

Curriculum Vitae

Dr. Gergely J. Szöllősi

Employment

- 2013 July - Researcher at MTA-TKI “GENESTORY” and ELTE-MTA “Biophysics” research groups.**
- 2011 - 2013 **Marie Curie fellow** at Lyon, Univ. Claude Bernard, Lyon, FRANCE
Probabilistic models of genome evolution, GENEFOREST project
- 2009 - 2011 **ANR Postdoctoral fellow** at CNRS UMR 5558, Lyon FRANCE
advisor: Vincent Daubin

Education & Research Training:

- 2009 Nov. 1. PhD in Biological Physics** from Eötvös University, Budapest Hungary
Thesis: *The effects of population structure and the genotype-phenotype map on evolutionary dynamics*. Grade: summa cum laude; supervisor: Imre Derényi
- 2008 (2 months) research affiliate at the Kavli Institute’s Genetics and Genomics Program at UCSB supervisor: Michael Lässig , topic: *Adaptation under linkage*
- 2008 (1 month) visiting PhD student at the Rockefeller University supervisor: Marcelo Magnasco; topic: *Damage and fluctuations in biological optimal transport networks*
- 2007 (2 months) visiting PhD student at Lässig Group at the Institute for Theoretical Physics, University of Cologne supervisor: Michael Lässig, topic: *Adaptation under linkage*
- 2004 M.Sc. in physics** from the Faculty of Sciences at Eötvös University
- 2004/05 I spent a semester at Kobenhavn University’s Niels Bohr Institute as a recipient of European Physical Society’s EMSPS scholarship to study biological physics.
- 2002/03 I spent a semester at Humboldt University Berlin’s Department of Physics as an ERASMUS student for the winter semester.
- 2000-2003 M.Eng. Program in Computer Science at Budapest University of Technology and Economics.
- 1994 - 98 Kossuth Lajos High School, (specialising in physics), Debrecen, Hungary.
- 1993 - 94 Raoul Wallenberg High School, San Francisco, California.

Curriculum Vitae

Involvement in major research projects (last five years):

2010 - 2011 [Phylariane](#) ANR project at LBBE (coordinator Vincent Berry, €700,000)
role: postdoc

2011-2013 [GENEFOREST](#) FP7-PEOPLE-IEF at LBBE (coordinator Gergely J Szöllősi, €170,000)
role: fellow

2012-2017 [ANCESTROME](#) ANR project at LBBE (coordinator Vincent Daubin €2,000,000)
role: coauthor

2013-2016 GENESTORY FP7-PEOPLE-CIG at MTA TKI (coordinator Gergely J Szöllősi, €87,500)

2014 “Thousands of trees for 4 billion years of life evolution on Earth” application to the Partnership for Advanced Computing in Europe (PRACE) awarded **36 000 000 hours computing time**. (coordinator Bastien Boussau)

Funding as PI

Dr. Gergely Szöllősi
(last five years)

duration	name	funding	
2011-2013	FP7-PEOPLE-IEF “GENEFOREST”	178 000 EUR	finished successfully (no rating)
2013-2016	FP7-PEOPLE-CIG “GENESTORY”	87 500 EUR	ends in 2016 see below
2013-2014	Albert Szentgyörgyi Fellowship	26 000 EUR	finished successfully (excellent/kiváló)
2014-2017	MTA Bolyai Fellowship	15 000 EUR	will be resigned if application is successful

The FP7-PEOPLE-CIG “GENESTORY” grant runs until 2016.12.31. It is concerned with the reconstruction of ancestral metabolic networks.

Curriculum Vitae

Publications

Dr. Gergely Szöllősi

I am a coauthor in 25 publications of which I am first author in 11 and last author in 3. The cumulative impact factor of my publications is 144.769 (and 87.713 as first or last author). The Hirsch index of my publications is 13 (and 10 as first or last author). For further citation and other information please see below.

Throughout my career I have tried to facilitate open access to my publications. During my PhD I regularly uploaded publication to the ArXiv preprint server (see arxiv.org/a/szollosi_g_1). In the last five years I have strived to publish all research I am involved in under an open access license (11 of 14 publications in the last five years have been published under an open access license).

