

Manolis Kellis - CV

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Date of Birth:	March 13, 1977	Web:	http://mit.edu/manoli
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Curriculum Vitae

Manolis Kellis is an Assistant Professor of Computer Science at MIT, a member of the Computer Science and Artificial Intelligence Laboratory, and associate member of the Broad Institute of MIT and Harvard.

Prof. Kellis is the recipient of a National Science Foundation Career Award (2007), the Karl Van Tassel 1925 Career Development Professorship, and the Distinguished Alumnus 1964 Career Development Professorship. He was selected as one of 35 top young innovators under the age of 35 by Technology Review Magazine, one of 20 young scientists recognized as the Principal Investigators of the Future by Genome Technology magazine, and one of three scientists representing the next generation in biotechnology by the Museum of Science in Boston. He obtained his Ph.D. from MIT, where he received the Sprowls award for the best doctorate thesis in Computer Science, the first Paris Kanellakis graduate fellowship, and the Chorafas Foundation award.

His research is in the field of computational biology, developing algorithms and machine learning techniques to interpret complete genomes, understand gene regulation, reconstruct cellular networks, and study genome evolution. Prior to computational biology, he worked on artificial intelligence, sketch and image recognition, robotics, and computational geometry, at MIT and at the Xerox Palo Alto Research Center. He was born in Greece, and lived in Greece and France before moving to the US.

Education

Massachusetts Institute of Technology, 2000-2003

Doctor of Philosophy (Ph.D.) in Computer Science. Profs. Eric Lander and Bonnie Berger.
Dissertation title: Computational Comparative Genomics: Genes, Regulation, Evolution.
Thesis earned MIT Sprowls award for best Ph.D. thesis in the field of Computer Science.

Massachusetts Institute of Technology, 1995-2000

Masters of Engineering (M.Eng.) in Electrical Engineering and Computer Science. Prof. Patrick Winston.
Dissertation title: Imagina: A cognitive abstraction approach to sketch-based image retrieval.
Bachelor of Science (B.S.) in Computer Science and Engineering.
Coursework includes Machine Learning, Robot Vision, Artificial Intelligence, Distributed Algorithms, Complexity, Probability, Statistics, Software Engineering, Programming Languages, Signal Processing, Computer Graphics, Microprocessor Design, Computer Architecture. GPA: 5.0 / 5.0.

Cold Spring Harbor Laboratory - Yeast Genetics, 2003

Foundations and principles of genetics, and current research topics.
Coursework includes: Immunofluorescence microscopy and cell staining, mutant isolation and complementation, tetrad analysis, recombinant DNA transformation, genome-wide synthetic lethal screens, targeted gene disruption, pathway suppressor analysis, transposon mutagenesis, two-hybrid protein-protein interactions, DNA precipitation and sequencing.

Awards Received

National Science Foundation CAREER Award, 2007-2011.
Karl Van Tassel (1925) Career Development Chair, 2007-2009.
Distinguished Alumnus (1964) Career Development Chair, 2005-2007.
Technology Review magazine, Top 35 Young Innovators under 35, TR35, 2006.
Genome Technology magazine, Top 20 Principal Investigators of the Future, 2006.
Museum of Science, Top 3 young scientists representing the next generation in biotech, 2004.
Service appreciation award, CSAIL Student Workshop, 2006.
MIT Sprowls award for the best Ph.D. thesis in Computer Science, 2003.
First recipient of Paris Kanellakis Fellowship, 2000.
NTT Fellowship for graduate studies, 1999.
Chorafas Foundation Award, 1999.
MassGrant Award for academic excellence, 1998.
Member of National Scientific and Engineering Honor Societies Sigma Xi, TBP, and Eta Kappa Nu.
First prize in the Tau Beta Pi Engineering Design Competition, representing MIT, Spring 1997.
French Baccalauréat with the Congratulations of the Jury, the highest distinction in France, June 1995.
First prize in South France in a country-wide math competition, 1993.

Students Supervised

Matthew D. Rasmussen, Master of Science, MIT - May 2006

Probabilistic model for genome-wide phylogeny and orthology determination.

