BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Russ B. Altman	Professor of Bioengineering, Genetics, & Medicine (and of Computer Science, by courtesy)
eRA COMMONS USER NAME Altman.Russ	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Harvard College	A.B.	06/83	Biochemistry & Molecular Biology
Stanford University Medical School	Ph.D.	06/89	Medical Information Sciences
Stanford University Medical School	M.D.	06/90	Medicine

A. Personal Statement

I am a Professor of Bioengineering, Genetics, Medicine and (by courtesy) Computer Science. My area of professional expertise is bioinformatics, the creation of methods to analyze molecular data of importance to problems in medicine and health. My specific application area of interest is drug action, including molecular analysis of protein structure and dynamics, datamining for discovery of unexpected drug actions, functional genomics (particularly pharmacogenomics) to understand drug action and the impact of human variation on drug response. The PharmGKB resource (http://www.pharmgkb.org/) is the premier repository of curated information about how human genetic variation impacts drug-response phenotypes. We use the contents of PharmGKB to create new applications in data mining, drug discovery and personal genomics. The Simbios resource is focused on physics-based simulation of biological structures, and I focus on GPCR structure and dynamics. I helped create simtk.org and my lab uses it as a place to store and disseminate source code for software, important data sets, and other information for distribution.

B. Positions and Honors.

RESEARCH AND/OR PROFESSIONAL EXPERIENCE

1982 Undergraduate Research Assistant. Supervisor: Prof. William N. Lipscomb, Nobel Laureate, Harvard Department of Chemistry
1982-1983 Undergraduate Research Assistant. Supervisor: Prof. Stephen C. Harrison, Harvard Department of Biochemistry and Molecular Biology
1984-1988 Graduate Research Assistant to Bruce G. Buchanan, Stanford Dept. of Computer Science
1989-1992 Post-Doctoral fellow (part time). Prof. Oleg Jardetzky, Stanford Magnetic Resonance Laboratory
1990-1992 Intern and Resident, Stanford University Medical Center
1992 Assistant Professor of Medicine (& Computer Science, by courtesy), Stanford University
1993-1997 Member, Executive Steering Committee, San Diego Supercomputer Center
1994-1995 Organizing Committee, 2nd & 3rd Intl. Conf. on Intelligent Systems for Molecular Biology
1996- Organizing Committee, Pacific Symposium on Biocomputing
1996 Founding Board of Directors, International Society for Computational Biology (ISCB)
1997 Molecular Science Thrust Leader, National Partnership for Advanced Computer Infrastructure
1999 Associate Professor of Medicine (& Computer Science, by courtesy) tenure, Stanford University
2000- Director, Biomedical Informatics Program, Stanford University
2000-2002 President, International Society for Computational Biology
2003 Professor of Genetics, Bioengineering, & Medicine (& Comp. Sci., by courtesy) Stanford University
2007 Chair, Department of Bioengineering, Stanford University
2009-2012 Guidant Chair of Bioengineering, Stanford University
2012 President-Elect, American Society for Clinical Pharmacology and Therapeutics
2013 President, American Society for Clinical Pharmacology and Therapeutics
2013- Chair, Science Board to the Food and Drug Administration

HONORS AND AWARDS

1983 Phi Beta Kappa, Harvard College Chapter
1983 Summa Cum Laude, Harvard College
1983 NIH Medical Scientist Training Program pre-doctoral fellowship at Stanford

1987 Departmental Ph.D. oral exams passed "with high distinction"
1991 Howard Hughes Fellowship for Physicians
1993 Charles E. Culpeper Scholarship in Medical Science
1996 National Science Foundation CAREER Award
1997 U.S. Presidential Early Career Award for Scientists and Engineers (NIH)
1998 Western Society for Clinical Investigation, Annual Young Investigator Award
1998 Fellow, American College of Medical Informatics
1999 Fellow, American College of Physicians
2000 Stanford Graduate Teaching Award
2005 General Internal Medicine, Honorable Mention for Clinical Teaching
2009 Fellow, American Institute of Medical and Biological Engineering
2009 Member, Institute of Medicine of the National Academies
2010 Fellow, International Society for Computational Biology

