
Curriculum Vitæ — Thomas Mailund (born 1975)

Academic Degrees

- PhD, Dept of Computer Science, University of Aarhus, May 2003
- MSc, Dept of Computer Science, University of Aarhus, December 2000

Academic Positions

- Research associate professor, Bioinformatics Research Center, University of Aarhus, Denmark, 2008–present.
- Assistant professor, Bioinformatics Research Center, University of Aarhus, Denmark, 2003–2008.
- Postdoc, Dept of Statistics, University of Oxford, UK, 2006–2007.
- Teaching assistant, Dept of Computer Science, University of Aarhus, Denmark, 1999–2002.

Other Positions

- CTO, Bioinformatics ApS, 2004–2005.
- Student programmer, Dept of Computer Science, University of Aarhus, 1997–1999.

Other Academic Activities

Referee for several journals, conferences and workshops in computer science and bioinformatics.

Invited Speaker

- *Mapping by Local Genealogies*, Workshop on Association Mapping and Linkage Analysis, Bioinformatics Research Center (BiRC) and Centre for Theory in Natural Science (CTN), University of Aarhus, Denmark, 2007.
- *Association Mapping—Searching for Disease Causing Genes*, Bioinformatics and Systems Biology, Bioinformatics Research Center (BiRC), University of Aarhus, Denmark, 2005.
- *Association Mapping—Searching for Disease Causing Genes*, Alexandra Institute, IT Solutions for Integrated Drug Discovery, 2005.

Teaching Experience

Lecturer

- *Mathematical Models in Systems Biology* (with C. Wiuf), Bioinformatics Research Center, University of Aarhus (2008).
- *Stochastic Models in Bioinformatics* (with F.B. Christiansen), Bioinformatics Research Center, University of Aarhus (2007).
- *String Algorithms* (with C.N.S. Pedersen), Dept of Computer Science, University of Aarhus (2004–2007).
- *Machine Learning* (with C.N.S. Pedersen), Dept of Computer Science, University of Aarhus (2007).
- *Genome Analysis* (with M.H. Schierup), Bioinformatics Research Center, University of Aarhus (2007).
- *Tool Building in Bioinformatics* (with S. Besenbacher), Bioinformatics Research Center, University of Aarhus (2007).
- *Script Programming*, Bioinformatics Research Center, University of Aarhus (2005).
- *Complex Software Systems* (with J. Fredslund), Bioinformatics Research Center, University of Aarhus (2003).

Tutorials

- *Association Mapping: Fundamental Principles and Applications* (with M.H. Schierup, J. Hein, L. Schausser, and J.N. Madsen), At Pacific Symposium on Biocomputing (PSB) 2006.
- *Association Mapping: Design Issues and Data Analysis Approaches* (with L. Schausser, J.N. Madsen, J. Hein and M.H. Schierup), At Pacific Symposium on Biocomputing (PSB) 2005.

Supervised Students

- Ricky Madsen (MSc):
Statistical Alignment for Accurate Parameter Inference.
Dept of Computer Science, University of Aarhus.
- Martin Stig Stissing (MSc):
Algorithms for Computing the Quartet Distance.
Dept of Computer Science, University of Aarhus.
Defended on February 24th 2006.
Co-supervised with C.N.S. Pedersen.

Grants

- **FNU grant 272-07-0380**; DKK 2 000 000; 2008–2011; *Computational Challenges in Disease Mapping*.
- **FTP grant 274-05-0365**; DKK 770 000; 2006–2008; *Tools for Fine-Scale and Whole-Genome Association Mapping*.
- **FNU grant 272-05-0283**; DKK 358 906; 2006–2007; *Tools for Fine-Scale and Whole-Genome Association Mapping*.

Awards

- **The Wellcome Trust Value in People Award**; £9486; 2006; For the project *Tools for Fine-Scale and Whole-Genome Association Mapping*.
- **The Danish Research Councils “Young Elite Investigator’s” award**; DKK 200 000; 2007; For the project *Computational Challenges in Disease Mapping*.

Research Projects

- *Computational Challenges in Disease Mapping* (2008–2011).

<http://www.daimi.au.dk/~mailund/association-mapping/>

The project concerns integrating various sources of data in disease mapping studies and the computational and informatics challenges in dealing with the both quantitatively and qualitatively change in data.

