

# CURRICULUM VITAE

OLIVER EULENSTEIN

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## CONTACT DETAILS

Oliver Eulenstein,  
Iowa State University,  
Department of Computer Science,  
Ames, IA 50011-1040 USA

phone: +1-515-294-2407

fax: +1-515-294-0258

e-mail: oeulnst@cs.iastate.edu

## RESEARCH INTERESTS

Computational Complexity, Discrete Algorithms, Computational Biology and Bioinformatics with particular interest in phylogenetics.

## PROFESSIONAL EXPERIENCE

### 1. IOWA STATE UNIVERSITY (USA)

2006 – present Associate Professor (tenured), Department of Computer Science.

2000 – 2006 Assistant Professor (tenure track), Department of Computer Science.

2002 – present Faculty member, Multidisciplinary Graduate Education Training.

2000 – present Faculty member, Ph.D. program for Bioinformatics & Computational Biology.

2000 – present Faculty member, L. H. Baker Center for Bioinformatics and Biological Statistics.

### 2. UNIVERSITY OF CALIFORNIA DAVIS (USA)

1998 – 2000 Postdoctoral Fellow with Dan Gusfield, Department of Computer Science.

1999 – 2000 Lecturer, Department of Computer Science.

### 3. UNIVERSITY OF BONN/GMD (GERMANY)

1993 – 1998 Ph.D. Research Assistant with Thomas Lengauer, Department of Computer Science and the National Research Center for Information Technology (GMD).

### 4. UNIVERSITY OF PADERBORN (GERMANY)

1992 – 1993 Ph.D. Research Assistant, Computer Aided Design Laboratory (CADLAB).

1989 – 1992 M.S. Research Assistant, Computer Aided Design Laboratory (CADLAB).

## EDUCATION

- 1998 Dr. rer. nat. (Ph. D.) with *cum laude* in Computer Science, University of Bonn.  
Advisor: Thomas Lengauer, Max Plank Institute for Computer Science, Saarbrücken.
- 1991 Diplom-Informatiker (M. S.) in Computer Science, University of Paderborn.
- 1987 Vordiplom (B. S.) in Computer Science, University of Paderborn.

## EXTRAMURAL FUNDING

- 2008 – 2011 \$800,000, Co-PI, *Collaborative Research: Phylogenetic Trees for Comparative Biology*.
- 2003 – 2009 \$976,520, PI, *AToL: Collaborative Research: A Phylogenomic Toolbox for Assembling the Tree of Life Molecular Sequence Databases*.
- 2000 – 2004 \$370,000, Co-PI, *Algorithms and Software for Phylogenetic Supertrees*.

## SYNERGISTIC ACTIVITIES

Pawel Górecki from the University of Warsaw together with Oliver Eulenstein organized the first international tree-reconciliation workshop in Germany (2009), which was supported by the Max-Planck Institute for molecular genetics in Berlin.

Oliver Eulenstein is a member of the PhyLoTA project ([loco.biosci.arizona.edu/phyloata](http://loco.biosci.arizona.edu/phyloata)) that aims to develop powerful computational tools for mining phylogenetic databases that support evolutionary biologists in their efforts to construct the tree of life.

Oliver Eulenstein is involved in the 1KP project ([www.onekp.com](http://www.onekp.com)), a public-private partnership with the challenging goal of generating large-scale gene sequence information for 1000 plant species. His specific task is to provide supertree methods to enable the construction of a robust phylogeny for these species. One motivation for building this phylogenetic tree is to use it in the design of novel plant-based drugs.

## ESSENTIAL COLLABORATORS

Evolutionary biology: Mike Sanderson (University of Arizona), Gordon Burleigh (University of Florida), Roland Krause (Max-Planck Institute for molecular genetics in Berlin).

Computer science: David Fernández-Baca (Iowa State University). Pawel Górecki (University of Warsaw, Poland).

## SERVICES

### CONFERENCE BOARDS

The International Society for Computational Biology (ISMB) in 2008; the Bioinformatics and Computational Biology (BICoB) conference in 2010, and 2009.

### REFeree ACTIVITIES

Refereed papers for numerous journals (Bioinformatics, BMC Bioinformatics, BMC Evolutionary Biology, IEEE Transactions on Computational Biology and Bioinformatics, Journal of Computational Biology, Mathematical Bioscience, Statistical Analysis and Data-mining, Systematic Biology,) and several proposals for the *National Science Foundation*.

## COMMITTEES

Oliver Eulenstein chaired the BCB admission committee for three years, and the scholarship and faculty awards committee in the Dept. of Computer Science for one year. He has also served on various committees at Iowa State University.

