

Andrea Califano, Dr.

Curriculum Vitae

Biographical data

Dr. Andrea Califano received the Laurea in Physics (*magna cum laude*) on the study of the chaotic behavior in high-dimensional dynamical systems from the University of Florence, Italy, in 1985. He was first a Research Associate at the Istituto Nazionale di Ottica in Florence, Italy and then a postdoc in the Information Mechanic Group at the Massachusetts Institute of Technology, Cambridge. From 1986 to 1990, he was a Research Staff Member in the Exploratory Computer Vision Group at the IBM T.J. Watson Research Center. In 1990 Dr. Califano started the IBM research initiative in Computational Biology, which culminated with the creation of the IBM Computational Biology Center in 1997, a worldwide organization that he directed until his departure. The center's activities spanned bioinformatics, chemo-informatics, protein structure prediction, and the modeling/simulation of complex biological system.

In 2000 he co-founded First Genetic Trust, Inc, a privately funded startup company, as Executive VP and Chief Technology Officer. Under his leadership, FGT built the first GxP compliant, integrated clinical-genomic trial management system and conducted several large scale Pharmacogenomic studies.

Finally, in 2003, he was appointed Professor of Biomedical Informatics at Columbia University, where he is currently Director of the Center for the Multiscale Analysis of Genetic Networks (MAGNet) – one of seven NIH-funded National Centers for Biomedical Computing, – Associate Director for Bioinformatics of the Herbert Irving Comprehensive Cancer Center (HICCC), and co-Director of the Center for Computational Biology and Bioinformatics (C2B2).

His scientific interests lay in the investigation of Systems Biology, using a variety of physics- and knowledge-based methods. Since 1998 he has been especially active in the development of integrative methodologies for the dissection of cancer phenotypes. His lab has pioneered a wide range of methodologies for the reverse engineering and biochemical validation of genome-wide gene regulatory networks in human cells – including transcriptional, post-transcriptional, and post-translational interactions – and in their use for the dissection of physiologic and pathologic phenotypes.

Education

1982 - University of Firenze, Italy, Dept. of Physics

Course requirements for the doctorate in Physics, (equivalent BS)

1985 - University of Firenze, Italy, Dept. of Physics

Laurea in Physics (Summa Cum Laude)

Post Doctoral Training

1985–1986 Universita' degli Studi, Firenze

Research Associate, Istituto Nazionale di Ottica

1986–1986 Massachusetts Institute of Technology

Visiting Scientist, Information Mechanics Group

Professional Organizations

Fellow of the Institute of Electrical and Electronics Engineers (IEEE)

Fellow of the New York Academy of Science,

Member of the American Association for the Advancement of Science

Member of the American Society of Human Genetics

Positions Held

1986–1993

IBM TJ Watson Research Center

Research Staff Member, Exploratory Computer Vision Group

1993–1997 IBM TJ Watson Research Center

Manager, Computational Biology Group

1997–2000 IBM TJ Watson Research Center

Program Director, IBM Computational Biology Center

2000–2002 First Genetic Trust Inc.

Founder, EVP and Chief Technology Officer

2003-present Columbia University

Professor of Biomedical Informatics

Dept. Biomedical Informatics

Institute of Cancer Genetics

Director, Center for the Multiscale Analysis of Genetic Networks (MAGNet)

Associate Director for Bioinformatics, Herbert Irving Comprehensive Cancer Ctr.

co-Director, Center for Computational Biology and Bioinformatics (C2B2)

Professional Honors

Fellow of the New York Academy of Science, since 2005

Fellow of the IEEE (since 1997)

2000 - Invited speaker, American and German National Academy of Engineering to the Frontiers of Engineering Symposium in Bremen

1999 – IBM Master Inventor

1998 - Young Engineer invited to the American National Academy of Engineering Symposium on Frontiers of Engineering

1997 – Member Elected, IBM Academy of Technology. The academy includes all IBM fellows and an approximately equivalent number of researchers that are the most scientifically and technically productive in the company (~ top 1%).

1997 - IBM Patent Award, US Patent 5,577,249 as top 5% most significant for IBM.

1994 - IBM Award for Outstanding Technical Achievement, “FLASH.”

1991 - IBM Research Accomplishment, “Data and Model Driven Foveation.”

1991 - IBM Computer Science Best Paper Award, “Data and Model Driven Foveation.”

