CURRICULUM VITAE

Russ Biagio Altman, MD, PhD

BIRTHPLACE: Brooklyn, New York
ETHNICITY: White
NATIONALITY: U.S.A.

LICENSURE:

1991	California State Medical Board, License G072413

EDUCATION:

1983 A.B.	Biochemistry and Molecular Biology, Harvard College; Cambridge, Massachusetts
1989 Ph.D.	Medical Information Sciences, Stanford University; Stanford, California
1990 M.D.	Stanford University; Stanford, California

POSTDOCTORAL TRAINING:

1990 - 91	Internship, Internal Medicine, Stanford University Medical School; Stanford, California
1991 - 92	Residency, Internal Medicine, Stanford University Medical School; Stanford, California

BOARD ELIGIBILITY:

1992	Diplomate, American Board of Internal Medicine, Certificate #142388. Certified 1992, Recertified 2002, 2012.
2014	Diplomate, American Board of Preventive Medicine, Clinical Informatics. Certified 2014.

NON-ACADEMIC APPOINTMENTS:

1982	Undergraduate Research Assistant, Professor William N. Lipscomb (Nobel Laureate), Department of Chemistry, Harvard University; Cambridge, Massachusetts
1982–83	Undergraduate Research Assistant, Professor Stephen C. Harrison, Department of Biochemistry and Molecular Biology, Harvard University; Cambridge, Massachusetts
1984–89	Doctoral Research, Preceptors: Professor Bruce G. Buchanan, Stanford Departments of Computer Science and Medicine; and Professor Oleg Jardetzky, Stanford Magnetic Resonance Laboratory; Stanford, California
1992	Research Assistant, Post-Doctoral, Professor Oleg Jardetzky, Stanford Magnetic Resonance Laboratory; Stanford, California
7/1/93–6/30/96	Assistant Director, Stanford Medical Scientist Training Program, Stanford University; Stanford, California

7/1/96–6/30/00	Associate Director, Stanford Medical Scientist Training Program, Stanford University; Stanford, California
4/1/00–	Director, Stanford Biomedical Informatics Training Program

ACADEMIC APPOINTMENTS:

9/1/92–4/30/99	Assistant Professor of Medicine (General Internal Medicine), Stanford University School of Medicine, Stanford, CA
1/1/93–4/30/99	Assistant Professor of Computer Science (by courtesy), Stanford University, Stanford, CA.
5/1/99–8/31/01	Associate Professor of Medicine (Medical Informatics, General Internal Medicine) with tenure
5/1/99 – 9/30/05	Associate Professor of Computer Science (by courtesy)
9/1/01–10/31/04	Associate Professor of Genetics and Medicine (Medical Informatics, General Internal Medicine), Stanford University School of Medicine, Stanford, CA
11/1/04–12/21/06	Professor of Genetics, Bioengineering, and Medicine (Medical Informatics, General Internal Medicine), and Computer Science, by courtesy, Stanford University School of Medicine, Stanford, CA
1/1/07–6/30/12	Professor & Chair, Department of Bioengineering. Professor, Departments of Genetics, Medicine (Biomedical Informatics, General Internal Medicine), and (by courtesy) Computer Science. Schools of Engineering & Medicine, Stanford University, CA
7/1/12-present	Professor, Departments of Bioengineering, Genetics, Medicine (Biomedical Informatics, General Internal Medicine), and (by courtesy) Computer Science. Schools of Engineering & Medicine, Stanford University, CA
7/1/13-present	Kenneth Fong Professor

HONORS AND AWARDS:

1979	Awards for General Excellence, Regis High School; NY, NY.
1979	Award for Excellence in Classical Greek Translation, Regis High School; New York, NY
1983	Phi Beta Kappa, Harvard College Chapter; Boston, MA
1983	Summa Cum Laude, Harvard College; Boston, MA
1983	Medical Scientist Training Program, NIH Predoctoral Fellowship
1987	Medical Information Sciences, Ph.D. oral exam passed *with distinction*
1991	Howard Hughes Institute Post-Doctoral Fellowship
1992	Finalist, Stanford Hospital Medical Resident Teaching Award
1993	Charles E. Culpeper Foundation Medical Scholar
1994	Nominated, Albert Gores University Teaching Award
1996	National Science Foundation CAREER Award
1997	Presidential Early Career Award for Scientists and Engineers

