

Curriculum Vitae

GILL BEJERANO

Assistant Professor, Dept. of Developmental Biology

Assistant Professor, Dept. of Computer Science

Stanford University

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A) ACADEMIC HISTORY

UNIVERSITIES AND DEGREES

Faculty of Science, Hebrew University, Jerusalem, Israel:

Three majors B.Sc. in Mathematics, Physics, and Computer Science (1992-1994; 1995-1997). Degree Average: 97/100.

M.Sc. studies, Computer Science Department. (1997-1999)

Advisor: Prof. Naftali Tishby. Courses average: 98/100.

Direct Ph.D., School of Computer Science & Engineering. (1999-2004)

Advisors: Prof. Naftali Tishby, School of Computer Science & Engineering,
Prof. Hanah Margalit, Hadassah Medical School.

Title: "Automata learning and stochastic modeling for biosequence analysis"

Courses average: 96/100.

ACADEMIC SCHOLARSHIPS AND HONORS

University tuition scholarship for high school and entry exams achievements, Hebrew

University (1992-1993).
 Rector Prize for undergraduate achievements, Hebrew University (1993).
 Dean's List for undergraduate achievements, Faculty of Science, Hebrew University (1993, 1994, 1996)
 Intel-Dean award for achievements, Intel and Faculty of Science, Hebrew University (1996).
 Member of the "Amirim" program for excellent student (1993-1994;1995-1997)
 B.Sc. *Summa Cum Laude* (1997)
 Graduate studies scholarship for achievements, Hebrew University (1998, 1999).
 Passed the qualification exam for a direct Ph.D. program (1999)
 Tuition scholarship, Rachel and Salim Banin fund (1999)
 Best paper by a young scientist award, 3rd annual international conference on research in computational molecular biology (1999)
 Rector Prize for graduate achievements, Hebrew University (1999)
 Levi Eshkol PhD fellowship recipient, Israeli Ministry of Science (1999-2002).
 Best poster award, 4th annual Israeli bioinformatics symposium (2002)
 Best paper by a young scientist award, 7th annual international conference on research in computational molecular biology (2003)

POSTDOCTORAL

Postdoc, School of Engineering, University of California, Santa Cruz, USA.
 Mentor: HHMI investigator Prof. David Haussler. (2003-2007).

OTHER STUDY AND RESEARCH OPPORTUNITIES

Advanced bioinformatic techniques in genomics, transcriptomics and proteomics, EMBO Practical Course, Linnaeus Centre for Bioinformatics, Sweden (2001)
 The GIF-Leibniz Workshop on Machine Learning for Bioinformatics, Germany (2000)
 Training and Research on Advanced Computing Systems program, The Edinburgh Parallel Computing Centre, Scotland (2000)
 Machine Learning and Applications, Advanced Course in Artificial Intelligence, Greece (1999)
 Thematic Summer in Mathematical Biology workshop on Genomics, Pacific Institute for the Mathematical Sciences, Canada (1999)
 Annual Complex Systems Summer School, Santa Fe Institute, New Mexico, USA (1998)
 Annual Karyn Kupcinet International Science School, Weizmann Institute, Israel (1994)

B) EMPLOYMENT HISTORY

1993 – 1994 Physics teacher. Mekif Gilo secondary school, Jerusalem.
 Part of an educational betterment project.
 1995 – 1996 Lecturer in Computer Science, Machon Ashrot . Programmers courses for the Israeli Ministry of Employment & Welfare, and the private sector.
 1996 – 1999 Lecturer, Computer Science Department, Open University, Israel.
 1997 – 1999 Teaching Assistant (frontal) to Prof. Catriel Beerli, Computer Science Department, Hebrew University, Israel.
 1997 – 2000 Lecturer, Jerusalem center for professional computer studies, Open University, Israel.
 1999 – 2001 Lecturer, Computer Science Department, Hadassah Academic College, Israel.

