Christian M. Zmasek, PhD | Curriculum Vitae

Personal Information

Name:	Zmasek, Christian Matthias
Highest Degree:	PhD in Biology and Biomedical Sciences (Molecular Genetics)
Birthplace:	Winterthur, Switzerland
Citizenship:	Swiss (permanent US resident through National Interest Waiver)

Work Address

Burnham Institute for Medical Research
10901 North Torrey Pines Road
La Jolla, CA 92037
USA
858-646-3100 x3077
czmasek at burnham dot org

Interests

- The evolution of regulatory pathways involved in development and defense (such as cell death and innate immunity)
- The evolutionary dynamics of protein and genome architectures
- Ancestral genome reconstruction and analysis
- The evolution of complexity
- Evolutionary developmental biology (evo-devo)
- Automated sequence function prediction
- Phylogeny reconstruction
- Systems biology; network analysis, reconstruction, and simulation
- Software and algorithm development, data visualization
- Experimental molecular biology

Research Experience

2006.06.26 – present: Burnham Institute for Medical Research: Post-doc with Prof. Adam Godzik
(10901 North Torrey Pines Road, La Jolla, CA 92037, USA)

- Reconstruction and functional analysis of ancestral eukaryotic genomes
- Evolution of signaling pathways, focusing on networks regulating development, cell death, and innate immunity
- Comparative analysis of protein domain architectures and their dynamics over time and taxonomic space
- Analysis of the origin of carbohydrate metabolism in human gut symbionts
- Cloning and sequence analysis of Bcl-2, Apaf-1, and Caspase family members from the sea anemone *Nematostella vectensis*
- Analysis of the evolution of protein structures and functions, development of empirical rules describing changes in protein structure accompanying functional changes
- Various software and algorithm development projects, including:
  - Design and Java-based implementation of phyloXML, an XML language for evolutionary biology and comparative genomics
  - Development, implementation, and analysis of an algorithm for protein domain phylogeny reconciliation
  - Development, implementation, and analysis of an algorithm for generalized gene duplication inference

- Development of Archaeopteryx – a sophisticated tool for phylogenetic tree visualization and interpretation
- Continued development of Forester – open source libraries of Java and Ruby software for phylogenomics and evolutionary biology research

2002.03.18 – 2006.06.23: Genomics Institute of the Novartis Research Foundation
(10675 John Jay Hopkins Drive, San Diego, CA 92121, USA)
Principal Investigator.
Select research/software development projects:

- Large scale phylogenetic analyses of multiple ion channel gene families from species ranging from *Ciona intestinalis* to mammals
- Phylogenetic analysis of non-protein kinases
- mRNA expression analysis
- Managed the full life cycle (design, develop, integrate, test, and user support) for three JavaEE/Oracle-based software projects:
  - Statistical analysis of high throughput functional cell based cDNA and siRNA screening experiments
  - DNA sequence/DNA sequencing management
  - Management of histology core services

1997.08 – 2002.03: Department of Genetics, Washington University School of Medicine
(Center for Genome Sciences, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA)
Graduate student in the research laboratory of Professor Sean Eddy. I performed research on the genome wide application of concepts and methods from molecular evolution for analyses in comparative functional genomics. In particular, I investigated the importance of gene duplications for protein function evolution and computational methods to detect them. Gene duplications are of interest in molecular evolution as they allow the evolution of novel functionality and because they complicate functional inferences. I developed an efficient algorithm to calculate gene duplications ("SDI"), as well as a system for automated sequence function prediction, based on orthology inference and suitable for large scale genome analyses ("RIO"; http://rio.janelia.org/).

1998.06 – 1998.08: Monsanto Company
(800 North Lindbergh Boulevard, St. Louis, MO 63167, USA)
Summer Internship.
Research project: Reconstruction of signaling pathways by automated mining of the knowledge present in scientific literature and databases.

1995.06 – 1997.08: Department of Cell Biology, Washington University School of Medicine
(660 South Euclid Avenue, St. Louis, MO 63110, USA)
Graduate research assistant with Professor Helen Piwnica-Worms.
Areas of work: cell biology and biochemistry of signal transduction, immuno-fluorescence and confocal microscopy, construction of a EMK/Par-1 protein kinase KO mouse.

1992; 1993: Institute of Microbiology, Swiss Federal Institute of Technology (ETH) in Zürich
(Wolfgang-Pauli-Strasse, CH-8093 Zürich, Switzerland)
Semester Work and Diploma Thesis work with Professor Gerhard Braus.
Analysis of the gene regulatory function of the yeast HIS7 promoter.

Teaching Experience

Summer 2009: Google Summer of Code 2009
Mentoring of a graduate student implementing phyloXML support in BioRuby.

2008/03; 2007/03: Burnham Institute for Medical Research
Taught 'Introduction to Phylogenetic Analysis' class.

1996.01 - 1996.05: Biology Department, Washington University
(One Brookings Drive, St. Louis, MO 63130, USA)
Teaching Assistant in Molecular Biology and Biochemistry.

1989 - 1994
Tutoring in Mathematics, Biology, and Physics.

Degrees

2002.05.10: **Doctor of Philosophy in Biology and Biomedical Sciences, Molecular Genetics Program**
Washington University School of Medicine, St. Louis, MO, USA
PhD advisor: Dr. Sean Eddy, Alvin Goldfarb Distinguished Professor of Computational Biology and assistant investigator of the Howard Hughes Medical Institute.

1994.05.03: **Diploma in Natural Sciences: Chemistry/Biology with emphasis on Biochemistry, Molecular Biology/Biophysics, Cell Biology**
Swiss Federal Institute of Technology (ETH) in Zürich, Switzerland.

