Artemis-Georgia Hatzigeorgiou

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Education

1993	MSE in Computer Science, University of Stuttgart, Germany.
2001	PhD in Molecular Biology, University of Jena, Germany.

Positions held

Research and Fellowship Appointments

1992	Research Assistant, Institute of Process Automation, Frauenhofer Gesellschaft, Stuttgart, Germany.
1993-96	Research Associate, German Cancer Research Center, Heidelberg, Germany.
1996	Fellowship, Gene prediction in Bacteria, Los Alamos National Laboratory, New Mexico.

Faculty Appointments

2001- 2007	Assistant Professor, Department of Genetics School of Medicine, University of Pennsylvania.
2001-2007	Assistant Professor, Department of Computer and Information Science, University of Pennsylvania (secondary appointment).
2007-	Principal Investigator, BSRC Alexander Fleming, Vari-Athens
2007-	Adjunct Assistant Professor, Department of Computer and Information Science, University of Pennsylvania

Administrative Appointments

1996-00	Chief scientist, Synaptic Ltd., Science and Technology Park of Crete, Heraklion, Greece.
2000-01	Group Leader, Bioinformatics, MetaGen GmbH, Berlin, Germany.

Honors and Awards

1995	Best Young Research Performance Award, German Cancer Research Center (DKFZ), Heidelberg, Germany.
1995	Neural Network Best Poster Paper Award, World Congress on Neural Networks, Washington D.C., USA.
2000	1st award New Entrepreneur of Heraklion County, Hellenic State Organization of Small and Medium Enterprise.
2003	National Science Foundation (NSF) Young Investigator Career Award.

Reviewer for

Journals:

Bioinformatics, BMC Bioinformatics, Genome Research, Genomics,
Journal of Biomolecular Structure and Dynamics,
International Journal of Computers, Systems and Signal, Nature,
Nature Genetics, Nature Methods, Nature Structural Biology
Neural Networks and Intelligent Systems for Biological Sequence Data Analysis,
Pattern Recognition, PLOS Computational Biology, PLOS Genetics,
Trends in Biotechnology.

Institutes

Welcome Trust Sanger Institute, Ηνωμένο Βασίλειο, 2005.
National Science Foundation (NSF), HPA 2005, 2008.
National Institute of Health (NIH), HPA, 2008.

Organizing Roles in Scientific Meetings

1996	*International Workshop on Computational Analysis of Eukaryotic Transcription Regulatory Elements*. German Cancer Research Center, Heidelberg, Germany
1999	*EST Data Analysis. BioStandarts Workshop*. European Molecular Biology Laboratory - European Bioinformatic Institute, Hinxton, UK.
2002	*Bioinformatics and Genomics: Methods, Data, and Prediction*. Institute for Mathematical Science, Singapore.
2005	*Workshop on miRNA target and gene prediction*. Foundation of Research and Technology Hellas, Crete, Greece.
2007	Fellowship committee member for the 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 6th European Conference on Computational Biology (ECCB), Vienna, Austria.

Memberships in Professional and Scientific Societies

Institute of Electrical and Electronics Engineers *(IEEE)*
International Society for Computational Biology *(ISCB)*
Association for Computing Machinery *(ACM)*

Teaching

At the University of Pennsylavania
Computational Biology/Genome Informatics (Fall 2002).
Computational Biology (Fall 2003).
Machine Learning For Bioinformatics (Spring 2004).
Advanced Computational Biology (Fall 2004).
Advanced Computational Biology (Fall 2005).

At the University of Athens
Teaching the graduate course of Bioinformatics
of the Master course Computer Science in Medicine and Biology (2008-2009)

PhD Students (Genetics and Computational Biology Graduate Program at Upenn)
Molly Megraw 2004 – 2007 Current Position PostDoc (Uwe Uhler Group) at Duke University, USA.
Praveen Sethupathy 2005 -20:08 Current Position PostDoc (Phill Green Group) at NIH, USA.
Axel Bernal 2003 – co-adviced with F. Perreira.

PhD students at BSRC Al. Fleming

Pangiotis Alexiou	2007 -
Manolis Maragakis	2007-
Giorgos Papadopoulos	2008 -.