The project is funded by FNU grant 272-07-0380.

- *PolyGene* (2006–2008)

<http://www.polygene.eu>

PolyGene is an EU-funded study that focuses on inherited predisposition to breast and prostate cancer. In the PolyGene project, genome-wide association studies of two European populations of different history and structure will be conducted in order to identify common variants that contribute to the risk of breast and prostate cancer. At the same time, statistical methods will be developed that will help identify the most important variants, direct the replication of positive findings and localize the causative genes.

- *Tools for Fine-Scale and Whole-Genome Association Mapping* (2006–2008).

<http://www.daimi.au.dk/~mailund/association-mapping/>

This project is concerned with development of computation methods and computer tools for locating disease genes. The amount of data and the complexity of the problems make computer tools essential for successful studies. With the recent improvements in genotyping technology that now allow simultaneous genotyping of hundreds of thousands of polymorphisms, the analysis of data is becoming the bottleneck of studies, and hence it is increasingly important to develop better and faster analysis methods.

The project is running in the period February 2006 – January 2007 at the Dept of Statistics, University of Oxford, (funded by FNU, grant 272-05-0283) and the period February 2007 – January 2008 at Bioinformatics Research Center, University of Aarhus (funded by FTP, grant 274-05-0365).

- *Faster Programs for reconstructing evolution* (2005–2007).

http://snf.formidling.dk/show_project.php?project_id=22

The aim of this project is to develop faster algorithms and computer tools for phylogenetic tree reconstruction and comparisons of phylogenetic trees. The project is funded by Statens Naturvidenskabelige Forskningsråd (SNF).

- *Computer based identification of disease genes (2004–2006).*

This project is a collaboration between the private company *Bioinformatics ApS* and *Bioinformatics Research Center, University of Aarhus* that is aimed at the development of IT-methods for identification of disease affecting genes. The project is partly funded by ISIS Katrinebjerg.

List of Publications — Thomas Mailund

Peer Reviewed Journal Papers

- [1] **The Effect of a Single Recombination Event** M.H. Schierup, T. Mailund, and C. Wiuf. To appear in *Genetics*.
- [2] **A coalescent model incorporating allele specific mutation rates: application to the estimation of effective population size from microsatellite polymorphism data** T. Bataillon, A.A.T. Smith, T. Mailund and A-C. Thuillet. To appear in *Genetics*.
- [3] **Computing the All-Pairs Quartet Distance on a Set of Evolutionary Trees.** M. Stissing, T. Mailund, C.N.S. Pedersen, G.S. Brodal, and R. Fagerberg. To appear in the *APBC 2007 Special Issue in Journal of Bioinformatics and Computational Biology*.
- [4] **On Recombination Induced Multiple and Simultaneous Coalescent Events** J. Davies, F. Simancik, R. Lyngsø, T. Mailund, and J. Hein. *Genetics* 2007, 177, 2151–2160; doi:10.1534/genetics.107.071126.
- [5] **Annotation of Selection Strengths in Viral Genomes.** S. McCauley, S. de Groot, T. Mailund, and J. Hein. *Bioinformatics* 2007, 23:22, 2978–2986; doi:10.1093/bioinformatics/btm472.
- [6] **Comparative Annotation of Viral Genomes with Non-Conserved Gene Structure.** S. de Groot, T. Mailund, and J. Hein. *Bioinformatics* 2007, 23:9, 1080–1089; doi:10.1093/bioinformatics/btm078.
- [7] **Genomic relationships and speciation times of human, chimpanzee and gorilla inferred from a coalescent hidden Markov model.** A. Hobolth, O.F. Christensen, T. Mailund, and M.H. Schierup. *PLoS Genetics* 2007, 3:2; doi:10.1371/journal.pgen.0030007.
- [8] **Experiences with GeneRecon on MiG.** T. Mailund, C.N.S. Pedersen, J. Bardino, B. Vinter, and H.H. Karlsen. *Future Generation Computer Systems*, 2007, 23, 580–586; doi:10.1016/j.future.2006.09.003.
- [9] **Whole genome association mapping by incompatibilities and local perfect phylogenies.** T. Mailund, S. Besenbacher, and M.H. Schierup *BMC Bioinformatics* 2006, 7:454; doi:10.1186/1471-2105-7-454.
- [10] **Fast Calculation of the Quartet Distance Between Trees of Arbitrary Degrees.** C. Christiansen, T. Mailund, C.N.S. Pedersen, M. Randers, and M. Stissing. *Algorithms for Molecular Biology* 2006, 1:16; doi:10.1186/1748-7188-1-16.
- [11] **GeneRecon—A Coalescent Based Tool for Fine-Scale Association Mapping.** T. Mailund, M.H. Schierup, C.N.S. Pedersen, J.N. Madsen, J. Hein, and L. Schausser. *Bioinformatics* 2006, 22:18: 2317–2318; doi:10.1093/bioinformatics/btl153.
- [12] **The effective size of the Icelandic population and the Prospects for LD Mapping: Inference from Unphased Microsatellite Markers.** T. Bataillon, T. Mailund, S. Thorlacius, E. Steingrimsson, T. Rafnar, M.M. Halldorsson, V. Calian, and M.H. Schierup. *European Journal of Human Genetics* 2006, 14, 1044–1053. doi:10.1038/sj.ejhg.5201669.