1998	Stanford School of Medicine Hume Faculty Scholar
1998	Western Society for Clinical Investigation, Young Investigator Award
1998	Fellow, American College of Physicians
1998	Fellow, American College of Medical Informatics
2000	Stanford Graduate Teaching Award (first time awarded)
2005	General Internal Medicine, Honorable Mention for Clinical Teaching
2009	Fellow, American Institute of Medical and Biological Engineering
2009	Member, Institute of Medicine (IOM) of the National Academies
2010	Fellow, International Society for Computational Biology
2014	Stanford Medical School Mentorship Award
2014	Fellow, American Association for the Advancement of Science
2014	Patient Service Award, Center for Pharmacogenomics & Individualized Therapy, University of North Carolina

MEMBERSHIPS:

1987-	American Association for Artificial Intelligence (AAAI)
1991- 1993	Biomatrix Society
1992- 2000	American Federation for Clinical Research (AFCR)
1992-	American Medical Informatics Association (AMIA)
1992-	American Association for the Advancement of Science (AAAS)
1992-	American College of Physicians
1993-	Protein Society
1993-	Physicians for a National Health Program
1993-	California Physician's Alliance
1994-	Association for Computing Machinery
1995- 1996	American Educational Research Association
1995-2010	RNA Society
1996-	Institute of Electrical and Electronic Engineers (IEEE)
1997-	International Society for Computational Biology (ISCB)
1997-2001	Society for General Internal Medicine (SGIM)
2003-	American Society for Clinical Pharmacology and Therapeutics (ASCPT)
2007	American Institute for Medical and Biological Engineering

RESEARCH INTERESTS:

Bioinformatics
Biomedical Informatics
Pharmacogenomics
Physics-based simulation
Functional genomics
Structural genomics
Probabilistic representations of molecular structure
Analysis of the biomedical literature
High performance computing

COMMITTEES, BOARDS, AND CONSULTANTSHIPS:

1991	Committee for Residency Training and Clinical Service
1991-1992	Physicians Advisory Committee to Stanford Hospital Information Systems
1991-	Admissions Committee, Stanford Medical Information Sciences Training Program (now Biomedical Informatics Training Program)
1992-1998	Consultant, Medicus Venture Partners; Menlo Park, California
1992-2001	Admissions Committee, Stanford Medical Scientist Training Program
1993-1997	Stanford University Department of Medicine Credentials Committee
1993-1997	Steering Committee, San Diego Supercomputer Center
1993-1994	Organizing Committee, International Symposium on NMR (in honor of Oleg Jardetzky)
1993-1994	Organizing Committee, Second International Conference on Intelligent Systems for Molecular Biology; Stanford CA
1994-1995	Organizing Committee, Third International Conference on Intelligent Systems for Molecular Biology; Cambridge, England
1995-1997	Executive Committee, San Diego Supercomputer Center
1995-1997	University Senate Committee on Computing and Academic Information Systems
1995-1997	Advisory Committee to Chairman of Department of Medicine
1995-1997	Steering Committee, Intelligent Systems for Molecular Biology
1995-1998	Faculty Senate Committee on Academic Information Systems (C-ACIS)
1995-1997	President's Commission on Technology in Teaching and Learning, Stanford University
1996-	Organizing Committee, Pacific Symposium on Biocomputing
1996	LCME Accreditation Project, Library and Computer Resources Subcommittee & Graduate Education Subcommittee
1997	Organizer, RNA Society Workshop on Online Resources for RNA Science
1997	Dean's Task Force on Alumni, Stanford Medical School
1997	Dean's Task Force on the Future of PhD Education, Stanford Medical School
1997- 2005	Board of Directors, International Society for Computational Biology
1997-2000	Chairman, Publications Committee, International Society for Computational Biology
1997-1998	Program Committee, AMIA Fall Symposium, 1998
1998-	Editorial Board, Journal of American Medical Informatics Association
1998-	Editorial Board, Bioinformatics
1998-2002	Thrust Leader, Molecular Sciences, NSF NPACI grant to San Diego Supercomputer Center
1999-2000	Member, National Research Council panel on Internet & Health