Lectures by Invitation:

1) Promoter recognition with neural networks.
SmithKline Beecham Pharmaceuticals. Philadelphia (1996)
2) Promoter recognition with neural networks.
National Center for Biotechnology Information (NCBI), Washington D.C. (1996)
3) Gene identification by neural networks.
Conference Industrial Applications of Neural Networks and Fuzzy logic,
IEEE Systems Man and Cybernetic Society, Lilly, France (1996)
4) Gene identification by neural networks.
Computer Science Department, University of Ioannina, Greece (1997)
5) Finding the correct amino acid sequence in EST's.
Max Delbrueck Zentrum, Berlin, Germany (1999).
6) Feature recognition on Expressed Sequence Tags in human DNA.
Center of Bioinformatics, University of Pennsylvania, Philadelphia, USA (1999).
7) Annotation of Expressed Sequence Tag’s.
European Bioinformatics Institute (EBI), Hinxton, UK (1999).

2000
8) An improved method for prediction of translation initiation sites in human cDNA's and EST's.
Deutsches Krebsforschungszentrum, Heidelberg, Germany
9) Computational analysis of mRNA sequences.
South African National Bioinformatics Institute, Cape Town, South Africa .
10) Prediction of translation initiation sites.
Center for Engineering Research, Technicon Natal, Durban, South Africa .

11) Prediction of translation initiation sites in human cDNA's. *SmithKline Beecham Pharmaceuticals, Philadelphia*, USA.
12) Prediction of translation initiation sites in human cDNA's.
Celera Genomics, Rockville, USA .
13) Translation initiation site Prediction.
Cold Spring Harbor Laboratory, Long Island .

2002
14) Artificial Neural Networks in gene prediction.
University of Patras, *Medichal School,* Greece .
15) Gene prediction in human sequences.
University of Thessaly, *Department of Computer Science*, Greece.

2003
16) Targets of miRNA's.
University of Athens, Department of Agriculture, Greece .
17) MiRNA genes and targets.
Drexel University, Philadelphia, USA .
18) MiRNA gene and target prediction.
Institute of Molecular Biology and Biotechnology,
Foundation of Research and Technology Hellas, Crete, Greece .

2004
19) MiRNA gene and target prediction*",*
Grup de Recerca en Informatica Biomedica (GRIB) - IMIM/UPF/CRG, Barcelona, Spain.
20) MiRNA target prediction.
European Molecular Biology Laboratory (EMBL), Heidelberg, Germany.
21) MiRNA gene and target prediction.
Cold Spring Harbor Laboratory, Long Island, USA .

2005
22) MiRNA target prediction on human genes.
NY Academy of Science, New York, USA.
23) MiRNA gene and target prediction.
Regeneron Pharmaceutical, Tarytown, USA.
24) MiRNA function.
Institute for plant Genetics, Gatersleben, Germany.
25) MiRNA function.
University of Patras, Patra, Greece.
26) MiRNA function.
IIBEAA, Academy of Athens, Athens, Greece.

2006
27) MiRNA biogenesis and function.
Meeting of the Teratology Society, Arizona, USA.
28) MiRNAs Biogenesis and Function: a computational experimental approach.
MRC Clinical Sciences Centre , Imperial College , London, UK.
29) MiRNAs Biogenesis and Function: a computational experimental approach.

Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge, UK.
30) Computational predictions of microRNA genes and targets: exploring the significance and validation of current approaches.
Frontiers In Science Events of New York Academy of Science, NY, USA (8.11.2006).
Audio, video & report available online at http://www.nyas.org/ebrief/miniEB.asp?eBriefID=623

2007
31) Identification and editing of microRNAs.
Workshop of Evolution of Molecular Networks, KITP, *University of Santa Barbara* (14.3.2007)
Audio, slides & video available online at http://online.kitp.ucsb.edu/online/evonet07/hatzigeorgiou/
32) Computational and experimental approaches for the analysis of microRNAs.
PICASso seminar, *Princeton University* (21.2.2007)
Video available online at http://www.cs.princeton.edu/picasso/bio_F06_S07.php
33) Computational/experimental approaches for microRNA biogenesis and function.
Current Topics Workshop: MicroRNA in Development and Cancer Schedule, MBI,
Ohio State University (12.4.2007).
34) Computational/experimental approaches for microRNA biogenesis and function.
29th Scientific Conference of the Greek Society for Biological Sciences, Kavala, Greece (17.05.07).
33) Identification and analysis of microRNAs: a computational/experimental interplay.
Moscow *Conference on Computational Molecular Biology* (MCCMB'07) (29.07.07).
34) Combination of computational and experimental approaches for analysis of microRNA function.
5th General meeting of the International Proteolysis Society, Bioinformatics - Computational Methods in Biological Data Mining, University of Patra, Greece (19.10.07).
35) Identifying microRNAs and their targets
The 6th Georgia Tech-Oak Ridge National Lab, International Conference on Bioinformatics, in silico Biology: Gene Discovery and Systems Genomics (17.11.07).
36) Identifying microRNAs and their targets
National Conference of Biochemistry and Molecular Biology, Athinais Complex, Athens (9.12.07)