## TEACHING SUMMARY (COURSES TAUGHT)

### 1. IOWA STATE UNIVERSITY (SEMESTER SYSTEM)

#### Graduate Courses

- Advanced Algorithms for Computational Biology (Com S 549).  
Currently teaching.
- Bioinformatics I (Fundamentals of Genome Informatics) (Com S 567).  
Taught in: Fall 09.
- Algorithms for Phylogenetic Problems (Com S 550).  
Taught in: Spring 04, and Fall 07.
- Advanced Algorithms in Computational Biology (Com S 549).  
Taught in Spring 06, 03, 01.
- Fundamental Algorithms in Computational Biology (Com S 548).  
Taught in Spring 03, 02, and Fall 06, 04.
- Design and Analysis of Algorithms (Com S 511).  
Taught in Fall 03.
- Discrete Algorithms in Computational Biology (seminar).  
Taught in Fall 00.

#### Undergraduate Courses

- Design and Analysis of Algorithms (Com S 311).  
Taught in Spring 07, 05, 04 (two sections), and Fall 07, 06, 01.

### 2. UNIVERSITY OF CALIFORNIA DAVIS (QUARTER SYSTEM)

#### Undergraduate Courses

- Introduction to the Theory of Computation (ECS 120).  
Taught in: Spring 00, Winter 01 and 00, Fall 99.

## COURSE CREATION

Com S 548      *Fundamental Algorithms for Computational Biology*. This course became a core course of the Bioinformatics and Computational Biology graduate program (BCB) at Iowa State University. Today, the course is taught in turns by different faculty from the engineering and computer science department.

## GRADUATE STUDENTS

Mukul Bansal, Com. Sci. PhD, 2009 (accepted a postdoctoral position in Ron Shamir's Computational Genomics group at Tel Aviv University); André Wehe, Com. Sci. PhD, Fall 2010 (expected); Wen-Chieh Chang, Com. Sci. PhD, 2011 (expected), Lee Younsook, BCB PhD, 2012 (expected); Wen-Chieh Chang, Com. Sci., MS 2005.

## Journal Articles

- [1] Mukul S. Bansal, J Gordon Burleigh, Oliver Eulenstein, and David Fernández-Baca. Robinson-foulds supertrees. *Algorithms Mol Biol*, 5(1):18, 2010.
- [2] André Wehe, Wen-Chieh Chang, Oliver Eulenstein, and Srinivas Aluru. A scalable parallelization of the gene duplication problem. *Journal of Parallel and Distributed Computing*, 70:237–244, 2010.
- [3] Mukul S. Bansal, J. Gordon Burleigh, and Oliver Eulenstein. Efficient genome-scale phylogenetic analysis under the duplication-loss and deep coalescence cost models. *BMC Bioinformatics*, 11(Suppl 1):S42, 2010.
- [4] J. Gordon Burleigh, Mukul S. Bansal, Oliver Eulenstein, Stephanie Hartmann, André Wehe, and Todd J. Vision. Genome-scale phylogenetics: Inferring the plant tree of life from 18,896 discordant gene trees. *Systematic Biology*, 2009 (to appear).
- [5] Mukul S. Bansal, Oliver Eulenstein, and André Wehe. The gene-duplication problem: Near-linear time algorithms for nni-based local searches. *IEEE/ACM Trans. Comput. Biology Bioinform.*, 6(2):221–231, 2009.
- [6] Harris T. Lin, J. Gordon Burleigh, and Oliver Eulenstein. Triplet supertree heuristics for the tree of life. *BMC Bioinformatics*, 10(S-1), 2009.
- [7] J G Burleigh, M S Bansal, A Wehe, and O Eulenstein. Locating large-scale gene duplication events through reconciled trees: implications for identifying ancient polyploidy events in plants. *J Comput Biol*, 16(8):1071–83, Aug 2009.
- [8] Cécile Ané, Oliver Eulenstein, Raul Piaggio-Talice, and Michael Sanderson. Groves of phylogenetic trees. *Annals of Combinatorics*, 13(2):139–167, August 2009.
- [9] Mukul S. Bansal and Oliver Eulenstein. An  $\Omega(n^2/\log n)$  speed-up of tbr heuristics for the gene-duplication problem. *IEEE/ACM Trans. Comput. Biology Bioinform.*, 5(4):514–524, 2008.
- [10] André Wehe, Mukul S. Bansal, J. Gordon Burleigh, and Oliver Eulenstein. Duptree: a program for large-scale phylogenetic analyses using gene tree parsimony. *Bioinformatics*, 24(13):1540–1541, 2008.