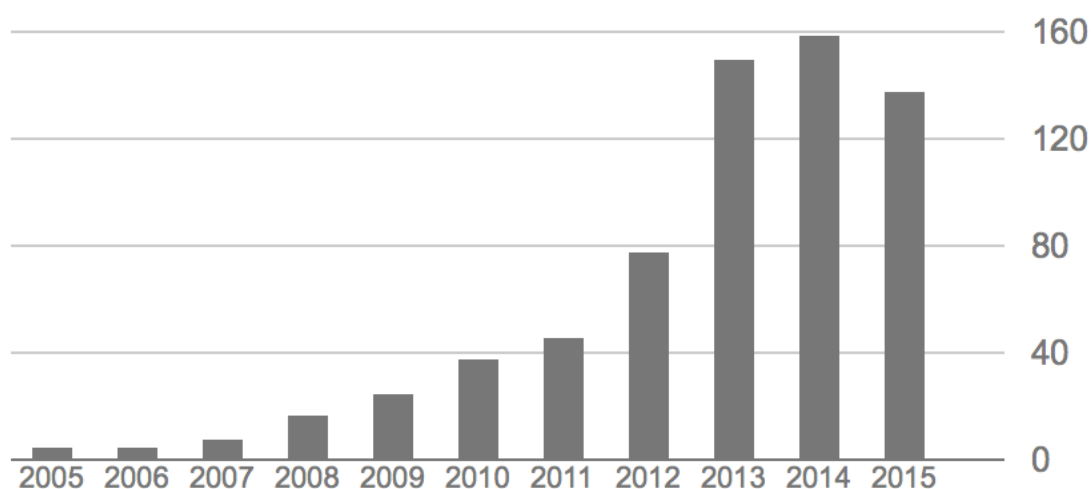
Citation statistics (based on Google Scholar):

	total	in the last five years
impact factor:	144	130
citations received:	671	614
H-index	13	N.A.
in peer reviewed journals	22	14
in peer reviewed proceedings	1	1
book chapter	2	2

Citations per year:

For a list of citations see:

Google Scholar : <http://scholar.google.hu/citations?user=sPrYT-oAAAAJ>.



Five most important publications in the last five years:

Szöllősi Gergely J., Tannier Eric, Lartillot Nicolas, Daubin Vincent

Lateral Gene Transfer from the Dead.

***SYSTEMATIC BIOLOGY* 62:(3) pp. 386-397. (2013)**

In this more theoretical work we derive the first complete minimal model of duplication, transfer and loss. Using this construction we demonstrate that under the sparse sampling assumption (relevant for most prokaryotic datasets) practically all transfers come from unsampled or more probably extinct species. We describe an approximation under using which the likelihood of a gene tree can be calculated efficiently.

Boussau Bastien, **Szöllősi Gergely J.**, Duret Laurent, Gouy Manolo, Tannier Eric, Daubin Vincent

Genome-scale coestimation of species and gene trees

***GENOME RESEARCH* 23:(2) pp. 323-330. (2013)**

In this paper, where I had the opportunity to collaborate with Bastien Boussau, we describe the first genome-scale reconstruction of species tree and gene trees based on a set of 36 mammalian genomes. We show that we are able to recover an accurate and well supported species tree together with gene trees that are significantly more accurate than those available from the pertinent reference database ENSEMBL.

Szöllősi Gergely J., Boussau Bastien, Abby Sophie S, Tannier Eric, Daubin Vincent

Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations

***PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA* 109:(43) pp. 17513-17518. (2012)**

In the paper we demonstrate that transfer events, encoded in the topologies of gene trees can be thought of as “molecular fossils” that record the order of speciation events. Using a maximum likelihood method we reconstruct the time ordered phylogeny of 36 cyanobacterial genomes from a genome-scale dataset of over 8000 homologous gene families. We show that the recovered timing information is fully consistent with the fossil record.

Schiffels Stephan*, **Szöllősi Gergely J.***, Mustonen Ville, Laessig Michael ***equal contrib.**

Emergent Neutrality in Adaptive Asexual Evolution

***GENETICS* 189:(4) pp. 1361-1375. (2011)**

In this paper, in which I share lead authorship with Stephan Schiffels, we develop a comprehensive model of adaptive evolution in linked genomes, which integrates interference interactions between multiple beneficial and deleterious mutations into a unified framework. By an approximate analytical solution, we predict the fixation rates of these mutations, as well as the probabilities of beneficial and deleterious alleles at fixed genomic sites. Our results suggest that interference can severely compromise biological functions in an adapting population, which sets viability limits on adaptive evolution under linkage.

