




## 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 HAI and Professor, by courtesy, of Computer Science

 NIH Biosketch available Online

 Curriculum Vitae available Online

### CONTACT INFORMATION

#### • Alternate Contact

Tiffany Murray - Administrative Associate

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**Tel** 650-725-0659

### Bio

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#### 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, Medicine - Biomedical Informatics Research
- Professor, 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 Committee 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**

- 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](http://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

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### 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

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### COURSES

#### 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, Win, 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)

#### **2021-22**

- 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**

Johnny Powell

### **Doctoral Dissertation Reader (AC)**

Matthew Aguirre, Andy Chen, Rastko Ciric, Ibtihal Elfaki, Elliot Hershberg, Jessica Kain, Ziv Lautman, Trang Le, Samson Mataraso, Akshat Nigam, Courtney Smith

### **Postdoctoral Faculty Sponsor**

Abdoul Jalil Djiberou Mahamadou, Artem Trotsyuk

### **Doctoral Dissertation Advisor (AC)**

Stephanie Arteaga, Kristy Carpenter, Henry Cousins, Gowri Nayar, Issah Samori, Delaney Smith, Betty Xiong

### **Master's Program Advisor**

Cathy Hou, Abhi Kumar, Nikhil Lyles, Eric Pan, Ashley Pournamdari, Priyanka Shrestha, Neha Srivathsa, Serena Zhang

### **Undergraduate Major Advisor**

John Wang

### **Doctoral (Program)**

Yasa Baig, Erin Craig, Aviv Korman, Ashley Lewis, Kara Liu, Janella Schwab Lizarraga

## **GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS**

- Bioengineering (Phd Program)

- Biomedical Informatics (Masters Program)
- Biomedical Informatics (Phd Program)
- Biophysics (Phd Program)
- Genetics (Phd Program)

## Publications

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### PUBLICATIONS

- **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
- **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
- **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., Moul, J., Repo, S., Hoskins, R. A., Andreoletti, G., Barsky, D., Chellapan, A., Chu, H., Dabir, N., Kollipara, et al  
2024; 25 (1): 53
- **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*  
Sosa, D. N., Hintzen, R., Xiong, B., de Giorgio, A., Fauqueur, J., Davies, M., Lever, J., Altman, R. B.  
2023: 104474
- **Genetic Correlations Among Corneal Biophysical Parameters and Anthropometric Traits.** *Translational vision science & technology*  
Cousins, H. C., Cousins, C. C., Valluru, G., Altman, R. B., Liu, Y., Pasquale, L. R., Ahmad, S.  
2023; 12 (8): 8
- **Integrative analysis of functional genomic screening and clinical data identifies a protective role for spironolactone in severe COVID-19.** *Cell reports methods*  
Cousins, H. C., Kline, A. S., Wang, C., Qu, Y., Zengel, J., Carette, J., Wang, M., Altman, R. B., Luo, Y., Cong, L.  
2023; 3 (7): 100503
- **Deep learning for localized detection of optic disc hemorrhages.** *American journal of ophthalmology*  
Brown, A., Cousins, H., Cousins, C., Esquenazi, K., Elze, T., Harris, A., Filipowicz, A., Barna, L., Yonwook, K., Vinod, K., Chadha, N., Altman, R. B., Coote, et al  
2023
- **Network-based machine learning for gene prioritization in primary open-angle glaucoma**  
Cousins, H., Altman, R. B., Pasquale, L. R.  
ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2023
- **Association between spironolactone use and COVID-19 outcomes in population-scale claims data: a retrospective cohort study.** *medRxiv : the preprint server for health sciences*  
Cousins, H. C., Altman, R. B.  
2023
- **Using GPT-3 to Build a Lexicon of Drugs of Abuse Synonyms for Social Media Pharmacovigilance.** *Biomolecules*  
Carpenter, K. A., Altman, R. B.  
2023; 13 (2)
- **Multilingual translation for zero-shot biomedical classification using BioTranslator.** *Nature communications*  
Xu, H., Woicik, A., Poon, H., Altman, R. B., Wang, S.  
2023; 14 (1): 738
- **Mapping transcriptional heterogeneity and metabolic networks in fatty livers at single-cell resolution.** *iScience*  
Coassolo, L., Liu, T., Jung, Y., Taylor, N. P., Zhao, M., Charville, G. W., Nissen, S. B., Yki-Jarvinen, H., Altman, R. B., Svensson, K. J.  
2023; 26 (1): 105802
- **Genetic association studies using disease liabilities from deep neural networks.** *medRxiv : the preprint server for health sciences*  
Yang, L., Sadler, M. C., Altman, R. B.  
2023
- **Detecting Contradictory COVID-19 Drug Efficacy Claims from Biomedical Literature**