Received William A. Martin Thesis Award for best M.S. thesis in Computer Science.

Michael Lin, Master of Engineering, MIT - May 2006

A classification approach to comparative gene identification.

Received Charles and Jennifer Johnson Thesis Award for best M.Eng. thesis in Computer Science.

Joshua Grochow, Master of Engineering, MIT - August 2006

Evolution and dynamics of biological networks.

Received Charles and Jennifer Johnson Thesis Award for outstanding M.Eng. thesis in CS.

Leopold Parts, Bachelor of Science, MIT, June 2006

Comparative RNA gene identification in the fly genome

Led to co-authored publications in Genome Research, Nature.

Ameya Deoras, Master of Science, MIT, June 2007

Gene Identification using Phylogenetic Metrics with Conditional Random Fields.

Led to co-authored publication in Nature.

Guilherme Issao Fujiwara, MIT, expected June 2008

De novo discovery of evolutionary signatures.

Pouya Kheradpour, MIT, expected June 2009

Regulatory network reconstruction in the human genome.

Giorgos Papachristoudis, MIT, expected June 2012

Phylogenetic models in complete genomes.

Rogério Candeias, expected June 2010

Regulatory genomics in human and fly.

Alexander Stark, Postdoctoral Fellow.

Regulatory genomics in flies.

Xiaohui Xie, Postdoctoral Associate.

Regulatory genomics in mammals.

Now an assistant professor at UC Irvine.

Positions held

MIT Computer Science and Artificial Intelligence Laboratory - since 2004 - Asst. Professor

Regulatory network discovery and dynamics in the fly genome, with Alex Stark.

Probabilistic framework for genome-wide phylogeny and orthology detection, with Matt Rasmussen.

Comparative gene identification using a classification approach, with Mike Lin.

Evolution of protein interaction networks in presence of duplication, with Aviva Presser.

Regulatory motif turnover and evolution, with Erez Lieberman.

Signal processing for DNA sequence analysis, with Ameya Deoras.

Broad Institute of MIT and Harvard - 2003-2004 - Post-doctoral fellow

Mammalian comparative genomics: genome-wide regulatory motif discovery, Spring 2004

microRNA regulation: post-transcriptional regulatory motifs and novel miRNA discovery, Fall 2004

Evolutionary genomics: proof of yeast genome duplication and emergence of new functions, Fall 2003

MIT/Whitehead Center for Genome Research - 2000-2003 - Biological Signal Discovery

Gene identification using cross-species comparison and re-annotation of the yeast genome, Fall 2002

Regulatory motif discovery using genome-wide conservation criteria, with Nick Patterson, Spring 2002

Automatic genome correspondence and alignment in a graph-theoretic framework, Spring 2001

Gene spacing constraints in the mammalian Hox developmental gene cluster, Ken Dewar, Fall 2000

MIT Learning and Vision Group - Fall 99 - Handwritten character recognition (*)

Introduced a curve-based representation for handwritten characters that facilitates online recognition and classification. The geometry-based representation matches shapes rather than pixels and is invariant to scaling and rotation. Wavelet-based smoothing reduces noise and facilitates recognition. w/ Paul Viola, MIT AI Lab.

Xerox Palo Alto Research Center (PARC) - 1999 - Video Analysis with Human Motion Primitives

Developed new angle-based representations for whole-body human motion, enabling time-warping of three-dimensional motion capture data and facilitating matching of gates across individuals. Worked towards an alphabet of human motions to be used in activity recognition and in combination with video data. M. Black.

MIT AI Lab - Masters Thesis - Spring 99 - Imagina: Sketch-based Image Retrieval (*)

Developed a system for content-based image retrieval from a sketch of the desired image. Matching focused on regions instead of global pixel metrics. Representation captured geometry and spatial organizations of regions within images, using a combination of shape and color representations at multiple levels of abstraction. Winston.

MIT Microprocessor Lab - 09/98 - RoboLogo: Programming Environment for Interactive Robots (*)

Co-developed an environment that enables children to program interactive robots in a high-level language that extends Logo. Compiler written in javacc, A51 assembly, printed circuit board designed on Protel.

