

CURRICULUM VITAE**PERSONAL INFORMATION**

SURNAME	PAVLIDIS
NAME	PAVLOS
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CURRENT POSITION(S)

2023 - Present	Associate Professor for Bioinformatics, Department of Biology, University of Crete, Greece
2023 - Present	Affiliated Researcher, CBML, ICS-FORTH

PREVIOUS POSITION(S)

2020 - 2023	Researcher B, Computational Population Genomics Group (EVOLAB), CBML, ICS-FORTH
2016 - 2020	Researcher C, ICS-FORTH, CBML, Heraklion, Greece Bioinformatics/Population Genetics
2014 - 2016	Marie Curie Postdoctoral Fellow IMBB-FORTH, Heraklion, Greece (group Dr. Panayiota Poirazi) Evolution of Gene Regulatory Networks
2013 - 2014	Postdoctoral fellow, BioComputing & Molecular Modeling IMBB-FORTH, Heraklion, Greece (group Prof. Michalis Kokkinidis) Population Genetics, Evolutionary Biology, Bioinformatics
2011 - 2013	Postdoctoral fellow in Phylogenetics and Population Genetics Project: High Performance Computing in Population Biology
2005 - 2007	Bioinformatician at Egeen (now Quretec) Tartu, Estonia Director: Dr. Jaak Vilo

EDUCATION

2007 - 2009	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 <i>Drosophila melanogaster</i> : Methods, applications, and extensions (summa cum laude)
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
2003- 2005	M.Sc. in Plant Molecular Biology and Biotechnology 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

PUBLICATIONS

- **The first 8 publications are recent** (within the last 7 years) and the PI is a main (first or last author).
- **Publications 9 - 10** are recent and related to the topic (human evolution). The PI had a main author as collaborator.
- **The remaining publications** are older **but important to the topic** since they **refer to tools and analyses** that will be used in the current proposal.

A list of publications is available at Google Scholar:

<https://scholar.google.com/citations?user=JW3CBlgAAAAJ&hl=en&oi=ao>

1. Koropoulis, A., Alachiotis, N. and Pavlidis, P., 2020. Detecting positive selection in populations using genetic data. *Statistical population genomics*, pp.87-123. DOI: [10.1007/978-1-0716-0199-0_5](https://doi.org/10.1007/978-1-0716-0199-0_5)

<p>2. Vasilarou, M., Alachiotis, N., Garefalaki, J., Beloukas, A., & Pavlidis, P. (2021). Population genomics insights into the first wave of covid-19. <i>Life</i>, 11(2), 1–19. https://doi.org/10.3390/life11020129 PDF</p>
<p>3. Primetis, E., Chavlis, S., & Pavlidis, P. (2021). Evolutionary models of amino acid substitutions based on the tertiary structure of their neighborhoods. <i>Proteins: Structure, Function and Bioinformatics</i>, September 2020, 1–12. https://doi.org/10.1002/prot.26178 PDF</p>
<p>4. Pavlidis, P., & Somel, M. (2020). Of dogs and men. - Perspective - <i>Science</i>, 370(6516), 522–523. https://doi.org/10.1126/science.abe7823 PDF</p>
<p>5. Alachiotis, N. & Pavlidis, P. RAI_{SD} detects positive selection based on multiple signatures of a selective sweep and SNP vectors. <i>Commun. Biol.</i> (2018). doi:10.1038/s42003-018-0085-8 PDF</p>
<p>6. Pavlidis, P. & Alachiotis, N. A survey of methods and tools to detect recent and strong positive selection. <i>J. Biol. Res.</i> 24, 7 (2017). DOI: 10.1186/s40709-017-0064-0 PDF</p>
<p>7. Papadantonakis, S., Poirazi, P. & Pavlidis, P. CoMuS: simulating coalescent histories and polymorphic data from multiple species. <i>Mol. Ecol. Resour.</i> 16, 1435–1448 (2016). DOI: 10.1111/1755-0998.12544</p>
<p>8. Alachiotis, N. & Pavlidis, P. Scalable linkage-disequilibrium-based selective sweep detection: A performance guide. <i>Gigascience</i> 5, (2016). DOI: 10.1186/s13742-016-0114-9</p>
<p>9. Koptekin, D., Yüncü, E., Rodríguez-Varela, R., Altınışık, N.E., Psonis, N., Kashuba, N., Yorulmaz, S., George, R., Kazancı, D.D., Kaptan, D. and Gürün, K... Pavlidis P., Storå J, Özer F, Götherström A, Somel M, 2023. Spatial and temporal heterogeneity in human mobility patterns in Holocene Southwest Asia and the East Mediterranean. <i>Current Biology</i>, 33(1), pp.41-57. DOI: 10.1016/j.cub.2022.11.034</p>
<p>10. Lin, Y.-L., Pavlidis, P., Karakoc, E., Ajay, J. & Gokcumen, O. The evolution and functional impact of human deletion variants shared with archaic hominin genomes. <i>Mol. Biol. Evol.</i> 32, (2015). DOI: 10.1093/molbev/msu405 PDF</p>

