KRISTOFFER SAHLIN, PHD

UPDATED: Dec 2, 2018

CONTACT INFORMATION

Tel: +1 814 777 8944
Email: kxs624@psu.edu / krsahlin@gmail.com
Web: http://ksahlin.github.io/

EDUCATION & TRAINING

Postdoctoral researcher *Oct 2015 -*
University: Pennsylvania State University
Advisor: Associate Professor Paul Medvedev

Ph.D. in Computer Science *Sept 2010 - Sept 2015*
University: Royal Institute of Technology (KTH), Sweden
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*
University: Stockholm University, Sweden
Thesis: Estimating convergence of Markov chain Monte Carlo simulations
Advisor: Assistant Professor Sebastial Höhna

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

VISITING RESEARCH 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.

PRESENTATIONS

- ISMB, HitSeq track (2018)
- Genome Informatics (2017)
- RECOMB (2016)
- WABI (2015)

AWARDS AND GRANTS

- KTH opportunities fund: Investing in research talent grant, 2014.
- Grant proposal finalist in the PacBio 2018 Iso-Seq SMRT Grant Program.

TEACHING

- Teaching assistant in Statistical Methods in Applied Computer Science at KTH (2012, 2013, 2014).

- Teaching assistant and assisting lecturer in graduate course Applied bioinformatics at KTH. I gave five lectures on introduction of python. TA throughout the course (2013).

- Teaching assistant and recitation session lecturer in courses: Programming Techniques and Matlab (Undergraduate level), Programming Techniques and C (Undergraduate level), and Bioinformatics and Biostatistics (graduate level), KTH (2013).

ADVISING

Josefine Röhss - Analysing k-mer distributions in a genome sequencing project. Bachelor's Thesis, March - June, 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 - 2019), RECOMB-seq (2018) WABI 2015

Peer reviewed publications

[1] **Kristoffer Sahlin** and Paul Medvedev. Quality-value based clustering of long-read transcriptome sequencing data. ***Manuscript in submission.***

[2] **Kristoffer Sahlin***, Marta Tomaszkiewicz*, Kateryna D. Makova, and Paul Medvedev. Deciphering highly similar multigene family transcripts from Iso-Seq data with IsoCon. ***Nature Communications***, 9(1):4601, 2018.

[3] **Kristoffer Sahlin**, Mattias Frånberg, and Lars Arvestad. Structural variation detection with read pair information: An improved null-hypothesis reduces bias. ***Journal of Computational Biology (also in RECOMB2016)***, 24(6):581–589, 2017.

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

[5] Leena Salmela, **Kristoffer Sahlin**, Veli Mäkinen, and Alexandru I. Tomescu. Gap filling as exact path length problem. In ***Research in Computational Molecular Biology (RECOMB2015)***, volume 9029 of *Lecture Notes in Computer Science*, pages 281–292. Springer International Publishing, 2015.

[6] **Kristoffer Sahlin**, Francesco Vezzi, Björn. Nystedt, Joakim Lundeberg, and Lars Arvestad. BESST - Efficient scaffolding of large fragmented assemblies. ***BMC Bioinformatics***, 15(1):281, 2014.

[7] **Kristoffer Sahlin**, Nathaniel Street, Joakim Lundeberg, and Lars Arvestad. Improved gap size estimation for scaffolding algorithms. ***Bioinformatics***, 28(17):2215–2222, Sep 2012.

[8] 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.