1989 - IBM Innovation Award, “High Dimensional Indexing.”

1989 - IBM Research Accomplishment, “The Multiple Window Parameter Transform.”

Other Professional activities

Since 2007: Data Analysis and Coordination Committee Member, The Serious Adverse Event Consortium.

Since 2007: Associate Editor, Journal of Biomedical Informatics

Since 2007: General Chair, RECOMB Satellite Conference on Systems Biology series.

Since 2007: Scientific Advisory Board, Skin Cancer SPORE, Yale University

Since 2006: Associate Editor, PLoS One

Since 2006: Scientific Advisory Board, CardioVascular Research Grid (CVRG), Johns Hopkins University

Since 2006: Scientific Advisory Board, Center for Systems and Computational Biology, Winstar Institute.

Since 2006: Executive Steering Committee, Herbert Irving Comprehensive Cancer Center

Since 2006: General Chair, DREAM Conference Series: Dialogue on Reverse Engineering Assessment and Methods

Since 2005: Permanent Member, NIH Study Section on Cancer Genetics

Since 2005: Scientific Advisory Board, Center for a Virtual Tumor (CViT), Harvard University

Since 2005: Co-Founder of the Intragen Program, a Translational Genomic Research platform for NY State.

Since 2004: Chair NYAS Special Interest Group in Systems Biology

Since 2000: Steering Committee, Special Interest Group on Biological Simulation (SIGBS), International Society of Computational Biology (ISCB)

2005: Program Committee of the RECOMB Conference

2005: Program Committee of the ISMB Conference

2001 – 2005: Editorial Board of Current Pharmacogenomics.

2004 – 2005: Director, AMDcC Bioinformatics Core and Integrated Genomics Core

2000 – 2004: Scientific Advisor, Novartis Functional Genomics

2003: National Dialogue on Cancer (NDC) – National Tissue Biobank Working Group

2000 – 2003: Steering Committee, DIMACS year on computational biology

2001: Steering Committee, Bioethics Consortium

2000 – 2001: Scientific Management Committee, The SNP Consortium

2000: Program Committee of the RECOMB Conference

2000: Editorial Advisory Board, “Bioinformatics: Getting Results in the Era of High-Throughput Genomics,” Cambridge Healthtech Institute

2000: Italian Post-Genome National Committee.

1999: Co-chair, Bioinformatics Workshop at CASCON

1997: Chair, IBM Academy Workshop on Emerging Applications of Biometry

1995: Advisory Committee for DAGS.

1994: General Chair, 1st IEEE Workshop on Shape and Pattern Matching in Computational Biology, Seattle, WA.

1993: Program Committee Member, International Conference on Computer Vision and Pattern Recognition, CVPR

**Presentations
2007 – 2008**

Invited Speaker (Jan 07): Gordon Conference on “New Frontiers in Cancer Detection and Diagnosis,”, Ventura, CA

Invited Seminar (Mar 07): Boston University, Boston MA

Invited Talk (Mar 07): Keystone Meeting on Systems Biology, Steamboat Springs, CO

Invited Seminar (Apr 07): Emory University, GA

Invited Talk (Apr 07): American Association for Cancer Research Annual

Meeting, Los Angeles, CA

Invited Speaker (May 07): Netsci 07, Queens NY

Invited Talk (Jun 07): CHI Meeting on Protein Kinase Targets, Boston, MA

Invited Seminar (Jun 07): Institute for Advanced Studies, Simon Center for Systems Biology, Princeton NJ

Invited Seminar (Jun 07): Rutgers University, New Brunswick NJ

Invited Speaker (Jun 07): Banft Conference on Allograft Pathology, Edmonton, AL

Invited Speaker (Aug 07): Cold Spring Harbor/Wellcome Trust Conference on Interactomes, Hinxton UK

Keynote Speaker (Sep 07): Spanish Conference on Clinical Pharmacology, Tenerife

Invited Speaker (Sep 07): Creative Leadership Forum, New York, NY

Invited Speaker (Oct 07): International Conference on Systems Biology, Long Beach CA

Invited Speaker (Oct 07): Aspen Health Forum, Aspen Institute, Aspen CO

Invited Speaker (Oct 07): Symposium on Clinical Applications of Genomics, University of Maryland Bicentennial Celebration, U. Maryland, Baltimore MA

