PERSONAL INFORMATION

Pavlos Pavlidis

Psomadaki 16, Mires 70400, Greece
☎ 6949243041
pavlidis@ics.forth.gr pavlidisp@gmail.com
www.pop-gen.eu

Sex M | Date of birth 15/07/1980 | Nationality GR

WORK EXPERIENCE

2020 -	ICS Group Leader, Researcher B; equivalent to Associate Professor grade ICS-FORTH, CBML, Heraklion, Greece
2016 - 2020	ICS Group Leader, Researcher C; equivalent to Assistant Professor grade
2014 - 2016	ICS-FORTH, CBML, Heraklion, Greece Population Genetics, Evolutionary Biology, Bioinformatics Population Genetics, Evolution of Gene Regulatory Networks
2013 - 2014	Postdoctoral fellow, BioComputing & Molecular Modeling IMBB-FORTH, Heraklion, Greece
2011 - 2013	PostDoc in Phylogenetics and Pop. Genetics Project: High Performance Computing in Population Biology Group Leader: Prof. Dr. Alexandros Stamatakis, Germany
2005 - 2007	Bionformatician at Egeen (now Quretec) Director: Dr. Jaak Vilo, Tartu, Estonia

EDUCATION AND TRAINING

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) Population Genetics, Programming, Statistics, Mathematics, Evolutionary Biology, Scientific Writing
2005-2007	PhD Student (not-complete) 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 Bioinformatics, Programming, Statistics
2003-2005	M.Sc. in 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
1998-2003	Diploma (5 years / MSc equivalent) 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

PERSONAL SKILLS

Communication skills	good communication skills gained through (i) PhD studies, (ii) Conferences/Presentations, (iii) interaction with students and colleagues, (iv) teaching

TEACHING	

	Introduction to R for Bioinformatics, MSc program in Bioinformatics, Medical School, University of Crete and FORTH Spring Semester (since 2016) Bioinformatics, MSc program Molecular Biomedicine, University of Crete Winter Semester (co-teaching with C. Nikolaou and I. Iliopoulos) Introduction to R for Bioinformatics, Elective course, Computer Science Department, University of Crete Spring Semester (since 2016) Computational Methods in Evolution. Elective course, Department of Biology, University of Crete Spring Semester (since 2018, with N. Poulakakis, C. Antoniou and M. Ladoukakis) Tutor Assistant in the Computational Molecular Evolution (CoME) workshop Since 2012 (every 2 years in HCMR, Heraklion Crete) February Days Workshop: Coalescent Theory and Bioinformatics using R (ΕΛΚΕΘΕ) Introduction to Bioinformatics (co-teacher with the group of A. Stamatakis) 2012 - 2013, KIT, Karlsruhe, Germany
WORKSHOPS & RESEARCH ACTIVITIES	Training in the group of Prof. Jan Komorowski on microarray classification methods Jun. 2005, University of Uppsala, Uppsala, Sweden Evolutionary Biology Course in Guarda Jun. 2006, University of Basel, Basel, Switzerland Summer Institute in Statistical Genetics Sep. 2007, University of Liege, Liege, Belgium
ORGANISATION OF WORKSHOPS	EuroXanth Training School 2018 (to be held in Heraklion, Greece, 12-16 February) Molecular and phenotypic evolution: theoretical and practical approaches (Serbia, June 2018) Workshop on Quantitative Evolutionary Biology (September 2018, Turkey) Hellenic Bioinformatics 10 - 2017, 6 - 9 September 2017; FORTH, Heraklion, Greece Smodia 2014: Statistical Methods for Omics Data Integration and Analysis Heraklion, Greece; 10-12 November 2014
HONORS & AWARDS	Award from Greek National Scholarship Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology. 2004, University of Crete, Heraklion, Greece Award from Greek National Scholarship Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology, 2003, University of Crete, Heraklion, Greece Award from Greek National Scholarship Foundation, 2nd in Panhellenic Entrance Exams, 1998, Athens, Greece
SELECTED PRESENTATIONS IN SYMPOSIA & CONFERENCES	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 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 Searching for coevolving sites between mitochondria and nuclear genes Papadantonakis Stefanos, Ladoukakis Em., and Pavlidis Pavlos, COME 2016

