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## Kort præsentation

Lektor i Bioinformatik. Mit forsknings område er ncRNA bioinformatik. Dette kan for eksempel være: Secondær struktur forudsigelse, strukturel ncRNA alignment, forudsigelse af RNA-RNA interaktioner, og ncRNA genom annotering.
Jeg underviser primært i programmering for begyndere og bioinformatik.

## Ansættelse

**Lektor**
Sektion, Preclinical Disease Biology
Københavns Universitet
Frederiksberg C, Danmark
30 apr. 2002 → nu

## Publikationer

**The Bacillaceae-1 RNA motif comprises two distinct classes**
González-Tortuero, E., Anthon, Christian, Havgaard, Jakob Hull, Geissler, Adrian Sven, Breüner, A., Hjort, C., Gorodkin, Jan & Seemann, Ernst Stefan, 2022, I: Gene. 841, 146756.

**Using GPU to accelerate the pairwise structural RNA alignment with base pair probabilities**
Sundfeld, D., Teodoro, G., Havgaard, Jakob Hull, Gorodkin, Jan & Melo, A. C. M. A., 2020, I: Concurrency Computation. 32, 10, e5468.

**Epigenetic and Transcriptomic Characterization of Pure Adipocyte Fractions From Obese Pigs Identifies Candidate Pathways Controlling Metabolism**
Jacobsen, M. J., Havgaard, Jakob Hull, Anthon, Christian, Mentzel, Caroline M. Junker, Cirera, Susanna, Krogh, P. M., Pundhir, Sachin, Karlskov-Mortensen, Peter, Bruun, C. S., Lesnik, P., Guerin, M., Gorodkin, Jan, Jørgensen, Claus Bøttcher, Fredholm, Merete & Barrès, Romain, 2019, I: Frontiers in Genetics. 10, 13 s., 1268.

**CRISPR-Cas9 off-targeting assessment with nucleic acid duplex energy parameters**
Alkan, F., Wenzel, Anne, Anthon, Christian, Havgaard, Jakob Hull & Gorodkin, Jan, 2018, I: Genome Biology. 19, 13 s., 177.

**Alignment-free comparative genomic screen for structured RNAs using coarse-grained secondary structure dot plots**
Kato, Y., Gorodkin, Jan & Havgaard, Jakob Hull, dec. 2017, I: BMC Genomics. 18, 1, 935.

**Assessing the miRNA sponge potential of RUNX1T1 in t(8;21) acute myeloid leukemia**
Junge, A., Zandi, R., Havgaard, Jakob Hull, Gorodkin, Jan & Cowland, J. B., 2017, I: Gene. 615, s. 35-40 6 s.

**CUDA-Sankoff: Using GPU to Accelerate the Pairwise Structural RNA Alignment**
Sundfeld, D., Havgaard, Jakob Hull, Gorodkin, Jan & De Melo, A. C. M. A., 2017, *Proceedings: 2017 25th Euromicro International Conference on Parallel, Distributed and Network-Based Processing, PDP 2017.* IEEE, s. 295-302 8 s. 7912663

**RNAscClust: Clustering RNA sequences using structure conservation and graph based motifs**
Miladi, M., Junge, A., Costa, F., Seemann, Ernst Stefan, Havgaard, Jakob Hull, Gorodkin, Jan & Backofen, R., 2017, I: Bioinformatics. 33, 14, s. 2089-2096 8 s.

**Adipocyte gene expression and DNA methylation patterns differ significantly between lean and obese pigs**
Jacobsen, M. J., Havgaard, Jakob Hull, Mentzel, Caroline M. Junker, Sørensen, P. M., Pundhir, Sachin, Anthon, Christian , Karlskov-Mortensen, Peter, Bruun, Camilla Vibeke Sichlau, Cirera, Susanna, Gorodkin, Jan, Jørgensen, Claus Bøttcher, Barrès, Romain & Fredholm, Merete, 9 nov. 2016, I: Journal of Animal Science. 94, Supplement 4, s. 46-47 2 s., P2019.

**Foldalign 2.5: multithreaded implementation for pairwise structural RNA alignment**
Sundfeld, D., Havgaard, Jakob Hull, de Melo, A. C. M. A. & Gorodkin, Jan, 2016, I: Bioinformatics. 32, 8, s. 1238-1240 3 s.

**Optimizing RNA structures by sequence extensions using RNAcop**
Hecker, N., Christensen-Dalsgaard, M., Seemann, Ernst Stefan, Havgaard, Jakob Hull, Stadler, P. F., Hofacker, I. L., Nielsen, Henrik & Gorodkin, Jan, 2015, I: Nucleic Acids Research. 43, 17, s. 8135-8145 11 s.

**RNA Structural Alignments, Part I: Sankoff-Based Approaches for Structural Alignments**
Havgaard, Jakob Hull & Gorodkin, Jan, 2014, *RNA Sequence, Structure, and Function: Computational and Bioinformatic Methods.* Gorodkin, J. & Ruzzo, W. L. (red.). s. 275-90 16 s. (Methods in molecular biology (Clifton, N.J.)).

