Pavlos Pavlidis

Evolutionary Biology and Bioinformatics Evolution Lab

Foundation for Research and Technology, Hellas

Institute of Computer Science (ICS)

Computational Biomedicine Laboratory (CBML)

Evolutionary Biology and Bioinformatics Group

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APPOINTMENTS

1. 2016- Researcher C, Institute of Computer Science (ICS), Foundation of Research and Technology (FORTH)
2. 2014-2016 Marie Curie Post-Doctoral Fellow: Evolution of Gene Regulatory Networks
   Group Leader: Dr. Panayota Poirazi
   Institute: IMBB, FORTH, Heraklion, Greece
3. 2013-2014 PostDoc in BioComputing & Molecular Modeling
   Project: InnovCrete (EU-funded FP7 REGPOT)
   Group Leader: Prof. Mike Kokkinidis
   Institute: IMBB, FORTH, Heraklion, Greece
4. 2011-2013 PostDoc in Phylogenetics and Pop. Genetics
   Project: High Performance Computing in Population Biology
   Group Leader: Prof. Dr. Alexandros Stamatakis

EDUCATION

1. 2007-2011 PhD in Evolutionary Biology
   Advisor: Prof. Dr. Wolfgang Stephan
   Institute: Ludwig-Maximilians-University, Munich, Germany
   Title of dissertation:
   Detecting selective sweeps in natural populations of *Drosophila melanogaster*: Methods, applications, and extensions (summa cum laude)
2. 2005-2007 PhD Student in Computer Science and Mathematics
   Advisor: Dr. Jaak Vilo
   Institute: University of Tartu, Tartu, Estonia
   Research topic: Detection and analysis of transcription factor binding sites
3. 2003-2005 M.Sc. of Biology
   Advisor: Dr. Panayiota Poirazi, Prof. Nikolaos Panopoulos
   Institute: University of Crete, Heraklion, Greece
   Title of dissertation: Analysis of microarrays: Finding informative genes, clustering and classification (9.55/10)
   General grade: 8.99/10
4. 1998-2003 Diploma in Agricultural Biotechnology
   Advisor: Prof. John Sourdis
   Institute: Agricultural University of Athens, Athens, Greece
   Title of dissertation: Evolutionary reconstruction in mitochondrial genomics (10/10)
   General grade: 8.05/10

WORKSHOPS & RESEARCH ACTIVITIES

1. Training in the group of Prof. Jan Komorowski on microarray classification methods
   Jun. 2005, University of Uppsala, Uppsala, Sweden
2. Evolutionary Biology Course in Guarda
   Jun. 2006, University of Basel, Basel, Switzerland
3. Summer Institute in Statistical Genetics
   Sep. 2007, University of Liege, Liege, Belgium

HONORS & AWARDS

1. Award from Greek National Scholarship Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology. 2004, University of Crete, Heraklion, Greece
2. Award from Greek National Scholarship Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology, 2003, University of Crete, Heraklion, Greece
3. Award from Greek National Scholarship Foundation, 2nd in Panhellenic Entrance Exams, 1998, Athens, Greece

SELECTED PRESENTATIONS IN SYMPOSIA & CONFERENCES

1. Searching for coevolving sites between mitochondria and nuclear genes
   Papadantonakis Stefanos, Ladoukakis Em., and Pavlidis Pavlos, COME 2016
2. Transcriptome Profiling by Next Generation Sequencing of Hematopoietic Progenitors in Murine Systemic Lupus Erythematosus (SLE)
   Banos A., Grigoriou M., Verginis P., Pavlidis P., Bertsias G., Boumpas DT., 36th EWRR
3. Detection of positive selection and demographic inference using SNP data, Jul. 2010, P. Pavlidis, S. Laurent, J.D. Jensen, and W. Stephan, SMBE 2010, Lyon, France
4. Detecting the signature of positive selection in genomes, May 2009 P. Pavlidis, and W. Stephan, VW 2009, Munster, Germany
5. Evolutionary conservation of BDNF gene coexpression network suggests potential regulators of BDNF gene expression, Jun. 2009 T. Aid-Pavlidis, P.Pavlidis, T.Timmusk, SMBE 2009, Barcelona, Spain

SCHOLARSHIPS & FUNDING

1. Marie-Curie IEF, Evolution of gene regulatory networks by means of natural selection and genetic drift (96.5/100)
2. Fellowship from the Volkswagen Stiftung, for Ph.D. studies. 2007-2010, Ludwig-Maximilians-University, Munich, Germany, Assistantship for foreign students (STIBET, DAAD) 2009