- [11] Mukul S Bansal and Oliver Eulenstein. The multiple gene duplication problem revisited. *Bioinformatics*, 24(13):i132–8, Jul 2008.
- [12] Duhong Chen, Oliver Eulenstein, David Fernández-Baca, and J Gordon Burleigh. Improved heuristics for minimum-flip supertree construction. *Evol Bioinform Online*, 2:391–400, 2006.
- [13] Duhong Chen, Oliver Eulenstein, David Fernández-Baca, and Michael Sanderson. Minimum-flip supertrees: Complexity and algorithms. *IEEE/ACM Trans. Comput. Biology Bioinform.*, 3(2):165–173, 2006.
- [14] Changhui Yan, J Gordon Burleigh, and Oliver Eulenstein. Identifying optimal incomplete phylogenetic data sets from sequence databases. *Mol Phylogenet Evol*, 35(3):528–35, Jun 2005.
- [15] Mark Wilkinson, James A Cotton, Chris Creevey, Oliver Eulenstein, Simon R Harris, Francois-Joseph Lapointe, Claudine Levasseur, James O McInerney, Davide Pisani, and Joseph L Thorley. The shape of supertrees to come: tree shape related properties of fourteen supertree methods. *Syst Biol*, 54(3):419–31, Jun 2005.
- [16] Oliver Eulenstein, Duhong Chen, J Gordon Burleigh, David Fernández-Baca, and Michael J Sanderson. Performance of flip supertree construction with a heuristic algorithm. *Syst Biol*, 53(2):299–308, Apr 2004.
- [17] Duhong Chen, Oliver Eulenstein, and David Fernández-Baca. Rainbow: a toolbox for phylogenetic supertree construction and analysis. *Bioinformatics*, 20(16):2872–2873, 2004.
- [18] Michael J Sanderson, Amy C Driskell, Richard H Ree, Oliver Eulenstein, and Sasha Langley. Obtaining maximal concatenated phylogenetic data sets from large sequence databases. *Mol Biol Evol*, 20(7):1036–42, Jul 2003.
- [19] Oliver Eulenstein, Boris Mirkin, and Martin Vingron. Duplication-based measures of difference between gene and species trees. *Journal of Computational Biology*, 5(1):135–148, 1998.
- [20] Oliver Eulenstein and Martin Vingron. On the equivalence of two tree mapping measures. *Discrete Applied Mathematics*, 88(1-3):103–128, 1998.
- [21] Yan P. Yuan, Oliver Eulenstein, Martin Vingron, and Peer Bork. Towards detection of orthologues in sequence databases. *Bioinformatics*, 14(3):285–289, 1998.

## Conference and Working Group Articles

- [22] Wiedenhopf John, Roland Krause, and Oliver Eulenstein. *Bioinformatics Research and Applications, 6th International Symposium, ISBRA 2010, Connecticut, CT, USA, May 23-26, 2010. Proceedings*, chapter Inferring Evolutionary Scenarios for Protein Domain Compositions. Lecture Notes in Computer Science. Springer Berlin / Heidelberg, 2010.
- [23] Homilius Max, J. Gordon Burleigh, and Oliver Eulenstein. Triplet-supertrees constructed from minimum triplet presentations. In Hisham Al-Mubaid, editor, *BICoB*, 2010.
- [24] Mukul S Bansal, J Gordon Burleigh, and Oliver Eulenstein. Efficient genome-scale phylogenetic analysis under the duplication-loss and deep coalescence models. In *8<sup>th</sup> Asian-Pacific Bioinformatics Conference (APBC 2010)*, 2010 (to appear).