**Structured RNAs and synteny regions in the pig genome**
Anthon, Christian, Tafer, H., Havgaard, Jakob Hull, Thomsen, B., Hedegaard, J., Seemann, Ernst Stefan, Pundhir, Sachin , Kehr, S., Bartschat, S., Nielsen, M., Nielsen, R. O., Fredholm, Merete, Stadler, P. F. & Gorodkin, Jan, 2014, I: BMC Genomics. 15, 27 s., 459.

**Comparative ncRNA gene and structure prediction using Foldalign and FoldalignM**
Havgaard, Jakob Hull, Kaur, S. & Gorodkin, Jan, 2012, I: Current Protocols in Bioinformatics. 39, s. 12.11.1-12.11.15 5 s.

***De novo* prediction of structured RNAs from genomic sequences**
Gorodkin, Jan, Hofacker, I. L., Þórarinsson, E., Yao, Z., Havgaard, Jakob Hull & Ruzzo, W. L., 2010, I: Trends in Biotechnology. 28, 1, s. 9-19 11 s.

**Structural profiles of human miRNA families from pairwise clustering**
Kaczkowski, B., Þórarinsson, E., Reiche, K., Havgaard, Jakob Hull, Stadler, P. F. & Gorodkin, Jan, 2009, I: Bioinformatics. 25, 3, s. 291-294 4 s.

**Fast pairwise structural RNA alignments by pruning of the dynamical programming matrix**
Havgaard, Jakob Hull, Torarinsson, E. & Gorodkin, Jan, 2007, I: PLoS Computational Biology. 3, 10, s. 1896-1908 13 s.

**Multiple structural alignment and clustering of RNA sequences: sequence analysis**
Torarinsson, E., Havgaard, Jakob Hull & Gorodkin, Jan, 2007, I: Bioinformatics. 23, 8, s. 926-32 7 s.

**Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags**
Gorodkin, J., Cirera, S., Hedegaard, J., Gilchrist, M. J., Panitz, F., Jørgensen, C., Scheibye-Knudsen, K., Arvin, T., Lumholdt, S., Sawera, M., Green, T., Nielsen, B., Havgaard, J. H., Rosenkilde, C., Wang, J., Li, H., Li, R., Liu, B., Hu, S., Dong, W. & 16 flere, Li, W., Yu, J., Wang, J., Staefeldt, H., Wernersson, R., Madsen, L. B., Thomsen, B. S., Hornshøj, H., Bujie, Z., Wang, X., Wang, X., Bolund, L., Brunak, Søren, Yang, H., Bendixen, C. & Fredholm, Merete, 2007, I: Genome Biology. 8, R45, s. R45 16 s.

**SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation**
Panitz, F., Stengaard, H., Hornshøj, H., Gorodkin, J., Hedegaard, J., Cirera, S., Thomsen, B. S., Madsen, L. B., Høj, A., Vingborg, R., Zahn, B., Wang, X., Wang, X., Wernersson, R., Jørgensen, C. B., Scheibye-Knudsen, K., Arvin, T., Lumholdt, S., Sawera, M., Green, T. & 5 flere, Nielsen, B., Havgaard, Jakob Hull, Brunak, Søren, Fredholm, Merete & Bendixen, C., 2007, I: Bioinformatics. 23, 13, s. i387-91 5 s.

**Semiautomated improvement of RNA alignments**
Andersen, E. S., Lind-Thomsen, A., Knudsen, B., Kristensen, S. E., Havgaard, Jakob Hull, Torarinsson, E., Larsen, N., Zwieb, C., Sestoft, P., Kjems, J. & Gorodkin, Jan, 2007, I: RNA: A publication of the RNA Society. 13, 11, s. 1850-1859

10 s.

**Structural alignment of RNA with FOLDALIGN**
Havgaard, Jakob Hull, 2007, Frederiksberg: Center for Skov, Landskab og Planlægning/Københavns Universitet. 128 s.

**MicroRNA sequence motifs reveal asymmetry between the stem arms**
Gorodkin, Jan, Havgaard, Jakob Hull, Ensterö, M., Sawera, M., Jensen, P., Öhman, M. & Fredholm, Merete, 2006, I: Computational Biology and Chemistry. 30, 4, s. 249-254 6 s.

**Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure**
Torarinsson, E., Sawera, M., Havgaard, Jakob Hull, Fredholm, Merete & Gorodkin, Jan, 2006, I: Genome Research. 16, 7 , s. 885-889 5 s.

**Pairwise local structural alignment of RNA sequences with sequence similarity less than 40%**
Havgaard, Jakob Hull, Lyngsø, R. B., Stormo, G. D. & Gorodkin, Jan, 2005, I: Bioinformatics. 21, 9, s. 1815-1824 10 s.

**The FOLDALIGN web server for pairwise structural RNA alignment and mutual motif search**
Havgaard, Jakob Hull, Lyngsø, R. B. & Gorodkin, Jan, 2005, I: Nucleic Acids Research. 33, s. W650-W653 4 s.