KRISTOFFER SAHLIN

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PERSONAL INFORMATION

Date of birth: March 05, 1984 Stockholm, Sweden
Nationality: Swedish
Website: `http://ksahlin.github.io/`

EDUCATION

Ph.D. in Computer Science *Sept 2010 - Sept 2015*
School: Royal institute of Technology (KTH)
Thesis: Algorithms and statistical models for scaffolding contig assemblies and detecting structural variants using read pair data
Advisor: Associate Professor Lars Arvestad
Co-advisor: Professor Joakin Lundeberg

M.Sc. in Mathematical Statistics *Aug 2008 - Sept 2010*
School: Stockholm University
Thesis: Estimating convergence of Markov chain Monte Carlo simulations
Advisor: Sebastial Höhna

B.S. in Mathematics *Aug 2005 - June 2008*
School: Stockholm University
Thesis: Splines: A theoretical and computational study
Advisor: Hans Rullgård

PROFESSIONAL EXPERIENCE

Postdoctoral researcher *Oct 2015 -*
School: Penn State University
Advisor: Assistant Professor Paul Medvedev

RESEARCH AREAS

Genome assembly, Structural variation, Transcriptomics, Phylogenetics, Cancer progression.

OTHER INTERESTS

- Statistics: Modeling, Inference, Stochastic processes
- Mathematics: Graph theory, Combinatorics, Probability theory

TEACHING

2014

· Teaching assistant (correcting homework assignments, general supervision) in Statistical Methods in Applied Computer Science at KTH Royal Institute of Technology, Stockholm, Sweden.

2013

· Lecturer on python (5 Lectures) in course Applied Bioinformatics at KTH Royal Institute of Technology, Stockholm, Sweden. Teachers assistant throughout the course.
· Teaching assistant (Lecturer at exercise sessions and computer lab assistant) in Programming Techniques and Matlab at KTH Royal Institute of Technology, Stockholm, Sweden
· Teaching assistant (Lecturer at exercise sessions and computer lab assistant) for Programming Techniques and C at KTH Royal Institute of Technology, Stockholm, Sweden
· Teaching assistant (for computer labs) for Bioinformatics and Biostatistics at KTH Royal Institute of Technology, Stockholm, Sweden
· Teaching assistant (correcting homework assignments, general supervision) for Statistical Methods in Applied Computer Science at KTH Royal Institute of Technology, Stockholm, Sweden.

2012

· Teaching assistant for course Algorithmic bioinformatics at KTH Royal Institute of Technology, Stockholm, Sweden.
· Teaching assistant for course Applied bioinformatics at KTH Royal Institute of Technology, Stockholm, Sweden.
· Teaching assistant (correcting homework assignments, general supervision) for Statistical Methods in Applied Computer Science at KTH Royal Institute of Technology, Stockholm, Sweden.

STUDENT SUPERVISION

Josefine Röhss - Analysing k-mer distributions in a genome sequencing project. Bachelor's Thesis, March - June, 2014.

EXPERIENCE

Helsinki University September 2014
Visiting researcher *Helsinki, Finland*

· Visiting Veli Mäkinen's lab for work on scaffolding and gapfilling of genome assemblies.

Penn State University November 2014
Visiting researcher *State college, PA, USA*

· Visiting Paul Medvedev's lab for work on Structural variation detection.

Conferences/Meetings

· ISMB: 2012 (Long beach), 2013 (Berlin), 2014 (Boston).
· RECOMB: 2016 (Santa Monica) **(Speaker)**.
· Genome informatics: 2013 (CSHL), 2014 (Cambridge).
· WABI: 2015 (Atlanta, GA, USA) **(Speaker)**.
· Assemblathon 1 satellite meeting for Genome informatics 2011 (CSHL).
· GATC Plant genomics symposium (2012).

AWARDS AND GRANTS

- KTH opportunities fund, Investing in research talent grant, 2014.

ACADEMIC SERVICE

- Reviewer for journals: BMC Bioinformatics
- Reviewer for conferences: RECOMB 2016, RECOMB 2014, WABI 2015

TECHNICAL STRENGTHS

Computer Languages	Python (Advanced), R (intermediate), MatLab (intermediate), C/C++ (basic - intermediate)
Tools	GitHub, Vi/Vim, Unix environment, LaTex, Snakemake

Publications

[1] B. Nystedt, N.R. Street, A. Wetterbom, A. Zuccolo, Y.C. Lin, D.G. Scofield, F. Vezzi, N. Delhomme, S. Giacomello, A. Alexeyenko, R. Vicedomini, **Sahlin, K.**, E. Sherwood, M. Elfstrand, L. Gramzow, K. Holmberg, J. Hallman, O. Keech, L. Klasson, M. Koriabine, M. Kucukoglu, M. Kaller, J. Luthman, F. Lysholm, T. Niittyla, A. Olson, N. Rilakovic, C. Ritland, J.A. Rossello, J. Sena, T. Svensson, C. Talavera-Lopez, G. Theissen, H. Tuominen, K. Vanneste, Z.Q. Wu, B. Zhang, P. Zerbe, L. Arvestad, R. Bhalerao, J. Bohlmann, J. Bousquet, R. Garcia Gil, T.R. Hvidsten, P. de Jong, J. Mackay, M. Morgante, K. Ritland, B. Sundberg, S. Lee Thompson, Y. Van de Peer, B. Andersson, O. Nilsson, P.K. Ingvarsson, J. Lundeberg, and S. Jansson. The norway spruce genome sequence and conifer genome evolution. ***Nature***, 497(7451):579–584, May 2013.

[2] **Sahlin, K.**, N. Street, J. Lundeberg, and L. Arvestad. Improved gap size estimation for scaffolding algorithms. ***Bioinformatics***, 28(17):2215–2222, Sep 2012.

[3] **Sahlin, K.**, F. Vezzi, B. Nystedt, J. Lundeberg, and L. Arvestad. BESST - Efficient scaffolding of large fragmented assemblies. ***BMC Bioinformatics***, 15(1):281, 2014.

[4] **Sahlin, Kristoffer**, Rayan Chikhi, and Lars Arvestad. Assembly scaffolding with pe-contaminated mate-pair libraries. ***Bioinformatics***, 2016.

[5] **Sahlin, Kristoffer**, Mattias Frånberg, and Lars Arvestad. Structural variation detection with read pair information—an improved null-hypothesis reduces bias. In Mona Singh, editor, ***Research in Computational Molecular Biology***, pages 176–188. Springer International Publishing, Cham, 2016.

[6] Salmela, Leena, **Kristoffer Sahlin**, Veli Mäkinen, and Alexandru I. Tomescu. Gap filling as exact path length problem. In ***Research in Computational Molecular Biology***, volume 9029 of *Lecture Notes in Computer Science*, pages 281–292. Springer International Publishing, 2015.