2008
37) Bioinformatic analysis of miRNAs and their targets,
EADGENE miRNAs workshop, University of Liège, Belgium (3.4.08).
38) Computational/experimental approaches for the functional analysis of microRNAs in diseases.
Workshop: miRNAs in Health & Disease 2, University of Liège, Belgium (4.4.08)
39) MiRNA genes and their targets.
The 3rd Warsaw-Berlin Workshop on Computational Biology, Max Planck Institute for Molecular Genetics, Berlin (7.04.08).
40) Computational/experimental approaches reveal function of microRNAs in disease.
Regeneron Pharmaceutical, Tarytown,NY. USA (6.6.08).
41) Computational/experimental approaches reveal function of microRNAs in disease.
Department of Bioingineering, Stanford University, CA, USA (10.6.08).
42) Computational/experimental approaches reveal function of microRNAs in disease.
New Ingland Biolabs Inc., Boston, USA (13.6.08).
43) Computational/experimental approaches reveal function of microRNAs in disease
International Epigenetic Symposium at Institute of Agrobiotechnology,
Center for Research and Technology, Thessaloniki, Hellas (27.6.08).
44) Computational/experimental approaches reveal function of microRNAs in disease
33rd Federation of European Chemical Society (FEBS) Congress, Athens, Greece. (2.7.08)

Bibliography

Refereed Journal articles

1. M. Reczko, A. Hatzigeorgiou, N. Mache, A. Zell and S. Suhai (1995) A Parallel Neural Network Simulator on the Connection Machine CM-5. ***Comp. Appl. in Biosci.***11:309-315.

2. J. Bolz, K. Zerfass, D. Spitkovsky, H.-J. Delius, B.Vogt, M. Eilers, A. Hatzigeorgiou and P. Jansen-Durr (1996) Cell cycle regulation of the murine Cylin E gene depends on an E2F binding cite in the promoter. ***Mol. Cell. Biol***., 16:3401-3409.

3. P. Bucher, J.W. Fickett and A. Hatzigeorgiou (1996) Computational analysis of transcriptional regulatory elements: a field in flux. ***Comp. Appl. In Biosci.,*** 12:361-362.

4. J.W. Fickett and A.C. Hatzigeorgiou (1997) Eukaryotic Promoter Recognition. ***Genome Research****,* 7:861-878.

5. S. Hannenhalli, W. Hayes, A. G. Hatzigeorgiou and J. W. Fickett (1999) Bacterial start site prediction*.* ***Nucl. Acid. Res***., 27:3577-3582.

6. A.G. Hatzigeorgiou, P. Vizief, M Reczko (2001) DIANA-EST: A statistical analysis. ***Bioinformatics***, Vol. 17, pp. 913-919.

7. A.G. Hatzigeorgiou (2002). Translation initiation site prediction in human cDNAs with high accuracy. ***Bioinformatics***, Vol. 17, pp. 913-919.

8. V. B. Bajic, S Tang, H. Han, V. Brusic and A. G. Hatzigeorgiou (2002) Artificial Neural Networks based systems for recognition of genomic signals and regions. ***Informatica,*** 26:389-400.

9. P.T. Nelson, AG. Hatzigeorgiou, Z. Mourelatos (2003) miRNP:miRNA association in polyribosomes, in a human neuronal cell line. ***RNA****,* 10(3):387-94.

10. M. Reczko, A.G. Hatzigeorgiou (2003) Prediction of the subcellular localization of eukaryotic proteins using sequence signals and composition. ***Proteomics,***4(6)¨1591-6.

11. Kiriakidou M., Nelson P.T., Kouranov A., Fitziev P., Bouyioukos C., Mourelatos Z. and A. Hatzigeorgiou (2004) A combined computational-experimental approach predicts human microRNA targets. ***Genes & Development***, 18(10):1165-78.

12. M. Yousef, A. Kouranov, Z. Mourelatos, A. Hatzigeorgiou (2004) Prediction of Human microRNA Targets using Parallel Computing. *WSEAS* ***Transactions on Information Science and Applications***, 1(1):581-586.