Invited Speaker (Dec 07): DREAM Conference, NY Academy of Science, New York NY

Invited Speaker (Dec 07): Symposium on microRNA in Biology and Disease, Padova, IT

Invited Seminar (Dec 07): TIGEM, Napoli, IT

Invited Speaker (Dec 07): Scientific Committee on Lymphocyte Biology, 49th American Society of Hematology Annual Meeting, Atlanta GA

Invited Speaker (Feb 08): NCI Workshop on Integrating and Leveraging the Physical Sciences to Open a New Frontier in Oncology, Arlington VA

Invited Speaker (Mar 08): Fourth Annual Pathway Analysis Meeting, Molecular Medicine Tri Conference, San Francisco, CA

Invited Speaker (Apr 08): ENFIN-DREAM Conference, Assessment of Computational Methods in Systems Biology, Madrid

Keynote Speaker (June 08): Applying Systems Biology, Beyond Genome 2008, San Francisco, CA

Invited Speaker (Sep 08): Creative Leadership Forum, New York, NY

Invited Speaker (Nov 08): Distinguished Speakers Symposium on Systems Biology and Human Disease, American Society of Human Genetics Annual Meeting, Philadelphia PA

Peer-reviewed, full-length articles in journals and conference proceedings

* Indicates co-first or co-corresponding authors.

- [1] Arecchi FT and **Califano A**, (1984) Low-frequency hopping phenomena in a nonlinear system with many attractors, Phys. Lett., 101A [9]:443-446.
- [2] Arecchi FT and **Califano A**, (1987) Noise-Induced Trapping at the Boundary between two Attractors: a source for 1/f spectra in Nonlinear Dynamics, Europhys. Lett.;3(1):5-10.
- [3] **Califano A** and Bolle RM, (1987) Localized Noise Propagation Effects in Parameter Transforms, in Proc. of SPIE Conf. Vol 848 Intell. Robots and Comp. Vision, pp. 93-101
- [4] **Califano A**, (1988) Feature Recognition Using Correlated Information Contained in Multiple Neighborhoods. In Proc. 7th AAAI Nat'l Conf. on Artificial Intell.; Vol. 2:831-836.
- [5] Kjeldsen R, **Califano A**, and Bolle RM, (1989) Evidence Integration for 3D Object Recognition: A Connectionist Framework. Proc. of the 5th Conf. on Artificial Intell. App.; pp. 55-63.
- [6] **Califano A**, Bolle RM, and Taylor RW, (1989) Generalized Neighborhoods: A New Approach to Complex Parameter Feature Extraction, in Proc. of the IEEE Conf. on Computer Vision and Pattern Recognition, pp.192-199.
- [7] Bolle RM, **Califano A**, Kjeldsen R, and Taylor RW, (1989) Visual recognition using concurrent and layered parameter networks, in Proc. IEEE Conf. on Computer Vision and Pattern Recognition, pp. 625-631.
- [8] Bolle RM, **Califano A**, Kjeldsen R, and Taylor RW, (1989) A Homogeneous Framework for Visual Recognition. In Proc. of the 11th. Int. Conf. on Artificial Intell.;pp.1571-7
- [9] **Califano A** and Mohan R, (1990) Generalized shape autocorrelation, in Proc. 8th Nat. Conf. on Artificial Intell. (AAAI 90), pp. 1067-1073.
- [10] Bolle RM, **Califano A**, and Kjeldsen R, (1990) A complete and scalable architecture for 3D model-based vision. In proc. of 5th IEEE Intl. Symposium on Intelligent Control; pp. 212-219.
- [11] Bolle RM, **Califano A**, and Kjeldsen R, (1990) Active 3D Object Models, in Proc. of 3rd Intl. Conf. on Computer Vision; pp.329-333.
- [12] **Califano A**, Bolle RM, and Kjeldsen R, (1990) Data and Model Driven Foveation, in Proc. of 10th Intl. Conf. on Pattern Recognition (ICPR90), pp. 1-7.
- [13] **Califano A** and Mohan R, (1991) Multidimensional Indexing for Recognizing Visual Shapes. In IEEE Transactions on Pattern Analysis and Machine Intelligence;16(4):373-392.
- [14] Bolle RM, **Califano A**, and Kjeldsen R, (1992) A complete and extendable approach to visual recognition, in IEEE Transactions on Pattern Analysis and Machine Intelligence; 14(5):534-8
- [15] **Califano A**, Bolle RM, (1992) The Multiple Window Parameter Transform. In IEEE Transactions on Pattern Analysis and Machine Intelligence;14(12):1157-1170.
- [16] **Califano A** and Mohan R, (1993) Systematic Design of Indexing Strategies. In Proceedings of IEEE Conf. on Computer Vision and Pattern Recognition; pp. 709-710.
- [17] **Califano A** and Rigoutsos I, (1993) FLASH: A Fast Look-up Algorithm for String Homology, in Proceedings of Symposium on Intelligent Systems for Molecular Biology; Vol. 1:56-64, also in Proceedings of International Conference on Computer Vision and Pattern Recognition, NY.
- [18] Rigoutsos I and **Califano A**, (1994) Fast Three-Dimensional Matching Using Very Large Databases of Conformationally Flexible Molecules. In Proceedings of the 207th American Chemical Society Conference.

