

# Curriculum Vitae

## RESEARCH VISION & STRATEGY

*Nothing in biology makes sense except in the light of Evolution. – Theodosius Dobzhansky*

*Nothing in Evolution makes sense except in the light of Population Genetics. – Michael Lynch*

My primary research goal is to understand the processes affecting the evolution of populations. Specifically, my goal is to obtain insights into the evolutionary forces that shape biodiversity. Biodiversity is organized at levels, forming a hierarchy: First, within a population, at the lowest level, alternative alleles affect the phenotypic traits. Genes form regulatory networks orchestrating their expression patterns. Biodiversity varies between different populations because of their adaptation to local environments. Gene flow between populations allows certain variants to spread throughout the whole species. At a higher organization level, species diverge from each other due to the limited exchange of genetic material between them and the adaptation to different environmental challenges. Species can interact by competing for resources or forming symbiotic communities. Because of the continuous biotic-biotic (e.g. between species) or biotic-abiotic (e.g. species-environment) interactions the genetic makeup is not isolated from ecological processes. During evolution, the genetic makeup is affected by ecological processes either because of the driving force of natural selection or the stochastic processes like random genetic drift. In order to understand the nature of forces that affect the evolutionary process it is necessary to successfully separate the natural selection from random genetic drift at various hierarchies, from the DNA-sequence level to the higher species-interaction level.

## RESEARCH EXPERIENCE

- Evolutionary biology and Population Genetics
- Bioinformatics

## JOB OFFERS

- Junior professorship, University of Goettingen, Germany, December 2012 (declined)

## PUBLICATION OUTPUT

- 3 full-papers published in Computer Science Conferences (Unlike in Biology, conference publications are important in computer science)
- 19 papers in peer-review journals.

## INVITED TALKS

10 invited talks (1 keynote speaker) in Germany, Switzerland, USA, Greece, Spain.

## Google profile, Scopus scores

- Google: Citations: 199, h-index: 9, i10-index: 8, publications: 22 (<http://scholar.google.gr/citations?user=JW3CBIgAAAAJ&hl=en>)
- Scopus: Citations: 139, h-index: 7, publications: 17

## CONTACT INFORMATION

### Address

IMBB-FORTH, CBL group  
Nikolaou Plastira 100, Vassilika Vouton  
GR - 711 10, Heraklion, Crete, Greece

### Email

pavlidis@imbb.forth.gr  
pavlidisp@gmail.com

### Web

[bio.lmu.de/~pavlidis/](http://bio.lmu.de/~pavlidis/)

## PERSONAL INFORMATION

### Nationality

Greek

### Date of Birth

15 July 1980

### Place of Birth

Amarousio, Athens

### Marital Status

Married, two children

## REFERENCES

### Prof. Dr. Wolfgang Stephan

address

LMU Munich, Grosshaderner Str. 2, 82152, Planegg-Martinsried, Germany

phone

+49 (0)89 / 2180-74102

fax

+49 (0)89 / 2180-74104

email

[stephan@bio.lmu.de](mailto:stephan@bio.lmu.de)

### Prof. Dr. Alexandros Stamatakis

address

Schloss-Wolfsbrunnenweg 35, 69118 Heidelberg, Germany

phone

+49 1511 7496080 (Mobile), +49 6221 533240 (Office)

fax

+49 6221 533298

email

[alexandros.stamatakis@h-its.org](mailto:alexandros.stamatakis@h-its.org)

### Prof. Dr. Jeffrey D. Jensen

address

EPFL-SV-IBI, Station 15, office AI 1 206, CH-1015 Lausanne, Switzerland

phone

+41 (0)21 693 96 68

fax

+41 (0)21 693 96 65

email: [jeffrey.jensen@epfl.ch](mailto:jeffrey.jensen@epfl.ch)

### Dr. Panayiota Poirazi

address

Computational Biology Lab, IMBB-FORTH, Nikolaou Plastira 100, 70013 Heraklion-Crete, GREECE

tel

+30-2810-39 11 39 (Office)

fax

+30-2810-39 11 01

email

[poirazi@imbb.forth.gr](mailto:poirazi@imbb.forth.gr)

## EDUCATION

<b>PostDoc in BioComputing &amp; Molecular Modelling</b>	<b>Jan 2013 -</b>
Project	InnovCrete (EU-funded FP7 REGPOT)
Group/advisor	M. Kokkinidis
Institute	IMBB, FORTH, <u>Heraklion, Greece</u>
<b>PostDoc in Phylogenetics and Pop. Genetics HPC)</b>	<b>Feb 2011-Dec 2012</b>
Title of the project	High Performance Computing (HPC) in population genetics and phylogenetics
Group/advisor	SCO Group, Alexis Stamatakis
Institute	HITS, <u>Heidelberg, Germany</u>
<b>PhD Student in Evolutionary Biology</b>	<b>2007-2011</b>
Advisor	Wolfgang Stephan
Institute	Ludwig-Maximilians-Universität, <u>Munich, Germany</u>
Title of dissertation	Detecting selective sweeps in natural populations of <i>Drosophila melanogaster</i> : Methods, applications, and extensions ( <i>summa cum laude</i> )
<b>PhD Student in Computer Science and Mathematics</b>	<b>2005–2007</b>
Advisor	Jaak Vilo
Institute	University of Tartu, <u>Tartu, Estonia</u>
Research topic	Detection and analysis of transcription factor binding sites
<b>M.Sc. of Biology</b>	<b>2003–2005</b>
Advisor	Yiota Poirazi
Institute	University of Crete, <u>Heraklion, Greece</u>
Title of dissertation	Analysis of microarrays: Finding informative genes, clustering and classification (9.55/10)
General grade	8.99/10
<b>Diploma in Agricultural Biotechnology</b>	<b>1998–2003</b>
Advisor	John Sourdis
Institute	Agricultural University of Athens, <u>Athens, Greece</u>
Title of dissertation	Evolutionary reconstruction in mitochondrial genomics (10/10)
General grade	8.05/10

