

MARINA AXELSON-FISK, Ph.D.

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Docent

Mathematical Sciences
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PROFESSIONAL EXPERIENCE

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|----------------------|---|
| Feb 2006 – present | VR Senior Researcher (Swedish Research Council)
Docent Dept of Mathematical Sciences, Chalmers, Sweden |
| Sep 2002 – Jan 2006 | Scientific Director in Bioinformatics
Fraunhofer-Chalmers Centre, Gothenburg, Sweden |
| Sep 2001 – Aug 2002 | Visiting research assistant
Dept of Mathematics, UC Berkeley |
| Sep 1999 – Aug 2001 | Postdoctoral fellow
Dept of Statistics, UC Berkeley |
| Aug 1995 – June 1999 | Graduate student
Dept of Math Statistics, Gothenburg University, Sweden
Adviser: Ziad Taib |
| Aug 1995 – June 1999 | Statistical consultant
Dept of Math Statistics, Gothenburg University, Sweden
Supervisor: Tommy Norberg |
| Jan 1995 – June 1995 | Technical translator
Wordworks AB, Gothenburg, Sweden
Supervisor: Lennart Widhe |

RESEARCH INTERESTS

Probability theory:

Stochastic processes: hidden Markov models, conditional random fields, branching processes, percolation theory.

Bioinformatics:

Comparative genomics, computational gene finding, biological sequence analysis, functional feature predictions, software design and programming.

Population dynamics:

Branching processes, cell population dynamics, cell cycle modeling.

EDUCATION

- M.Sc., Department of Mathematical Statistics, Gothenburg University 1995
 Thesis: *Multivariat kalibrering*
 Adviser: Ziad Taib
- Ph.Lic., Department of Mathematical Statistics, Gothenburg University 1998
 Thesis: *Branching Processes and Cell Populations*
 Adviser: Ziad Taib
- Ph.D., Department of Mathematical Statistics, Gothenburg University 1999
 Thesis: *Branching Processes and Cell Populations*
 Adviser: Ziad Taib
- Docent, Mathematical Sciences, Chalmers University of Technology 2004

TEACHING EXPERIENCE

Lecturer of various courses in Mathematical Statistics, Probability Theory and Bioinformatics since 1998.

SUPERVISING EXPERIENCE

Assistant adviser, Ph.D student Malin Östensson, Aug 2008 – present.

Co-adviser, M.Sc. thesis project, Aug 2002 – Aug 2003.

Title: *Optimal evolutionary distance for cross-species gene finding and alignment.*

PUBLICATIONS

Note: In 2005 my last name changed from Alexandersson to Axelson-Fisk.

Books

1. Axelson-Fisk, M. (2010) *Comparative Gene Finding: Models, Algorithms and Implementation*. Springer Verlag, London.

Refereed journal articles

2. Axelson-Fisk, M., Häggström, O. (2009) Biased random walk in a one-dimensional percolation model. *Adv. Appl. Prob.* **41**(4), 1102 – 1122.
3. Axelson-Fisk, M., Häggström, O. (2009) Conditional percolation on one-dimensional lattices. *Stoch. Proc. Appl.* **119**(10), 3395 – 3415.
4. Alexandersson, M. (2005). The Cell Cycle. In *Branching Processes: Variation, Growth, and Extinction of Populations*, pp. 218-225. Editors: Haccou, P., Jagers, P., Vatutin, V. Cambridge University Press.
5. Rat Genome Sequencing Project Consortium. (2004). Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **428**, 493 – 521.
6. Dewey, C., Wu, J.Q., Cawley, S., Alexandersson, M., Gibbs, R., Pachter, L. (2004). Accurate Identification of Novel Human Genes Through Simultaneous Gene Prediction in Human, Mouse and Rat. *Genome Res.* **14**(4), 661 – 664.

7. Lang, T., Alexandersson, M., Hansson, G.C., Samuelsson, T. (2004). Bioinformatic identification of polymerizing and transmembrane mucins in the puffer fish *Fugu rubripes*. *Glycobiology* **14**(6), 521 – 527.
8. Lam, F., Alexandersson, M., Pachter, L. (2003). Picking Alignments from (Steiner) Trees. *J. Comp. Bio.*, **10**(3-4), 509 – 520.
9. Cawley, S., Pachter, L., Alexandersson, M. (2003). SLAM webserver for comparative gene finding and alignment. *Nucl. Ac. Res.*, **31**(13), 3507 – 3509.
10. Alexandersson, M., Cawley, S., Pachter, L. (2003). SLAM: Cross-species Gene Finding and Alignment with a Generalized Pair Hidden Markov Model. *Genome Res.*, **13**(3), 496 – 502.
11. Waterston, R.H., Lindblad-Toh, K., Birney, E., Rogers, J., Abril, J.F., Agarwal, P., Agarwala, R., Ainscough, R., Alexandersson, M., An, P., *et al.* (2002). Initial sequencing and comparative analysis of the mouse genome. *Nature*, **420**(6915), 520 – 562.
12. Pachter, L., Alexandersson, M., Cawley, S. (2002). Applications of Generalized Pair Hidden Markov Models to Alignment and Gene Finding Problems. *J. Comp. Bio.*, **9**(2), 389 – 399.
13. Alexandersson, M. (2001). Existence of the Stable Birth Type Distribution in a General Branching Process Cell Cycle Model with Unequal Cell Division. *J. Appl. Prob.*, **38**(3), 673 – 685.
14. Alexandersson, M. (1998). An Application of General Branching Processes to a Cell Cycle Model with Two Uncoupled Subcycles and Unequal Cell Division. *Int. J. Appl. Math. and Comp. Sci.*, **1**, 131-145.

Book chapters

15. Alexandersson, M., Bray, N., Pachter, L. (2005). Pair hidden Markov models. Special review in *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*. John Wiley & Sons, Ltd. Editors: Jorde, L.B., Little, P., Dunn, M. and Subramanian, S.
16. Axelson-Fisk, M., Sunnerhagen, P. (2005). Gene finding in fungal genomes. In *Topics in Current Genetics: Comparative genomics using fungi as models*. Springer Verlag. Editors: Sunnerhagen, P. and Piskur, J.

Conference proceedings

17. Alexandersson, M. (2003). Gene Finding, Alignments, and Generalized Pair Hidden Markov Models. *Proceedings of the 54th ISI session*, ISI Berlin 2003, 1 – 4.
18. Pachter, L., Lam, F., Alexandersson, M. (2002). Picking Alignments from (Steiner) Trees. *RECOMB 2001: Proceedings of the Sixth International Conference on Computational Molecular Biology*.
19. Pachter, L., Alexandersson, M., Cawley, S. (2001). Applications of Generalized Pair Hidden Markov Models to Alignment and Gene Finding Problems. *RECOMB 2001: Proceedings of the Fifth International Conference on Computational Molecular Biology*.

Ph.D. Thesis

20. Alexandersson, M. (1998). *Branching Processes and Cell Populations.*, Ph.D. thesis, Dept. Mathematics, Gothenburg University.

Software

21. Alexandersson, M., Cawley, S., Pachter, L. *SLAM*: A cross-species gene finding and alignment tool based on generalized pair hidden Markov models.
<http://bio.math.berkeley.edu/slam/>
22. Alexandersson, M., Lang, T., Hansson, G.C., Samuelsson, T. *MPRED*: A mucin domain prediction software.