KRISTOFFER SAHLIN

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+8147778944 ⋄ krsahlin@gmail.com

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 Joakim 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: Associate Professor Paul Medvedev

RESEARCH AREAS

Genome assembly, Structural variation detection, Transcriptome assembly and analysis, Phylogenetics.

PROFESSIONAL INTERESTS

Statistical modeling and inference, stochastic processes, 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 in course Applied Bioinformatics at KTH Royal Institute of Technology, Stockholm, Sweden. I taught five lectures on introduction of python. 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, 2013, 2014.
- RECOMB: 2016 (**Speaker**).
- Genome informatics: 2013, 2014, 2017 (**Speaker**).
- WABI: 2015 (**Speaker**).
- Assemblathon 1 satellite meeting for Genome informatics 2011.
- GATC Plant genomics symposium (2012).

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

ACADEMIC SERVICE
- Reviewer for journals: BMC Bioinformatics, Bioinformatics, GigaScience, Communications in statistics - Simulation and Computation.
- Reviewer for conferences: ISMB (2017, 2018), RECOMB (2014, 2016, 2017, 2018), WABI 2015

TECHNICAL STRENGTHS

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

Selected publications

[1] **Sahlin, Kristoffer**, Marta Tomaszkiewicz, Kateryna D Makova, and Paul Medvedev. Isocon: Deciphering highly similar multigene family transcripts from iso-seq data. *bioRxiv*, 2018.

[2] **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.

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

[4] 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.

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

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

[7] 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.