Xerox PARC Smart Matter Area - 06/98 - PolyBot: Distributed Control for Reconfigurable Robots

Worked on a new control architecture to allow many identical robotic modules to communicate, share state information, arbitrate decisions based on local rules, message-passing, and environmental stimuli. Mark Yim.

MIT AI Lab - Spring 98 - Mood: Music Classification using Patterns of Attentional State (*)

Co-developed a new architecture for music classification, integrating a low-level note observer with a music classifier that observes high-level patterns in the routines used by the note observer. P. Winston.

AI in Practice Project - Spring 98 - Invest: Applications of AI to Stock Market Prediction (*)

Applied Artificial Intelligence methods to the study of the stock market. Co-developed neural network, pattern saliency, and nearest neighbor predictors and applied them to real stock market data. Tomás Lozano-Perez.

MIT Machine Vision Group- 09/97 - EciMorph: Curve Morphing in Extended Gaussian Space (*)

Developed a morphing method for convex two-dimensional curves, as projected in their Extended Gaussian Image representation, originally used in machine vision for object recognition. Prof. Berthold Horn.

MIT Lab for Computer Science - Fall 97 - 3DMorph: Polygon Model Morphing (*)

Co-developed a morphing algorithm for three-dimensional models, which directly alters the surface mesh to interpolate shapes rather than pixels or volumes. Matching methods are applicable beyond morphing. Teller.

Xerox PARC Computer Science Lab - 06/97 - Crust: Voronoi-Based 3D Surface Reconstruction (*)

Co-developed the Crust algorithm for 3D reconstruction of surfaces from unorganized sample points. Algorithm runs on a desktop rather than movie studio supercomputers and has provable guarantees of its performance. ACM Siggraph publication has been influential in the field, cited in 78 papers. Marshall Bern and Nina Amenta.

World Wide Web Consortium - Summer 96 - WebBot: Constraint Model for a Web Robot (*)

Proposed and implemented a modular rule-based constraint language for automatic web traversal. The model allows a recursive definition of arbitrarily complex rules and constraints. Henrik Frystyk Nielsen.

Consulting and Advisory Record:

Galleries Lafayette Information Technology Strategy, July 1999

Novartis Pharmaceuticals, Nov. 2003

Interim Advisory Board Member, National Human Genome Research Institute (NHGRI), NIH, Jan. 2002

Advisory Member, Planning meeting for Project ENCODE for the Human Genome, NIH, June 2002

Advisory Member, NHGRI council meeting for planning mammalian comparative sequencing, NIH, 2004

Advisory Member, NHGRI/NIAID selection and planning of sequencing for Pathogen and Disease Vectors, 2006

Advisory Member, Saccharomyces Genome Database (SGD) planning meeting in the yeast community, Aug. 2002

Broad Scientific Council Meeting Participant, Broad Institute, Jan. 2007

Professional service:

RECOMB 2004 Satellite Meeting on Gene Regulation, Program Committee Member, Dec 2004.

RECOMB 2006, Program Committee Member.

ISMB 2007, Program Committee Member, Regulatory Genomics, Aug. 2006

Nature, Nature Genetics, PLoS Biology, Genome Research, Genome Biology, Referee, May 2004-present

CSHL, The Biology of Genomes, Program Committee Co-Chair for Computational Genomics, May 2006

RECOMB 2007, Program Committee Member, Sept. 2006

ISMB 2006, Program Committee Co-Chair, Comparative Genomics, Nov. 2006

Genome Research, Member of Editorial Board, Aug. 2007

CSHL Genome Informatics, Co-Chair for Comparative Genomics, Oct. 2007

RECOMB Satellite on Regulatory Genomics, Conference Organizer and Chair, Oct. 2007