- 2000 – 2003 Senior Lecturer, Software Engineering Department, Jerusalem Academic College of Engineering, Israel.
- 2003 – 2007 Postdoc, School of Engineering, University of California, Santa Cruz, USA.
Mentor: Prof. David Haussler.
- 01/02/2007- Assistant Professor, Department of Developmental Biology and Department of Computer Science, Stanford University, California, USA.

C) PROFESSIONAL ACTIVITIES

Workshop Organizer:

Barbados workshop on Genomics and Gene Regulation: Development, Barbados 2007

Technical Advisory Board: Numenta 2008 - 2011

Program Committee Member:

IEEE symposium on biological data visualization (BioVis) 2012

Int'l conf. on Intelligent Systems for Molecular Biology (ISMB) 2004, 2007, 2009

Int'l conf. on Research in Computational Molecular Biology (RECOMB) 2007, 2009

Automated Function Prediction Special Interest Group (AFP-SIG) 2005, 2006

Italian Bioinformatics Symposium (BITS) 2007

Editorial Board: GENE 2007 – 2008

PLoS Genetics, guest associated editor, 2012

Service as Journal Scientific Reviewer:

Nature	Bioinformatics
Science	Journal of Computational Biology
Cell	Journal of Virology
Nature Biotechnology	IEEE/ACM Transactions Comp. Biology & Bioinformatics
Nature Genetics	IEEE Transactions on Signal Processing
Nature Reviews Genetics	IEEE Signal Processing Letters
Genome Research	Acta Biotheoretica
Trends in Genetics	BMC Bioinformatics
PLoS Biology	Journal of Computational and Graphical Statistics
PLoS Genetics	Journal of Proteome Research
PLoS Computational Biology	British Journal of Mathematical and Statistical Psychology
Gene	Carcinogenesis
Nucleic Acids Research	etc.

D) POST-DEGREE HONORS AND AWARDS

SciFoo Camp (Nature, O'Reilly, Google) Invitee, 2006.

Edward Mallinckrodt, Jr. Foundation Junior Faculty Grant recipient, 2007

Japanese-American National Academy of Science Kavli Symposium Invitee, 2007

Searle Scholar, Searle Scholars Program, 2008

Young Investigator Award, Human Frontier Science Program, 2008

Fellow, Alfred P. Sloan Foundation, 2008

Tomorrow's Principal Investigator, Genome Technology magazine, 2008

Okawa Foundation Research Grant recipient, 2008
Packard Fellowship for Science and Engineering, 2008
Microsoft New Faculty Fellowship, 2009
Stanford High Performance Computing Day keynote speaker, 2010
University of Chicago Committee on Genetics, Genomics & Systems Biology student invited speaker, 2010
Pinkham Basic Sciences Lectureships invited speaker, 2011
Weizmann Institute Student Conference invited speaker, 2012

ADDITIONAL ACTIVE GRANTS

NIH / NICHD R-01 Multiple PI (Ahituv / Bejerano; Scored 122/1.6%), 2009
NIH / NHGRI R-01 Multiple PI (Bejerano / Ahituv), 2009
NSF “Emerging Frontiers of the Science of Information” Science and Technology Center (STC; Stanford team: Goldsmith / Bejerano / Weissman), 2010

ADDITIONAL COMPLETED GRANTS

Bioinformatics specialist support (Crabtree / Bejerano), 2009
KAUST Research Grant 2008-09
Bio-X IIP4 (Baker / Bejerano / Penn), 2009
Burroughs Wellcome Preterm Disease Planning (Baker/Bejerano/McKenney/Palmer/Penn), 2009

INVITED PAPERS AND LECTURES (SINCE 2005)

Bay Area Bioinformatics Discussion Group, Stanford, California. 2005
“Ultraconservation and Function in the Human Genome”
Washington University Genetics Department, St. Louis, Missouri.
“Ultraconserved Elements in the Human Genome”
Applied Biosystems, California.
“Conservation and function in the human genome”