3. Scholarship from the Estonian government for Ph.D. studies, 2005-2007, University of Tartu, Tartu, Estonia

INVITED TALKS

1. Advanced tools to detect selective sweeps in whole-genomes and extensions of the sweep model. University of Sussex, April 2016

2. Detecting selective sweeps in full genome-data and populations that have experienced demographic events, January 2015, MPI for developmental biology, Cologne, Germany

3. The problem of detecting selective sweeps April 2012, MPI for Dev. Biology, Tuebingen, Germany

4. Detecting positive selection: i) Machine-learning and Bayesian approaches ii) Selection in multiple-locus models September 2011, HCMR, Heraklion, Greece

5. Detecting selective sweeps in natural populations of D. melanogaster June 2011, UPF, Barcelona, Spain

6. The problem of detecting selective sweeps in bottlenecked populations May 2010, HCMR, Heraklion, Greece

7. Combining SFS and LD to detect selective sweeps: a machine learning approach Apr. 2010, University of Vanderbilt, Nashville, TN, USA

8. Detecting selective sweeps in natural populations of D. melanogaster Apr. 2010, MPI for Evolutionary Anthropology, Leipzig, Germany

9. A novel approach for detecting selective sweeps in whole genome data, using machine learning techniques Jun. 2009, University of Zuerich, Zuerich, Switzerland

10. Detecting sweeps in whole genome data Apr. 2009, Evolutionary Genomics: the impact of next generation sequencing technologies, Wittenberg, Germany

TEACHING

1. Bioinformatics for Graduate students, MSc program Molecular Biomedicine, University of Crete

2. Bioinformatics for Undergraduate students, Computer Science Department, University of Crete

3. Tutor Assistant in the Computational Molecular Evolution (CoME) workshop

4. February Days Workshop: Coalescent Theory and Bioinformatics using R (ΕΛΚΕΘΕ)

5. Introduction to Bioinformatics (co-teacher with the group of A. Stamatakis)

6. R for molecular biologists (co-teacher with Vincenzo Lagani)

PUBLISHED IN CONFERENCE PROCEEDINGS

1. Duo Xu, Pavlos Pavlidis, Colin Flanagan, Supaporn Thamadilok, Emilie Redwood, Sara Fox, Ran Blekhman, Stefan Ruhl, Omer Gokcumen, Evolution of MUC7: Insights into human salivary adaptation, AMERICAN JOURNAL OF PHYSICAL ANTHROPOLOGY 159, 339-340
2. YL Lin, P Pavlidis, E Karakoc, J Ajay, O Gokcumen, Human structural variants shared with Neandertal and Denisovan genomes, AMERICAN JOURNAL OF PHYSICAL ANTHROPOLOGY 159, 209-210

PUBLISHED IN PEER-REVIEWED CONFERENCES (FULL-PAPERS)*

1. Alachiotis N., Pavlidis P., Stamatakis A. Exploiting Multi-grain Parallelism for efficient Selective Sweep Detection, ICA3PP-2012, Fukuoka, Japan, September 2012, to appear in Springer LNC

2. S. Pissis, A. Stamatakis and P. Pavlidis MoTeX: an HPC word-based tool for MoTif eXtractioN ACM-BCB 2013

** For computer-science publications Peer-Reviewed Conference Papers are usually more important than Journal Papers*

PUBLISHED IN PEER-REVIEWED JOURNALS

3. Duo Xu, Pavlos Pavlidis, Supaporn Thamadilok, Emilie Redwood, Sara Fox, Ran Blekhman, Stefan Ruhl, and Omer Gokcumen Recent evolution of the salivary mucin MUC7, accepted at Scientic Reports (July 2016)

4. Papadantonakis S, Poirazi P, Pavlidis P, CoMuS: Simulating coalescent histories and polymorphic data from multiple

species, accepted at Molecular Ecology Resources (May 2016)