1. Galagan, Calvo, Borkovich, Selker, Read, Jaffe, *et al.*, “The Genome Sequence of the Filamentous Fungus *Neurospora crassa*,” *Nature*, v. 422, p. 859-868, Apr 24, 2003.
2. Kellis, Patterson, Endrizzi, Birren, Lander, “Sequencing and Comparison of Yeast Species to Identify Genes and Regulatory Motifs,” *Nature*, v. 423 p. 241-254. May 15, 2003.
Cited in 746 publications and featured in numerous reviews, magazines and newspapers.
3. Chiang, Moses, Kellis, Lander, Eisen, “Phylogenetically and Spatially Conserved Word Pairs Associated with Gene-Expression Changes in Yeasts,” *Genome Biology*, 4(7):R43, 19 pages, June 26, 2003.
4. Moses, Chiang, Kellis, Lander, Eisen. “Position Specific Variation in the Rate of Evolution in Transcription Factor Binding Sites,” *BMC Evolutionary Biology*, 3:19, 13 pages, Aug 28, 2003.
5. Kellis, Patterson, Birren, Berger, Lander, “Methods in comparative genomics: genome correspondence, gene identification, regulatory motif discovery,” *Journal of Computational Biology*, v. 11, Numbers 2-3, p. 319-55, 2004.
6. Kellis, Birren, Lander, “Proof and Evolutionary Analysis of Ancient Genome Duplication in Yeast,” *Nature*, 428 pp. 617-624, Apr 8, 2004.
Cited in 313 publications and featured in numerous reviews, magazines and newspapers.
7. Harbison, Gordon, Lee, J.Rinaldi, Macisaac, Danford, Hannett, Tagne, Reynolds, Yoo, Jennings, Zeitlinger, Kellis, Rolfe, Takusagawa, Gifford, Fraenkel, Young, “Transcriptional regulatory code of a eukaryotic genome,” *Nature*, 431 pp. 99-104, Sep 2, 2004.
Cited in 460 publications.
8. Jaillon *et al.*, “Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals the early vertebrate proto-karyotype,” *Nature*, 431 pp. 946-957, Oct 21, 2004.
Cited in 278 publications.
9. Xie, Lu, Kulbokas, Golub, Mootha, Lindblad-Toh, Lander, Kellis, “Systematic discovery of regulatory motifs in human promoters and 3' UTRs by comparison of several mammals,” *Nature*, 434 p. 338-345, Mar 17, 2005.
Cited in 424 publications.
10. Lindblad-Toh, *et al.*, “Genome sequence, comparative analysis and haplotype structure of the domestic dog,” *Nature*, 438 p.803-819, Dec 8, 2005.
11. Zeitlinger, Zinzen, Stark, Kellis, Zhang, Young, Levine, “Genome-wide binding of *Drosophila* developmental factors shows integration of diverse patterning processes,” *Genes & Development*, 21(4):385-90, Feb 15, 2007.
12. Brennecke, Arabin, Stark, Dus, Kellis, Sachidanandam, Hannon, “Discrete small RNA-generating loci as master regulators of transposon activity in *Drosophila*,” *Cell*, 128(6): 1089-103, Mar 23, 2007.
13. Xie, Mikkelsen, Gnirke, Lindblad-Toh, Kellis, Lander, “Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites,” *PNAS*, 104:7145-50, Apr 24, 2007.
14. Stark, Kheradpour, Ruby, Bartel, Hannon, Kellis, “Systematic discovery and characterization of fly microRNAs using 12 *Drosophila* genomes,” 14 pages, early online access, Nov 7, 2007, [Genome Research](#).
15. Stark, Lin, Kheradpour, Pedersen, Parts, Carlson, Crosby, Rasmussen, Roy, Deoras, Ruby, Brennecke, FlyBase curators, Berkeley *Drosophila* Genome Project, Hodges, Hinrichs, Caspi, Paten, Park, Han, Maeder, Polansky, Robson, Aerts, vanHelden, Hassan, Gilbert, Eastman, Rice, Weir, Hahn, Park, Dewey, Pachter, Kent, Haussler, Lai, Bartel, Hannon, Kaufman, Eisen, Clark, Smith, Celniker, Gelbart, Kellis, “Discovery of functional elements in 12 *Drosophila* genomes using evolutionary signatures,” *Nature*, 450:219-232, Nov 8, 2007.
16. *Drosophila* 12 Genomes Consortium, “Evolution of genes and genomes in the *Drosophila* Phylogeny,” *Nature*, 450:203-218, Nov 8, 2007.
17. Lin, Carlson, Crosby, Matthews, Yu, Park, Wan, Schroeder, Gramates, Pierre, Roark, Wiley, Kulathinal, Zhang, Myrick, Antone, Celniker, Gelbart, Kellis, “Revisiting the protein-coding gene catalog of *Drosophila melanogaster* using twelve fly genomes,” [Genome Research](#), early online access, Nov 7, 2007.
18. Ruby, Stark, Johnston, Kellis, Bartel, Lai, “Evolution, biogenesis, expression, and target predictions of a substantially expanded set of *Drosophila* microRNAs,” [Genome Research](#), early online access, Nov 7, 2007.
19. Kheradpour, Stark, Roy, Kellis, “Reliable prediction of regulator targets using 12 *Drosophila* genomes,” [Genome Research](#), early online access, Nov 7, 2007.