NSF Advisory Committee, Princeton, New Jersey. 2006
“Deciphering the human genome - computational insights & opportunities”
Google, California.
“Ultraconservation and Living Fossils: Mysteries of the Human Genome”
INSERM Workshop on Identification of Non-Coding Funct. Regions in Genomes, France.
“The Human Genome: Computational Insights & Challenges”
Int'l Conf. on Genomic Impact of Eukaryotic Transposable Elements, California.
“Origins of ultraconservation and distal cis-regulation in vertebrates”
Genentech, California
“Dark Matter! On the Evolution & Function of Conserved Elements in the Human Genome”

Tokyo Institute of Technology, Japan. 2007
“Dispensability of Mammalian DNA”
Gordon Conference on Bioinformatics, New Hampshire.
“Dispensability of Mammalian DNA”,
FASEB Research Conference, Mobile Elements in Mammalian Genomes, Arizona.

- “A survey of exaptation in the human genome”
Seminar on Bioinformatics, UC Santa Cruz, California
"Coming under the auspices of purifying selection"
- Guest Seminar, Dept. of Zoology, University of Otago, New Zealand 2008
"Ultraconserved Elements in the Human Genome: The Hip & The Hype"
UC Berkeley Computational Biology Retreat Keynote, San Carlos, California
"Ultraconservation: The Hip & The Hype"
- Guest Seminar, Dept. of Molecular Genetics, University of Toronto, Canada
"Ultraconserved Elements and Dispensability of Mammalian DNA"
- Dahlem Colloquium, Max Planck Institute of Molecular Genetics Berlin, Germany
"Ultraconserved Elements and Dispensability of Mammalian DNA"
- PhD Student Retreat, Max Planck Institute, Berlin, Germany
"Ultraconserved Elements: The Hip and the Hype"
- Blue Seminar, EMBL, Heidelberg, Germany
“Dispensability of Mammalian DNA”
- Evolutionary Genetics Seminar, University of California, Davis, California.
“Dispensability of Mammalian DNA”
- Bioinformatics Seminar, University of California Los Angeles, California
“Dispensability of Mammalian DNA”
- Genomic Impact of Eukaryotic Transposable Elements, 2nd Int'l Conf., California. 2009
"In Search of Regulatory Co-option in the Human Genome"
RECOMB Satellite Conference on Bioinformatics Education, UC San Diego, CA
“All Your Base Are Belong To Us: Thoughts on Genome Conservation”
- Center for Algorithmic and Systems Biology CASB-20 Meeting, UC San Diego, CA
“Whole Genome Reconstruction”
- Microsoft Research Faculty Summit, Bellevue, Washington
“Needles in a Haystack: Reading Human Evolution in the Human Genome”
- Jackson Laboratory, Bar Harbor, Maine
“Regulatory Mutations in Mice & Human: In search of the Phenotype”
- University of Southern California, Los Angeles, CA
“Genomics and the evolution of human-specific traits”
- Weizmann Institute of Science, Rehovot, Israel
“Comparative & Functional Genomics of the evolution of human-specific traits”
- Hebrew University of Jerusalem, Israel
“Comparative & Functional Genomics of the evolution of human-specific traits”
- University of California San Francisco (UCSF), San Francisco, CA 2010
“Comparative & Functional Genomics of the Evolution of Human-Specific Traits”
- Duke University, Durham, NC
“Comparative & Functional Genomics of the Evolution of Human-Specific Traits”
- Georgia-Tech Distinguished Lecture in Bioinformatics, Atlanta, GA
“Conservation & Function in the Human Genome”
- Okinawa Institute of Science and Technology (OIST) QECG 2010 Summer School, Japan
“Ultraconservation: the hip and the hype”

