Bent Petersen, Curriculum Vitae

CONTACT DETAILS:	Center for Biological Sequence Analysis, Technical University of Denmark, Kemitorvet bygning 208, DK-2800 Kongens Lyngby, Denmark Mobile: (+45) 2084 7492 bentpetersen@gmail.com, bent@cbs.dtu.dk, bent@bison-seqtech.dk
DATE OF BIRTH:	October 9, 1979

ENTREPRENEURSHIP

June 2014 - Present
Co-Founder / CEO Bison SeqTech - http://www.bison-seqtech.dk
Bison SeqTech is a bioinformatics company with a solid scientific foundation.
Bison Seqtech offers a wide range of bioinformatic services customised to the specific needs of our clients. The services include experimental design, data cleaning and preparation, genome assembly and profiling, transcriptomics and metatranscriptomics.

EDUCATION AND EMPLOYMENT

May 2015 - Present
Associate Professor, Department of Systems Biology, Technical University of Denmark
Continuing working within the area of metagenomics using Next Generation Sequencing technologies. I have worked on many exciting projects spanning from Ancient horses to modern breeds, Extinct animals, Malaria parasites, metagenomics samples from exotic places, Cochineals and many other so far unpublished projects.

May 2013 - April 2015
Assistant Professor, Department of Systems Biology, Technical University of Denmark
Continuing working within the area of metagenomics using Next Generation Sequencing technologies.

May 2011 - April 2013
Post.Doc, CBS, DTU.
Working in the Meta-genomics group with projects related to Next-Generation-Sequencing data.

February 2008 – March 2011
Ph.D, CBS, DTU.
Thesis: “Prediction of protein structural features by use of artificial neural networks.”
Supervisors: Claus Lundegaard and Thomas Nordahl Petersen.

September 2000 – September 2007
Cand. Polyt. (Master of Science) in biotechnology, DTU, CBS.
Thesis: “Prediction of local structure elements using artificial neural networks”.
Supervisors: Claus Lundegaard and Thomas Nordahl Petersen.

RESEARCH GRANTS

2015 - Danish Agency for Science, Technology and Innovation framework grant *“Deciphering Amazon endemic plants with omics tools. Utilising Bioinformatics for faster description of endemic plant species.”* (€19.324)

TEACHER TRAINING COURSES

uDTU - Education in University Teaching at DTU:
Module 1 - Teaching and learning - September 2012
Module 2 - Teaching Methods and course planning - February 2013
Module 3 - Teaching and teacher Development - April 2013

TEACHING AND SUPERVISION

2012 - Ongoing: Introduction to Bioinformatics, 13-weeks Bachelor course (DTU #27611)
2014 - 2015 - Teaching in Introduction to bioinformatics and Next Generation Sequencing for master students in China attending Omics course, SDC
2015 - Metagenomics course, Belo Horizonte, Brazil
2011 - 2013: Introduction to Bioinformatics - Turbo version, 3-weeks Master course (DTU #27622)

TEACHING RESPONSIBILITIES

I am responsible for the 13-weeks course 27611 with ~100 students every spring semester and for the 3-weeks course 27622 with ~20 students every summer including teaching, preparing and correcting exercises/exams and final grading.

STUDENTS AND MENTORING

1 bachelor student project, 9 special projects students and mentoring of 3 PhD students.

INTERNATIONALLY GIVEN TALKS

2016

BioVisionAlexandria (BVA) 2016 conference on the 13th April
http://www.bibalex.org/bva2016/home/home.aspx

Faculty of Pharmacy- Cairo University Seventh International Scientific Conference on the 16th April with the title: “From sequence to knowledge: How DNA sequencing is changing science”
http://www.pharma.cu.edu.eg/conference.aspx

Aimst University, Malaysia at the 3rd Regional Conference on Biosensors, Biodiagnostics and Biotechnology 2016 on the 21th April with the title: “Supercomputing in Biotechnology industry: making big data widely applicable”.
http://www.aimst.edu.my/3rdRC4Bs-2016/index.html

2015

DeiC Conference 2015 - Supercomputer kortlægger danskernes arvemasse

2014

March 2014 - Metagenomics Workshop - III International Workshop on Environmental Microbiology, Brazil

EDITORIAL COMMITMENTS

March 2014 - February 2016
Assistant Editor - De Gruyter Open
Journal:Methods in Next Generation Sequencing

Since 2010 have been acting as reviewer for:

- Amino Acids
- Bioinformatics
- Immunome Research
- Journal of Theoretical Biology
- International Journal of Molecular Sciences
- PLOS ONE
- Molecular Ecology Resources
- ISMB 2014/2015 – Travel fellowships

BIOLOGICAL SKILLS: Bioinformatics, Computational biology, DNA Sequencing, NGS data analysis, metagenomics, protein structure prediction, Genomics, Genome assembly of: Bacteria, insects, mammals, metagenomics samples, parasites and highly complex organisms.

