Curriculum Vitae

Ketil Malde, dr.scient.

Personalia

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Current activities

I am employed at the Institute of Marine Research, where I am the senior of three people responsible for bioinformatics data management, analysis, and research. I have contributed to several genome and transcriptome projects, including the cod genome project (codgenome.no), and lead bioinformatics in the sea louse genome project. I have experience with a broad field of technologies and methods, including hands-on experience with second generation sequencing data (454, Illumina, and SOLiD).

I currently manage one project, *Analysis of high-throughput sequencing data*, where we investigate the error characteristics of 454 data. This project has lead to the publication of several research papers and software utilities.

I am involved in several other projects spanning a diversity of fields, including developmental studies of cod and salmon, fisheries-induced evolution of cod, the effect of seismics on larvae, and population structure and disease resistance of sea lice. I have also participated in the application process for several projects, most recently the infrastructure projects NMDC and Elixir.

As part of my work, I have developed several open-source software tools and libraries, mainly using the functional programming language Haskell. I am initiator and one of the main contributors to the Biohaskell effort to introduce and apply functional programming methods and concepts to bioinformatics, and I occasionally publish commentary on a blog.

Peer-reviewed publications

Unpublished

Susanne Balzer, **Ketil Malde**, Markus Grohme, and Inge Jonassen. *Filtering duplicate reads from 454 pyrosequencing data*. Submitted.

Christiane Eichner, Rasmus Skern-Mauritzen, Sussie Dalvin, Heidi Kongshaug, **Ketil Malde**, and Frank Nilsen. *Characterisation of a Novel RXR Receptor in the Salmon Louse (Lepeophtheirus Salmonis, Crustacea) Regulating Growth and Reproduction in Adult Female Lice.*Submitted.

2013 Ketil Malde. Can Software Transactional Memory make concurrent programs simple and safe?

Accepted, Bioinformatics 2013, BIOSTEC.

Ketil Malde and Tomasz Furmanek. *Increasing sequence search sensitivity with transitive alignments.*

Accepted for publication, PLoS ONE.

2012 Rasmus Skern, **Ketil Malde**, *et al. How does sample sequence variability affect* de novo *assembly quality?*

ICOC 2012/Journal of Natural History.

Lene Kleppe, Rolf B Edvardsen, Heiner Kuhl, **Ketil Malde**, Tomasz Furmanek, Øyvind Drivenes, Richard Reinhardt, Geir Lasse Taranger and Anna Wargelius. *Maternal 3'UTRs: from egg to onset of zygotic transcription in Atlantic cod* Cell and Tissue Research, 346(2):191-202.

2011 Anita Sagstad, Sindre Grotmol, Harald Kryvi, Christel Krossoy, Geir Totland, Ketil Malde, Shou Wang, Tom Hansen, and Anna Wargelius. *Identification of* vimentin- and elastin-like transcripts specifically expressed in developing notochord of Atlantic salmon (Salmo salar L.).

Cell and Tissue Research, 346(2):191-202.

Bastiaan Star, Lex Nederbragt, et al. The genome sequence of Atlantic cod reveals a unique immune system.

Nature, 477:207-210.

Susanne Balzer, **Ketil Malde**, and Inge Jonassen. *Systematic exploration of error sources in pyrosequencing flowgram data.* ISMB 2011.

Bioinformatics 27(13):i304-i309

Ketil Malde. Flower: extracting information from pyrosequencing data. Bioinformatics, 27(7):1041-1042

Rolf B Edvardsen, **Ketil Malde**, Christian Mittelholzer, Knut Jørstad, Geir-Lasse Taranger, and Frank Nilsen. *EST resources and establishment and validation of a 16k cDNA microarray from Atlantic cod (Gadus morhua).*

Comp Biochem Physiol Part D Genomics Proteomics, 6(1):23-30

2010 Susanne Balzer, **Ketil Malde**, Anders Lanzén, Animesh Sharma, and Inge Jonassen. *Characteristics of 454 pyrosequencing data - Enabling realistic simulation with FlowSim.* ECCB 2010.

Bioinformatics, 26(18):i420-i425.

Marian K Malde, Susanne Bügel, Mette Kristensen, Ingvild E Graff, **Ketil Malde**, and Jan I Pedersen. *Calcium absorption and retention from fish bones assessed by whole-body radioisotope retention method.*

Nutrition & Metabolism, 7:61.

2009 Sonal Patel, Ketil Malde, Anders Lanzén, Rolf H Olsen, and Audun H Nerland. *Identification of immune related genes in Atlantic halibut (Hippoglossus hippoglossus L.) following in vivo antigenic and in vitro mitogenic stimulation.* Fish and Shellfish Immunology, 27(6):729-38

Ketil Malde and Bryan O'Sullivan. Using Bloom Filters for Large Scale Gene Sequence Analysis in Haskell. PADL 2009.

LNCS 5418:183-194.

2008 Ketil Malde and Inge Jonassen. *Repeats and EST analysis for new organisms.* BMC Genomics, 9:23.

Ketil Malde. The effect of sequence quality on sequence alignment. Bioinformatics, 24(7):897-900.

2006 Ketil Malde, Korbinian Schneeberger, Eivind Coward, and Inge Jonassen. *RBR: Library-less repeat detection for ESTs.*

Bioinformatics, 22(18):2232-2236.

Ketil Malde and Robert Giegerich. *Calculating PSSM Probabilities with Lazy Dynamic Programming.*

Journal of Functional Programming, 16(1):75-81.