20. Rasmussen, Kellis, "Accurate gene-tree reconstruction by learning gene- and species-specific substitution rates across multiple complete genomes," Genome Research, early online access, Nov 7, 2007.
21. Zeitlinger, Zinzen, Stark, Kellis, Young, Levine, "RNA Polymerase Stalling at Developmental Control Genes in the *Drosophila* Embryo," Nature Genetics, Nov 11, 2007, early online access.
22. Clamp, Fry, Kamal, Xie, Cuff, Lin, Kellis, Lindblad-Toh, Lander, "Distinguishing protein-coding and noncoding genes in the human genome," PNAS 49:19428-33, Dec 4, 2007.
23. Stark, Bushati, Jan, Kheradpour, Hodges, Brennecke, Bartel, Cohen, Kellis, "A single Hox locus in *Drosophila* produces functional microRNAs from opposite DNA strands," Genes & Development, Jan 1, 2008, in press.
24. Presser, Elowitz, Kellis, Kishony, "Evolutionary dynamics of the *Saccharomyces cerevisiae* protein interaction network following duplication," PNAS, 6 pages, in press.

Proceedings of Refereed Conferences

25. Amenta, Bern, Kellis (Kamvysselis), "Crust: A new Voronoi-Based Surface Reconstruction Algorithm," ACM SIGGRAPH, v. 32, p. 415-421, Jul 19, 1998.
Cited in 447 publications.
26. Kellis, Patterson, Birren, Berger, Lander, "Whole-Genome Comparative Annotation and Motif Discovery in Multiple Yeast Species," ACM RECOMB, p. 157-166, Apr 13, 2003.
27. Chiang, Moses, Kellis (Kamvysselis), Lander, Eisen. "Phylogenetically and Spatially Conserved Word Pairs Associated with Gene-Expression Changes in Yeasts," ACM RECOMB, p. 84-93, Apr 13, 2003.
28. Grochow, Kellis, "Network motif discovery using motif enumeration and symmetry conditions," ACM RECOMB, p. 92-106, Apr 21, 2007.

Other Major Publications.

