Kristoffer Sahlin, PhD

CONTACT INFORMATION

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CURRENT APPOINTMENTS

Assistant Professor *Jan 2020 -*
Institution: Department of Mathematics, Stockholm University
SciLifeLab Fellow *Jan 2020 -*
Institution: Science for Life Laboratory, Solna

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

RESEARCH GRANTS

- 2021-2024: 4 MSEK (0.4M€). Start-up grant from The Swedish Research Council, Sweden (VR) (13% acceptance rate)

- 2020-2025: 16 MSEK (1.6M€). Start-up funding from Strategiska forskningsområden, Sweden (SFO).

- 2014: 12,500 SEK (1,250€). KTH opportunities fund: Investing in research talent grant. Grant supported travel and accommodation for one month's collaboration in Helsinki, Finland.

AWARDS AND DISTINCTIONS

- 2020: Scilifelab fellowship.

- 2019: RECOMB Travel fellowship award.

- 2018: Top five grant proposal finalist in the PacBio 2018 Iso-Seq SMRT Grant Program.

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

Conferences

- RECOMB-Seq (Online, 2021). Title: "Accurate spliced alignment of long RNA sequencing reads."

- ISMB, HitSeq track (Online, 2021). Title: "Strobemers: an alternative to k-mers for sequence comparison"

- SMRT Leiden 2021 (Online, May 2021). Title: "uLTRA: Accurate spliced alignment of long RNA sequencing reads." (Invited talk)

- ISMB, HitSeq track (Online, 2020). Title: "Error correction enables use of Oxford Nanopore technology for reference-free transcriptome analysis."

- RECOMB (Washington D.C., 2019). Title: "De novo clustering of long-read transcriptome data using a greedy, quality-value based algorithm."

- ISMB, HitSeq track (Chicago, 2018). Title: "IsoCon: Deciphering highly similar multi-copy gene transcripts from PacBio Iso-Seq data."

- Genome Informatics (Cold Spring Harbour, 2017). Title: "IsoCon: Deciphering highly similar multi-copy gene transcripts from PacBio Iso-Seq data."

- RECOMB (Los Angeles, 2016). Title: "Structural variation detection with read pair information: An improved null-hypothesis reduces bias."

- WABI (Atlanta, 2015). Title: "Genome scaffolding with PE-contaminated mate-pair libraries"

Seminars/Workshops

- Lille Computational seminar series (Online, 2021) Title: "Strobemers: an alternative to k-mers for sequence comparison"

- SciLifeLab Seminar Series (Stockholm, 2020). Title: Computational methods for analysis of genome and transcriptome sequencing data.

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

- Weekly Wednesday Wartik Genomics Lecture Series (PennState, 2016). 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

TEACHING

- Lecturer and responsible for course contents
  - Programming Techniques for Mathematicians, Stockholm University. Undergraduate level, 7.5 ECTS. (Spring 2020, Autumn 2020, Autumn 2021)
  - Applied programming for Life Science 2, Stockholm University. Graduate level, 1.5 ECTS. (Spring 2020, Spring 2021)
- 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

- Alexander Petri - PhD student. Date: September 2020 -
- Natasha Stopa - Using Female Alignment Features to Identify Reads from the Y Chromosome in Nanopore Whole Genome Sequencing Data, Master's Thesis. Date: January 2019 - January 2020.
- Josefine Röhss - Analysing k-mer distributions in a genome sequencing project. Bachelor's Thesis, Date: March 2014 - June 2014.

ACADEMIC SERVICE

- Program committee appointments:
  - RECOMB-Seq (2020, 2021)
- Panel session:
  - Panel member on ' Round table discussion - Young Investigator experiences' (SMRT Leiden 2021)
- Reviewer for journals (number of manuscripts):
  - Nature Computational Science (1)
  - Nature communications (1)
  - Genome Research (3)
  - Bioinformatics (8)
  - BMC Bioinformatics (2)
  - BMC Genomics (1)

- Frontiers in Plant Science (1)
- GigaScience (2)
- NAR Genomics and Bioinformatics (1)
- Communications in Statistics - Simulation and Computation (1)

- Reviewer for conferences:
    - Intelligent Systems for Molecular Biology (ISMB) (2017 - 2019)
    - Research in Computational Molecular Biology (RECOMB) (2014, 2016 - 2021)
    - RECOMB-seq (2018 - 2020)
    - Workshop on Algorithms in Bioinformatics (WABI) (2015)