Kristoffer Sahlin, PhD

CONTACT INFORMATION

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CURRENT APPOINTMENT

Assistant Professor   *Jan 2020 -*
Institution: Department of Mathematics, Stockholm University

EDUCATION & TRAINING

Postdoctoral researcher   *July 2019 - Dec 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

- Bioinformatics afternoon (Helsinki, 2019). Title: Computational methods for analysis of genome and transcriptome sequencing data.

- 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 (PennState, 2019), 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 (PennState, 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 (PennState, 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

- Lecturer and responsible for course contents
  - Programming Techniques for Mathematicians, Stockholm University, Spring 2020. Undergraduate level, 7.5 ECTS.
  - Applied programming for Life Science 2, Stockholm University, Spring 2020. Graduate level, 1.5 ECTS.
- Teaching assistant
  - 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

- Program committee appointments:
  - RECOMB-Seq (2020)
- Reviewer for journals:
  - Bioinformatics
  - BMC Bioinformatics
  - GigaScience
  - NAR Genomics and Bioinformatics
  - 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)