1. Zhang, J., Kapli, P., Pavlidis, P. & Stamatakis, A. A General Species Delimitation Method with Applications to Phylogenetic Placements. *Bioinformatics* 29, 2869–2876 (2013).
[PDF](#)
2. Alachiotis, N., Vogiatzi, E., Pavlidis, P. & Stamatakis, A. ChromatoGate : A Tool for Detecting Base Mis-Calls in Multiple Sequence Alignments by Semi-Automatic Chromatogram Inspection. *Comput. Struct. Biotechnol. J.* 6, 1–16 (2013).
[PDF](#)
3. Pissis, S. P., Stamatakis, A. & Pavlidis, P. MoTeX: A word-based HPC tool for MoTif extraction. in 2013 ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, ACM-BCB 2013 (2013). doi:10.1145/2506583.2506587
[PDF](#)
4. Gokcumen, O. et al. Primate genome architecture influences structural variation mechanisms and functional consequences. *Proc. Natl. Acad. Sci.* 10, 15764–15769 (2013).
[PDF](#)
5. Werzner, A., Pavlidis, P., Ometto, L., Stephan, W. & Laurent, S. Selective Sweep in the Flotillin-2 Region of European *Drosophila melanogaster*. *PLoS One* 8, (2013).
[PDF](#)
6. Pavlidis P., Zivkovic D, Stamatakis A. & Alachiotis N. SweeD : Likelihood-Based Detection of Selective Sweeps in Thousands of Genomes. *Mol. Biol. Evol.* 30, 2224–2234 (2013).
[PDF](#)
7. Pavlidis, P., Jensen, J. D., Stephan, W. & Stamatakis, A. A critical assessment of storytelling: gene ontology categories and the importance of validating genomic scans. *Mol. Biol. Evol.* 29, 3237–48 (2012).
[PDF](#)
8. Alachiotis, N., Pavlidis, P. & Stamatakis, A. Exploiting multi-grain parallelism for efficient selective sweep detection. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)* 7439 LNCS, (2012).
[PDF](#)
9. Alachiotis, N., Stamatakis, A. & Pavlidis, P. OmegaPlus: A Scalable Tool for Rapid Detection of Selective Sweeps in Whole-Genome Datasets. *Bioinformatics* 28, 2274–2275 (2012).
[PDF](#)
10. Pavlidis, P., Metzler, D. & Stephan, W. Selective sweeps in multilocus models of quantitative traits. *Genetics* 192, 225–39 (2012).
[PDF](#)
11. Bousios, A. et al. The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. *Plant J.* 69, 475–88 (2012).
[PDF](#)
12. Svetec, N. et al. Identification of X-linked quantitative trait loci affecting cold tolerance in *Drosophila melanogaster* and fine mapping by selective sweep analysis. *Mol. Ecol.* 20, 530–44 (2011).
[PDF](#)
13. 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, 17052–7 (2011).
[PDF](#)
14. Saminadin-Peter, S. S., Kemkemer, C., Pavlidis, P. & Parsch, J. Selective Sweep of a cis-Regulatory Sequence in a Non-African Population of *Drosophila melanogaster*. *Mol. Biol. Evol.* 29, 1167–74 (2011).
[PDF](#)
15. Tsuchimatsu, T. et al. Evolution of self-compatibility in *Arabidopsis* by a mutation in the male specificity gene. *Nature* 464, 1342–6 (2010).
[PDF](#)
16. Pavlidis, P., Laurent, S. & Stephan, W. msABC: a modification of Hudson’s ms to facilitate multi-locus ABC analysis. *Mol. Ecol. Resour.* 10, 723–7 (2010).
[PDF](#)
17. Pavlidis, P., Jensen, J. D. & Stephan, W. Searching for footprints of positive selection in whole-genome SNP data from nonequilibrium populations. *Genetics* 185, 907–22 (2010).
[PDF](#)