- [19] Rigoutsos I and **Califano A**, (1994) Searching in Parallel for Similar Strings [biological sequences], in IEEE Journal of Computational Science and Engineering;1(2):60-75.
- [20] **Califano A**, Kjeldsen R, and Bolle RM, (1996) Data- and model-driven multiresolution processing, in Journal of Computer Vision and Image Understanding;63(1):27-49.
- [21] Germain RS, **Califano A**, and Colville S, (1997) Fingerprint Matching Using Transformation Parameter Clustering, in IEEE Journal of Computational Science & Engineering;4(4):42-49.
- [22] **Califano A**, Germain B, and Colville S, (1997) A High-Dimensional Indexing Scheme for Scalable Fingerprint-Based Identification, in Lecture Notes in Computer Science;1351:32-39.
- [23] **Califano A**, (2000) SPLASH: structural pattern localization analysis by sequential histograms, Bioinformatics;16(4):341-357.
- [24] **Califano A**, Stolovitzky G, and Tu Y, (2000) Analysis of Gene Expression Microarrays for Phenotype Classification, in Proc. of the 8th Symposium on Intelligent Systems for Molecular Biology; Vol. 8:75-85.
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- [26] Liu A and **Califano A**, (2001) Functional Classification of Proteins by pattern discovery and top-down clustering of primary sequences, in IBM Systems Journal, special issue on Deep Computing for the Life Sciences; 40(2):379-393.
- [27] **Califano A**, (2001) Advances in sequence analysis. Curr Opin Struct Biol;11(3):330-3.
- [28] Klein U, Tu Y, Stolovitzky G, Mattioli M, Cattoretti G, Husson H, Freedman A, Inghirami G, Cro L, Baldini L, Neri A, **Califano A**, Dalla-Favera R, (2001) Gene expression profiling of B cell chronic lymphocytic leukemia reveals a homogeneous phenotype related to memory B cells. J Exp Med.;194(11):1625-38.
- [29] Pomeroy SL, Tamayo P, Gaasenbeek M, Sturla LM, Angelo M, McLaughlin ME, Kim JY, Goumnerova LC, Black PM, Lau C, Allen JC, Zagzag D, Olson JM, Curran T, Wetmore C, Biegel JA, Poggio T, Mukherjee S, Rifkin R, **Califano A**, Stolovitzky G, Louis DN, Mesirov JP, Lander ES, Golub TR, (2002) Prediction of central nervous system embryonal tumour outcome based on gene expression. Nature;415(6870):436-42. **Selected by the Faculty of 1000**
- [30] Buchanan A, **Califano A**, Kahn J, McPherson E, Robertson J, Brody B. (2002) Pharmacogenetics: ethical issues and policy options. Kennedy Inst Ethics Journal;12(1):1-15.
- [31] Liu A and **Califano A**, (2003) CASTOR: Clustering Algorithm for Sequence Taxonomical Organization and Relationship, Journal of Computational Biology;10(1):21-45.
- [32] Liu A, Zhang X, Stolovitzky G, **Califano A**, and Firestein S, (2003) Motif-Based Construction of a Functional Map for Mammalian Olfactory Receptors, Genomics;81(5):443-56.
- [33] Klein U, Tu Y, Stolovitzky GA, Keller JL, Haddad Jr. J, Miljkovic V, Cattoretti G, **Califano A**, Dalla-Favera R, (2003) Transcriptional analysis of the germinal center reaction. Proc. Natl. Acad. Sci USA;100(5):2639-2644.
- [34] Küppers R, Klein U, Schwering I, Distler V, Bräuninger A, Cattoretti G, Tu Y, Stolovitzky GA, **Califano A**, Hansmann M-L, Dalla-Favera R, (2003) Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. J. Clin. Invest;111(4):529-537.