	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 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 Detecting the signature of positive selection in genomes, May 2009 P. Pavlidis, and W. Stephan, VW 2009, Munster, Germany 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	2019 - 2020 Forth Synergy Grant (EVO-NMDA) 2017-2018 Participation in ELIXIR with the software SweeD 2017-2018 Participation in POLITEIA II National Grant Marie-Curie IEF, Evolution of gene regulatory networks by means of natural selection and genetic drift (96.5/100) Fellowship from the Volkswagen Stiftung, for Ph.D. studies. 2007-2010, Ludwig-Maximilians-University, Munich, Germany, Assistantship for foreign students (STIBET, DAAD) 2009 Scholarship from the Estonian government for Ph.D. studies, 2005-2007, University of Tartu, Tartu, Estonia
INVITED TALKS	Advanced tools to detect selective sweeps in whole-genomes and extensions of the sweep model. University of Sussex, April 2016 Detecting selective sweeps in full genome-data and populations that have experienced demographic events, January 2015, MPI for developmental biology, Cologne, Germany The problem of detecting selective sweeps April 2012, MPI for Dev. Biology, Tuebingen, Germany Detecting positive selection: i) Machine-learning and Bayesian approaches ii) Selection in multiple-locus models September 2011, HCMR, Heraklion, Greece Detecting selective sweeps in natural populations of D. melanogaster June 2011, UPF, Barcelona, Spain The problem of detecting selective sweeps in bottlenecked populations May 2010, HCMR, Heraklion, Greece Combining SFS and LD to detect selective sweeps: a machine learning approach Apr. 2010, University of Vanderbilt, Nashville, TN, USA Detecting selective sweeps in natural populations of D. melanogaster Apr. 2010, MPI for Evolutionary Anthropology, Leipzig, Germany A novel approach for detecting selective sweeps in whole genome data, using machine learning techniques Jun. 2009, University of Zuerich, Zuerich, Switzerland Detecting sweeps in whole genome data Apr. 2009, Evolutionary Genomics: the impact of next generation sequencing technologies, Wittenberg, Germany
STUDENTS SUPERVISION	2019- PhD Student (Nikolaos Fikas, Plant Microbiome) 2018-2019 2 MSc Students (Bioinformatics) 2017-2018 3 MSc Students (Bioinformatics, Microbial Population Genetics) 2016-2017 1 MSc Student 2015-2016 2 MSc Students (Population Genetics)

PREPRINTS

https://scholar.google.gr/citations?user=JW3CBIgAAAAJ&hl=en

1. Population genomics insights into the recent evolution of SARS-CoV-2. M Vasilarou, N Alachiotis, J Garefalaki, A Beloukas, P Pavlidis, BioRxiv

2. ERCC1-XPF Interacts with Topoisomerase IIβ to Facilitate the Repair of Activity-induced DNA Breaks. G Chatzinikolaou, K Stratigi, K Agathangelou, M Tsekrekou, … Pavlidis P., … bioRxiv

3. Kapopoulou, A, Kapun, M, Pavlidis, P, Pieper, B, & ... 2018, 'Early split between African and European populations of Drosophila melanogaster', *bioRxiv*
4. Pajic, P, Pavlidis, P, Dean, K, Neznanova, L, & ... 2018, 'Amylase copy number analysis in several mammalian lineages reveals convergent adaptive bursts shaped by diet', *bioRxiv*
5. Kioukis, A, & Pavlidis, P 2018, 'Evolution of gene regulatory networks by means of selection and random genetic drift', *bioRxiv*
6. Primetis, E, Chavlis, S, & Pavlidis, P 2018, 'Evolutionary Models of Amino Acid Substitutions Based on the Tertiary Structure of their Neighborhoods', *bioRxiv*

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

1. Bozikas, D., Alachiotis, N., Pavlidis, P., Sotiriades, E., & Dollas, A. (2017). Deploying FPGAs to future-proof genome-wide analyses based on linkage disequilibrium. In 2017 27th International Conference on Field Programmable Logic and Applications (FPL) (pp. 1–8). IEEE.
2. S. Pissis, A. Stamatakis and P. Pavlidis MoTeX: an HPC word-based tool for MoTif eXtractioN ACM-BCB 2013
3. 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

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

BOOK CHAPTERS

4. Detecting positive selection in populations using genetic data. Accepted for publication in Statistical Population Genetics (Springer). Edited by Julien Dutheil