COMPUTATIONAL SKILLS: Shared Memory architecture Machines, Massive data handling, Super computing expertise, Moab/Torque resource manager, Neural networks, machine learning, experience with Perl, Unix Scripting and basic knowledge of MySQL databases

INTERPERSONAL SKILLS: Team-worker, networking, extrovert, hard-working, efficient, analytical, disciplined, inter-cultural, flexible, open-minded

PUBLIC PROFILES:

Blog: http://www.bpetersen.dk/blog
Linkedin: https://www.linkedin.com/in/bentpetersen
Twitter: https://twitter.com/bentpetersen
Company: http://bison-seqtech.dk

PUBLICATIONS:

1. **A generic method for assignment of reliability scores applied to solvent accessibility predictions.**
   Petersen, B., Petersen, T., Andersen, P., Nielsen, M. & Lundegaard, C.
   BMC Structural Biology 9**,** 51 (2009)
2. **NetTurnP - Neural Network Prediction of Beta-turns by Use of Evolutionary Information and Predicted Protein Sequence Features.**
   Petersen, B., Lundegaard, C. & Petersen, T. N.
   PLoS One **5,** e15079 (2010).
3. **Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse.**
   Ludovic Orlando, Aurélien Ginolhac, Guojie Zhang, Duane Froese, Anders Albrechtsen, Mathias Stiller, Mikkel Schubert, Enrico Cappellini, **Bent Petersen**, Ida Moltke, Philip L. F. Johnson, Matteo Fumagalli, Julia T. Vilstrup, Maanasa Raghavan, Thorfinn Korneliussen, Anna-Sapfo Malaspinas, Josef Vogt, Damian Szklarczyk, Christian D. Kelstrup, Jakob Vinther, Andrei Dolocan, Jesper Stenderup, Amhed M. V. Velazquez, James Cahill, Morten Rasmussen et al.,
   Nature Letters, Nature 499, 74–78 (04 July 2013) doi:10.1038/nature12323
4. **Speciation with gene flow in equids despite extensive chromosomal plasticity.**
   Hákon Jónsson, Mikkel Schubert, Andaine Seguin-Orlando, Aurélien Ginolhac, Lillian Petersen, Matteo Fumagalli, Anders Albrechtsen, **Bent Petersen**, Thorfinn S. Korneliussen, Julia T. Vilstrup, Teri Lear, Jennifer Leigh Myka, Judith Lundquist, Donald C. Miller, Ahmed H. Alfarhan, Saleh A. Alquraishi, Khaled A. S. Al-Rasheid, Julia Stagegaard, Günter Strauss, Mads Frost Bertelsen, Thomas Sicheritz-Ponten, Douglas F. Antczak, Ernest Bailey, Rasmus Nielsen, Eske Willerslev, and Ludovic Orlando
   PNAS 2014 ; published ahead of print December 1, 2014, doi:10.1073/pnas.1412627111
5. **Whole Genome Analyses Resolve Early Branches in the Tree of Life of Modern Birds.**
   Jarvis ED, Mirarab S, Aberer AJ, Li B, Houde P, Li C, Ho SYW, Faircloth BC, Nabholz B, Howard JT, Suh A, Weber CC, Fonseca RRd, Li J, Zhang F, Li H, Zhou L, Narula N, Liu L, Ganapathy G, Boussau B, Bayzid MdS, Zavidovych V, Subramanian S, Gabaldón T, Capella-Gutiérrez S, Huerta-Cepas J, Rekepalli B, Munch K, Schierup M, Lindow B, Warren WC, Ray D, Green RE, Bruford M, Zhan X, Dixon A, Li S, Li N, Huang Y, Derryberry EP, Bertelsen MF, Sheldon FH, Brumfield RT, Mello CV, Lovell PV, Wirthlin M, Schneider MPC, Prosdocimi F, Samaniego JA, Velazquez AMV, Alfaro-Núñez A, Campos PF, **Petersen B**, Sicheritz-Ponten T, Pas A, Bailey T, Scofield P, Bunce M, Lambert DM, Zhou Q, Perelman R, Driskell AC, Shapiro B, Xiong Z, Zeng Y, Liu S, Li Z, Liu B, Wu K, Xiao J, Yinqi X, Zheng Q, Zhang Y, Yang H, Wang J, Smeds L, Rheindt FE, Braun M, Fjeldsa J, Orlando L, Barker K, Jønsson KA, Johnson W, Koepfli KP, OBrien S, Haussler D, Ryder OA, Rahbek C, Willerslev E, Graves GR, Glenn TC, McCormack J, Burt D, Ellegren H, Alström P, Edwards SW, Stamatakis A, Mindell DP, Cracraft J, Braun EL, Warnow T, Jun W, Gilbert MTP, Zhang G
   Science 12 December 2014: 1320-1331
6. **Prehistoric genomes reveal the genetic foundation and cost of horse domestication.**
   Mikkel Schubert, Hákon Jónsson, Dan Chang, Clio Der Sarkissian, Luca Ermini, Aurélien Ginolhac, Anders Albrechtsen, Isabelle Dupanloup, Adrien Foucal, **Bent Petersen**, Matteo Fumagalli, Maanasa Raghavan, Andaine Seguin-Orlando, Thorfinn S. Korneliussen, Amhed M. V. Velazquez, Jesper Stenderup, Cindi A. Hoover, Carl-Johan Rubin, Ahmed H. Alfarhan, Saleh A. Alquraishi, Khaled A. S. Al-Rasheid, David E. MacHugh, Ted Kalbfleisch, James N. MacLeod, Edward M. Rubin, Thomas Sicheritz-Ponten, Leif Andersson, Michael Hofreiter, Tomas Marques-Bonet, M. Thomas P. Gilbert, Rasmus Nielsen, Laurent Excoffier, Eske Willerslev, Beth Shapiro, and Ludovic Orlando
   PNAS 2014 - published ahead of print December 15, 2014, doi:10.1073/pnas.1416991111
7. ***Structural Conservation Despite Huge Sequence Diversity Allows EPCR Binding by the PfEMP1 Family Implicated in Severe Childhood Malaria**
   Clinton K.Y. Lau, Louise Turner, Jakob S. Jespersen, Edward D. Lowe, **Bent Petersen,** Christian W. Wang, Jens E.V. Petersen, John Lusingu, Thor G. Theander, Thomas Lavstsen, Matthew K. Higgins
   Cell Host & Microbe, Available online 4 December 2014, ISSN 1931-3128, http://dx.doi.org/10.1016/j.chom.2014.11.007
8. **Evolutionary genomics and conservation of the endangered Przewalski's horse**
   Sarkissian CD, Ermini L, Schubert M, Yang MA, Librado P, Fumagalli M, Jónsson H, Bar-Gal GK, Albrechtsen A, Vieira FG, **Petersen B**, Ginolhac A, Seguin-Orlando A, Magnussen K, Fages A, Gamba C, Lorente-Galdos B, Polani S, Steiner C, Neuditschko M, Jagannathan V, Feh C, Greenblatt CL, Ludwig A, Abramson NI, Zimmermann W, Schafberg R, Tikhonov A, Sicheritz-Ponten T, Willerslev E, Marques-Bonet T, Ryder OA, McCue M, Rieder S, Leeb T, Slatkin M, Orlando L
   Current Biology - Current Biology 25 (19), 2577-2583
9. **Within-host microevolution of Pseudomonas aeruginosa in Italian cystic fibrosis patients**
   Rasmus Lykke Marvig, Daniela Dolce, Lea M. Sommer, **Bent Petersen,** Oana Ciofu, Silvia Campana, Søren Molin, Giovanni Taccetti and Helle Krogh Johansen
   BMC Microbiology 2015, 15:218 doi:10.1186/s12866-015-0563-9