13. H. Miller … A.G. Hatzigeorgiou…. International Chicken Genome Sequencing Consortium (2004) Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. ***Nature,*** 432(7018).

14. P. Sethupathy, B. Corda and A.G. Hatzigeorgiou (2006) TarBase: A comprehensive database of experimentally supported animal microRNA targets. ***RNA****,* 12: 192-197.

15. L. Zhang. J. Huang, N. Yang, M. Megraw, S. Liang, T. Naylor, A. Bachetti, A. Giannakakis, G. Yao, S. Liang, A. Medina, D. Katsaros, A. Hatzigeorgiou, P. Gimotty, B. Weber, G. Coukos (2006) MicroRNAs and their associate genes exhibit high frequency genomic alteration in human epithelial cancers ***PNAS****, USA* 13;103(24):9136-41.

16. M. Megraw, V. Baev, V. Rusinov, S. Jensen, K. Kalantidis, A. G. Hatzigeorgiou (2006) MicroRNA Promoter Element Discovery in Arabidopsis. ***RNA,*** 12: 1612:1619.

17. P. Sethupathy, J. Hirel,, A. G. Hatzigeorgiou (2006) A comparative analysis of mammalian microRNA target prediction programs. ***Nature Methods****,* 3(11):881-6.

18. W. Kang, R. Mukerjee, J. J. Gartner, A. G. Hatzigeorgiou, R. M. Sandri-Goldin, N. W. Fraser (2006) Characterization of the Spliced Exon Product of Herpes Simplex Type-1 Latency Associated Transcript in Productively Infected Cell. ***Virology****,* Dec 5-20;356(1-2):106-14.

19. M. Megraw, P. Sethupathy, B. Corda, A.G. Hatzigeorgiou (2007). miRGen: A database for the study of animal microRNA genomic organization and function. ***Nucleic Acids Research***, Jan;35:D149-55.

20. Y. Kawahara, B. Zinshteyn, P.Sethupathy, H. Iizasa, A.G. Hatzigeorgiou, K. Nishikura (2007) Dictation of silencing targets by adenosine-to-inosine editing of microRNAs. ***Science,*** Feb 23;315(5815):1137-40.

21. A. Bernal, K. Crammer, A.G. Hatzigeorgiou, F. Pereira (2007) Global Discriminative Learning for Higher-Accuracy Computational Gene Prediction. ***PLoS Comput Biol.***, Mar 16;3(3):e54.

22. P. Sethupathy, C. Borel, M. Gagnebin, G.R. Grant, Artemis G. Hatzigeorgiou, S.E. Antonarakis Human mir-155 on chromosome 21 differentially interacts with its polymorphic targets in the AGTR1 3'UTR- a mechanism for functional SNPs related to phenotypes. ***American Journal of Human Genetics***, 2007 Aug;81(2):405-13. Epub 2007 Jul 12 (corresponding author).

23. Giannakakis A, Coukos G, Hatzigeorgiou A, Sandaltzopoulos R, Zhang L. miRNA genetic alterations in human cancers. ***Expert Opin Biol Ther***. 2007 Sep;7(9):1375-86. Review.

24. L. Zhang**,** S. Volinia, T. Bonome, G.A. Calin, J. Greshock, N. Yang **,** C. Liu, A. Giannakakis**,** P. Alexiou, K. Hasegawa, C. N. Johnstone, M. S. Megraw, S. Adams, H. Lassus, J. Huang, S. Kaur, S. Liang, P. Sethupathy, A. Leminen, V.A. Simossis, R. Sandaltzopoulos, Y. Naomoto, D. Katsaros, P.A. Gimotty, A. DeMichele, Q. Huang, R. Bützow, A.K. Rustgi, B.L. Weber, M.J. Birrer, A.G. Hatzigeorgiou, C.M. Croce and G. Coukos (2008) Genomic and Epigenetic Alterations Deregulate microRNA Expression in Human Epithelial Ovarian Cancer, ***PNAS****,* (May 13;105(19):7004-9. Epub 2008 May 5)(co-corresponding author).

25. Y. Kawahara, M. Megraw, E. Kreider, H. Iizasa, L. Valente, A. G. Hatzigeorgiou, K. Nishikura (2008) Frequency and Fate of microRNA Editing in Human Brain. ***Nucleic Acids Research*** Sep;36(16):5270-80. Epub 2008 Aug 6.