Szöllősi G.J., Derényi I

Congruent Evolution of Genetic and Environmental Robustness in Micro-RNA

***MOLECULAR BIOLOGY AND EVOLUTION* 26:(4) pp. 867-874. (2009)**

In the paper we reexamine the results of Borenstein and Ruppin (PNAS vol.103 pp.6593-8, 2006), which presented evidence of the direct evolution of genetic robustness in microRNA sequences. Our results, based on the analysis of an exhaustive set of miRNA sequences, establishes the existence of a previously unreported level of correlation between mutational and environmental robustness induced by the biophysics of RNA folding. These results allow us to demonstrate that the results of Borenstein and Ruppin, one of the very few results concerning genetic robustness that manage to step beyond computer simulations, must be fundamentally reexamined. Our results further reveal the presence of a structural similarity threshold necessary for functional stem loop structure that may have important implications for the future of secondary structure based miRNA prediction.

Curriculum Vitae

List of Publications:

(citations from Google Scholar, first or last authorship in bold)

Submitted

Groussin M, Boussau B, Szöllősi GJ, Eme L, Gouy M, Brochier-Armanet C, Daubin V
Origins of major archaeal clades do not correspond to gene acquisitions from bacteria
MOLECULAR BIOLOGY AND EVOLUTION under review;

Jacox E, Chauve C, Szöllősi GJ, Ponty J, Scornavacca C
TERA: Comprehensive gene tree-species tree reconciliation using parsimony
BIOINFORMATICS under review;

2015

Szöllősi Gergely J, Adrien Arellano Davin, Tannier Eric, Daubin Vincent, Boussau Bastien
Genome-scale phylogenetic analysis finds extensive gene transfer among Fungi.
Philosophical Transactions of the Royal Society B in press (2015)
IF: 6.314, Citations: -;

Scornavacca Celine, Jacox Edwin, Szöllősi Gergely J
Joint Amalgamation of Most Parsimonious Reconciled Gene Trees
BIOINFORMATICS 31(6) pp. 841-8. (2015)
IF: 4.621, Citations: 2;

Derényi Imre, Szöllősi Gergely J
The effective temperature of mutations
PHYSICAL REVIEW LETTERS 114(5) pp. 058101 (2015)
IF: 7.728, Citations: 0;

Groussin Mathieu, Hobbs Joanne K, Szöllősi Gergely J, Gribaldo Simonetta, Arcus Vickery L, Gouy Manolo
Towards more accurate ancestral protein genotype–phenotype reconstructions with the use of species tree-aware gene trees.
MOLECULAR BIOLOGY AND EVOLUTION 32:(1):pp 13-22. (2015)
IF: 14.308, Citations: 1;

Szöllősi Gergely J, Tannier Eric, Daubin Vincent, Boussau Bastien
The inference of gene trees with species trees
SYSTEMATIC BIOLOGY 64:(1):pp. 42-62. (2015)
IF: 11.532, Citations: 11;

2013

Szöllősi Gergely J, Tannier Eric, Lartillot Nicolas, Daubin Vincent
Lateral Gene Transfer from the Dead.
SYSTEMATIC BIOLOGY 62:(3) pp. 386-397. (2013)
IF: 11.532, Citations: 18;

Szöllősi Gergely J, Rosikiewicz Wojciech, Boussau Bastien, Tannier Eric, Daubin Vincent
Efficient Exploration of the Space of Reconciled Gene Trees
SYSTEMATIC BIOLOGY 62:(6) pp. 901-912. (2013)
IF: 11.532, Citations: 15;

Patterson Murray, Szöllősi Gergely J, Daubin Vincent, Tannier Eric
Lateral gene transfer, rearrangement, reconciliation
BMC BIOINFORMATICS 14:(Supplement 15) p. S4. 7 p. (2013)
IF: 2.672, Citations: 6;

Curriculum Vitae

Boussau Bastien, Szöllősi Gergely J, Duret Laurent, Gouy Manolo, Tannier Eric, Daubin Vincent
Genome-scale coestimation of species and gene trees
GENOME RESEARCH **23**:(2) pp. 323-330. (2013)
IF: 13.852, Citations: 64;

2012

Szöllősi Gergely J, Boussau Bastien, Abby Sophie S, Tannier Eric, Daubin Vincent
Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations
PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA
109:(43) pp. 17513-17518. (2012)
IF: 9.737, Citations: 54;
Berard Severine, Gallien Coralie, Boussau Bastien, Szöllősi Gergely J, Daubin Vincent, Tannier Eric
Evolution of gene neighborhoods within reconciled phylogenies
BIOINFORMATICS **28**:(18) pp. 1382-1388. (2012)
IF: 5.323, Citations: 20;