- [25] Harris Lin, J Gordon Burleigh, and Oliver Eulenstein. Triplet supertree heuristics for the tree of life. In *7<sup>th</sup> Asian-Pacific Bioinformatics Conference (APBC 2009)*, 2009.
- [26] Mukul S. Bansal, Wen-Chieh Chang, Oliver Eulenstein, and David Fernández-Baca. Generalized binary tanglegrams: Algorithms and applications. In Sanguthevar Rajasekaran, editor, *BICoB*, volume 5462 of *Lecture Notes in Computer Science*, pages 114–125. Springer, 2009.
- [27] J. Gordon Burleigh, Mukul S. Bansal, André Wehe, and Oliver Eulenstein. Locating multiple gene duplications through reconciled trees. In Martin Vingron and Limsoon Wong, editors, *RECOMB*, volume 4955 of *Lecture Notes in Computer Science*, pages 273–284. Springer, 2008.
- [28] Mukul S. Bansal and Oliver Eulenstein. The gene-duplication problem: Near-linear time algorithms for nni based local searches. In Ion I. Mandoiu, Raj Sunderraman, and Alexander Zelikovsky, editors, *ISBRA*, volume 4983 of *Lecture Notes in Computer Science*, pages 14–25. Springer, 2008.
- [29] Mukul S. Bansal and Oliver Eulenstein. The multiple gene duplication problem revisited. In *ISMB*, pages 132–138, 2008.
- [30] Mukul S. Bansal and Oliver Eulenstein. An  $\Omega(n^2/\log n)$  speed-up of tbr heuristics for the gene-duplication problem. In Raffaele Giancarlo and Sridhar Hannenhalli, editors, *WABI*, volume 4645 of *Lecture Notes in Computer Science*, pages 124–135. Springer, 2007.
- [31] Mukul S. Bansal, J. Gordon Burleigh, Oliver Eulenstein, and André Wehe. Heuristics for the gene-duplication problem: A  $\Theta(n)$  speed-up for the local search. In Terence P. Speed and Haiyan Huang, editors, *RECOMB*, volume 4453 of *Lecture Notes in Computer Science*, pages 238–252. Springer, 2007.
- [32] Wen-Chieh Chang and Oliver Eulenstein. Reconciling gene trees with apparent polytomies. In Danny Z. Chen and D. T. Lee, editors, *COCOON*, volume 4112 of *Lecture Notes in Computer Science*, pages 235–244. Springer, 2006.
- [33] Duhong Chen, Lixia Diao, Oliver Eulenstein, David Fernández-Baca, and Michael J Sanderson. Flipping: A supertree construction method. In M. F Janowitz, editor, *Bioconsensus*, volume 37 of *DIMACS Series in Discrete Mathematics and Theoretical Computer Science*, pages 135–169, Providence, RI, March 2003. American Mathematical Society.
- [34] J. Schonfeld, Oliver Eulenstein, Kent Vander Velden, and Gavin J. P. Naylor. Investigating evolutionary lines of least resistance using the inverse protein-folding problem. In *Pacific Symposium on Biocomputing*, pages 613–624, 2002.
- [35] Duhong Chen, Oliver Eulenstein, David Fernández-Baca, and Michael Sanderson. Supertrees by flipping. In Oscar H. Ibarra and Louxin Zhang, editors, *COCOON*, volume 2387 of *Lecture Notes in Computer Science*, pages 391–400. Springer, 2002.
- [36] Oliver Eulenstein, Boris Mirkin, and Martin Vingron. Comparison of annotating duplication, tree mapping, and copying as methods to compare gene trees with species trees. In Boris Mirkin, Fed R. McMorris, Fred S. Roberts, and Andrey Rzhetsky, editors, *Mathematical Hierarchies and Biology*, volume 37 of *DIMACS Series in Discrete Mathematics and Theoretical Computer Science*, pages 71–94, Providence, RI, 1997. American Mathematical Society.

- [37] Yan P. Yuan, Oliver Eulenstein, Martin Vingron, and Peer Bork. Towards detection of sequence orthologs. In *German Conference on Bioinformatics*, pages 25–30, 1997.

## Book Chapters

- [38] O. Eulenstein, S. Huzurbazar, and D. Liberles. *Evolution after gene duplication*, chapter Reconciling phylogenetic trees. Wiley, New York, 2010 (to appear).
- [39] Michael J Sanderson, Cécile Ané, Oliver Eulenstein, David Fernández-Baca, Kim Junhyong, Michelle M. McMahon, and Piaggio-Talice Raul. Fragmentation of large data sets in phylogenetic analyse. In Olivier Gascuel and Mike Steel, editors, *Reconstructing Evolution*, pages 199–216. Oxford University Press, August 2007.
- [40] Oliver Eulenstein. Consensus trees and supertrees. In Alurtu Srinivas, editor, *Handbook of Computational Molecular Biology*, Chapman & Hall/Crc Computer and Information Science Series, chapter 20. Chapman & Hall/CRC, 2005.
- [41] Raul Piaggio-Talice, J Gordon Burleigh, and Oliver Eulenstein. Quartet supertrees. In Olaf Bininda-Emonds, editor, *Phylogenetic supertrees: combining information to reveal the tree of life*, pages 173–192. Kluwer, 2004.
- [42] J Gordon Burleigh, Oliver Eulenstein, David Fernández-Baca, and Michael J Sanderson. Mrf supertrees. In Olaf Bininda-Emonds, editor, *Phylogenetic supertrees: combining information to reveal the tree of life*, pages 65–86. Kluwer, 2004.