2000-2005	Associate Editor, Bioinformatics
2000-2002	President, International Society for Computational Biology
2000-2010	Steering Committee member and Coordinating Committee member, NIH Pharmacogenetics Research Network.
2000	Review panel, Burroughs Wellcome Functional Genomics Initiative
2000-2001	Advisor, Cambridge HealthTech Inc. Professional Meetings.
2001-	Editorial Board, Pharmacogenetics & Genomics
2003-	Associate Editor, Briefings in Bioinformatics
2003-2010	Associate Editor, Genomics
2005-2007	Chair, Stanford Digital Repository Faculty Advisory Committee
2006-	Editor, Journal of Biomedical Informatics
2007-2011	Advisor, 23andme, Inc.
2007-	Scientific Advisor, Chicago Biomedical Consortium
2008-2015	Editorial Board, BMC Medical Genomics
2008-	Editorial Board, Genome Medicine
2008-	Associate Editor, PLoS Computational Biology
2008-	Member, MIT Biological Engineering Visiting Committee
2009	Ad hoc Advisor, Novartis Pharmaceuticals
2009-2011	Steering Committee, IEEE/ACM Transactions on Computational Biology and Bioinformatics
2011	Editorial Board, Clinical Pharmacology & Therapeutics
2012	Co-Founder and Scientific Advisor, Personalis Inc.
2012	President-elect, American Society for Clinical Pharmacology and Therapeutics
2013-	Review panel, Burroughs Wellcome Foundation Careers at the Scientific Interface (CASI) Program
2013-2014	President, American Society for Clinical Pharmacology and Therapeutics
2013-2014	Chair, Science Board to the Food and Drug Administration Commissioner
2012-	Advisory Committee to NIH Director (ACD), Francis Collins
2014-	Vanderbilt University, Biomedical Science Advisory Board
2014-	Faculty Director, 100 Year Study of Artificial Intelligence (AI100)
2015-	Director, Stanford Predictives and Diagnostics Accelerator
2015-	Acting Chief, Systems Medicine Division, Department of Pediatrics
2016-	International Advisory Board, UK Biobank
2016 -	Founding Co-Editor, Annual Review of Biomedical Data Science
2016-	Co-Chair, Institute of Medicine Drug Forum
2016-	Co-Chair, Burroughs Wellcome Foundation Careers at the Scientific Interaface (CASI) Program
2017-	International Advisory Board, Swiss Personalized Health Network

BIBLIOGRAPHY

PEER REVIEWED JOURNAL PUBLICATIONS:

1. **Altman, R.**, Ladner, J., Lipscomb, W. (1982). Quartenary Structural Changes in Aspartat Carbamoyltransferase of E. Coli at pH 8.3 and pH 5.8. *Biochemical and Biophysical Research Communications*, 108(2), 592–596.
2. **Altman, R.** and Jardetzky, O. (1986). New Strategies for the Determination of Macromolecular Structure in Solution. *Journal of Biochemistry*, 100, 1403–1423.
3. Duncan, B., Buchanan, B., Hayes-Roth, B., Lichtarge, O., **Altman, R.**, Brinkley, J., Hewett, M., Cornelius, C., Jardetzky, O. (1986). PROTEAN: A New Method of Deriving Solution Structures of Proteins. *Bulletin of Magnetic Resonance,* 8, 111–119.
4. Brinkley, J., **Altman, R.**, Duncan, B., Buchanan, B., Jardetzky, O. (1988). The Heuristic Refinement Method for the Derivation of Protein Solution Structures: Validation on Cytochrome-b562. *Journal of Chemical Info. & Computer Sciences*, 28(4), 194–210.
5. Jardetzky, O., **Altman, R.**, Madrid, M. (1989). NMR and Protein Structure. *Biofizika*, 34(5), 763–771.
6. Carrara, E., Brinkley, J., Cornelius, C., **Altman, R.**, Brugge, J., Pachter, R., Buchanan, B., Jardetzky, O. (1990). PROTEAN - Part I: Generating Ensembles of Stylized Molecular Fragments using Uncertain Constraints. *Quantative Computer Program Exchange Bulletin*, 10(4), Program 596.
7. **Altman, R.**, Pachter, R., Carrara, E., Jardetzky, O. (1990). PROTEAN - Part II: Molecular Structure Determination from Uncertain Data. *Quantitative Computer Program Exchange Bulletin,* 10(4), Program 596.
8. Arrowsmith, C., Pachter, R., **Altman, R.**, Iyer, S., Jardetzky, O. (1990). Sequence Specific 1H-NMR Assignments and Secondary Structure of E. Coli trp Repressor. *Biochemistry*, 29, 6332–6341.
9. Pachter, R., **Altman, R.**, Jardetzky, O. (1990). The Dependence of a Protein Solution Structure on the Quality of the Input NMR data. Application of the Double-Iterated Kalman Filter Technique to Oxytocin. *Journal of Magnetic Resonance*, 89, 578–584.
10. Pachter, R., **Altman, R.**, Czaplicki, J., Jardetzky, O. (1991). Comparison of the NMR Solution Structure of Cyclosporin A Determined by Different Techniques. *Journal of Magnetic Resonance*, 92, 468–479.
11. Arrowsmith, C., Pachter, R., **Altman, R.**, Jardetzky, O. (1991). The Solution Structures of E. Coli trp Repressor and trp Aporepressor at an Intermediate Resolution. *European Journal of Biochemistry*, 202(2), 53–66.
12. Liu, Y., Zhao, D., **Altman, R.**, Jardetzky, O. (1992). A Systematic Comparison of Three Structure Determination Methods from NMR Data: Dependence upon Quality and Quantity of Data. *Journal of Biomolecular NMR*, 2, 373–388.
13. **Altman, R.**, Pachter, R., Jardetzky, O. (1993). Structural Uncertainty of Proteins in Solution by NMR. A Re-evaluation of the Structure of the Lac Repressor Headpiece, *Journal of Applied Magnetic Resonance*, 4, 441–460.