Microsoft Research Faculty Summit, Bellevue, WA
 “Genomic Data Interpretation and Dissemination”
 University of Washington, Seattle, WA
 “Interpreting ChIP-Seq peaks and similar glimpses of human cis-regulation”
 High Performance Computing Day keynote speaker, Stanford, CA
 “Understanding the Machine Code of the Human Genome: No HPC = No Understanding”
 Genomics and Genetics of human Health and Disease Symposium, Oslo, Norway
 “Studies of the Cis-regulatory Basis of Recent Human Evolution and Human Disease”
 University of Bergen, Norway
 “Studies of the Cis-regulatory Basis of Recent Human Evolution and Human Disease”
 University of Chicago Committee on Genetics, Genomics & Systems Biology student invited speaker, Chicago, IL
 “The Cis-regulatory Landscape in Development and in Recent Human Evolution”
 NSF Science of Information STC Kick Off Meeting, Chicago, IL
 “Small Alphabet Sequence Transmission in Time and Space”
 Microsoft eScience Workshop, Berkeley, CA
 “Generating Functional Hypotheses from Genome-Wide Measurements of Mammalian Cis-Regulation”
 Chance and Necessity in Evolution, Ravello, Italy
 “Studies of Change and Constancy in the Evolution of the Human Genome”

National Center for Biomedical Ontology (NCBO) NIH review meeting, Stanford, CA 2011
 “<http://GREAT.stanford.edu> and the NCBO”
 X-GEN Congress and Expo, San Diego, CA
 “Using GREAT.stanford.edu to interpret cis-regulatory rich datasets”
 University of California San Diego (UCSD), San Diego, CA
 “The cis-regulatory landscape during mammalian development and in recent human evolution”
 Annual Stanford Symposium for Genomics and Personalized Medicine, Stanford, CA
 “Gene regulation: looking at the logic in the cis-tem”
 Annual Searle Scholars meeting, Chicago, IL
 “Human-specific Loss of Regulatory DNA and the Evolution of Human-specific Traits”
 Guest Seminar, University of Oregon, Eugene, OR
 “Exploring the vertebrate cis-regulatory landscape”
 SMBE Symposium: Present and future of the neutral theory, Kyoto, Japan
 “Mutation & function in the human genome cis-regulatory landscape”

etc. to be updated...

TEACHING

CS273A “A Computational Tour of the Human Genome”
 Spring 2006/07, Fall 2007/08, Fall 2008/09, Fall 2009/10, Fall 2010/11, Fall 2011/12
 DB210 “Developmental Biology”
 Spring 2007/08, Spring 2008/09, Spring 09/10, Spring 2010/11, Spring 2011/12
 Also lectured in CS262 (2011), CS 279 (2006), Biochem 218 (2007), BMI 205 (2008, 2009, 2010), EE477 (2012), HumBio 109A (2008, 2009)

MENTORING

Current Students

Shoa Clarke – PhD student, Medical Scientist Training Program/Genetics, HHMI Gilliam Fellow (5 yrs)

Harendra Guturu – PhD student, Electrical Engineering, NSF Graduate Fellow (3 yrs)

Jim Notwell - PhD student, Computer Science, NSF Graduate Fellow (3 yrs)

Current postdocs

Geetu Tuteja, PhD (U. Pennsylvania) – Stanford School of Medicine Dean’s Fellow (1 yr), A.P. Giannini Fellow (3 yrs)

Zaneta Odrowaz, PhD (Manchester)

Current Staff

Tisha Chung – Life Sciences Research Associate

Karen Moreira, PhD - Life Sciences Research Associate

Current Other

Ravi Parikh - Computer Science Co-Term

Emily Cheng - Computer Science Undergraduate

Lab Alumni

Adam Adler (PhD, Stanford) – Postdoc

Saatvik Agarwal – Computer Science Co-Term, Stya Paul Scholar

Cory Barr - Masters Student, Computer Science

Abraham Bassan – Masters, Developmental Biology, joint with David Kingsley, NSF Graduate Fellow

Dave Bristor – Software Engineer

Jenny Chen – Biomedical Informatics Co-Term

Andrew Doxey (PhD, Waterloo, Governor General Gold Medal, top PhD graduate of 2010) – NSERC Postdoc Fellow (2 yrs), Now Assistant Prof., Waterloo (2013)

Michael Hiller (PhD, Freiburg) – Postdoc, German Research Foundation Scholar (2 yr), Human Frontiers Long Term Fellow (3 yrs), Now Research Group Leader, Max Planck Institute

Janet Jin (Phd, Stanford) - Life Sciences Research Associate

Cory McLean – PhD student, Computer Science, First Year Fellowship (1 yr), Bio-X Graduate Fellow (3yrs)

