

BIOGRAPHICAL SKETCH

NAME Russ B. Altman		POSITION TITLE Professor of Bioengineering, Genetics, & Medicine (and of Computer Science, by courtesy)	
eRA COMMONS USER NAME Altman.Russ			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Harvard College	A.B.	1983	Biochemistry & Molecular Biology
Stanford University Medical School	Ph.D.	1989	Medical Information Sciences
Stanford University Medical School	M.D.	1990	Medicine

A. 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, Stanford University Medical School
- 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 (and Computer Science, by courtesy) with tenure, Stanford University Medical School
- 2000-2002 President, International Society for Computational Biology
- 2004 Professor of Genetics, Bioengineering, & Medicine (and Computer Science, by courtesy) with tenure, Stanford University Medical School
- 2007 Chair, Department of Bioengineering, Stanford University

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

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

- Bagley, SC, Altman, RB, "Characterizing the microenvironment surrounding protein sites." Protein Science, 4(4) p. 622-635, 1995.
- Wei, L, Huang, ES, Altman, RB, "Are Predicted Structures Good Enough to Preserve Functional Sites?" Structure 7 p. 643-650, 1999.
- Altman, RB, Bada, M, Chai, XJ, Carillo, MW, Chen, RO, Abernethy, NF. "RiboWeb: An Ontology-Based System for Collaborative Molecular Biology." IEEE Intelligent Systems and Their Applications 14(5):68-76, 1999.
- Troyanskaya OG, Garber ME, Brown PO, Botstein D, Altman RB. Nonparametric methods for identifying differentially expressed genes in microarray data. Bioinformatics. 2002 Nov;18(11):1454-61.
- Chang JT, Schutze H, Altman RB. Creating an online dictionary of abbreviations from MEDLINE. J Am Med Inform Assoc. 2002 Nov-Dec;9(6):612-20
- Yeh I, Karp PD, Noy NF, Altman RB. Knowledge acquisition, consistency checking and concurrency control for Gene Ontology (GO). Bioinformatics. 2003 Jan 22;19(2):241-8.
- Troyanskaya, OG, Dolinski, K, Owen, AB, Altman, RB, Botstein, D. A Bayesian framework for combining heterogeneous data sources for gene function prediction (in *Saccharomyces cerevisiae*). Proc Natl Acad Sci U S A. 2003 Jul 8;100(14):8348-53. Epub 2003 Jun 25.
- 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.
- Gabashvili IS, Whirl-Carrillo M, Bada M, Banatao DR, Altman RB. Ribosomal dynamics inferred from variations in experimental measurements. RNA. 2003 Nov;9(11):1301-7.
- Dugan JM, Altman RB Using surface envelopes for discrimination of molecular models. Protein Sci. 2004 Jan;13(1):15-24.
- Chang JT, Schutze H, Altman RB. GAPSCORE: finding gene and protein names one word at a time. Bioinformatics. 2004 Jan 22;20(2):216-25.
- Lin Z, Owen AB, Altman RB. Genetics. Genomic research and human subject privacy. Science. 2004 Jul 9;305(5681):183.
- Kohane, I., Altman, R. Health-information altruists--a potentially critical resource. N Engl J Med. 2005 Nov 10;353(19):2074-7.
- Kohane, I, Masys, D, Altman, R. The incidentalome: a threat to genomic medicine. JAMA. 2006 Jul 12;296(2):212-5. Erratum in: JAMA. 2006 Sep 27;296(12):1466.
- Laederach, A, Shcherbakova, I, Liang, M, Brenowitz, M, Altman, R. Local kinetic measures of macromolecular structure reveal partitioning among multiple parallel pathways from the earliest steps in the folding of a large RNA molecule. J Mol Biol. 2006 May 12;358(4):1179-90.
- Tang S, Liao JC, Dunn AR, Altman RB, Spudich JA, Schmidt JP. Predicting allosteric communication in myosin via a pathway of conserved residues. J Mol Biol. 2007 Nov 9;373(5):1361-73. Epub 2007 Aug 31.
- 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
- Poulter, GL, Rubin, DL, Altman, RB, Seoighe, C. MScanner: a classifier for retrieving Medline citations. BMC Bioinformatics. 2008 Feb 19;9:108.
- Hillenmeyer, ME, Fung, E, Wildenhain, J, Pierce, SE, Hoon, S, Lee, W, Proctor, M, St Onge, RP, Tyers, M, Koller, D, Altman, RB, Davis RW, Nislow C, Giaever G. The chemical genomic portrait of yeast: uncovering a phenotype for all genes. Science. 2008 Apr 18;320(5874):362-5.
- Altman RB. PharmGKB: a logical home for knowledge relating genotype to drug response phenotype. Nat Genet. 2007 Apr;39(4):426.
- Jonikas MA, Radmer RJ, Laederach A, Das R, Pearlman S, Herschlag D, Altman RB. Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters. RNA. 2009 Feb;15(2):189-99.
- Ebert JC, Altman RB. Robust recognition of zinc binding sites in proteins. Protein Sci. 2008 Jan;17(1):54-65.
- Hansen N, Brunak S, Altman R. Generating Genome-Scale Candidate Gene Lists for Pharmacogenomics. Clin Pharmacol Ther. 2009 Apr 15.
- Glazer DS, Radmer RJ, Altman RB. Improving structure-based function prediction using molecular dynamics. Structure, *in press*, 2009.