26. G. Papadopoulos, M. Reczko, V. Simossis, P. Sethupathy, A. Hatzigeorgiou, The database of experimentally supported targets: a functional update of TarBase5.0 (2009) ***Nucleic Acids Research*** Jan;37(Database issue):D155-8. Epub 2008 Oct 27.

27. M. Megraw, F. Perreira, S. Jense, U. Ohler, A.G. Hatzigeorgiou. A Transcription Factor Affinity Based Code for Mammalian Transcription Initiation (2009) ***Genome Res***. Jan 13. [Epub ahead of print].

Complete Articles in Refereed Conferences

1. A. Hatzigeorgiou, N. Mache, J. Wieland, M. Reczko, A. Zell, P. Levi, S. Suhai(1994) Recognition of promoters and coding region on eukaryotic sequences with neural networks. *In Proceedings of the Workshop in Bioinformatics*, 70-74, Institute for Molecular Biology.

2. M. Reczko, H. Bohr, S. Subramaniam, S. Pamidighantam, and A. Hatzigeorgiou (1994) Fold class Prediction by neural networks. *In Protein Structure by Distance Analysis*, eds. S. Brunak and H. Bohr, 227-286, IOS Press.

3. A. Hatzigeorgiou, T. Harrer, N. Mache, M. Reczko (1995) The gene sequence analysis system DIANA. *In Bioinformatics: from Nucleic Acids and Proteins to Cell Metabolism.* 19-28, ed. D. Schomburg and U. Lessel, GBF Braunschweig, VCH press.

4. A. Hatzigeorgiou and M. Reczko (1996) Gene identification with Neural Networks. *In Symposium on Control, Optimization and Supervision - IMACS Multiconference,* (1):140-143, Lilly, IEEE-SMC.

5. A. Hatzigeorgiou, N. Mache and M. Reczko (1996) Functional site prediction on the DNA sequence by Artificial Neural Networks. *In Proceedings IEEE International Joint Symposia in Intelligence and Systems,*. 12-17, IEEE Computer Society Press.

6. A.G. Hatzigeorgiou, H. Papanikolaou and M. Reczko (1999) Finding the reading frame in protein coding regions on DNA sequences: a combination of statistical and Neural Network methods. *In Computational Intelligence: Neural Networks & Advanced Control Strategies* ed. M. Mohammadian,. 148-153, Vienna, IOS Press.

7. M Reczko, P. Viziev, E. Staub, A.G. Hatzigeorgiou (2002) Finding signal peptides in human protein sequences using recurrent neural networks. *2nd Workshop on Algorithms in Bioinformatics,* Springer Verlag, 60-67.

8. A. G. Hatzigeorgiou and M. Reczko (2004) Signal peptide prediction on DNA sequences with Artificial Neural Networks. In *Proc. of IEEE International Workshop on BioMedical Circuits & Systems* IEEE press.

9. P. Sethupathy, M. Megraw, I.M. Barrasa, A.G. Hatzigeorgiou (2005) Computational identification of regulatory factors involved in microRNA transcription. Proceedings of PCI 2005. In Lecture Notes in Computer Science.

10. H. Hinsch, A. G. Hatzigeorgiou (2006) Simple methods of finding short protein coding sequences using multiple species alignments. Proceedings of BIOCOMP 06, pp. 17-23.

11. K. Szafranski, M. Megraw, M. Reczko, A. G. Hatzigeorgiou (2006) Support Vector Machines for Predicting microRNA Hairpins. Proceedings of BIOCOMP 06, pp. 270-276.

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Book chapters

1. A.G Hatzigeorgiou, M. Megraw (2005) Analysis of DNA Sequences: Hunting for Genes, in Information Processing & Living Systems, ed. VB. Bajic, T. Wee, World Scientific Publishing.

2. P. Sethupathy, M. Megraw and A.G. Hatzigeorgiou (2006). Computational approaches to elucidate microRNA biology. In microRNAs: From Basic Science to Disease Biology, ed. Krishnarao Appasani, Cambridge University Press.

3. .P. Sethupathy, M. Megraw and A.G. Hatzigeorgiou (2008). A suite of resources for the study of miRNA ontology and function. Ed. R. Gaur. CRC press (in press).

4. M. Megraw and A.G. Hatzigeorgiou (2008) MicroRNA Promoter Analysis. Ed. B Meyer & P. Green. In Plant miRNA methods. Methods in Molecular Biology series, Humana Press, USA (in press).