C. Selected peer-reviewed publications (in chronological order).

1. Raychaudhuri S, Chang JT, Imam F, Altman RB. The computational analysis of scientific literature to define and recognize gene expression clusters. Nucleic Acids Res. 2003 Aug 1;31(15):4553-60. PMID: 12888516, PMCID: PMC169898
2. Wu S, Liang MP, Altman RB. The SeqFEATURE library of 3D functional site models: comparison to existing methods and applications to protein function annotation. Genome Biol. 2008 Jan 16;9(1):R8. PMID: 18197987, PMCID: PMC2395245
3. Hansen N, Brunak S, Altman R. Generating Genome-Scale Candidate Gene Lists for Pharmacogenomics. Clin Pharmacol Ther. 2009 Apr 15. PMID: 19369935, PMCID: PMC2729176
4. Liu T, Altman RB. Prediction of calcium-binding sites by combining loop-modeling with machine learning. BMC Struct Biol. 2009 Dec 11;9:72. PMID: 20003365, PMCID: PMC2808310
5. Glazer DS, Radmer RJ, Altman RB. Improving structure-based function prediction using molecular dynamics. Structure. 2009 Jul 15;17(7):919-29. PMID: 19604472, PMCID: PMC2748254
6. Coulet A, Shah NH, Garten Y, Musen M, Altman RB. Using text to build semantic networks for pharmacogenomics. J Biomed Inform. 2010 Aug 17. PMID: 20723615, PMCID: PMC2991587
7. Engreitz JM, Daigle BJ Jr, Marshall JJ, Altman RB. Independent component analysis: Mining microarray data for fundamental human gene expression modules. J Biomed Inform. 2010 Jul 7. PMID: 20619355, PMCID: PMC2991480
8. Wu S, Liu T, Altman RB. Identification of recurring protein structure microenvironments and discovery of novel functional sites around CYS residues. BMC Struct Biol. 2010 Feb 2;10:4. PMID: 20122268, PMCID: PMC2833161.
9. Tatonetti NP, Fernald GH, Altman RB.A novel signal detection algorithm for identifying hidden drug-drug interactions in adverse event reports. J Am Med Inform Assoc. 2011 Jun 14. PMID: 21676938, PMCID: PMC3240755.
10. Capriotti E, Altman RB. Improving the prediction of disease-related variants using protein three-dimensional structure. BMC Bioinformatics. 2011;12 Suppl 4:S3. PMCID: PMC3194195.
11. Tang GW, Altman RB. Remote thioredoxin recognition using evolutionary conservation and structural dynamics. Structure. 2011 Apr 13;19(4):461-70. PMID: 21481770, PMCID: PMC3075543.
12. Liu T, Altman RB. Using multiple microenvironments to find similar ligand-binding sites: application to kinase inhibitor binding. PLoS Comput Biol. 2011 Dec;7(12):e1002326. PMCID: PMC3248393.
13. Delp SL, Ku JP, Pande VS, Sherman MA, Altman RB. Simbios: an NIH national center for physics-based simulation of biological structures. J Am Med Inform Assoc. 2012 Mar-Apr;19(2):186-9. PMCID: PMC3277621
14. Tatonetti NP, Ye PP, Daneshjou R, Altman RB. Data-driven prediction of drug effects and interactions. Sci Transl Med. 2012 Mar 14;4(125):125ra31. PMCID: PMC3382018.
15. Lahti JL, Tang GW, Capriotti E, Liu T, Altman RB. Bioinformatics and variability in drug response: a protein structural perspective. J R Soc Interface. 2012 Jul 7;9(72):1409-37. PMCID: PMC3367825.

D. Research Support

2 R01 LM05652 (PI: Altman) 09/01/04 – 08/31/14
NIH / NLM
Annotating Functional Sites in 3D Biological Structures
The main goal is to apply methods and develop methods for annotating biological structures so that active sites, binding sites and interaction sites in biological structures can be automatically identified and annotated.
Role: PI

5 U01 GM061374 (PI: Altman) 08/08/05-06/30/15
NIH / NIGMS
The Stanford Pharmacogenetics Knowledge Base
The Stanford PharmacoGenetic Knowledge Base (PharmGKB), an integrated data resource to support the NIGMS Pharmacogenetic Research Network and Database Initiative focuses on how genetic variation contributes to variation in the response to drugs, and will produce data from a wide range of sources, therefore interlinking genomic, molecular, cellular and clinical information about gene systems important for modulating drug responses.
Role: PI

U54 GM072970 (PI: Altman) 09/15/04-8/31/14
NIH/NIGMS
Physics-Based Simulation of Biological Structures
The goal of this project is to establish a National Center for Simulation of Biological Structures (Simbios). The center develops, disseminates, and supports a simulation toolkit (SimTK) that enables users to create and visualize accurate models and simulations of biological structures at a large range of scales–from molecules to organisms.
Role: PI

PARSA Community Foundation (PI: Altman) 11/01/10 - 10/31/13
Iranian Genome Project
An initiative for better understanding of the genes of the Iranian population.
Role: PI

1 P01 CA139490 (PI: Clarke) 05/27/10-4/30/14
NIH / NCI
Tumor Stem Cells in Cancer Biology, Prevention, and Therapy
Investigate methods for analyzing high throughput data for understanding tumor biology.
Role: Co-Investigator

NIH/University of Florida 08/01/10 - 07/31/15
Subcontract
Pharmacogenomic Evaluation of Antihypertensive Drugs
Role: PI

1 P50 MH094267
NIH/University of Chicago 09/22/11 - 06/30/16
Subcontract
Conte Center for Computational Systems Genomics of Neuropsychiatric Phenotypes
The goal is to consolidate in a single modeling framework a number of disparate approaches for analysis of complex neuropsychiatric disorders.
Role: PI

U10 HL105198
NIH/University of Maryland, Baltimore 8/30/2011 – 6/30/2015
Subcontract

Translational Pharmacogenetics Program
The overall goal of the TPP is to operationalize the work of the PGRN Clinical Pharmacogenomics Implementation Committee (CPIC) by translating widely accepted actionable pharmacogenetic discoveries into real-world clinical practice.
Role: PI

U54-HL117798
NIH/University of Pennsylvania 08/01/2012-05/31/2014
Subcontract
Personalization of Therapeutic Efficacy and Risk
The goal is to build an integrated network of genes, drugs and phenotypes that will be an important asset in integrating information from multiple integrated efforts to understand the individual response to NSAIDs.
Role: PI