C. Research Support

ACTIVE

2 R01 LM05652-11 (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 GM061374-07 (PI: Altman) 08/08/05-06/30/10
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 GM072970-03 (PI: Altman) 09/15/04-07/31/10
NIH / NCRR

Physics-based simulation of biological structures

The main goals are to create a follow on to the planning grant listed above that will focus on physics-based simulation of biological structures ranging from atomic scale to organismal scale. This is a response to the roadmap call for proposals in National Centers for Biomedical Computing.

Role: PI

1 P01 GM66275-04 (PI: Herschlag) 06/06/03-05/31/10
NIH / NIGMS (Project Director of project 3: Altman)
(Project Director of project 8: Altman)

Folding of Tetrahymena Group 1 Ribozyme

This grant addresses the mechanism by which the RNA folds to active and inactive structures using a battery of physical and computational approaches.

Role: Co-PI

COMPLETED

Roche Bioscience (PI: Altman) 11/1/06 - 10/31/08
Computational Genetic Analysis of Large Data Sets

Small collaboration to fund travel for a student working on methods for analyzing mouse pharmacogenomics.

University of Edinburgh (PI: Altman) 10/01/02-03/31/07
Enhancing the Ability of the Biomedical Literature to Support Biomedical Discovery

The goal of this project is to assess the incremental benefit of adding shallow parsing and language models to statistical natural language processing techniques in assigning functions to genes based on text. Edinburgh has expertise with language models and will collaborate to re-analyze the data published by Stanford to see if performance can be improved with their technologies.

Role: PI

5 P20 EM000265-03 (PI: Altman) 09/20/01-02/28/07

NIH / NIBIB

Planning the Stanford Center for Biomedical Computation

The major goal of this proposal is to plan the process for the Stanford Center for Biomedical Computation (CBMC) with joint leadership from the Schools of Medicine and Engineering; the CBMC comprises structures that will allow Stanford scientists to create new methodologies in biomedical computation and apply these to the most difficult unsolved problems in biomedicine. The CBMC mission includes the creation of shared computational infrastructure, joint training of young scientists, and interdisciplinary collaborations falling outside traditional departmental boundaries.

Role: PI

Burroughs Wellcome Fund (PI: Altman)

07/01/99-06/30/05

Programs in Emerging Infectious Diseases

A Knowledge Base of Biological Function for Malaria

The main goal of this project is to build a bioinformatics repository of information about the functions (both known and inferred) of *Plasmodium falciparum*; as the genome sequencing projects for other organisms have progressed, it has become clear that the volume of information available from these projects stresses current computational methods for organization and analysis and the malaria community can be the first to have an integrated, knowledge-based environment for organizing the data into computer-readable and human-browsable formats.

Role: PI

5 R01 LM06244-05 (PI: Altman)

05/15/96-11/14/02

NIH NLM

Representing Biological Data for Modeling Function

Building upon my recent work in producing preliminary models of the 30S subunit we are building a system called RiboWeb to focus on the structure of the 30S ribosomal subunit in procaryotes, and to make this resource available to our collaborators in the field of ribosomal structural biology on the Internet, and to test it by creating new models of the 30S subunit that better integrate the existing body of structural data.

Role: PI

DBI-9600637 (PI: Altman)

08/15/96-07/31/02

NSF

Representing Biological Structure Information for Multiple Uses

This grant focused on developing methods for building ontologies of biological experimental data, with a particular emphasis on representations that allowed re-use. The application area was RNA structure.

Role: PI