10. **Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments**
    Pablo Librado, Clio Der Sarkissian, Luca Ermini, Mikkel Schubert, Hákon Jónsson, Anders Albrechtsen, Matteo Fumagalli, Melinda A. Yang, Cristina Gamba, Andaine Seguin-Orlando, Cecilie D. Mortensen, **Bent Petersen**, Cindi A. Hoover, Belen Lorente-Galdos, Artem Nedoluzhko, Eugenia Boulygina, Svetlana Tsygankova, Markus Neuditschko, Vidhya Jagannathan, Catherine Thèves, Ahmed H. Alfarhan, Saleh A. Alquraishi, Khaled A. S. Al-Rasheid, Thomas Sicheritz-Ponten, Ruslan Popov, Semyon Grigoriev, Anatoly N. Alekseev, Edward M. Rubin, Molly McCue, Stefan Rieder, Tosso Leeb, Alexei Tikhonov, Eric Crubézy, Montgomery Slatkin, Tomas Marques-Bonet, Rasmus Nielsen, Eske Willerslev, Juha Kantanen, Egor Prokhortchouk, and Ludovic Orlando
    PNAS 2015 ; published ahead of print November 23, 2015, doi:10.1073/pnas.1513696112
11. **Using expected sequence features to improve basecalling accuracy of amplicon pyrosequencing data**
    Thomas S. Rask, **Bent Petersen**, Donald S. Chen, Karen P. Day and Anders Gorm Pedersen
    BMC Bioinformatics, 201617:176 DOI: 10.1186/s12859-016-1032-7