14. **Altman, R.**, Hughes, C., Jardetzky, O. (1994). Compositional Characteristics of Disordered Regions in Proteins. *Protein and Peptide Letters*, 1(2), 120–127.
15. **Altman, R.**, Hughes, C., and Gerstein, M. (1995). Methods for Displaying Macromolecular Structural Uncertainty: Application to the Globins. *Journal of Molecular Graphics*, 13, 142–152.
16. **Altman, R.** (1995). A Probabilistic Approach to Determining Biological Structure: Integrating Uncertain Data Sources. *International Journal of Human Computer Studies*, 42, 593–616.
17. Bagley, S. and **Altman, R.** (1995). Characterizing the Microenvironment Surrounding Protein Sites. *Protein Science*, 4, 622–635.
18. Gerstein, M. and **Altman, R.** (1995). Average Core Structures and Variability Measures for Protein Families: Application Immunoglobulins. *Journal of Molecular Biology*, 251, 161–175.
19. Gerstein, M. and **Altman, R.** (1995). Using a Measure of Structural Variation to Define a Core for the Globins. *CABIOS Computer Applications in the Biosciences*, 11, 633–644.
20. **Altman, R.** and Merino, J. (1996). Images in clinical medicine. Knotted umbilical cord.. *New England Journal of Medicine,* 334(9), 573.
21. Chen, C., Chen, R., **Altman, R.** (1996). Constraining Volume by Matching Moments of a Distance Distribution. *Computer Applications in the Biosciences,* 12(4), 319–326.
22. Fink, D., Chen, R., Noller, H., **Altman, R.** (1996). Computational Methods for Defining the Allowed Conformational Space of 16S rRNA Based on Chemical Footprinting Data. *RNA* 2(9), 851–866. PMCID: PMC1369421.
23. Bagley, S. and **Altman, R.** (1996). Conserved Features in the Active Site of Nonhomologous Serine Proteases. *Folding & Design*, 1(5), 371–379.
24. Felciano, R. and **Altman, R.** (1996). LAMPREY: Tracking Users on the World Wide Web. In: Proceedings of the 1996 AMIA Fall Symposium (pp. 757-761). Philadelphia: Hanley & Belfus Publishers. PMCID: PMC2233185.
25. Wei, L., **Altman, R.**, Chang, J. (1997). Using the Radial Distribution of Physical Features to Compare Amino Acid Environments. In: R. Altman, K. Dunker, L. Hunter, T. Klein (eds.), Pacific Symposium on Biocomputing 1997 (pp. 465–476). Singapore: World Scientific Publishing Co.
26. **Altman, R.**, Abernethy, N., Chen, R. (1997), Standardized Representations of the Literature: Combining Diverse Sources of Ribosomal Data. In: Proceedings of the Fifth International Conference on Intelligent Systems in Molecular Biology (pp. 15-24). Menlo Park: AAAI Press.
27. Chen, R., Felciano, R., **Altman, R.** (1997). RiboWeb: Linking Structural Computations to a Knowledge Base of Published Experimental Data. In: Proceedings of the Fifth International Conference on Intelligent Systems in Molecular Biology (pp. 84-87). Menlo Park: AAAI Press.
28. Schmidt, R., Gerstein, M., **Altman, R.** (1997). LPFC: An Internet Library of Protein Family Core Structures. *Protein Science,* 6, 246–248. PMCID: PMC2143520.
29. **Altman, R.** (1997). Informatics in the Care of Patients: Ten Notable Challenges. *Western Journal of Medicine* 166(2), 118–122. PMCID: PMC1304028