- [13] **Recrafting the Neighbor-Joining Method.** T. Mailund, G.S. Brodal, R. Fagerberg, C.N.S. Pedersen, and D. Phillips. *BMC Bioinformatics* 2006, 7:29. doi:10.1186/1471-2105-7-29.
- [14] **CoaSim: A Flexible Environment for Simulating Genetic Data under Coalescent Models.** T. Mailund, M.H. Schierup, C.N.S. Pedersen, P.J.M. Mechlenborg, J.N. Madsen, and L. Schausser. *BMC Bioinformatics* 2005, 6:252. doi:10.1186/1471-2105-6-252.
- [15] **Pigs in Sequence Space: A 0.66X Coverage Pig Genome Survey based on Shotgun Sequencing.** R.Wernersson, M.H. Schierup, F.G. Jørgensen, J. Gorodkin, F. Panitz, H.H. Staerfeldt, O.F. Christensen, T. Mailund, H. Hornshøj, A. Klein, W. Jun, B. Liu, S. Hu, W. Dong, W. Li, G.K.-S. Wong, J. Yu, J. Wang, C. Bendixen, M. Fredholm, S. Brunak, H. Yang and L. Bolund. *BMC Genomics* 2005, 6:70. doi:10.1186/1471-2164-6-70.
- [16] **RBT—A Tool for Building Refined Buneman Trees,** S. Besenbacher, T. Mailund, L. Westh-Nielsen, C.N.S. Pedersen. *Bioinformatics*, Vol. 21, no. 8, pp. 1711–1712, 2005.
- [17] **QuickJoin—Fast Neighbour-Joining Tree Reconstruction.** T. Mailund og C.N.S. Pedersen. *Bioinformatics*, Vol. 20, no. 17, pp. 3261–3262, 2004.
- [18] **QDist—Quartet Distance between Evolutionary Trees.** T. Mailund og C.N. S. Pedersen. *Bioinformatics*, Vol. 20, no. 10, pp. 1636–1637, 2004.
- [19] **Exploiting Equivalence Reduction and the Sweep-Line Method for Detecting Terminal States,** J. Billington, G.E. Gallasch, L.M. Kristensen, og T. Mailund, *IEEE Transactions on Systems, Man, and Cybernetics, Part A: Systems and Humans*. Vol. 34, No. 1, pp. 23–37, 2004.