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- [37] Basso K, Klein U, Niu H, Stolovitzky GA, Tu Y, **Califano A**, Cattoretti G, Dalla-Favera R., (2004) Tracking CD40 signaling during germinal center development. *Blood*; 104(13):4088-96.
- [38] Basso K, Klein U, Niu HF, **Califano A**, et al. "Tracking CD40 signaling during normal germinal center development by gene expression profiling" *ANNALS OF THE NEW YORK ACADEMY OF SCIENCES* 987: 288-290 2003
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- [41] Poppema S, Kluiver JL, Atayar C, van den Berg A, Rosenwald A, Hummel M, Lenze D, Lammert H, Stein H, Joos S, Barth T, Dyer M, Lichter P, Klein U, Cattoretti G, Ghoghini A, Tu Y, Stolovitzky GA, **Califano A**, Carbone A, Dalla-Favera R, Melzner I, Bucur AJ, Bruderlein S, Dorsch K, Hasel C, Barth TF, Leithauser F, Moller P., (2005) Report: workshop on mediastinal grey zone lymphoma. *Eur J Haematol Suppl.* 2005 Jul;(66):45-52.
- [42] Wang K, Banerjee N, Margolin AA, Nemenman I, **Califano A**, (2006) Genome-wide discovery of modulators of transcriptional interactions in human B lymphocytes, in *Lecture Notes in Computer Science*, Vol. 3909:348-362, Proceedings of the 10th Annual International Conference on Research in Computational Molecular Biology (RECOMB).
- [43] Margolin AA, Wang K, Lim WK, Kustagi M, Nemenman I, **Califano A** (2006). "Reverse engineering cellular networks." *Nature Protocols*; 1(2): 662-671.
- [44] Margolin AA, Nemenman I, Basso K, Wiggins C, Stolovitzky G, Dalla Favera R and **Califano A**, (2006) ARACNE: An Algorithm for the Reconstruction of Gene Regulatory Networks in a Mammalian Cellular Context, *BMC Bioinformatics*;7(Suppl.1):S7, also arXiv.org/abs/q-bio.MN/0410037. **Selected by the Faculty of 1000**
- [45] Palomero T, Lim WK, Odom DT, Sulis ML, Real PJ, O'Neal J, Neuberg D, Margolin AA, Weng A, Aster JC, Sigaux F, Soulier J, Look AT, Young R, **Califano A*** and Ferrando A, (2006) NOTCH1 directly regulates MYC expression and controls oncogenic cell growth, *Proc. Natl. Acad. Sci USA*; 103 (48): 18261-18266 NOV 28 2006.
- [46] Banerjee N. and **Califano A**, (2006) Transcription Factor Centric Discovery of Regulatory Elements in Mammalian Genomes Using Alignment- Independent Conservation Maps, in *Lecture Notes in Computer Science* Vol. 4205: 200-214, Springer Verlag, ISBN 978-3-540-44529-6. Proceedings of the 4th RECOMB Comparative Genomics Satellite Workshop, Montreal (CA).
- [47] Lefebvre C, Lim WK, Basso K, Dalla Favera R, and **Califano A** (2006), "A context-specific network of protein-DNA and protein-protein interactions reveals new regulatory motifs in human B cells" in *Lecture Notes in Computer Science*, Vol. 4532 Springer Verlag, ISBN: 978-3-540-73059-0. Proceedings of the 2006 RECOMB Satellite Workshop on Systems Biology, San Diego.
- [48] Sosinsky A., Honig B*, Mann R.S.* and **Califano A**, (2007) "Discovering transcriptional regulatory regions in Drosophila by a nonalignment method for phylogenetic footprinting" *Proc Natl Acad Sci U S A*. 2007 Apr 10;104(15):6305-10. Epub 2007 Mar 29.