2011

Schiffels Stephan*, Szöllősi Gergely J*, Mustonen Ville, Laessig Michael *equal contrib.
Emergent Neutrality in Adaptive Asexual Evolution
GENETICS **189**:(4) pp. 1361-1375. (2011)
IF: 4.007, Citations: 38;

Rauscher AA, Simon Z, Szöllősi GJ, Graf L, Derenyi I, Malnasi-Csizmadia A
Temperature dependence of internal friction in enzyme reactions
FASEB JOURNAL **25**:(8) pp. 2804-2813. (2011)
IF: 5.712, Citations: 3

Czovek A, Szöllősi GJ, Derenyi I
Neck-Linker Docking Coordinates the Kinetics of Kinesin's Heads
BIOPHYSICAL JOURNAL **100**:(7) pp. 1729-1736. (2011)
IF: 3.653, Citations: 6

2010

Katifori Eleni, Szöllősi Gergely J, Magnasco Marcelo O
Damage and Fluctuations Induce Loops in Optimal Transport Networks
PHYSICAL REVIEW LETTERS **104**:(4) Paper 048704. (2010)
IF: 7.621, Citations: 77;

2009

Szöllősi G.J., Derenyi I
Congruent Evolution of Genetic and Environmental Robustness in Micro-RNA
MOLECULAR BIOLOGY AND EVOLUTION **26**:(4) pp. 867-874. (2009)
IF: 9.872, Citations: 36;

2008

Szöllősi G.J., Derényi I
Evolutionary games on minimally structured populations
PHYSICAL REVIEW E - STATISTICAL, NONLINEAR AND SOFT MATTER PHYSICS **78**:(3) 031919. (2008)
IF: 2.508, Citations: 9;

Szöllősi G.J., Derenyi I
The effect of recombination on the neutral evolution of genetic robustness
MATHEMATICAL BIOSCIENCES **214**:(1-2) pp. 58-62. (2008)
IF: 1.148, Citations: 19;

Czovek A, Szöllősi GJ, Derenyi I
The relevance of neck linker docking in the motility of kinesin
BIOSYSTEMS **93**:(1-2) pp. 29-33. (2008)
IF: 1.477, Citations: 10;

2006

Curriculum Vitae

Szöllősi G.J., Derenyi I, Vellai T

The maintenance of sex in bacteria is ensured by its potential to reload genes

GENETICS **174**:(4) pp. 2173-2180. (2006)

IF: 4.242, Citations: 16;

Szabo B, **Szöllősi G.J.**, Gonci B, Juranyi Z, Selmeczi D, Vicsek T

Phase Transition in The Collective Migration of Tissue Cells: Experiment And Model

PHYSICAL REVIEW E - STATISTICAL, NONLINEAR AND SOFT MATTER PHYSICS **74**:(6) Paper 061908. (2006)

IF: 2.438, Citations: 156;

2004

Szöllősi G.J., Derenyi I, Voros J

Reversible mesoscopic model of protein adsorption: From equilibrium to dynamics

PHYSICA A - STATISTICAL MECHANICS AND ITS APPLICATIONS **343**: pp. 359-375. (2004)

IF: 1.369, Citations: 23;

Conference Proceedings

Doyon Jean-Philippe, Scornavacca Celine, Gorbunov K Yu, **Szöllősi Gergely J.**, Ranwez Vincent, Berry Vincent

An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers

In: Tannier Eric (szerk.)

Lecture Notes in Computer Science.

IF: N/A, Citations: 68;

Book chapters

Daubin Vincent, **Szöllősi Gergely J.**

Horizontal gene transfer and the history of life. In: Howard Ochman (ed.)

Microbial Evolution. New York: Cold Spring Harbour Press, Woodbury, New York, 2015. in press

IF: N/A, Citations: -;

Szöllősi Gergely J., Daubin Vincent

Modeling gene family evolution and reconciling phylogenetic discord. In: Maria Anisimova (ed.)

Evolutionary Genomics: Statistical and Computational Methods, Volume 2. New York: Humana Press, 2012. pp. 29-51.

