


Thies Gehrman M.Sc Curriculum Vitæ

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Personal profile

Currently, I am a Postdoc in the Bioinformatics group at the KNAW/Westerdijk Institute of Fungal Biodiversity (formerly CBS). Having been raised in Norway, among people from all over the world, I am accustomed to an international, multicultural environment. Academically, machine learning techniques are interesting to me, and bioinformatics presents a splendid opportunity to develop and apply them. I am looking for a position where challenging problems, involving many different skills and team work, allow me to contribute positively to society, and further develop my skills.

Employment

Nov. 2016 - Present

Postdoc at KNAW/Westerdijk Institute
Project involving novel product discovery

Nov. 2012 - Nov. 2016

PhD Researcher
During my PhD, I conducted research and performed teaching duties, including Bachelor and Master's level courses, and student supervision.

Education

2012-Present

Pattern Recognition and Bioinformatics group, TU Delft, The Netherlands
PhD in Bioinformatics.
Gene regulation in mushroom formation.

2010-2012

Leiden University, Leiden, The Netherlands (In cooperation with TU Delft)
MSc Computer Science Track Bioinformatics.
Thesis on protein function prediction using Conditional Random Fields.

2008-2010

Heriot Watt University, Edinburgh, Scotland
BSc (Ord) Computer Science
Graduated with distinction.

Skills

Technical Skills

Python, Scala, C/C++, Java, Shell, Matlab, R
Experience with schedulers (SLURM, PDB) and version control software, (SVN, Git).
SQL, XML (and related technologies), \LaTeX .
Pipeline development and management (Snakemake, Jupyter Notebook, Anaconda).
Experienced with Unix environments (primarily Linux).
Machine learning, comparative genomics, RNA-Seq analysis and algorithm development.

Languages

Fluent in Norwegian, German and English.
High level Dutch. Beginners French.

Referees

Upon request

| Contact Thies for referee contact details.

Teaching

MSc Courses

Functional Genomics and Systems Biology: Lecturer and teaching assistant. Fall 2014, 2015, 2016 at TU Delft
Computational Molecular Biology: Teaching assistant. Spring 2012 at Leiden University

BSc Courses

Life Science and Technology Bioinformatics: Teaching assistant and course content creator. Spring 2016 at TU Delft.
Genome Scale Data Analysis: Lecturer and teaching assistant. Fall 2014 at TU Delft

External Courses

Quantitative biology summer school: Lectured on computational aspects of synten and alternative splicing in fungi. Summer 2015 at Utrecht University.

Supervision

Arlin Keo

MSc Student 2014-2016
Detecting mixed Mycobacterium tuberculosis infections and differences in drug susceptibility with WGS data.

André Vollering

MSc Student 2014-2015
Heterosis: Finding Associated Genomic Regions.

Valerie Pourquie

BSc Student 2015
Conservation of polarization proteins in yeast and fungi.

Dimitris Palachanis

MSc Student 2013-2014
Using the Multiple Instance Learning framework to address differential regulation.

Other activities/skills/information

Awards

TU Delft Graduate school event 2013 'Best poster presentation award'.
Scott Logic Computer Science Prize 2010.

Reviewing

Nucleic Acid Research (2016)

Volunteering

International Student Network (Leiden) 2013-2016. Theatre set construction and management.
Dutch Red Cross (Den Haag) 2014-2015. First Aid worker for events and refugee camps.

Special Interests

Theatre acting, Sailing, Cycling, Climbing/Bouldering, Swimming, Skiing and Hiking.

Publications

Journal publications

Conference publications

In progress/ Under Review

- [1] Abigail L Manson, Thomas Abeel, James E Galagan, Jagadish Chandrabose Sundaramurthi, Alex Salazar, Thies Gehrman, Siva Kumar Shanmugam, Kannan Palaniyandi, Sujatha Narayanan, Soumya Swaminathan, et al. Mycobacterium tuberculosis whole genome sequences from southern india suggest novel resistance mechanisms and the need for region-specific diagnostics. *Clinical Infectious Diseases*, 64 (11):1494–1501, 2017
- [2] Jordi F Pelkmans, Mohini B Patil, Thies Gehrman, Marcel JT Reinders, Han AB Wösten, and Luis G Lugones. Transcription factors of schizophyllum commune involved in mushroom formation and modulation of vegetative growth. *Scientific Reports*, 7(1):310, 2017
- [3] Thies Gehrman, Jordi F Pelkmans, Luis G Lugones, Han AB Wösten, Thomas Abeel, and Marcel JT Reinders. Schizophyllum commune has an extensive and functional alternative splicing repertoire. *Scientific reports*, 6, 2016
- [4] Jordi F Pelkmans, Aurin M Vos, Karin Scholtmeijer, Ed Hendrix, Johan JP Baars, Thies Gehrman, Marcel JT Reinders, Luis G Lugones, and Han AB Wösten. The transcriptional regulator c2h2. *Applied microbiology and biotechnology*, 100(16):7151–7159, 2016
- [5] Thies Gehrman and Marcel JT Reinders. Proteny: discovering and visualizing statistically significant syntenic clusters at the proteome level. *Bioinformatics*, 31(21):3437–3444, 2015
- [6] Thies Gehrman, Marco Loog, Marcel JT Reinders, and Dick de Ridder. Conditional random fields for protein function prediction. In *IAPR International Conference on Pattern Recognition in Bioinformatics*, pages 184–195. Springer, Berlin, Heidelberg, 2013
- [7] Thies Gehrman, Jordi F Pelkmans, Robin A Ohm, Aurin M Vos, Anton SM Sonnenberg, Johan JP Baars, Han AB Wosten, Marcel JT Reinders, and Thomas Abeel. Nucleus specific expression in the multinucleated mushroom-forming fungus agaricus bisporus reveals different nuclear regulatory programs. *bioRxiv*, page 141689, 2017
- [8] Eveline T Diepeveen, Valerie Pourquie, Thies Gehrman, Thomas Abeel, and Liedewij Laan. Patterns of conservation and diversification in the fungal polarization network. *bioRxiv*, page 154641, 2017
- [9] Variants in RNA-Seq data show a continued mutation rate during strain preservation of *Schizophyllum commune*