- [49] Piccaluga PP, Agostinelli C, **Califano A**, Rossi M, Basso K, Zupo S, Went P, Klein U, Zinzani PL, Baccarani M, Dalla Favera R, and Pileri SA, (2007) " Gene expression analysis of peripheral T cell lymphoma, unspecified, reveals distinct profiles and new potential therapeutic targets. *J Clin Invest*. 2007 Mar;117(3):823-34. Epub 2007 Feb 15
- [50] Mani K, Lefebvre C, Wang K, Lim WK, Margolin AA, Basso K, Dalla-Favera R, and **Califano A**, (2007) "A Systems Biology Approach to the Identification of Causal Somatic Mechanisms in Cancer Phenotypes." In Press, Proceedings of RECOMB Computational Cancer Biology.
- [51] Lim WK, Wang K, Lefebvre C, and **Califano A**, (2007) "Comparative analysis of microarray normalization procedures: effects on reverse engineering gene networks" in *Bioinformatics* 23(13):i282-i288.
- [52] Li Z, Zheng T, **Califano A**, and Floratos A (2007), "Pattern-based mining strategy to detect multi-locus association and gene-environment interaction" in press *BMC Genetics*.
- [53] Margolin AA, Palomero T, Ferrando A*, **Califano A***, and Stolovitzky G* (2007), "ChIP-on-chip significance analysis reveals large scale transcription factor activity" (Best student paper award at ISMB 2007), in press *Bioinformatics*.
- [54] Stolovitzky G, Monroe D, and **Califano A** (2007) "Dialogue on Reverse-Engineering Assessment and Methods: The DREAM of High-Throughput Pathway Inference," *Ann N Y Acad Sci*. 2007 Oct 9.
- [55] Margolin A and **Califano A** (2007) "Theory and Limitations of Genetic Network Inference from Microarray Data," *Ann N Y Acad Sci*. 2007 Oct 9.
- [56] Mani K, Lefebvre C, Wang K, Lim WK, Basso K, Dalla-Favera R, and **Califano A**, (2007) "A Systems Biology Approach to the Prediction of Causal Oncogenic Mechanisms and Drug Mechanism-of-Action Profiles in Cancer Phenotypes," *Molecular Systems Biology*, in press.
- [57] Piccaluga PP, Agostinelli C, **Califano A**, Carbone A, Fantoni L, Ferrari S, Gazzola A, Gloghini A, Righi S, Rossi M, Tagliafico E, Zinzani PL, Zupo S, Baccarani M, Pileri SA, (2007) "Gene expression analysis of angioimmunoblastic lymphoma indicates derivation from T follicular helper cells and vascular endothelial growth factor deregulation" *Cancer Res*. 2007 Nov 15;67(22):10703-10.
- [58] Lim WK, Wang K, Lefebvre C, and Califano A (2007), "Comparative analysis of microarray normalization procedures: effects on reverse engineering gene networks." Vol. 23 *ISMB/ECCB* 2007, pages i282-i288.
- [58] Carro MS*, Lim WK*, Snyder E, Colman H, Aldape K, Lasorella A, **Califano A***, and Iavarone A*, (2007) "A transcriptional regulatory network initiates and maintains the mesenchymal phenotype of human malignant glioma." submitted (in review at *Science*)
- [59] Wang K, Saito M*, Nemenman I, Basso K, Margolin AA, Klein U, Dalla-Favera R*, and **Califano A***, (2007), "Genome-wide identification of transcriptional network modulators in human B cells," submitted (second round of review at *Nature*).
- [60] Margolin AA*, Palomero T, Sumazin P, **Califano A***, Ferrando A*, Stolovitzky G*, (2007) "ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes" submitted (*Nature Biotechnology*)