29. Kellis (as 'Kamvysselis'), Marina, "Imagina: Sketch-based Image Retrieval using Cognitive Abstraction," MIT Masters Thesis, 157 pages, June 1999.
30. Kellis (Kamvysselis), "Computational Comparative Genomics: Genes, Regulation, Evolution," MIT Ph.D. Thesis, 100 pages, May 25, 2003.
31. Batzoglou, Kellis, Xing, "Computational Biology: Genomes, Networks, Evolution (Book)," Cambridge University Press, In preparation.
32. Kellis, "The changing face of genomics," Genome Biology, 5(5):324, 3 pages, Apr 30, 2004.
33. Bernstein, Kellis, "Large-scale discovery and validation of functional elements in the human genome," Genome Biology 6(3):312, 2 pages, Mar 1, 2005.
34. Kellis. "Gene finding using multiple related species: a classification approach," Encyclopedia of Genetics, Genomics, Proteomics, John Wiley & Sons, 7 pages, 2005.
35. Heintzman, Hon, Kheradpour, Stark, Ching, Stuart, Harp, Hawkins, Ching, Liu, Zhang, Green, Crawford, Kellis, Ren, "A genome-wide map of human transcriptional enhancers," 7 pages, in revisions, Nature.
36. Lin, Deoras, Rasmussen, Kellis, "Performance and scalability of discriminative metrics for comparative gene identification in 12 *Drosophila* genomes," 6 pages, In revisions, PLoS Computational Biology.
37. Murchison, Kheradpour, Sachidanandam, Smith, Xuan, Grutzner, Stark, Kellis, Hannon, "Small RNA pathways in platypus," 7 pages, in review, Genome Research.
38. Rasmussen, Kellis, "SPiML: a machine learning approach to phylogenomics," 12 pages, in review, RECOMB 2008.
39. Kheradpour, Stark, Kellis, "Genome-wide motif discovery in fly promoters, enhancers, UTRs, coding and non-coding regions," 6 pages, in submission to Genome Research.
40. Pedersen, Kellis, Haussler, "Systematic discovery and characterization of RNA genes in *Drosophila* using comparative genomics," In preparation.
41. Lieberman, Kellis "Regulatory motif turnover and evolution," In preparation.
42. Kellis, "Biological Signal Discovery: The Power of Multiple Genomes," Fungal comparative genomics, Springer Verlag, invited book chapter.

Internal Memoranda and Progress Reports.

1. Kellis (as 'Kamvysselis'), Nielsen, "WebBot: Constraint Model for a Web Robot," World Wide Web Consortium, Aug 1996.
2. Kellis (as 'Kamvysselis'), "EciMorph: Curve Morphing in Extended Gaussian Space," MIT Machine Vision Group, Dec 1997.
3. Kellis (as 'Kamvysselis'), Gajos, Blum, Vassef, "3DMorph: Polygon Model Morphing," MIT Lab for Computer Science, Dec 1997.
4. Kellis (as 'Kamvysselis'), Lueck, Rohrs, "RoboLogo: Programming Environment for Interactive Robots," MIT Microprocessor Lab, Dec 1998.
5. Kellis (as 'Kamvysselis'), Yim, "PolyBot: Distributed Control for Reconfigurable Robots," Xerox PARC Smart Matter Area, Aug 1998.
6. Kellis (as 'Kamvysselis'), Marina, Vassef, Carter, "Mood: Music Classification using Patterns of Attentional State," MIT AI Lab, May 1998.
7. Kellis (as 'Kamvysselis'), Mehrotra, Warshawsky, "Invest: Applications of AI to Stock Market Prediction," AI in Practice Project, May 1998.
8. Kellis (as 'Kamvysselis'), "Handwritten character recognition using wavelets," MIT AI Lab, Dec 1999.
9. Kellis (as 'Kamvysselis'), Black, "Video Analysis with Human Motion Primitives," Xerox Palo Alto Research Center (PARC), Jul 1999.
10. Kellis, Dewar, "Gene spacing constraints in the mammalian Hox developmental gene cluster," Dec 2000.

Invited Lectures

1. Jun. 2002, "Yeast Comparative Genomics," Whitehead Institute First Symposium on Genomics, Cambridge, MA.
2. Aug. 2002, "Yeast Comparative Genomics," Harvard Institute of Proteomics Joint Colloquium, Cambridge, MA.
3. Mar. 2003, "Yeast Comparative Genomics," Harvard Center for Genomics Research, Lectures on Genomics, Cambridge, MA.
4. Mar. 2004, "Computational Biology: Challenges and Opportunity," Tufts Medical School Faculty Lectures on Computational Biology, Boston, MA.
5. Apr. 2004, "Extracting functional information from genome comparisons," Human Genome Discovery and Gene Functional Analysis meeting, San Francisco, CA.
6. May 2004, "Regulatory motif discovery using comparative genomics," Harvard Medical School Conference on Analysis of Genomic Data, Cambridge MA.
7. Jun. 2004, "Comparative genomics in *Saccharomyces cerevisiae*," Gordon Conference Invited Plenary Lecture on Phylogenomics, Plymouth NH.
8. Dec. 2004, "Revisiting the yeast genome," From Genome Sequencing to Biological Systems, ORFeome Meeting, Dana Farber.
9. May 2005, "Regulatory motif discovery using comparative genomics," First Proteomics Meeting of the Hellenic Proteomics Society, Athens Greece.
10. Jun. 2005, "Comparative genomics: Genes, Networks, Evolution," Bertinoro Meeting on Comparative Genomics, Invited Lecture, Italy.
11. Jun. 2005, "Computational Comparative Genomics," Advanced Course in Functional Genomics, Invited Keynote Lecture, Sanger Center.
12. Jun. 2005, "Comparative genomics: Genes, Networks, Evolution," Intelligent Systems for Molecular Biology, Invited Lecture, ISCB Student Council.
13. Aug. 2005, "Comparative Genomics in Yeast," International Meeting on Yeast Genetics Keynote Lecture, Bratislava, Slovakia.
14. Oct. 2005, "Computational Comparative Genomics," Princeton University, Quantitative and Computational Biology series, Lewis-Singler Institute.

