enhances performance and interpretability of biological classification tasks.** *Bioinformatics (Oxford, England)*
  Kim, J. W., Altman, R. B.
  2025; 41 (Supplement_1): i373-i381
- **Identifying DNA methylation sites affecting drug response using electronic health record-derived GWAS summary statistics.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Smith, D. A., Arteaga, S. A., Sadler, M. C., Altman, R. B.
  2025; 30: 457-472
- **Detecting clinician implicit biases in diagnoses using proximal causal inference.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Liu, K., Altman, R., Syrgkanis, V.
  2025; 30: 330-345
- **CRISPR-GPT: LLM Agents for Automated Design of Gene-Editing Experiments**
  Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H., Johnson, W., Wang, X., Altman, R., Zhou, D., Wang, M., Cong, et al
  CELL PRESS.2025
- **Which social media platforms facilitate monitoring the opioid crisis?** *PLOS digital health*
  Carpenter, K. A., Nguyen, A. T., Smith, D. A., Samori, I. A., Humphreys, K., Lembke, A., Kiang, M. V., Eichstaedt, J. C., Altman, R. B.
  2025; 4 (4): e0000842
- **Pool PaRTI: A PageRank-Based Pooling Method for Identifying Critical Residues and Enhancing Protein Sequence Representations.** *bioRxiv : the preprint server for biology*
  Tartici, A., Nayar, G., Altman, R. B.
  2025
- **The E2F4 transcriptional repressor is a key mechanistic regulator of colon cancer resistance toirinotecan(CPT-11).** *bioRxiv : the preprint server for biology*
  Matsubara, J., Li, Y. F., Koul, S., Mukohyama, J., Valencia Salazar, L. E., Isobe, T., Qian, D., Clarke, M. F., Sahoo, D., Altman, R. B., Dalerba, P.
  2025
- **Heterogeneous network approaches to protein pathway prediction** *COMPUTATIONAL AND STRUCTURAL BIOTECHNOLOGY JOURNAL*
  Nayar, G., Altman, R. B.
  2024; 23: 2727-2739
- **Heterogeneous network approaches to protein pathway prediction.** *Computational and structural biotechnology journal*
  Nayar, G., Altman, R. B.
  2024; 23: 2727-2739
- **Databases of ligand-binding pockets and protein-ligand interactions.** *Computational and structural biotechnology journal*
  Carpenter, K. A., Altman, R. B.
  2024; 23: 1320-1338
- **Toward a framework for risk mitigation of potential misuse of artificial intelligence in biomedical research** *NATURE MACHINE INTELLIGENCE*

Trotsyuk, A. A., Waeiss, Q., Bhatia, R., Aponte, B. J., Heffernan, I. M. L., Madgavkar, D., Felder, R., Lehmann, L., Palmer, M. J., Greely, H., Wald, R., Goetz, L., Trengove, et al

2024

- **Which social media platforms facilitate monitoring the opioid crisis?** *medRxiv : the preprint server for health sciences*

  Carpenter, K. A., Nguyen, A. T., Smith, D. A., Samori, I. A., Humphreys, K., Lembke, A., Kiang, M. V., Eichstaedt, J. C., Altman, R. B.

  2024

- **Prospector Heads: Generalized Feature Attribution for Large Models & Data.** *ArXiv*

  Machiraju, G., Derry, A., Desai, A., Guha, N., Karimi, A. H., Zou, J., Altman, R. B., Ré, C., Mallick, P.

  2024

- **Unsupervised network learning enables systematic characterization of genetic risk pathways for primary open-angle glaucoma**

  Cousins, H., Altman, R. B., Pasquale, L. R.

  ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2024

- **Elucidating the semantics-topology trade-off for knowledge inference-based pharmacological discovery.** *Journal of biomedical semantics*

  Sosa, D. N., Neculae, G., Fauqueur, J., Altman, R. B.

  2024; 15 (1): 5

- **Computational Approaches to Drug Repurposing: Methods, Challenges, and Opportunities.** *Annual review of biomedical data science*

  Cousins, H. C., Nayar, G., Altman, R. B.

  2024

- **Leveraging large-scale biobank EHRs to enhance pharmacogenetics of cardiometabolic disease medications.** *medRxiv : the preprint server for health sciences*

  Sadler, M. C., Apostolov, A., Cevallos, C., Ribeiro, D. M., Altman, R. B., Kutalik, Z.

  2024

- **CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods** *GENOME BIOLOGY*

  Jain, S., Bakolitsa, C., Brenner, S. E., Radivojac, P., Moult, J., Repo, S., Hoskins, R. A., Andreoletti, G., Barsky, D., Chellapan, A., Chu, H., Dabbiru, N., Kollipara, et al

  2024; 25 (1): 53

- **CRISPR-GPT: an LLM agent for automated design of gene-editing experiments** *bioRxiv: the preprint server for biology*

  Qu, Y., Huang, K., Cousins, H., Johnson, W., Yin, D., Shah, M., Zhou, D., Altman, R., Wang, M., Cong, L.

  2024

- **DEEP LEARNING FOR LOCALIZED DETECTION OF OPTIC DISC HEMORRHAGES (vol 255, pg 161, 2023)** *AMERICAN JOURNAL OF OPHTHALMOLOGY*

  Brown, A. C., Cousins, H., Cousins, C. C., Esquenazi, K., Filipowicz, A., Barna, L., Kim, Y., Vinod, K., Chadha, N., Altman, R. B., Coote, M., Elze, T., Topouzis, et al

  2024; 257

- **A mitochondrial inside-out iron-calcium signal reveals drug targets for Parkinson's disease.** *Cell reports*

  Bharat, V., Durairaj, A. S., Vanhauwaert, R., Li, L., Muir, C. M., Chandra, S., Kwak, C. S., Le Guen, Y., Nandakishore, P., Hsieh, C. H., Rensi, S. E., Altman, R. B., Greicius, et al

  2023; 42 (12): 113544

- **Integrative analyses highlight functional regulatory variants associated with neuropsychiatric diseases.** *Nature genetics*

  Guo, M. G., Reynolds, D. L., Ang, C. E., Liu, Y., Zhao, Y., Donohue, L. K., Siprashvili, Z., Yang, X., Yoo, Y., Mondal, S., Hong, A., Kain, J., Meservey, et al

  2023

- **Explainable protein function annotation using local structure embeddings.** *bioRxiv : the preprint server for biology*

  Derry, A., Altman, R. B.

  2023

- **A Holy Grail - The Prediction of Protein Structure.** *The New England journal of medicine*

  Altman, R. B.

2023

- **Stronger regulation of AI in biomedicine.** *Science translational medicine*
  Trotsyuk, A. A., Federico, C. A., Cho, M. K., Altman, R. B., Magnus, D.
  2023; 15 (713): eadi0336
- **The phenotype-genotype reference map: Improving biobank data science through replication.** *American journal of human genetics*
  Bastarache, L., Delozier, S., Pandit, A., He, J., Lewis, A., Annis, A. C., LeFaive, J., Denny, J. C., Carroll, R. J., Altman, R. B., Hughey, J. J., Zawistowski, M., Peterson, et al
  2023
- **Associating biological context with protein-protein interactions through text mining at PubMed scale.** *Journal of biomedical informatics*
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PRESENTATIONS

- TedMed 2015 Talk: What really happens when you mix medications? - TedMED 2015 (11/2015 - 11/1/2015)
- TedxStanford Talk: Personlized prescriptions - Stanford (6/2013 - 6/2013)