IF: N/A, Citations: 12;

Recent and upcoming talks at major international conferences

Invited keynote speaker at upcoming **Jacques Monod Conference** “50 years of molecular phylogeny” in Roscoff, **2016** France.

Invited speaker at upcoming **Evolution 2016** Austin, Texas.

Efficient Exploration of the Space of Reconciled Gene Trees

SMBE 2014 San Juan, Puerto Rico, USA. (**Selected abstract**)

Inferring gene trees with species trees

at Statistical Methods for Post Genomic Data, **SMPGD 2014**.

in Paris, France. (**Invited talk**)

Horizontal gene transfer as a molecular clock

at Theoretical and empirical advances in evolutionary genomics

Jacques Monod Conference in Roscoff, **2012** France. (**Selected abstract**)

Horizontal gene transfer as a molecular clock

SMBE 2010 in Lyon, France. (**Selected abstract**)

Curriculum Vitae

Other talks with a large audience

Inferring gene trees with species trees

https://www.youtube.com/watch?v=ivxnXZQ7_xY

Invited seminar on phyloseminar.org, as part of the

Mini-course on genome-scale phylogeny. 2014, online.

Media coverage of work

Our paper “Damage and Fluctuations Induce Loops in Optimal Transport Networks” received was covered both online and in print:

[Leaves Show Looped Networks May Be Better Than Branched](#)

appeared online 2010 Feb. 4. in wired.com (see also [video](#))

[Stressz mellett ideálisak a hurkok: Rózsalevélből hálózat kutatás](#)

appeared 2010 feb. 19. in Népszabadság a major Hungarian daily newspaper

Teaching and supervision of students

- 4 semesters during 2005-2008 teaching the *Molecular Modelling* practical course in Biological Physics for physics M.Sc. students (weekly, five hours per week)
- 2 semesters from 2014 fall and ongoing teaching “”
- I supervised the thesis work of several M.Sc. students at the Laboratoire de Biométrie et Biologie Évolutive in Lyon and at the Biological Physics department at Eötvös university in Budapest:
 1. **2010. Wojciech Roskiewicz** (Bioinformatics M.Sc. Univ. Lyon 1 Claude Bernard). The thesis, who I co-supervised with Vincent Daubin was ranked in the top 10% of his class;
 2. **2013. Kéri Zsófia** (Physics B.Sc. Eötvös University, Budapest) The thesis received a score of 5 out of 5.;
 3. **2013-2015 Kéri Zsófia** (Biological Physics M.Sc. Eötvös University, Budapest) Ms. Kéri completed her M.Sc. thesis under my supervision, her thesis received a score of 5 out of 5;
 4. **2014 Benjamin Horvilleur** (Bioinformatics M.Sc. Univ. Lyon 1 Claude Bernard) joint supervision with Dr. Nicolas Lartillot.

Awards

I was ranked 13th and 8th in two successive years of the Hungarian National High School Physics competition (Fizika OKTV). I have also been awarded a number of fellowships from agencies ranging from the European Commissions (under FP7) to the Burroughs Wellcome Fund.

Membership

I am a member of the Hungarian Academy of Sciences General Assembly since 2014.

I am a member of the Society for Molecular Evolution since 2010, the Society of Systematic Biologists since 2014, the American Biophysical Society since 2014, the Hungarian Society of Biochemistry since 2009, the Hungarian Society of Biophysics since 2014.

Professional service

Curriculum Vitae

I have reviewed several dozen papers for a range of journals including:

Reviewer for Systematic Biology

Reviewer for Genome Biology and Evolution

Reviewer for BioMed Central's journal BMC Evolutionary Biology

Reviewer for the Public Library of Science's journal PLoS Computational Biology

Reviewer for the Public Library of Science's journal PLoS One

Reviewer for Physical Review Letters and Physical Review E

Reviewer for the Journal of Statistical Physics

Collaboration with industry

1. During the summer of 2006, I participated in a project led by Miklós István (Rényi Institute of Mathematics, Hungarian Academy of Sciences) that test a wide range of machine learning approaches for selecting candidate kinase inhibitors in collaboration with Vichem, a Hungarian pharmaceutical start-up.

2. In 2006, I participated in the EURESCOM project NEW DIMENSIONS (NEtWork DIMENSIONing baSed on modeling of Internet traffic), funded by Ericsson Hungary at the Budapest University of Technology and Economics, where I worked on a stochastic timer approach to feedback optimization of multicast networks.

I also worked for a small programming company during my university studies.