15. Nov. 2005, "Computational genomics," Tufts University Computer Science colloquium, Invited Lecture, Medford MA.
16. Dec. 2005, "Regulatory genomics," RECOMB Satellite meeting on Regulatory Genomics, Invited Lecture, San Diego, CA.
17. Mar. 2006, "Regulatory Networks in the fly," Systems Biology: Global Regulation of Gene Expression, Invited Lecture, Cold Spring Harbor, NY.
18. May 2006, "Fly Comparative Genomics," Cold Spring Harbor Laboratory (CSHL), The Biology of Genomes, Invited Lecture, CSHL, NY.
19. Nov. 2006, "Discovering the human gene set using comparative genomics," Sanger Institute, BioSapiens workshop, Invited Lecture, Wellcome Trust.
20. Nov. 2006, "Interpreting the human genome," The Institute for Advanced Study, Simons Center for Systems Biology, Invited Lecture, Princeton, NJ.
21. Oct. 2006, "Interpreting the human genome," Stanford University, Frontiers in Biology lecture series, Invited Lecture, Palo Alto, CA.
22. Nov. 2006, "Interpreting the human genome," Algorithmic Biology, Cal(IT)2, UC San Diego, Invited Keynote Lecture, San Diego, CA.
23. Mar. 2007, "Biological signal discovery in 12 *Drosophila* genomes," *Drosophila* 2007 meeting, Invited Lecture, Philadelphia, PA.
24. Jul. 2007, "Phylogenomics in mammalian, fly, and fungal genomes," ISMB 2007 SIG, Invited Lecture, Vienna, Austria.
25. Oct. 2007, "Systematic discovery of protein-coding genes using evolutionary signatures," BioCuration meeting, Invited Keynote Lecture, San Jose, CA.
26. Oct. 2007, "Phylogenomics of mammalian, fly, and fungal genomes," Harvard OEB, Invited Lecture, Cambridge MA.
27. Oct. 2007, "Computational Comparative Genomics," Columbia C2B2, Invited Lecture, New York, NY.
28. Oct. 2007, "Systems Biology of gene regulation," Linnaeus Tricentennial Workshop, Uppsala, Sweden.
29. Nov. 2007, "Machine learning for Phylogenomics," CSHL Genome Informatics, Invited Lecture, Cold Spring Harbor, NY.
30. Dec. 2007, "Algorithms for regulatory network discovery using comparative genomics," RECOMB Satellite on Systems Biology, Invited Keynote Lecture, San Diego, CA.
31. Dec. 2007, "Comparative genomics in flies and mammals: signal discovery, regulatory networks, and evolutionary dynamics," NIPS 2008, Machine Learning in Computational Biology, Invited Keynote Lecture, Vancouver, Canada.
32. Mar. 2008, "Regulatory genomics of 12 *Drosophila* species," *Drosophila* 2008, Invited Keynote Lecture, San Diego, CA
33. May 2008, "Regulatory logic in *Drosophila* developmental enhancers," HHMI Janelia Farms meeting, Invited Lecture, Chevy Chase, DC.
34. July 2008, "Genome Interpretation using comparative Genomics," ISMB 2008, SIG, Invited Lecture, Toronto, Canada.