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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

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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, 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 Sichelau, 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.)).

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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.

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Gorodkin, Jan, Hofacker, I. L., Þórarinnsson, 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

Kaczowski, B., Þórarinnsson, 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

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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

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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

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Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure

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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.