Hrysoula Papadakis - Computer Science Co-Term

Fah Sathirapongsasuti – Undergraduate, Mathematical and Computational Science

Bruce Schaar, PhD – Senior Research Scientist

Sushant Shankar – Computer Science Masters

Aaron Wenger – PhD student, Computer Science, Stanford Graduate Fellow (3 yrs), Stanford Interdisciplinary Graduate Fellow (3yrs)

Undergraduate advisees

Junichi Tsutsui (Computer Science)

Yoon Seuk Kim (Computer Science)

E) BIBLIOGRAPHY

PEER-REVIEWED

Refereed journal papers

1. A. Apostolico and **G. Bejerano**. Optimal amnesic probabilistic automata, or, how to learn and classify proteins in linear time and space, *J. Computational Biology*, 7(3-4): 381-393, 2000. [[pdf](#)]
2. R. Hershberg, **G. Bejerano**, A. Santos-Zavaleta and H. Margalit. PromEC: An updated database of Escherichia coli mRNA promoters with experimentally identified transcriptional start sites, *Nucleic Acids Research*, 29(1): 277, 2001. [[pdf](#)] [[website](#)]
3. **G. Bejerano** and G. Yona. Variations on probabilistic suffix trees - a new tool for statistical modeling and prediction of protein families, *Bioinformatics*, 17(1): 23-43, 2001. [[pdf](#)] [[code](#)]
4. L. Argaman, R. Hershberg, J. Vogel, **G. Bejerano**, G. Wagner, H. Margalit and S. Altuvia. Novel small RNA-encoding genes in Escherichia coli, *Current Biology*, 11(12): 941-950, 2001. [[pubmed](#)]
5. **G. Bejerano**, Y. Seldin, H. Margalit and N. Tishby. Markovian domain fingerprinting: Statistical segmentation of protein sequences, *Bioinformatics* 17(10): 927-934, 2001. [[pdf](#)] [[poster](#)]
6. N. Slonim, **G. Bejerano**, S. Fine and N. Tishby. Discriminative feature selection via multiclass variable memory Markov models, *EURASIP J. Applied Signal Processing*, 2: 93-102, 2003. [[pdf](#)]
7. O. Lartillot, S. Dubnov, G. Assayag and **G. Bejerano**. A system for computer music generation by learning and improvisation in a particular style, *IEEE Computer J.*, 36(10): 73-80, 2003. [[pdf](#)] [[music](#)]
8. **G. Bejerano**. Algorithms for variable length Markov chain modeling. *Bioinformatics*, 20(5): 788-789, 2004. [[pdf](#)] [[code](#)]
9. **G. Bejerano**, M. Pheasant, I.V. Makunin, S. Stephen, W.J. Kent, J.S. Mattick and D. Haussler. Ultraconserved elements in the human genome. *Science*, 304(5675): 1321-1325, 2004. [[pdf](#)] [[suppl](#)] [[website](#)] *Quoted by Science in Breakthrough of the Year 2004, 5th runner up.*
10. **G. Bejerano**, D. Haussler and M. Blanchette. Into the heart of darkness: large-scale clustering of human non-coding DNA. *Bioinformatics*, 20: 140-148, 2004. [[pdf](#)] [[website](#)]
11. International Chicken Genome Sequencing Consortium. Sequencing and comparative analysis of the chicken genome, *Nature*, 432(7018): 695-716, 2004. [[pubmed](#)]
12. **G. Bejerano**, N. Friedman and N. Tishby. Efficient exact p-value computation for small sample, sparse and surprising categorical data, *J. Computational Biology*, 11(5): 867-886, 2004. [[pdf](#)] [[code](#)]
13. E.A. Glazov, M. Pheasant, E.A. McGraw, **G. Bejerano** and J.S. Mattick. Ultraconserved elements in insect genomes: a highly conserved intronic sequence implicated in the control of homothorax mRNA splicing. *Genome Research*, 15(6):800-808, 2005. [[pubmed](#)]
14. A. Siepel, **G. Bejerano**, J.S. Pedersen, A. Hinrichs, M. Hou, K. Rosenbloom, H. Clawson, J. Spieth, L.W. Hillier, S. Richards, G.M. Weinstock, R.K. Wilson, R.A. Gibbs, W.J. Kent, W. Miller, and D. Haussler. Evolutionarily Conserved Elements in Vertebrate, Fly, Worm, and Yeast Genomes. *Genome Research*, 15(8):1034-1050, 2005. [[pubmed](#)]
15. **G. Bejerano**, A.C. Siepel, W.J. Kent and D. Haussler. Computational screening of conserved genomic DNA in search of functional non-coding elements. *Nature Methods*, 2(7):535-545, 2005. [[pdf](#)]
16. UCSC Genomics Group. The UCSC Genome Browser Database: Update 2006. *Nucleic Acids Res.*, 34:D590-D598, 2006. [[pubmed](#)]