#### WORKSHOPS & RESEARCH ACTIVITIES

<b>Training in the group of Prof. Jan Komorowski on microarray classification methods</b>	<b>Jun. 2005</b>
University of Uppsala	<u>Uppsala, Swedem</u>
<b>Evolutionary Biology Course in Guarda</b>	<b>Jun. 2006</b>
University of Basel	<u>Basel, Switzerland</u>
<b>Summer Institute in Statistical Genetics</b>	<b>Sep. 2007</b>
University of Liege	<u>Liege, Belgium</u>

#### SUPERVISION

**Stefanos Papadantonakis (Undergrad in UOC)**

**Computational Methods in Evolution** 2013

**Loukas Theodosiou (MSc Student in LMU, Munich)**

**Analysis of rtPCR data and introduction to population genetics** Aug-Sept 2013

## TEACHING

1. Bioinformatics course for MSc students (UOC; with Y. Poirazi and I. Iliopoulos)
2. February Days Workshop: Coalescent Theory and Bioinformatics using R (HCMR; Feb 2012)
3. Introduction to Bioinformatics (KIT, Karlsruhe Germany; with A. Stamatakis, A. Aberer, T. Flouri)

## SELECTED PRESENTATIONS IN SYMPOSIA & CONFERENCES

**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, Münster, 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

## HONORS & AWARDS

**Award from Greek National Scholarship's Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology**

**2004**, University of Crete, Heraklion, Greece

**Award from Greek National Scholarship's Foundation for the M.Sc. program in Plant Molecular Biology and Biotechnology**

**2003**, University of Crete, Heraklion, Greece

**Award from Greek National Scholarship's Foundation, 2nd in Panhellenic Entrance Exams**

**1998**, Athens, Greece

## SCHOLARSHIPS

**Marie Curie IEF Fellowship 2014 - 2016**, for postdoctoral research, IMBB, Forth

**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

### **Learning about evolution with computational tools**

**June 2013** (Keynote Speaker) COST Meeting Berlin

### **Macroevolutionary processes of RNA viruses**

**September 2012** 9. Jahrestagung Deutsche Vereinte Gesellschaft für Klinische Chemie und Laboratoriumsmedizin, Mannheim, 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 Zürich, Zürich, Switzerland

### **Detecting sweeps in whole genome data**

**Apr. 2009**, Evolutionary Genomics: the impact of next generation sequencing technologies, Wittenberg, Germany

## PUBLICATIONS

### In Preparation

**Detecting functionally important aminoacids by analyzing the 3D protein structure (with K. Rousaki and M. Kokkinidis)**

### Submitted

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

### Published in Peer-Reviewed Conferences

Solon Pissis, Alexandros Stamatakis and Pavlos Pavlidis **MoTeX: an HPC word-based tool for MoTif eXtraction** *ACM-BCB 2013*

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** *submitted to HSCBB 2012*

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 LNCS*

### Published in Peer-Reviewed Journals

Pybus M., Dall'Olio G., Luisi P., Uzkudun M., Carreno-Torres A., Pavlidis P., Laayouni H., Bertranpetit J., Engelken J. **1000 Genomes Selection Browser: a genome browser dedicated to signatures of natural selection in humans** *Nucleic Acids Res. 2014 42:D903-9*

J. Zhang, P. Kapli, P. Pavlidis, A. Stamatakis **A general species delimitation method with applications to phylogenetic placement** *accepted in Bioinformatics*

Omer Gokcumen, Verena Tischler, Jelena Tica, Qihui Zhu, Rebecca Iskow, Eunjung Lee, Markus Hsi-Yang Fritz, Amy Langdon, Adrian M. Sttz, Pavlos Pavlidis, Vladimir Benes, Ryan Mills, Peter Park, Charles Lee, Jan O. Korbel **Primate genome architecture linked with formation mechanisms and functional consequences of structural variation** *accepted, in PNAS*

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)*

Wertzner A., Pavlidis P., Ometto L., Stephan W., and Laurent S. **Multiple selective sweeps in the Flotillin-2 region of European *Drosophila melanogaster*.** *PLoS ONE*

Pavlidis P., Metzler D., Stephan W. **Selective sweeps in multi-locus models of quantitative traits** *Genetics*

Alachiotis N., Stamatakis A., Pavlidis P. **OmegaPlus: A Parallel Tool for Rapid & Scalable Detection of Selective Sweeps in Genome Datasets** *Bioinformatics, in print*

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** *Molecular Biology and Evolution*, in print

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

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

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]

Svetec N, Werzner A, Wilches R, Pavlidis P, Álvarez-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

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.

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

Tsuchimatsu T, Suwabe K, Shimizu-Inatsugi R, Isokawa S, Pavlidis P, Städler 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

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, \*authors have contributed equally

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.** *Molecular Biology and Evolution* 26:1549–1556

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.** *Molecular Biology and Evolution* 26:567–578

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

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