PUBLISHED IN PEER-REVIEWED JOURNALS

5. Intraspecific diversification of the crop wild relative Brassica cretica Lam. using demographic model selection. A Kioukis, VA Michalopoulou, L Briers, S Pirintsos, DJ Studholme, … Pavlidis P. Sarris P. BMC Genomics 21 (1), 48

6. Analysis of Haplotypic Variation and Deletion Polymorphisms Point to Multiple Archaic Introgression Events, Including from Altai Neanderthal Lineage. O Taskent, YL Lin, I Patramanis, P Pavlidis, O Gokcumen. Genetics

7. Phylogenomics investigation of sparids (Teleostei: Spariformes) using high-quality proteomes highlights the importance of taxon sampling. P Natsidis, A Tsakogiannis, P Pavlidis, CS Tsigenopoulos, T Manousaki. Communications biology 2 (1), 1-10

8. Petar Pajic, Pavlos Pavlidis, Kirsten Dean, Lubov Neznanova, …, Stefan Ruhl, Omer Gokcumen, Independent amylase gene copy number bursts correlate with dietary preferences in mammals (*accepted in ELife*).

9. Ndjiondjop, M.N., Alachiotis, N., Pavlidis, P., Goungoulou, A., Kpeki, S.B., Zhao, D. and Semagn, K., 2018. Comparisons of molecular diversity indices, selective sweeps and population structure of African rice with its wild

progenitor and Asian rice. *Theoretical and Applied Genetics*, pp.1-14.

10. Alachiotis, N. and Pavlidis, P., 2018. RAiSD detects positive selection based on multiple signatures of a selective sweep and SNP vectors. *Communications biology*, *1*(1), p.79.
11. Xu D, Pavlidis P, Taskent RO, Alachiotis N, Flanagan C, DeGiorgio M, Blekhman R, Ruhl S, Gokcumen O. Archaic hominin introgression in Africa contributes to functional salivary MUC7 genetic variation. Molecular biology and evolution. 2017 Jul 21;34(10):2704-15.
12. Xu, D., Jaber, Y., Pavlidis, P., & Gokcumen, O. (2017). VCFtoTree: a user-friendly tool to construct locus-specific alignments and phylogenies from thousands of anthropologically relevant genome sequences. BMC Bioinformatics, 18(1), 426.
13. Kapli, P., Lutteropp, S., Zhang, J., Kobert, K., Pavlidis, P., Stamatakis, A., & Flouri, T. (2017). Multi-rate Poisson Tree Processes for single-locus species delimitation under Maximum Likelihood and Markov Chain Monte Carlo. Bioinformatics, 33(11)
14. Pavlidis, P., & Alachiotis, N. (2017). A survey of methods and tools to detect recent and strong positive selection. Journal of Biological Research-Thessaloniki, 24(1), 7.
15. Xu, D., Pavlidis, P., Taskent, R. O., Alachiotis, N., Flanagan, C., DeGiorgio, M., … Gokcumen, O. (2017). Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. Molecular Biology and Evolution, 34(10),
16. Xu, D., Pavlidis, P., Thamadilok, S., Redwood, E., Fox, S., Blekhman, R., … Gokcumen, O. (2016). Recent evolution of the salivary mucin MUC7. Scientific Reports, 6(1), 31791.
17. Papadantonakis S, Poirazi P, Pavlidis P, CoMuS: Simulating coalescent histories and polymorphic data from multiple species, accepted at Molecular Ecology Resources (May 2016)
18. N Alachiotis, P Pavlidis, Scalable linkage-disequilibrium-based selective sweep detection: a performance guide, GigaScience 5 (1), 1
19. Eaaswarkhanth Muthukrishnan, Pavlos Pavlidis, Omer Gokcumen, Geographic Distribution And Adaptive Significance Of Genomic Structural Variants: An Anthropological Genetics, Human Biology 86 (4), 3
20. 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
21. 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.
22. 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)
23. 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
24. 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
25. Pavlidis P., Metzler D., Stephan W. Selective sweeps in multi-locus models of quantitative traits. Genetics 2012 192:225-239

26. 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.

27. 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

28. 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

29. 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

30. 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]

31. 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

32. 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.

33. 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

34. 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

35. 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

36. 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

37. 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

38. Pavlidis P, Hutter S, Stephan W. 2008, A population genomic approach to map recent positive selection in model species. Molecular Ecology 17:3585–3598

39. Pavlidis P, Poirazi P. 2006, Individualized markers optimize class prediction of microarray data. BMC Bioinformatics, 7:345-358