17. J.S. Pedersen, **G. Bejerano**, A. Siepel, K. Rosenbloom, K. Lindblad-Toh, E.S. Lander, W.J. Kent, W. Miller and D. Haussler. Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. *PLoS Computational Biology*, 2(4):e33, 2006. [[pubmed](#)]
18. **G. Bejerano**, C.B. Lowe, N. Ahituv, B. King, A. Siepel, S.R. Salama, E.M. Rubin, W.J. Kent and D. Haussler. A Distal Enhancer and an Ultraconserved Exon are Derived From a Novel Retroposon. *Nature*, 441(7089):87-90, 2006. [[pdf](#)] [[suppl](#)] [[website](#)] *Quoted by a Nature editorial, 2007.*
19. **G. Bejerano**. Branch and bound computation of exact P-values, *Bioinformatics*, 22(17):2158-2159, 2006. [[pdf](#)] [[code](#)]
20. K.S. Pollard, S.R. Salama, B. King, A.D. Kern, T. Dreszer, S. Katzman, A. Siepel, J.S. Pedersen, **G. Bejerano**, R. Baertsch, K.R. Rosenbloom, J. Kent and D. Haussler. Forces Shaping the Fastest Evolving Regions in the Human Genome. *PLoS Genetics* 2(10): e168, 2006. [[pubmed](#)]
21. UCSC Genomics Group. The UCSC genome browser database: update 2007. *Nucleic Acids Research*, 35:D668-73, 2007. [[pubmed](#)]
22. C.B. Lowe, **G. Bejerano*** and D. Haussler. Thousands of human mobile element fragments undergo strong purifying selection near developmental genes. *Proc. Nat'l Acad. Sci. USA*. 104(19):8005-8010, 2007. *Corresponding author (Direct submission) [[pdf](#)] [[suppl](#)] [[website](#)]
23. S. Katzman, A.D. Kern, **G. Bejerano**, G. Fewell, L. Fulton, R.K. Wilson, S.R. Salama, and D. Haussler. Human Genome Ultraconserved Elements Are Ultraselected. *Science* 317(5840): 915, 2007. [[abstract](#)]
24. C. McLean and **G. Bejerano**. Dispensability of Mammalian DNA. *Genome Research* 18(11):1743-1751, 2008. [[pdf](#)] [[suppl](#)]
25. C.B. Lowe, **G. Bejerano**, S.R. Salama and D. Haussler. Endangered Species Hold Clues to Human Evolution. *J. Heredity* 101(4):437-47, 2010. [[pubmed](#)]
26. C.Y. McLean, D. Bristor, M. Hiller, S.L. Clarke, B.T. Schaar, C.B. Lowe, A.M. Wenger and **G. Bejerano**. GREAT improves functional interpretation of cis-regulatory regions. *Nature Biotechnology* 28(5):495-501, 2010. [[journal](#)] [[website](#)]
27. X. Fan, P. Ren, S. Dhal, **G. Bejerano**, S.B. Goodman, M.L. Druzin, S.S. Gambhir and N.R. Nayak. Noninvasive monitoring of placenta-specific transgene expression by bioluminescence imaging. *PLoS One*, 6(1):e16348, 2011. [[pubmed](#)]
28. C.Y. McLean, P.L. Reno, A.A. Pollen, A.I. Bassan, T.D. Capellini, C. Guenther, V.B. Indjeian, X. Lim, D.B. Menke, B.T. Schaar, A.M. Wenger, **G. Bejerano*** and D.M. Kingsley*. Human-specific loss of regulatory DNA and the evolution of human-specific traits. *Nature*, 471:216-219, 2011. [[pdf](#)] [[suppl](#), [lists](#)] *Corresponding authors
29. T.D. Capellini, K. Handschuh, L. Quintana, E. Ferretti, G. Di Giacomo, S. Fantini, G. Vaccari, S.L. Clarke, A.M. Wenger, **G. Bejerano**, J. Sharpe, V. Zappavigna and L. Selleri. Control of pelvic girdle development by genes of the Pbx family and Emx2. *Dev Dyn.*, 240:1173-89 2011. [[pubmed](#)]
30. R.Y. Birnbaum, Clowney EJ, Agamy O, Kim MJ, Zhao J, Yamanaka T, Pappalardo Z, Clarke SL, Wenger AM, Nguyen L, Gurrieri F, Everman DB, Schwartz CE, Birk OS, **Bejerano G**, Lomvardas S and Ahituv N. Coding exons function as tissue-specific enhancers of nearby genes. *Genome Res*. 22(6):1059-68, 2012. [[pubmed](#)]
31. Laurell T, Vandermeer JE, Wenger AM, Grigelioniene G, Nordenskjöld A, Arner M, Ekblom AG, **Bejerano G**, Ahituv N, Nordgren A. A novel 13 base pair insertion in the sonic hedgehog ZRS limb enhancer (ZRS/LMBR1) causes preaxial polydactyly with triphalangeal thumb. *Hum Mutat*. 2012 Jul;33(7):1063-6. [[pubmed](#)]
32. S.L. Clarke, J.E. VanderMeer, A.M. Wenger, B.T. Schaar, N. Ahituv and **G. Bejerano**. Human developmental enhancers conserved between deuterostomes and protostomes. 2012, *PLoS Genetics*, In

