Kristoffer Sahlin, PhD

CONTACT INFORMATION

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EDUCATION & TRAINING

Postdoctoral researcher *July 2019 -*
University: University of Helsinki
Mentor: Professor Veli Mäkinen

Postdoctoral researcher *Oct 2015 - June 2019*
University: Pennsylvania State University
Mentor: 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

- RECOMB (2019). Title: De novo clustering of long-read transcriptome data using a greedy, quality-value based algorithm.
- ISMB, HitSeq track (2018). Title: IsoCon: Deciphering highly similar multi-copy gene transcripts from PacBio Iso-Seq data.
- CCBB, workshop on emerging methods for sequence analysis (2018). Title: IsoCon: Deciphering highly similar multi-copy gene transcripts from PacBio Iso-Seq data.

- Genome Informatics (2017). Title: IsoCon: Deciphering highly similar multi-copy gene transcripts from PacBio Iso-Seq data.
- RECOMB (2016). Structural variation detection with read pair information: An improved null-hypothesis reduces bias
- Weekly Wednesday Wartik Genomics Lecture Series (2016). Title: Genome scaffolding with PE-contaminated mate-pair libraries
- WABI (2015). Title: Genome scaffolding with PE-contaminated mate-pair libraries
- Weekly Wednesday Wartik Genomics Lecture Series (2014). Title: An investigation of bias in methods using insert size for inference

AWARDS AND GRANTS

- RECOMB Travel fellowship award. (2019)
- Top five grant proposal finalist in the PacBio 2018 Iso-Seq SMRT Grant Program. (2018)
- KTH opportunities fund: Investing in research talent grant. Grant supported travel and accommodation for one month's collaboration in Helsinki, Finland. (2014)

TEACHING

- Statistical Methods in Applied Computer Science, KTH (graduate level). Teaching assistant 2012, 2013, and 2014.
- Applied Bioinformatics, KTH (graduate level). Assisting lecturer and teaching assistant. I gave five lectures on introduction of python (2013).
- Programming Techniques and Matlab, KTH (undergraduate level). Teaching assistant and recitation session lecturer (2013).
- Programming Techniques and C, KTH (undergraduate level). Teaching assistant and recitation session lecturer (2013).
- Bioinformatics and Biostatistics, KTH (graduate level). Teaching assistant (2013).

ADVISING

- Josefine Röhss - Analysing k-mer distributions in a genome sequencing project. Bachelor's Thesis, Date: March - June, 2014.
- I am currently supervising Natasha Stopa, a graduate student, on Genome assembly and sequence classification using Machine Learning approaches. Date: January 2019 - .

ACADEMIC SERVICE

- Reviewer for journals:
  - Bioinformatics
  - BMC Bioinformatics
  - GigaScience
  - Communications in Statistics - Simulation and Computation
- Reviewer for conferences:
  - Intelligent Systems for Molecular Biology (ISMB) (2017 - 2019)

- Research in Computational Molecular Biology (RECOMB) (2014, 2016 - 2019)
- RECOMB-seq (2018, 2019)
- Workshop on Algorithms in Bioinformatics (WABI) (2015)

Selected papers

[1] **Kristoffer Sahlin**† and Paul Medvedev. De novo clustering of long-read transcriptome data using a greedy, quality-value based algorithm. In Lenore J. Cowen, editor, ***Research in Computational Molecular Biology***, pages 227–242, Cham, 2019. Springer International Publishing.

[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 RECOMB-2016)***, 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 (RECOMB-2015)***, Lecture Notes in Computer Science, pages 281–292. Springer International Publishing.

[6] **Kristoffer Sahlin**†, Mattias Frånberg, and Lars Arvestad. Structural variation detection with read pair information—an improved null-hypothesis reduces bias. In ***Research in Computational Molecular Biology (RECOMB-2016)***, Lecture Notes in Computer Science, pages 176–188. Springer International Publishing, 2016.

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

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

[9] 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, **K. Sahlin**, 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.

[10] Leena Salmela, **Kristoffer Sahlin**, Veli Mäkinen†, and Alexandru I Tomescu†. Gap filling as exact path length problem. ***Journal of Computational Biology (also in RECOMB-2015)***, 23(5):347–361, May 2016.