Book Chapters, and Editorials

- [61] Califano A and Savorelli S, "Caos" (Chaos), *Science* '85, 1st. Ed., May 1985.
- [62] Califano A and Bolle RM, "A Layered Multi Resolution Approach to 3D Vision," in J.K. Aggarwal (ed.), *Multisensor Fusion for Computer Vision*, NATO ASI Series F, Springer Verlag (1990).
- [63] Bolle RM and Califano A: "A framework for 3D recognition," in *Machine Vision for Three-Dimensional Scenes*, H. Freeman (ed.). New York: Academic Press, 1990, pp. 1-24.

- [64] Bolle RM, Califano A, Kjeldsen R: "Constraint Satisfaction Networks for 3D object recognition," book chapter in Progress in Neural Networks: Neural Networks in Vision, R. Mohan and O.M. Omidvar (Ed.), Ablex Publishing, 1992
- [65] Bolle RM, Califano A, Kjeldsen R, Mohan R: "Active 3D object model networks ," book chapter in 3D Object Recognition Systems, A. Jain and P. Flynn (ed.), New York: Academic Press, 1992.
- [66] Califano A, Kjeldsen R, Bolle RM: "Data and Model Driven Active Vision," in a special issue on Active Vision of the International Journal of Computer Vision, M. Swain (ed.).

Invited papers, Research Reports, and abstracts

- [67] **Califano A**, "Use of Correlated Information for Feature Recognition," IBM Tech. Rep. RC 14116 (#62148)(1988) Computer Science.
- [68] Bolle RM, **Califano A**, Kjeldsen R, and Taylor RW, "Computer Vision Research at the IBM T.J. Watson Research Center," in Proc. DARPA Image Understanding Workshop, May 1989, pp. 471-478.
- [69] Bolle RM and **Califano A**, "Data and model driven multiresolution," SIAM Conf. on Nonlinear Dynamical Systems, Orlando, FL,(5/8/90).
- [70] Bolle RM, **Califano A**, Kender J, Kjeldsen R, and Mohan R: "Computer vision research at the IBM T.J. Watson Research Center, anno 190" IBM RC 15915, (7/11/90).
- [71] Bolle RM, **Califano A**, "Multilevel evidence fusion for the recognition of 3D objects," in SPIE Proc. Vol. 1383, Sensor Fusion III: 3-D Perception and Recognition, (invited paper) November 1990
- [72] **Califano A** and Mohan R: "High dimensional indexing for shape acquisition and recognition," in Proc. of 1991 Workshop on Computer Vision, Capri, Italy, May 1991
- [73] **Califano A** and Bolle RM: "Multiresolution and Tractability," IBM Research Report RC 17359, October 1991.
- [74] Rigoutsos I and **Califano A**, "dFLASH: A distributed Fast Look-up Algorithm for String Homology," in Proceedings of the 1994 Dartmouth Advanced Institute for Parallel Computing, Hanover, NH
- [75] Germain RS, Bolle RM, **Califano A**, Colville S, Pankanti S and Ratha N, "Issues in large scale automatic biometric identification," in Proceedings of the Workshop on Automatic Identification Advanced Technologies, Stony Brook, NY (1997)
- [76] **Califano A** and Stolovitzky G, "Pattern Relevance in Biological Datasets," Tenth International Genome Sequencing and Analysis Conference, Fontainebleau FL, 1998, also available as IBM RC at <http://www.research.ibm.com/splash/Papers/Pattern%20Statistics.pdf>
- [77] Royyuru AK and **Califano A**, "Novel Approach to Identification of Functional Similarity in Protein Structures" in Structure Based Functional Genomics Conference, Avalon NJ, 1998
- [78] Piccaluga P, Agostinelli C, Zupo S, ... **Califano A**, et al., "Gene expression analysis of peripheral T-cell lymphoma not otherwise specified reveals the existance of two subgroups related to different cellular counterparts" ANNALS OF ONCOLOGY 16: 74-75 125 Suppl. 5 JUN 2005
- [79] Piccaluga PP, Agostinelli C, Zupo S, ... **Califano A**, et al. "Gene expression analysis of peripheral T-cell lymphoma not otherwise specified reveals the existance of two subgroups related to different cellular counterparts and recurrent PDGFRA deregulation" BLOOD 106 (11): 354A-354A 1217 Part 1 NOV 16 2005
- [80] Palomero T, Odom DT, Margolin A, ... **Califano A***, and Ferrando A*, "Transcriptional regulatory networks downstream of NOTCH1 in T-cell acute lymphoblastic leukemia" BLOOD 106 (11): 219A-219A 740 Part 1 NOV 16 2005

- [81] Deng MC, Cadeiras M, Lim WK, ... and **Califano A**, "Calcium responsive element binding protein CREB molecular network is differentially enriched during rejection and quiescence in heart transplant recipients" CIRCULATION 114 (18): 55-55 Suppl. S OCT 31 2006
- [82] Gangadin AR, Cadeiras M, Sinha A, ... **Califano A***, and Deng M. "Gene expression profiling in patients with antibody mediated rejection" JOURNAL OF HEART AND LUNG TRANSPLANTATION 26 (2): S136-S137 215 Suppl. S FEB 2007
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