press. [[journal](#)]

Refereed conference papers (8-12 pages)

1. **G. Bejerano** and G. Yona. Modeling protein families using probabilistic suffix trees, Proceedings of the 3rd annual international conference on research in computational molecular biology (RECOMB), 1999. [[pdf](#)] *Best paper by a young scientist award*.
2. A. Apostolico and **G. Bejerano**. Optimal amnesic probabilistic automata, or, how to learn and classify proteins in linear time and space, Proceedings of the 4th annual international conference on research in computational molecular biology (RECOMB), 2000.
3. Y. Seldin, **G. Bejerano** and N. Tishby. A variable memory Markovian modeling approach to unsupervised sequence segmentation, Proceedings of 33rd Symposium on the Interface of Computing Science and Statistics (Interface), 2001.
4. Y. Seldin, **G. Bejerano** and N. Tishby. Unsupervised sequence segmentation by a mixture of switching variable memory Markov sources, Proceedings of 18th International Conference on Machine Learning (ICML), 2001.
5. Y. Barash, **G. Bejerano** and N. Friedman. A Simple Hyper-Geometric Approach for Discovering Putative Transcription Factor Binding Sites, 1st Workshop on Algorithms in Bioinformatics (WABI), 2001. Lecture Notes in Computer Science, 2149: 278-293.
6. O. Lartillot, S. Dubnov, G. Assayag, and **G. Bejerano**. Automated modeling of musical style, Proceedings of the International Computer Music Conference (ICMC), 2001.
7. N. Slonim, **G. Bejerano**, S. Fine and N. Tishby. Discriminative feature selection via multiclass variable memory Markov models, Proceedings of 19th International Conference on Machine Learning (ICML), 2002.
8. **G. Bejerano**. Efficient exact p-value computation and applications to biosequence analysis. Proceedings of the 7th annual international conference on research in computational molecular biology (RECOMB), 2003. [[pdf](#)] *Best paper by a young scientist award*.
9. I.V. Makunin, S. Stephen, M. Pheasant, **G. Bejerano**, W.J. Kent, D. Haussler and J.S. Mattick. Extremely conserved non-coding sequences in the vertebrate genomes. Proceedings of 4th International Conference on Bioinformatics of Genome Regulation and Structure (BGRS), 2004.