30. Felciano, R., Chen, R., **Altman, R.** (1997). RNA Secondary Structure as a Reusable Interface to Biological Information Resources, *Gene* 190, 59–70.
31. Chen, C., Singh, J., **Altman, R.** (1998). The Hierarchical Organization of Molecular Structure Computations. *Journal of Computational Biology,* 5(3), 409–422.
32. Gennari, J., Cheng, H., **Altman, R.**, Musen M. (1998). Reuse, CORBA, and Knowledge-Based Systems, *International Journal of Human-Computer Studies,* 49(4), 523–546.
33. **Altman, R.** (1998). A Curriculum for Bioinformatics: The Time is Ripe. *Bioinformatics,* 14(7), 549–550.
34. Wei, L. and **Altman, R.** (1998). Recognizing Protein Binding Sites Using Statistical Descriptions of Their 3D Environments. In: R. Altman, K. Dunker, L. Hunter, T. Klein (eds.), Pacific Symposium on Biocomputing 1998 (pp. 497–508). Singapore, World Scientific Publishing Co.
35. Felciano, R. and **Altman, R.** (1998). Graphical Style Sheets: Towards Reusable Representations of Biomedical Graphics. In: Computer-Human Interactions (CHI) Conference (pp. 48–49). New York: ACM Press.
36. Chen, C., Singh, J., **Altman, R.** (1998). The Hierarchical Organization of Molecular Structure Computation. In: RECOMB-98 (pp. 51–59). New York: ACM Press.
37. Schmidt, J., Chen, C., Cooper, J., **Altman, R.** (1998). A Surface Measure for Probabilistic Structural Computations. In: ISMB 98 (pp. 148-156). Menlo Park: AAAI Press.
38. Liu, X. and **Altman, R.** (1998). Updated Bibliography Using the RELATED ARTICLES Function within PubMed. In: 1998 AMIA Fall Symposium (pp. 750-754). Philadelphia: Hanley & Belfus Publishers.PMCID: PMC2232162
39. Hon, L., Abernethy, N., Brusic, V., Chai, J., **Altman, R.** (1998). MHCWeb: Converting a WWW Database into a Knowledge-based Collaborative Environment. In: 1998 AMIA Fall Symposium (pp. 947-951). Philadelphia: Hanley & Belfus Publishers. PMCID: PMC2232088.
40. Abernethy, N. and **Altman, R.** (1998). SOPHIA: Providing Basic Knowledge Services with a Common DBMS. In: A. Borgida, V. Chaudhri, M. Staudt (eds.), KRDB-98 Conference (pp. 1-6).
41. **Altman, R.** (1998). Bioinformatics in Support of Molecular Medicine. In: 1998 AMIA Fall Symposium (pp. 53–61). Philadelphia: Hanley & Belfus Publishers.
42. Wei, L., Chang, J., **Altman, R.** (1998). Probabilistic and Statistical Descriptions of Protein Structure. In: S. Salzberg, D. Searls, and S. Kasif (eds.), Computational Biology: Pattern Analysis and Machine Learning Methods (pp. 207-225). London, UK: Elsevier Science.
43. Chen, C., Singh, J., **Altman, R.** (1999). Using Imperfect Secondary Structure Predictions to Improve Molecular Structure Computations, *Bioinformatics*, 15(1), 53-65.
44. **Altman, R.**, Chen, R., Abernethy, N., Bada, M. (1999). RiboWeb: An Ontology-Based System for Collaborative Molecular Biology. *IEEE Intelligent Systems and Their Application,* 14(5), 68-76.