2005 Korbinian Schneeberger, **Ketil Malde**, Eivind Coward, and Inge Jonassen. *Masking Repeats while Clustering ESTs.*

Nucleic Acids Research, 33(7):2176-2180

Ketil Malde, Eivind Coward, and Inge Jonassen. A graph based algorithm for generating EST consensus sequences.

Bioinformatics, 21(8):1371-1375.

Ketil Malde. Algorithms for the Analysis of Expressed Sequence Tags. Ph.D. (*dr. scient*) thesis. University of Bergen.

2003 Ketil Malde, Eivind Coward, and Inge Jonassen. Fast sequence clustering using a suffix array algorithm.

Bioinformatics, 19(10):1221-1226.

Other contributions

I participated in the organizing of Bioinformatics in Bergen in 2005, and BFYS in 2003.

I have contributed at the following conferences with posters/abstracts: WABIo2, BREWo3, RECOMBo4, BFYSo5, GCBo7, ECCBo8, and also participated at several hackathons, most recently at BOSC11.

Student supervision

I'm currently supervising one Ph.D. student (Susanne Balzer), and co-supervising another (Animesh Sharma). Both are scheduled to complete their Ph.D.s in 2012.

I have previously participated in the supervision of three M.Sc. students.

Education and work experience

2007- Research scientist at the Institute of Marine Research in Bergen.

2005-2007 Working as a scientist at the Computational Biology Unit, Bergen Centre for Computational Science. Research and software development. Highperformance computing

2004 Three month stay with prof. Giegerich's group at the University of Bielefeld.

2003 Participation in the summer school for computational biology, ISSCB03, Warzaw.

2002-2004 Ph.D. (*dr.scient.*) studies at the Department of Informatics, University of Bergen. The topic for the thesis is sequence analysis, with the main focus on EST sequences and processing (clustering, masking, and assembly).

Bioinformatics, Haskell

1998-2001 Employment at Nera Networks AS as programmer. The work consisted of maintenance, support and development of software for management of telecommunications equipment.

C++, software engineering, large projects

1997-1998 Working as programmer and consultant for STEP Infotek AS, where I developed solutions for document management based on SGML and XML.

Java, SGML, XML, document management Unix, scripting

1996-1997 Employed as systems administrator at the IT department at the Institute of Marine Research in Bergen. Planning, installation, administration and maintenance of approximately 70 servers running Solaris or HP-UX.

C++, numerical

analysis

1995-1996 Master's degree (*siv.ing.*) at the Department of Informatics, University of Bergen. The thesis, titled *Permutations in Structured Numerical Problems* analyzes FFT, wavelets, multigrid, and cyclic reduction with respect to data permutations. Part of the thesis was the implementation a C++ library for parallel implementation of the algorithms.

Entrepreneurship

1994 Co-founded Vestnett, the first commercial Internet service provider in Bergen. Tasks consisted of management of Unix server and workstations, modem pool, and development of systems for logging and accounting.
Studies in Latin and Scientific Theory at the University of Bergen.

1993 Military service in the Royal Norwegian Coastal Artillery. BSKA (OCS) training and subsequent service as NCO, instructor, and squad leader at Nes fort.

Leadership and instruction

1989-1992 Undergraduate studies in informatics and mathematics at the University of Bergen. Bachelor's degree (*cand.mag.*) attained in 1992.

1985-1989 Attending Grimstad Videregående Skole (high school)

1987-1988 Exchange student at Novato High School, Marin county, California.

English

Skills

Languages

Native Norwegian, fluent written and spoken English, written Latin, some German and French.

Informatics

Experience with various programming languages, e.g. C++, C, Java, Pascal, Lisp, Python, Haskell and scripting languages, with good knowledge of different paradigms like object orientation and functional programming. Good knowledge of Unix and associated tools.

Systems administration

I have been managing Unix and Linux desktop and server systems since 1992. Familiar with common Internet services and protocols.

Bioinformatics

Good knowledge of sequence analysis algorithms and practical use of common tools. Experience dealing with second generation sequencing data (454, Illumina, SOLiD), and microarray probe design (cDNA and Agilent oligo-arrays).

Teaching and supervision

Instruction and teaching experience from BSKA, as teaching assistant at University. Supervision of Ph.D. and graduate students.

Leadership and management

Project manager responsibility in projects at IMR. Attended courses in project management (2000 and 2006).

Other activities

Current activities

For the last ten years I've been practicing orienteering, and have worked my way up to compete in the A class. I enjoy occasional sailing and recreational floorball and skiing.

I generally try to be involved in the local community, and am currently elected FAU (similar to PTA) representative.

Previous activities

Leader of the local FAU.

Board member and chairman, Bildeleringen BA.

Member of the organizing committee and VP for the Nera Sports Team.

Elected representative for the class at BSKA.

Participation in Realistforeningen and the organizing committee for Hulen.

Steering committee member of Fribyte, the computer science students' organization for social activities.

References

- 1. Helge Sagen, group leader at the Norwegian Data Centre at IMR. helge.sagen@imr.no, tel: +47 5523 8447.
- 2. Inge Jonassen, professor at the Department of Informatics, University of Bergen, inge@ii.uib.no, tel: +47 5558 4713 .
- 3. Henrik Thorsen, manager at the *Element Management* department at Nera.
- 4. Magnus Alvestad, CEO, Vestnett, magnus.alvestad@gmail.com, tel: +47 9829 8004.