Peer Reviewed Conference and Workshop Papers

- [1] **Computing the Quartet Distance between Evolutionary Trees of Bounded Degree,** M. Stissing, C.N.S. Pedersen, T. Mailund, G.S. Brodal, and R. Fagerberg Proceedings of the *Asia-Pacific Bioinformatics Conference (APBC) 2007*, 91–100. Series on Advances in Bioinformatics and Computational Biology, Imperial College Press.
- [2] **Computing the All-Pairs Quartet Distance on a set of Evolutionary Trees,** M. Stissing, T. Mailund, C.N.S. Pedersen, G.S. Brodal, and R. Fagerberg Proceedings of the *Asia-Pacific Bioinformatics Conference (APBC) 2007*, 101–110. Series on Advances in Bioinformatics and Computational Biology, Imperial College Press.
- [3] **Algorithms for Computing the Quartet Distance Between Trees of Arbitrary Degree,** C. Christiansen, T. Mailund, C.N.S. Pedersen, and M. Randers. In *Proceedings of Workshop on Algorithms in Bioinformatics (WABI) 2005*, LNBI 3692, pp. 77–88 © Springer-Verlag.
- [4] **Quartet Distance Between General Trees,** C. Christiansen, T. Mailund, C.N.S. Pedersen, and M. Randers. In *Proceedings of International Conference on Numerical Analysis and Applied Mathematics (ICNAAM) (2005)*, pp. 796-799 © Wiley-VCH Verlag GmbH & Co.
- [5] **Initial Experiences with GeneRecon on MiG,** T. Mailund, C.N.S. Pedersen, J. Bardino, B. Vinter, and H.H. Karlsen. In *Proceedings of The 2005 International Conference on Grid Computing and Applications (GCA'05)*.
- [6] **Obtaining Memory-Efficient Reachability Graph Representations Using the Sweep-Line Method,** T. Mailund and M. Westergaard. *Proceedings of Tools and Algorithms for the Construction and Analysis of Systems (TACAS 2004)*, LNCS 2988 pp. 177–191, Springer-Verlag.

- [7] **Efficient Path Finding with the Sweep-Line Method using External Storage**, L.M. Kristensen and T. Mailund. *Proceedings of International Conference on Formal Engineering Methods (ICFEM 2003)* LNCS 2885 pp. 319–337, Springer-Verlag.
- [8] **A Compositional Sweep-Line State Space Exploration Method**, L.M. Kristensen and T. Mailund, In *Proceedings of Formal Description Techniques for Distributed Systems and Communication Protocols (FORTE 2002)*, LNCS 2529 pp. 327–343, Springer-Verlag.
- [9] **A Generalised Sweep-Line Method for Safety Properties**, L.M. Kristensen and T. Mailund, In *Proceedings of Formal Methods Europe (FME 2002)*, LNCS 2391 pp. 549–567, Springer-Verlag.
- [10] **Analysing Infinite-State Systems by Combining Equivalence Reduction and the Sweep-Line Method**, T. Mailund, In *Proceedings of International Conference on Application and Theory of Petri Nets (ICATPN 2002)*, LNCS 2360 pp. 314–333, Springer-Verlag.
- [11] **Sweep-Line State Space Exploration for Coloured Petri Nets**, G.E. Gallasch, L.M. Kristensen, and T. Mailund, In *Proceedings of Fourth Workshop on Practical Use of Coloured Petri Nets and the CPN Tools (CPN 2002)*. DAIMI PB-560 pp. 101–119, Aarhus, Denmark, 2002.
- [12] **Condensed State Spaces for Timed Petri Nets**, S. Christensen, L.M. Kristensen, and T. Mailund, In *Proceedings of International Conference on Application and Theory of Petri Nets (ICATPN 2001)*, LNCS 2075 pp. 101–120, Springer-Verlag.
- [13] **A Sweep-Line Method for State Space Exploration**, S. Christensen, L.M. Kristensen, and T. Mailund, In *Proceedings of Tools and Algorithms for the Construction and Analysis of Systems (TACAS 2001)*, LNCS 2031 pp. 450–464, Springer-Verlag.
- [14] **State Space Methods for Timed Coloured Petri Nets**, S. Christensen, K. Jensen, T. Mailund and L.M. Kristensen, In *Proceedings of 2nd International Colloquium on Petri Net Technologies for Modelling Communication Based Systems*, pp. 14–15, Berlin Germany, September 2001.
- [15] **Separation of Style and Content with XML in an Interchange Format for High-level Petri Nets**, T. Mailund and K.H. Mortensen, In *Proceedings of the Meeting on XML/SGML based Interchange Formats for Petri Nets*, pp. 7–12, Aarhus, Denmark, 2000.
- [16] **Parameterised Coloured Petri Nets**, T. Mailund, In *Proceedings of Second Workshop on Practical Use of Coloured Petri Nets and Design/CPN*, DAIMI PB-541 pp. 133–151, Aarhus, Denmark, 1999.
- [17] **Textual Interchange Format for High-Level Petri Nets**, R.B. Lyngsø and T. Mailund, In *Proceedings of First Workshop on Practical Use of Coloured Petri Nets and Design/CPN*, DAIMI PB-532 pp. 47–64 Aarhus, Denmark, 1998.