45. Abernethy, N. and **Altman, R.** (1999). SOPHIA: A Flexible, Web-Based Knowledge Server. *IEEE Intelligent Systems and Their Applications,* 14(4), 79-85.
46. Chen, R. and **Altman, R.** (1999). Automated Diagnosis of Data-Model Conflicts Using Metadata. *J Am Med Inform Assoc*, 6(5), 374-392. PMCID: PMC61381.
47. Wei, L., Huang, E., **Altman, R.** (1999). Are Predicted Structures Good Enough to Preserve Functional sites? *Structure (with Folding & Design),* 7(6), 643-650.
48. **Altman, R.** (1999). AI in medicine: The spectrum of challenges from managed care to molecular medicine. *AI Magazine*, 20(3), 67-77.
49. Bada, M. and **Altman, R.** (2000). Computational Modeling of Structured Experimental Data. *Methods in Enzymology*, 317, 470-491.
50. Joseph, S., Carrillo, M., Kondo, H., Noller, H., **Altman, R.** (2000). Calculation of the relative geometry of tRNAs in the ribosome from directed hydroxyl-radical probing data. *RNA* 6, 220-232. PMCID: PMC1369908.
51. **Altman, R.** (2000). The interactions between clinical informatics and bioinformatics: a case study. *J Am Med Inform Assoc.,* 7(5), 439-443. PMCID: PMC79038.
52. Raychaudhuri, S., Sutphin, P., Chang, J., **Altman, R.** (2001). Basic microarray analysis: grouping and feature reduction. *Trends in Biotechnology,* 19(5), 189-193.
53. **Altman, R.** (2000). Biomedical computation at Stanford University: A larger umbrella for the future. *MD Comput*., 17(6), 35-37.
54. Raychaudhuri, S., Stuart, J., Liu, X., Small, P., & **Altman, R.** (2000). Pattern recognition of genomic features with microarrays: Site typing of Mycobacterium tuberculosis strains. In: ISMB 2000 (pp. 286-295). Menlo Park: AAAI Press. PMCID: PMC2865887.
55. Raychuaduri, S., Stuart, J. & **Altman, R.** (2000). Principal components analysis to summarize microarray experiments: application to sporulation time series. In: R. Altman, K. Dunker, L. Hunter, K. Lauderdale, T. Klein (eds.), Pacific Symposium on Biocomputing 2000 (pp. 455-466). Singapore: World Scientific Publishing, Co. PMCID: PMC2669932.
56. Pulavarthi, P., Chiang, R., & **Altman, R.** (2000). Generating interactive molecular documentaries using a library of graphical actions. In: R. Altman, K. Dunker, L. Hunter, K. Lauderdale, T. Klein (eds.), Pacific Symposium on Biocomputing 2000 (pp. 266-277). Singapore: World Scientific Publishing, Co.
57. **Altman, R.** (2000). Bioinformatics. In: T. Shortliffe, G. Wiederhold, and L. Fagan (eds.), Medical Informatics: Computer Applications in Health Care (pp. 638-660), Heidelberg: Springer-Verlag.
58. Troyanskaya, O., Cantor, M., Sherlock G., Brown P., Hastie, T., Tibshirani, R., Botstein, D., **Altman, R.** (2001). Missing value estimation methods for DNA microarrays. *Bioinformatics,* 17(0), 1-6.
59. **Altman, R.**, Raychaudhuri, S. (2001). Whole-genome expression analysis: challenges beyond clustering. *Curr Opin Struct Biol*., 11(3), 340-347.
60. Williams, G., Dugan, J., **Altman, R.** (2001). Constrained global optimization for estimating molecular structure from atomic distances. *J Comput Biol*., 8(5), 523-547.

61. Garber, M., Troyanskaya, O., Schluens, K., Petersen, S., Thaesler, Z., Pacyna-Gengelbach, M., van de Rijn, M., Rosen, G., Perou, C., Whyte, R., **Altman, R.**, Brown, P., Botstein, D., Petersen, I. (2001). Diversity of gene expression in adenocarcinoma of the lung. *Proc Natl Acad Sci USA*, 98(24), 13784-13789. PMCID: PMC61119.
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63. **Altman, R.** (2001). Challenges for intelligent systems in biology. *IEEE Intelligent Systems*, 16(6), 14-18.
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65. Waugh, A., Williams, G., Wei, L. & **Altman, R.** (2001). Using metacomputing tools to facilitate large scale analyses of biological databases. In: R. Altman, K. Dunker, L. Hunter, K. Lauderdale, T. Klein (eds.), Pacific Symposium on Biocomputing 2001 (pp. 360-371). Singapore: World Scientific Publishing, Co.
66. Chang, J., Raychaudhuri, S. & **Altman, R.** (2001). Including biological literature improves homology search. In: R. Altman, K. Dunker, L. Hunter, K. Lauderdale, T. Klein (eds.), Pacific Symposium on Biocomputing 2001 (pp. 374-383). Singapore: World Scientific Publishing, Co. PMCID: PMC2671075.
67. Hewett, M., Oliver, D., Rubin, D., Easton, K., Stuart, J., **Altman, R.**, Klein, T. PharmGKB: the Pharmacogenetics Knowledge Base. *Nucleic Acids Res*., 30(1), 163-165. PMCID: PMC99138.
68. Raychaudhuri, S., Chang, J., Sutphin, P., **Altman, R.** (2002). Associating genes with gene ontology codes using a maximum entropy analysis of biomedical literature. *Genome Res*., 12(1), 203-214. PMCID: PMC155261.
69. **Altman, R.**, Klein, T. (2002). Challenges for biomedical informatics and pharmacogenomics. *Annu Rev Pharmacol Toxicol*., 42, 113-133.
70. Rubin, D., Shafa, F., Oliver, D., Hewett, M., **Altman, R.** (2002). Representing genetic sequence data for pharmacogenomics: an evolutionary approach using ontological and relational models. *Bioinformatics*, 18 Suppl 1, S207-S215.
71. Waugh, A., Gendron, P., **Altman, R.**, Brown, J., Case, D., Gautheret, D., Harvey, S., Leontis, N., Westbrook, J., Westhof, E., Zuker, M., Major, F. (2002). RNAML: a standard syntax for exchanging RNA information. *RNA*, 8(6), 707-717. PMCID: PMC1370290.
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73. Kivi, M., Liu, X., Raychaudhuri, S., **Altman, R.**, Small, P. (2002). Determining the genomic locations of repetitive DNA sequences with a whole-genome microarray: IS6110 in Mycobacterium tuberculosis. *J Clin Microbiol*., 40(6), 2192-2198. PMCID: PMC130717.