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- Sosa, D. N., Suresh, M., Potts, C., Altman, R. B., Boyd-Graber, J., Okazaki, N., Rogers, A.  
ASSOC COMPUTATIONAL LINGUISTICS-ACL.2023: 694-713
- **Promises and challenges in pharmacoepigenetics.** *Cambridge prisms, Precision medicine*  
Smith, D. A., Sadler, M. C., Altman, R. B.  
2023; 1: e18
  - **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
  - **Gene set proximity analysis: expanding gene set enrichment analysis through learned geometric embeddings, with drug-repurposing applications in COVID-19.** *Bioinformatics (Oxford, England)*  
Cousins, H., Hall, T., Guo, Y., Tso, L., Tzeng, K. T., Cong, L., Altman, R. B.  
2022
  - **Functional genomics of OCTN2 variants informs protein-specific variant effect predictor for Carnitine Transporter Deficiency.** *Proceedings of the National Academy of Sciences of the United States of America*  
Koleske, M. L., McInnes, G., Brown, J. E., Thomas, N., Hutchinson, K., Chin, M. Y., Koehl, A., Arkin, M. R., Schlessinger, A., Gallagher, R. C., Song, Y. S., Altman, R. B., Giacomini, et al  
2022; 119 (46): e2210247119
  - **A cis-regulatory lexicon of DNA motif combinations mediating cell-type-specific gene regulation.** *Cell genomics*  
Donohue, L. K., Guo, M. G., Zhao, Y., Jung, N., Bussat, R. T., Kim, D. S., Neela, P. H., Kellman, L. N., Garcia, O. S., Meyers, R. M., Altman, R. B., Khavari, P. A.  
2022; 2 (11)
  - **A network paradigm predicts drug synergistic effects using downstream protein-protein interactions.** *CPT: pharmacometrics & systems pharmacology*  
Wilson, J. L., Steinberg, E., Racz, R., Altman, R. B., Shah, N., Grimes, K.  
2022
  - **Contexts and contradictions: a roadmap for computational drug repurposing with knowledge inference.** *Briefings in bioinformatics*  
Sosa, D. N., Altman, R. B.  
2022
  - **Genetic Correlations between Corneal Biophysical Parameters and Anthropomorphic Traits**  
Cousins, H., Cousins, C., Valluru, G., Liu, Y., Ahmad, S., Altman, R. B., Pasquale, L. R.  
ASSOC RESEARCH VISION OPHTHALMOLOGY INC.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
  - **Protein sequence design with a learned potential.** *Nature communications*  
Anand, N., Eguchi, R., Mathews, I. I., Perez, C. P., Derry, A., Altman, R. B., Huang, P.  
2022; 13 (1): 746
  - **Training data composition affects performance of protein structure analysis algorithms.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Derry, A., Carpenter, K. A., Altman, R. B.  
2022; 27: 10-21
  - **Recommendations for achieving interoperable and shareable medical data in the USA.** *Communications medicine*  
Szarfman, A., Levine, J. G., Tonning, J. M., Weichold, F., Bloom, J. C., Soreth, J. M., Geanacopoulos, M., Callahan, L., Spotnitz, M., Ryan, Q., Pease-Fye, M., Brownstein, J. S., Ed Hammond, et al