Refereed Podium Presentation Abstracts (1-2 pages)

1. **G. Bejerano**, H. Margalit and N. Tishby. Using variable length Markov models to study DNA and protein sequences. Multinational Conference on Foundations of Statistical Inference: Applications and the Interface with Computer Science, 2000.
2. A. Siepel, **G. Bejerano**, M. Blanchette, K. Pollard, K. Roskin, R. Weber, D. Thomas, B. Raney, K. Rosenbloom, H. Clawson, J. Kent, W. Miller and D. Haussler. Comparative analysis of complete mammalian genomes: multiple alignment, phylogenetic analysis, and detection of functional elements. 17th Cold Spring Harbor meeting on the Biology of Genomes, 2004.
3. **G. Bejerano**, S. Mahadevan, B. Rattitch, E. Blais, D. Precup, D. Haussler and M. Blanchette. Similarity measures and clustering for regulatory modules. Cold Spring Harbor Genomics Workshop on Identification of Functional Elements in Mammalian Genomes, 2004.
4. **G. Bejerano**, S. Salama, W.J. Kent and D. Haussler. Candidate Non-Coding Functional RNAs among the Human Ultraconserved Elements and Related Genomic Regions. Keystone Symposium on Diverse Roles of RNA in Gene Regulation, 2005.

5. **G. Bejerano**, D. Haussler and M. Blanchette. Computational analysis of the regulatory potential of non-coding regions conserved in vertebrates. 3rd Cold Spring Harbor conference on Systems Biology: Global Regulation of Gene Expression, 2005.
6. **G. Bejerano**, C.B. Lowe, N. Ahituv, B. King, A. Siepel, S.R. Salama, E.M. Rubin, W.J. Kent and D. Haussler. A tetrapodal distal enhancer and a mammalian ultraconserved exon are both derived from a novel "living fossil" retroposon. 19th Cold Spring Harbor meeting on the Biology of Genomes, 2006.
7. **G. Bejerano**. Empirical challenges in the evolution of the human genome. 7th joint Australia-New Zealand Mathematical Convention, Christchurch, New Zealand 2008.
8. **G. Bejerano**. Human-specific regulatory DNA mutation and the evolution of human-specific traits. Gordon Research Conference on Human Genetics and Genomics, Biddeford, Maine 2009.
9. **G. Bejerano**. Human-specific regulatory DNA mutation and the evolution of human-specific traits. American Society of Human Genetics annual meeting, Honolulu, Hawaii 2009.
10. **G. Bejerano**. Human-specific regulatory DNA mutation and the evolution of human-specific traits. Systems Biology: Global Regulation of Gene Expression bi-annual meeting, Cold Spring Harbor, New York, 2010.
11. **G. Bejerano**. Generating functional hypotheses from measurements of the mammalian cis-regulatory genome in action. Santa Cruz Developmental Biology Meeting, Santa Cruz, CA, 2010.
12. **G. Bejerano**. Annotating the Zebrafish Genome Cis-Regulatory Landscape. 4th Strategic Conference of Zebrafish Investigators, Asilomar, CA, 2011.

etc. to be updated...

Book Chapters

1. D. Karolchik, **G. Bejerano**, A.S. Hinrichs, R.M. Kuhn, W. Miller, K.R. Rosenbloom, A.S. Zweig, D. Haussler and W.J. Kent. Comparative Genomic Analysis Using the UCSC Genome Browser. *Methods Mol Biol.* 395:17-34, 2007. [[pubmed](#)]

NON-PEER REVIEWED

Patents

1. N. Tishby, Y. Seldin, **G. Bejerano** and H. Margalit. Markovian Domain Fingerprinting in Statistical Segmentation of Protein Sequences. 2002. [[link](#)]