Awards

8th International Conference on Intelligent Systems for Molecular Biology (2000; San Diego, USA): **Best of Conference: Poster**
For the poster entitled: Automated Sequence Function Prediction Based on Phylogenetic Inference.

Publications (peer reviewed)

Tegla TJ, **Zmasek** CM, Batalov S, and Nayak SK (2009).
Evolution of the human ion channel set.
Combinatorial Chemistry & High Throughput Screening, 12, 2-23.

Zhang Q, **Zmasek** CM, Dishaw LJ, Mueller MG, Ye Y, Litman GW, and Godzik A (2008).
Novel genes dramatically alter regulatory network topology in amphioxus.
Genome Biology, 9:R123.

Holland LZ, Albalat R, Azumi K, ..., **Zmasek** CM, ..., and Holland PW (2008).
The amphioxus genome illuminates vertebrate origins and cephalochordate biology.
Genome Research, 18, 1100-1111.

Zmasek CM, Zhang Q, Ye Y, and Godzik A (2007). Surprising complexity of the ancestral apoptosis network. *Genome Biology*, 8:R226.

Lapp H, Bala S, ..., **Zmasek** CM, ..., and Vision TJ (2007).
The 2006 NESCent phyloinformatics hackathon: A field report.
Evolutionary Bioinformatics, 2007:3 287-296.

Leebens-Mack J, Vision T, …, and **Zmasek** C (2006). Taking the first steps towards a standard for reporting on phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). *OMICS*, 10, 231-237.

Lawrence CJ, **Zmasek** CM, Kelly Dawe R, and Malmberg RL (2004). LumberJack: a heuristic tool for sequence alignment exploration and phylogenetic inference. *Bioinformatics*, 20, 1977-1979.

Zmasek CM and Eddy SR (2002). RIO: Analyzing proteomes by automated phylogenomics using resampled inference of orthologs. *BMC Bioinformatics*, 3:14.

Zmasek CM and Eddy SR (2001). A simple algorithm to infer gene duplication and speciation events on a gene tree. *Bioinformatics*, 17, 821-828.

Zmasek CM and Eddy SR (2001). ATV: display and manipulation of annotated phylogenetic trees. *Bioinformatics*, 17, 383-384.

Hurov JB, Stappenbeck TS, **Zmasek** CM, White LS, Ranganath SH, Russell JH, Chan AC, Murphy KM, and Piwnica-Worms H (2001). Immune system dysfunction and autoimmune disease in mice lacking Emk (Par-1) protein kinase. *Molecular and Cellular Biology*, 21, 3206-3219.

Springer C, Krappmann S, Künzler M, **Zmasek** C, and Braus GH (1997). Activation of the HIS7 gene by the global transcription factor Abf1p. *Molecular and General Genetics*, 256, 136-146.

Invited Presentations

Invited Speaker:
Biodiversity Information Standards (TDWG) Annual Conference 2008, Fremantle (Perth), Australia.
Zmasek CM (2008). Emerging data standards for phylogenomics research.

Society Memberships

- American Society for Cell Biology (ASCB) (Bethesda, MD, USA)
- Society for Developmental Biology (Bethesda, MD, USA)
- Society for Molecular Biology and Evolution (SMBE) (Athens, GA, USA)
- Society for Integrative and Comparative Biology (McLean, VA, USA)
- International Society for Computational Biology (ISCB) (La Jolla, CA, USA)

Education (only relevant experiences listed)

1994.06 – 2002.03.01: Washington University School of Medicine: Molecular Genetics Graduate Program
(660 South Euclid Avenue, St. Louis, MO 63110, USA)
Biology and Biomedical Sciences.
Degree: Doctor of Philosophy in Biology and Biomedical Sciences, Molecular Genetics Program

1999.08: Marine Biological Laboratory: Workshop on Molecular Evolution
(7 MBL Street, Woods Hole, MA 02543, USA)
In-depth course in the theory and applications of molecular evolution.

1989.10 – 1994.05: Swiss Federal Institute of Technology in Zürich: Natural Sciences (Chemistry/Biology)
(ETH Zentrum, Rämistrasse 101, CH-8092 Zürich, Switzerland)
Degree: Diploma in Natural Sciences: Chemistry/Biology with emphasis on Biochemistry, Molecular Biology/Biophysics, Cell Biology.

1985.04 – 1989.09: Kantonsschule im Lee: Mathematics/Natural Sciences
(Rychenbergstrasse 140, CH-8400 Winterthur, Switzerland)
Degree: Matura Type C (Mathematics/Natural Sciences)

Distributed Software Packages (partial list)

RIO: System to analyze proteomes by automated phylogenomics using resampled inference of orthologs (available at: http://www.phylosoft.org/forester/; RIO webserver at: http://rio.janelia.org/).

SDI: Implementation of an algorithm developed by me for speciation - duplication inference (available at: http://www.phylosoft.org/forester/).

ATV: Java application for the visualization and manipulation of annotated phylogenetic trees, as well as a platform for phylogenomics analyses (available at: http://www.phylosoft.org/atv/).

Technical Experiences

Molecular Evolution: Extensive experience in phylogenetic analysis, gene duplication inference, genome-wide functional analysis, and phylogenetic protein family analysis.

Genomics, Computational Biology: Experienced in algorithm development and testing, DNA and protein sequence analysis, genome-wide data analysis and management, strong skills in object oriented software engineering.

Molecular Biology, Biochemistry, and Cell Biology: Experienced in DNA isolation, manipulation, and analysis; protein expression, purification, and analysis; microscopy techniques (immuno-fluorescence and confocal); and embryonic stem (ES) cell culture.

Genetics: Familiar with mouse, yeast, and *E. coli* genetics.

Computer programming languages: Java, Ruby, C++, Perl, SQL.

References

Available upon request.