2022; 2: 86

- **Challenges and opportunities in network-based solutions for biological questions.** *Briefings in bioinformatics*  
Guo, M. G., Sosa, D. N., Altman, R. B.  
2021
- **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., Karkani, J., Altman, R. B.  
2021; 12 (1): 5556
- **PhenClust, a standalone tool for identifying trends within sets of biological phenotypes using semantic similarity and the Unified Medical Language System metathesaurus.** *JAMIA open*  
Wilson, J. L., Wong, M., Stepanov, N., Petkovic, D., Altman, R.  
2021; 4 (3): ooab079
- **Genome-wide Association Studies in Pharmacogenomics.** *Clinical pharmacology and therapeutics*  
McInnes, G., Yee, S. W., Pershad, Y., Altman, R. B.  
2021
- **Distinct clinical phenotypes for Crohn's disease derived from patient surveys.** *BMC gastroenterology*  
Liu, T., Han, L., Tilley, M., Afzelius, L., Maciejewski, M., Jelinsky, S., Tian, C., McIntyre, M., 23andMe Research Team, Bing, N., Hung, K., Altman, R. B., Agee, M., et al  
2021; 21 (1): 160
- **Opportunities and challenges for the computational interpretation of rare variation in clinically important genes.** *American journal of human genetics*  
McInnes, G., Sharo, A. G., Koleske, M. L., Brown, J. E., Norstad, M., Adhikari, A. N., Wang, S., Brenner, S. E., Halpern, J., Koenig, B. A., Magnus, D. C., Gallagher, R. C., Giacomini, et al  
2021; 108 (4): 535–48
- **Large-scale labeling and assessment of sex bias in publicly available expression data.** *BMC bioinformatics*  
Flynn, E., Chang, A., Altman, R. B.  
2021; 22 (1): 168
- **Search and visualization of gene-drug-disease interactions for pharmacogenomics and precision medicine research using GeneDive.** *Journal of biomedical informatics*  
Wong, M., Previde, P., Cole, J., Thomas, B., Laxmeshwar, N., Mallory, E., Lever, J., Petkovic, D., Altman, R. B., Kulkarni, A.  
2021: 103732
- **Modeling drug response using network-based personalized treatment prediction (NetPTP) with applications to inflammatory bowel disease.** *PLoS computational biology*  
Han, L., Sayyid, Z. N., Altman, R. B.  
2021; 17 (2): e1008631
- **A New Era in Pharmacovigilance: Towards real world data and digital monitoring.** *Clinical pharmacology and therapeutics*  
Lavertu, A., Vora, B., Giacomini, K. M., Altman, R., Rensi, S.  
2021
- **Repurposing Biomedical Informaticians for COVID-19.** *Journal of biomedical informatics*  
Sosa, D. N., Chen, B., Kaushal, A., Lavertu, A., Lever, J., Rensi, S., Altman, R.  
2021: 103673
- **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)

- **Drug Response Pharmacogenetics for 200,000 UK Biobank Participants**  
McInnes, G., Altman, R. B., Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2021: 184-195
- **Pharmacogenetics at Scale: An Analysis of the UK Biobank.** *Clinical pharmacology and therapeutics*  
McInnes, G., Lavertu, A., Sangkuhl, K., Klein, T. E., Whirl-Carrillo, M., Altman, R. B.  
2020
- **Transfer learning enables prediction of CYP2D6 haplotype function.** *PLoS computational biology*  
McInnes, G., Dalton, R., Sangkuhl, K., Whirl-Carrillo, M., Lee, S., Tsao, P. S., Gaedigk, A., Altman, R. B., Woodahl, E. L.  
2020; 16 (11): e1008399
- **OrderRex clinical user testing: a randomized trial of recommender system decision support on simulated cases.** *Journal of the American Medical Informatics Association : JAMIA*  
Kumar, A., Aikens, R. C., Hom, J., Shieh, L., Chiang, J., Morales, D., Saini, D., Musen, M., Baiocchi, M., Altman, R., Goldstein, M. K., Asch, S., Chen, et al  
2020
- **MARS: discovering novel cell types across heterogeneous single-cell experiments.** *Nature methods*  
Brbic, M., Zitnik, M., Wang, S., Pisco, A. O., Altman, R. B., Darmanis, S., Leskovec, J.  
2020
- **PharmGKB tutorial for pharmacogenomics of drugs potentially used in the context of COVID-19.** *Clinical pharmacology and therapeutics*  
Huddart, R., Whirl-Carrillo, M., Altman, R. B., Klein, T. E.  
2020
- **Sex-specific genetic effects across biomarkers.** *European journal of human genetics : EJHG*  
Flynn, E., Tanigawa, Y., Rodriguez, F., Altman, R. B., Sinnott-Armstrong, N., Rivas, M. A.  
2020
- **Scientific considerations for global drug development.** *Science translational medicine*  
Wilson, J. L., Cheung, K. W., Lin, L., Green, E. A., Porras, A. I., Zou, L., Mukanga, D., Akpa, P. A., Darko, D. M., Yuan, R., Ding, S., Johnson, W. C., Lee, et al  
2020; 12 (554)
- **Gaussian embedding for large-scale gene set analysis** *NATURE MACHINE INTELLIGENCE*  
Wang, S., Flynn, E. R., Altman, R. B.  
2020; 2 (7): 387-95
- **Gaussian Embedding for Large-scale Gene Set Analysis.** *Nature machine intelligence*  
Wang, S., Flynn, E. R., Altman, R. B.  
2020; 2 (7): 387-395
- **Homology modeling of TMPRSS2 yields candidate drugs that may inhibit entry of SARS-CoV-2 into human cells.** *ChemRxiv : the preprint server for chemistry*  
Rensi, S., Keys, A., Lo, Y. C., Derry, A., McInnes, G., Liu, T., Altman, R.  
2020
- **PharmGKB summary: lamotrigine pathway, pharmacokinetics and pharmacodynamics.** *Pharmacogenetics and genomics*  
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- TedxStanford Talk: Personalized prescriptions - Stanford (6/2013 - 6/2013)