Reports

1. A. Hatzigeorgiou (1992) The learning algorithm Backpercolation. *In Proceedings of the Simulation of Neural Networks Workshop,* 112-120, University of Stuttgart Institute of Parallel and Distributed High-Performance Systems.

2 A. Hatzigeorgiou (1993) Texture recognition with neural networks. *In Proceedings of the Simulation of Neural Networks Workshop,* 50-58, University of Stuttgart Institute of Parallel and Distributed High-Performance Systems.

3. A. Zell, G. Mamier, M. Vogt, N. Mache, R. Huebner, S. Doering, K. U. Herrmann, T. Soyez, M. Schmalzl, T. Sommer, A. Hatzigeorgiou, D. Posselt, T. Schreiner, B. Kett, G. Clemente, M. Reczko, M. Riedmiller M. Seemann, M. Ritt, J.DeCoster, J. Biedermann, J. Danz, C. Wehrfritz, R. Werner and M. Berthold (1995) *Stuttgart Neural Network Simulator (SNNS) User Manual,* Vers. 4.0 University of Stuttgart, Institute of Parallel and Distributed High-Performance, Report No. 6/95, 265 pages
SNNS is a widely used open source software for simulating Artificial Neural Networks worldwide. As such it is part of the software that is provided with the open source Red Hut Linux operating.

4. A. Hatzigeorgiou, F. Hermann, M. Reczko, S. Suhai, J. G. Reich, J. Hanke, N. Mache, A. Zell and P. Levi (1996) Project Neurogen: neuronal and genetic algorithms for parallel computers applied *in the genome research. Statusseminar Informationstechnology* 195-220, Braunschweig, German Ministry of Research.

Completed Grants

1999-2001 *Physical mapping and transcript analysis of the gene-dense human chromosome band 10q24, for the identification of familial epilepsy (EPT) and ectrodactylsplit hand-split foot malformation type 3 (SHSF3) disease genes.* (in collaboration with the CNR Institute of Molecular Genetics, Alghero, Italy, and the Institute of Molecular Biology and Biotechnology, FORTH, Greece), funded by the Bilateral Cooperation Division, International Cooperation Directorate, General Secretariat of Research and Technology, Ministry of Development of Greece (Principal investigator for the Synaptic Ltd. contribution).

1999-2001 *Physical mapping and transcript analysis of the gene-dense human chromosome band 10q24, for the identification of familial epilepsy (EPT) and ectrodactylsplit hand-split foot malformation type 3 (SHSF3) disease genes.* (in collaboration with the CNR Institute of Molecular Genetics, Alghero, Italy, and the Institute of Molecular Biology and Biotechnology, FORTH, Greece), funded by the Bilateral Cooperation Division, International Cooperation Directorate, General Secretariat of Research and Technology, Ministry of Development of Greece (Principal investigator for the Synaptic Ltd. contribution).

1999-2001 *Computational functional sequence mapping of Drosophila DNA.*
(in collaboration with the Institute of Protein Research, Russian Academy of Sciences and the Institute of Molecular Biology and Biotechnology, FORTH, Greece), funded by the Bilateral Cooperation Division, International Cooperation Directorate, General Secretariat of Research and Technology, Ministry of Development of Greece.(Principal investigator for the Synaptic Ltd. contribution).

1999-2001 *Development and progress of the nucleotide sequence methodology:*
Analysis of the transcription factors of the IRF family (Interferon Regulatory Factors) and of the STAT1 (Signal Transducer and Activator of Transcription 1) in the chronic myeologenic leukemia (in collaboration with the Institute of Molecular Biology and Biotechnology, the Institute of Computer Science, Foundation of Research and Technology Hellas, Greece, the Aristotele's University of Thessalonika, Greece and the Dimokritios University of Thracien, Greece), funded by the Program for the Amplification of the Research Potential from the General Secretariat of Research and Technology, Ministry of Development of Greece. (Co-Investigator for the Institute of Computer Science, FORTH contribution).

2000-2005 The European Wolbachia Project:
Towards novel biotechnological approaches for control of arthropod pests and modification of beneficial arthropod species by evdosymbiotic bacteria.,(with the IMBB-FORTH, the Upsala University, the Copenhagen University, the University of Wales, the University of Cambridge, the Wageningen University and the University de Poitiers funded by the Commission of the European Communities (Principal investigator for the Synaptic Ltd. contribution).

2003-2005 Co-PI Penn Genomics Institute Prediction of miRNA binding sites.

2003-2008 PI National Science Foundation (NSF) Career Award: Gene Prediction the final step.