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75. Han, J., **Altman, R.**, Kumar, V., Mannila, H., Pregibon, D. (2002). Emerging Scientific Applications in Data Mining. *Communications of the ACM*, 45(8), 54-58.
76. Chang, J., Schuetze, H., **Altman, R.** (2002). Creating an Online Dictionary of Abbreviations from MEDLINE. *J Am Med Inform Assoc.*, Nov-Dec;9(6), 612-620. PMCID: PMC349378.
77. Troyanskaya, O., Garber, M., Brown, P., Botstein, D., **Altman, R.** (2002). Nonparametric Methods for Identifying Differentially Expressed Genes in Microarray Data. *Bioinformatics*, 18(11), 1454-1461.
78. Yeh, I., Karp, P., Noy, N., **Altman, R.** (2002). Knowledge Acquisition, Consistency Checking and Concurrency Control for Gene Ontology. *Bioinformatics*, 19(2), 241-248.
79. Chang, J., **Altman, R.** (2002). Promises of text processing: natural language processing meets AI. *Drug Discov Today*, 7(19), 992-993.
80. Raychaudhuri, S., Schuetze, H., **Altman, R.** (2002). Using text analysis to identify functionally coherent gene groups. *Genome Research*, 12(10), 1582-1590. PMCID: PMC187532.
81. Rubin, D., Hewett, M., Oliver, D., Klein, T., **Altman, R.** (2002). Automating data acquisition into ontologies from pharmacogenetics relational data sources using declarative object definitions and XML. In: R. Altman, K. Dunker, L. Hunter, K. Lauderdale, T. Klein (eds.), Pacific Symposium on Biocomputing 2002 (pp. 88-99). Singapore: World Scientific Publishing, Co.
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83. Lin, Z., Hewett, M., **Altman, R.** (2002). Using Binning to Maintain Confidentiality of Medical Data. In: 2002 AMIA Fall Symposium (pp. 454-458). Philadelphia: Hanley & Belfus Publishers. PMCID: PMC2244360.
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INVITED LECTURES AND PRESENTATIONS (selected from over 100):

