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Preclinical Disease Biology
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Short presentation

Associate professor in Bioinformatics. My research area is ncRNA bioinformatics. This includes: Secondary structure prediction, structural ncRNA alignment, prediction of RNA-RNA interactions, and ncRNA genome annotation. I primarily teach programming for beginners and bioinformatics.

Employment

Associate Professor

Preclinical Disease Biology

Frederiksberg C, Denmark

30 Apr 2002 → nu

Research outputs

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, In: *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, In: *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, In: *Frontiers in Genetics*. 10, 13 p., 1268.

CRISPR-Cas9 off-targeting assessment with nucleic acid duplex energy parameters

Alkan, F., Wenzel, Anne, Anthon, Christian, Havgaard, Jakob Hull & Gorodkin, Jan, 2018, In: *Genome Biology*. 19, 13 p., 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, In: *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, In: *Gene*. 615, p. 35-40 6 p.

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, p. 295-302 8 p. 7912663

RNAAscClust: 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, In: *Bioinformatics*. 33, 14, p. 2089-2096 8 p.

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, In: Journal of Animal Science. 94, Supplement 4, p. 46-47 2 p., 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, In: Bioinformatics. 32, 8, p. 1238-1240 3 p.

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, In: Nucleic Acids Research. 43, 17, p. 8135-8145 11 p.

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. (eds.). p. 275-90 16 p. (Methods in molecular biology (Clifton, N.J.)).

Structured RNAs and syntenic 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, In: BMC Genomics. 15, 27 p., 459.

Comparative ncRNA gene and structure prediction using Foldalign and FoldalignM

Havgaard, Jakob Hull, Kaur, S. & Gorodkin, Jan, 2012, In: Current Protocols in Bioinformatics. 39, p. 12.11.1-12.11.15 5 p.

De novo prediction of structured RNAs from genomic sequences

Gorodkin, Jan, Hofacker, I. L., Þórarinnsson, E., Yao, Z., Havgaard, Jakob Hull & Ruzzo, W. L., 2010, In: Trends in Biotechnology. 28, 1, p. 9-19 11 p.

Structural profiles of human miRNA families from pairwise clustering

Kaczkowski, B., Þórarinnsson, E., Reiche, K., Havgaard, Jakob Hull, Stadler, P. F. & Gorodkin, Jan, 2009, In: Bioinformatics. 25, 3, p. 291-294 4 p.

Fast pairwise structural RNA alignments by pruning of the dynamical programming matrix

Havgaard, Jakob Hull, Torarinsson, E. & Gorodkin, Jan, 2007, In: PLoS Computational Biology. 3, 10, p. 1896-1908 13 p.

Multiple structural alignment and clustering of RNA sequences: sequence analysis

Torarinsson, E., Havgaard, Jakob Hull & Gorodkin, Jan, 2007, In: Bioinformatics. 23, 8, p. 926-32 7 p.

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 others, 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, In: Genome Biology. 8, R45, p. R45 16 p.

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 others, Nielsen, B., Havgaard, Jakob Hull, Brunak, Søren, Fredholm, Merete & Bendixen, C., 2007, In: Bioinformatics. 23, 13, p. i387-91 5 p.

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, In: RNA: A publication of the RNA Society. 13, 11, p. 1850-1859 10 p.

Structural alignment of RNA with FOLDALIGN

Havgaard, Jakob Hull, 2007, Frederiksberg: Center for Skov, Landskab og Planlægning/Københavns Universitet. 128 p.

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, In: Computational Biology and Chemistry. 30, 4, p. 249-254 6 p.

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, In: Genome Research. 16, 7, p. 885-889 5 p.

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, In: Bioinformatics. 21, 9, p. 1815-1824 10 p.

The FOLDALIGN web server for pairwise structural RNA alignment and mutual motif search

Havgaard, Jakob Hull, Lyngsø, R. B. & Gorodkin, Jan, 2005, In: Nucleic Acids Research. 33, p. W650-W653 4 p.