18. Aid-Pavlidis, T., Pavlidis, P. & Timmusk, T. Meta-coexpression conservation analysis of microarray data: a 'subset' approach provides insight into brain-derived neurotrophic factor regulation. *BMC Genomics* 10, 420 (2009).
[PDF](#)

CONFERENCES/WORKSHOPS/etc

- 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., Bertias 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

MEMBERSHIPS & REVIEWING ACTIVITIES (if applicable)

2017 - Present	Founding member of the Greek Evolutionary Society (EΛEΞE)
2021 – 2022	ESEB Membership
2007 - Present	<i>Reviewer in multiple Peer Review Journals for evolutionary biology and/or bioinformatics For example, Genetics, Molecular Biology and Evolution, Heredity, JEB, GBE, Bioinformatics, BMC Bioinformatics, etc.</i>

TEACHING ACTIVITIES *(if applicable)*

- **2021** - Computational Biology (2021 - Present; Department of Biology; Spring Semester)
- **2024** - Genetic analysis with R (Department of Biology; Spring Semester)
- **2023** - Introduction to R and Linux (Department of Biology; Fall Semester)
- **2023** - Introduction to Programming with Python (Department of Biology; Fall Semester)
- **2016 - 2023** Introduction to R for Bioinformatics, MSc program in Bioinformatics, Medical School, University of Crete and FORTH
Spring Semester
- **2016** - Bioinformatics, MSc program Molecular Biomedicine, University of Crete
Winter Semester (co-teaching with M. Lavigne and I. Iliopoulos)
- **2016** - Introduction to R for Bioinformatics, Elective course, Computer Science Department, University of Crete
Spring Semester
- **2018** - Computational Methods in Evolution. Elective course, Department of Biology, University of Crete
Spring Semester (with N. Poulakakis, C. Antoniou and M. Ladoukakis)
- Tutor Assistant in the Computational Molecular Evolution (CoME) workshop
Since 2012 (2010, 2012)
- Introduction to Bioinformatics (co-teacher with the group of A. Stamatakis)
2012 - 2013, KIT, Karlsruhe, Germany

Insert row below to add information

SUPERVISION OF GRADUATE STUDENTS & POSTDOCTORAL FELLOWS *(if applicable)*

Completed Theses

- 8 **Undergraduate** Theses (3 Biology Department, 5 Computer Science Department)
- 10 **M.Sc.** Theses (6 Bioinformatics, 3 Biology Department, 1 Computer Science Department)

Moreover, I am **currently** supervising (not yet completed):

- 1 **M.Sc.** Theses (1 Bioinformatics)
- 3 **Ph.D.** Theses (Biology Department, 1 is co-supervised with Prof. John Vontas)

FELLOWSHIPS and AWARDS (if applicable)

2014 - 2016	<ul style="list-style-type: none"> Marie Curie IEF Fellowship
2004	<ul style="list-style-type: none"> Award from Greek National Scholarship Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology. 2004, University of Crete, Heraklion, Greece
2003	<ul style="list-style-type: none"> Award from Greek National Scholarship Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology, 2003, University of Crete, Heraklion, Greece
1998	<ul style="list-style-type: none"> Award from Greek National Scholarship Foundation, 2nd in Panhellenic Entrance Exams, 1998, Athens, Greece

RESEARCH GRANTS (if applicable)

Please add indicative research projects (international or national) in which you have participated (in any role).