1. "AI in Medicine: Challenges from managed care to molecular medicine." Annual Conference of American Association for Artificial Intelligence, Invited Talk, Madison, WI, July 29, 1998.
2. "Bioinformatics in support of molecular medicine." Annual Conference of the American Medical Informatics Association, Invited Talk, Orlando, FL, November 9, 1998.
3. "Challenges for Discovery in Molecular Biology." Knowledge Discovery and Data Mining Conference, 2001, San Francisco, CA, August 28, 2001.
4. "Challenges for Knowledge Management in Bioinformatics." IEEE Computer Society Bioinformatics Conference, August 16, 2002.
5. "AI in Biomedicine: helping scientists reason about genomes, drugs and diseases." American Association for Artificial Intelligence (AAAI) 2004, San Jose, CA, July 28, 2004.
6. "Challenges for Informatics & Medicine in the Post-Genome Era." Medinfo 2004, San Francisco, CA, September 10, 2004.
7. "Building genotype-phenotype data resources for pharmacogenomics." Frontiers in Bioinformatics: Unsolved Problems and Challenges, Arthur M. Sackler Colloquia of the National Academy of Sciences, Irvine, CA, October 16, 2004.
8. "Challenges for knowledge management in biomedical informatics." IEEE Computational Systems Bioinformatics Conference, Stanford, CA, August 11, 2005.
9. "PharmGKB: is sharing pharmacogenomics information worthwhile?" Pharmacogenomics Meeting at Sanger Centre/Cold Spring Harbor, Hinxton, UK. September 15, 2005.
10. "Simbios: creating an infrastructure for physics-based simulation of biological structure." American Medical Informatics Association (AMIA) Annual Meeting, Washington, DC, October 24, 2005.
11. "Annual Review of Translational Bioinformatics." American Medical Informatics Association (AMIA) Summit on Translational Bioinformatics, San Francisco, CA, March 12, 2008.
12. "Annual Review of Translational Bioinformatics." American Medical Informatics Association (AMIA) Summit on Translational Bioinformatics, San Francisco, CA, March 17, 2009.
13. "Annual Review of Translational Bioinformatics." American Medical Informatics Association (AMIA) Summit on Translational Bioinformatics, San Francisco, CA. March 12, 2010.
14. "Translational Bioinformatics: Challenges for the AMIA community." Semi-Plenary Session, American Medical Informatics Association Fall Symposium, Washington, DC. November 10, 2008.
15. "Genes & Drugs." Columbia University Department of Biomedical Informatics Colloquium, New York, Oct 16, 2009.
16. "Systems approaches for Pharmacogenomics." Scripps Genomic Medicine Conference, San Diego, CA, March 6, 2010.

17. “Translational Bioinformatics Year-in-Review.” American Medical Informatics Association (AMIA) Joint Summits on Translational Science, San Francisco, CA, March 9, 2011
18. “7th annual Grant R. Wilkinson Distinguished Lecture in Clinical Pharmacology.” Vanderbilt University, Nashville, TN, April 14, 2011.
19. "The emerging network of data for understanding the interactions of genes and drugs.” Dewitt Stetten Jr. 2011 Lecture, NIGMS, October 12, 2011.
20. “Translational Bioinformatics Year-in-Review.” American Medical Informatics Association (AMIA) Joint Summits on Translational Science, San Francisco, CA, March 21, 2012
21. “Integrating Multiple Sources of Information to Understand Drug Action: From Molecular Structure to Clinical Population Data.” American Society for Clinical Pharmacology & Therapeutics (ASCPT) and Food and Drug Administration William B. Abrams Lecture, FDA White Oak Campus, Silver Spring, MD, March 23, 2012.
22. "Understanding drug action over 17 orders of magnitude—from molecular to global." Mario Stefanelli Memorial Lecture, The National Congress of Italian Group of Bioengineering Annual Meeting, Rome, Italy, June 28, 2012.
23. "Dealing with biomedical knowledge explosion for better healthcare: identifying actionable knowledge items at the point of care." International Center for Scientific Debate (Inbiomedvision), Barcelona, Spain, July 3, 2012
24. Three invited lectures at the Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) 2012, Long Beach, CA, July 15-17, 2012.
25. “The Network of Data for Understanding Drug Response.” The Oxford-Stanford Conference on Big Data: Challenges & Opportunities for Human Health, Oxford University, Oxford, United Kingdom, November 29, 2012.
26. “Translational Bioinformatics Year-in-Review.” AMIA Joint Summits on Translational Science, San Francisco, CA, March 20, 2013
27. "Systems pharmacology methods for linking drugs to genetic networks." Leon I Goldberg Memorial Lectures in Clinical Pharmacology, Department of Medicine, University of Chicago, Chicago, IL, December 10, 2013.
28. “Big data for drug repurposing, druggability, drug design & side effect prediction.” The Flexner Discovery Series, Vanderbilt University Medical Center, Nashville, TN, February 6, 2014.
29. “Translational Bioinformatics Year-in-Review.” AMIA Joint Summits on Translational Science, San Francisco, CA, April 9, 2014
30. “Informatics for understanding drug response at all scales.” 2014 International Society for Computational Biology Fellows Keynote, Boston, MA, July 15, 2014.
31. “Translational Bioinformatics Year-in-Review.” AMIA Joint Summits on Translational Science, San Francisco, CA, March 26, 2015
32. “Translational Bioinformatics Year-in-Review.” AMIA Joint Summits on Translational Science, San Francisco, CA, March 21, 2016

PATENTS

1. Tatonetti, N., **Altman, R**., Fernald, G. *Signal detection algorithms to identify drug effects and drug interactions.* April 5, 2016. US Patent 9,305,267 B2.