5. N Alachiotis, P Pavlidis, Scalable linkage-disequilibrium-based selective sweep detection: a performance guide, GigaScience 5 (1), 1
6. Eaaswarkhanth Muthukrishnan, Pavlos Pavlidis, Omer Gokcumen, Geographic Distribution And Adaptive Significance Of Genomic Structural Variants: An Anthropological Genetics, Human Biology 86 (4), 3
7. Yen-Lung Lin,Pavlos Pavlidis, Emre Karakoc, Jerry Ajay, Omer Gokcumen The evolution and functional impact of human deletion variants shared with archaic hominin genomes accepted at MBE
8. Marc Pybus, Giovanni M Dall'Olio, Pierre Luisi, Manu Uzkudun, Angel Carreño-Torres, Pavlos Pavlidis, Hafid, Laayouni, Jaume Bertranpetit, Johannes Engelken, 1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans, accepted in NAR.
9. Pavlidis P., Zivkovic D., Stamatakis A., Alachiotis N. SweeD: Likelihood-based detection of selective sweeps in thousands of genomes. MBE, in print (online advanced access)
10. Werzner A., Pavlidis P., Ometto L., Stephan W., and Laurent S. Multiple selective sweeps in the Flotillin-2 region of European Drosophila melanogaster. PLoS ONE
11. O. Gokcumen, V. Tischler, J. Tica, Q. Zhu, R. Iskow, E. Lee, M. Fritz, A. Langdon, A. Sttz, P. Pavlidis, V. Benes, R. Mills, P. Park, C. Lee, J. Korbel Primate genome architecture linked with formation mechanisms and functional consequences of structural variation, accepted in PNAS
12. Pavlidis P., Metzler D., Stephan W. Selective sweeps in multi-locus models of quantitative traits. Genetics 2012 192:225-239
13. Alachiotis N., Stamatakis A., Pavlidis P. OmegaPlus: A Parallel Tool for Rapid & Scalable Detection of Selective Sweeps in Genome Datasets Bioinformatics 28(17):2274-5.
14. Pavlidis P., Jensen J.D., Stephan W., Stamatakis A. A Critical Assessment of Story-Telling: Gene Ontology categories and the importance of validating genomic scans. MBE 29(10):3237-48
15. Bousios, A.; Kourmpetis, Y.; Pavlidis, P.; Minga, E. ;Tsaftaris, A.; Darzentas, N. The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story Plant J. 2012 Feb;69(3):475-88

16. Tellier A., Laurent S.J.Y., Lainer H., Pavlidis P., Stephan W. Inference of Seed Bank Parameters in Two Wild Tomato Species Using Ecological and Genetic Data Proc Natl Acad Sci U S A. 108(41):17052-7
17. Saminadin-Peter SS, Kemkemer C, Pavlidis P, Parsch J. Selective Sweep of a cis-Regulatory Sequence in a Non-African Population of Drosophila melanogaster. Mol Biol Evol. 2011 Dec 22. [Epub ahead of print]
18. Svetec N, Werzner A, Wilches R, Pavlidis P, Alvarez-Castro J, Broman K, Metzler D, Stephan W. 2011, Identification of X-linked quantitative trait loci affecting cold tolerance in Drosophila melanogaster and fine-mapping by selective sweep analysis. Molecular Ecology, 20:530–544
19. Pavlidis P, Jensen JD, Stephan W. 2010, Searching for footprints of positive selection in whole-genome SNP data from nonequilibrium populations. Genetics, 185:907–922.
20. Pavlidis P*, Laurent S*, and Stephan W. 2010, msABC: a modification of Hudson’s ms to facilitate multi-locus ABC analysis. Molecular Ecology Resources, 10:723–727, *authors have contributed equally
21. Tsuchimatsu T, Suwabe K, Shimizu-Inatsugi R, Isokawa S, Pavlidis P, Staedler T, Suzuki G, Takayama S, Watanabe M, Shimizu KK. 2010, Evolution of self-compatibility in Arabidopsis by a mutation in the male specificity gene. Nature, 464:1342–1346
22. Aid-Pavlidis T*, Pavlidis P*, Timmusk T. 2009, Meta-coexpression conservation analysis of microarray data for studying the regulation of a single gene - BDNF gene case study. BMC Genomics, 10:420
23. Svetec N, Pavlidis P, Stephan W. 2009, Recent strong positive selection on Drosophila melanogaster HDAC6 , a gene encoding a stress surveillance factor, as revealed by population genomic analysis. MBE 26:1549–1556
24. Johnsen JM, Teschke M, Pavlidis P, McGee BM, Tautz D, Ginsburg D, Baines JF. 2009, Selection on cis-regulatory variation at B4galnt2 and its influence on von Willebrand Factor in house mice. MBE 26:567–578
25. Pavlidis P, Hutter S, Stephan W. 2008, A population genomic approach to map recent positive selection in model species. Molecular Ecology 17:3585–3598
26. Pavlidis P, Poirazi P. 2006, Individualized markers optimize class prediction of microarray data. BMC Bioinformatics, 7:345-358