Project Title	Funding source	Period	Role of the PI
PhylProGramm	EU-ERC Advanced Grant	2024 -	Team member
NEOMATRIX (Twinning)	EU	2020 - 2024	Collaborator
EVONMDA	FORTH	2019 - 2021	PI
MobiVirus	FORTH	2021 - 2023	PI
Nativine	GR- Ερευνώ Καινοτομώ	2022 - 2025	Collaborator
FOTOMELO	GR	2023	Collaborator
MODELGLOSS	GR-ELIDEK	2021	Collaborator

GRANT APPLICATIONS OF RELATED PROJECTS (if applicable)

Please add other Research Proposals/Projects **related to the proposed research project** in which you are involved in any role.

Project Title	Funding source	Submission date	Role of the PI

The PI should list his/her activity regarding (if applicable):

Up to ten (10) representative publications, from the last ten (10) years, as main author

Please see in the section “Publications”, the first part of the table, where 10 representative and recent publications are listed. In these publications, the main topic is the implementation of software for the analysis of population genetics data, especially detection and localization of Selective Sweeps and inference of the demographic model. Especially the inference of demography is related to the topic of the proposal because a scientific question of the proposal is the co-analysis of genetic and linguistics data.

Research monographs

PhD Dissertation: Pavlidis, Pavlos (2011): Detecting selective sweeps in natural populations of *Drosophila melanogaster*: Methods, applications, and extensions. Dissertation, LMU München: Faculty of Biology

Granted patents: -

Invited presentations to international conferences and/or advanced schools

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

Organization of international conferences

- EuroXanth Training School 2018 (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

Prizes/Awards/Academy memberships

Please refer to the previous sections of the CV

Major contributions to the early careers of excellent researchers

Since 2014, I have been supervising undergraduate students on topics related to computational population genetics. Several of them have continued their studies as PhD Students or their scientific career as postdoctoral fellows (1 in UK, 2 in Austria, 2 in Germany, 2 in Greece).

National and international collaborations

During the last 10 years, I have established a number of scientific collaborations with national and international groups:

Group: aDNA Lab (IMBB-FORTH)

Topics: analysis of aDNA data

We have established a collaboration with the aDNA Lab of IMBB-FORTH to analyze aDNA data that was derived from individuals who were mainly located in Greece in order to obtain insights into the recent evolutionary history of the populations that lived in Greece for the last 10,000 years.

Group: Prof. Emmanouil Ladoukakis, Prof. Elena Anagnostopoulou, Dr. Dimitris Michelioudakis (UoC, Heraklion, Greece)

Topics: Evolution of Languages

We study language as an evolvable system. We apply phylogenetics/population genetics methods to understand the evolution of Indo-European Languages.

Group: Prof. Alexandros Stamatakis (HITS, Heidelberg, Germany)

Topics: Phylogenetics, High Performance Computing in Population genetics

We have established a long-term collaboration (since 2011) with the group of Prof. Alexandros Stamatakis (during 2011-2013, I was a postdoctoral fellow in his group) to develop new methods in phylogenetics and population genomics aiming at high performance software.

Group: Prof. Omer Gokcumen (Buffalo University, NY, USA)

Topics: Evolutionary Anthropology

Since 2012 we have published together a series of papers to provide insights into the recent evolutionary history of modern humans and hominids. Our findings have been published in prestigious journals in the field of evolutionary biology (MBE, PNAS, etc).

Group: Prof. Mehmet Somel (METU, Ankara, Turkey)

Topics: Neolithic expansion from Anatolia to Europe

We are collaborating in a multitude of topics (e.g. kinship inference, demography and selection inference) of the Anatolian Neolithic populations and their expansion to the European Continent. Currently, we have **earned a TWINNING Grant (NEOMATRIX)** to study the Neolithic expansion from Anatolia to Europe.

Group: Prof. Helen Papadaki (UoC, Heraklion, Greece)

Topics: The HLA diversity in the Cretan population

In an effort to understand the HLA diversity in the Cretan population and propose novel ways to build improved and more efficient cord-blood banks we assess the HLA diversity of the Cretan population using population genetics methodologies.

Group: Prof. Nikolaos Alachiotis (University of Twente, The Netherlands)

Topics: Implementation of High Performance Tools in population genetics

With Nikolaos Alachiotis, I have implemented high performance tools in population genetics (SweeD, OmegaPlus, quickLD, RAiSD) to facilitate the analysis of large genomic data.