

Curriculum Vitae and Publication List

Prof. Dr. Jens Stoye
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Jens Stoye is a professor for Genome Informatics at the Faculty of Technology, Bielefeld University, Germany. His research interest is the development of algorithms and software for the analysis of genomic and post-genomic data in molecular biology and evolution, from the low level of DNA sequence comparison up to the higher levels of comparative genomics, metagenomics and phylogenetics.

Academic background:

1990-1995 Studies of Informatics in the Natural Sciences at Bielefeld University, Germany
1997 Dissertation at the Faculty of Technology, Bielefeld University, Germany;
supervisors: Robert Giegerich and Andreas Dress

Professional career:

1995-1997 Staff researcher at Bielefeld University, Germany
03-09/1997 Postdoctoral researcher at Bielefeld University, Germany
1997-1998 Postdoctoral researcher at the University of California at Davis, CA, USA
1998-2001 Postdoctoral researcher at the German Cancer Research Center, Heidelberg, Germany
2001-2002 Group leader at the Max Planck Institute for Molecular Genetics, Berlin, Germany
2002-present Professor for Genome Informatics, Bielefeld University, Germany
2015-2018 Special Visiting Researcher, Universidade Federal Fluminense (UFF), Niterói, Brazil

Community service:

since 2004 Associate editor of IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)
2010-2013 Associate editor of BMC Bioinformatics

Theses advised:

44 Bachelor Theses
63 Master and Diploma Theses
32 PhD Theses

Member of conference steering committees:

since 09/2012 Workshop on Algorithms in Bioinformatics (WABI)
since 10/2014 Bioinformatics Research and Education Workshop (BREW)

Member of conference program committees:

GCB: 2000 (co-chair), 2004 (co-chair), 2010, 2011, 2012, 2013, 2014
WABI: 2002, 2003, 2004, 2005, 2007, 2008, 2009, 2010, 2011, 2012, 2013 (co-chair), 2014, 2015, 2016, 2017
ISMB: 2003, 2004, 2009, 2010, 2012, 2013, 2014, 2015, 2016, 2017

RECOMB: 2004, 2006, 2008, 2009, 2012, 2017
ECCB: 2004, 2005, 2009, 2012, 2013, 2014, 2015, 2016, 2017
RECOMB-CG: 2005, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015 (co-chair), 2016, 2017
IWBRA/ISBRA: 2006, 2007, 2008, 2009, 2010, 2011
CPM: 2006, 2010, 2012 (co-chair), 2013, 2014, 2015
SPIRE: 2006, 2010, 2011, 2017
ALENEX: 2007
IEEE BIBM: 2007, 2013
SHORT-SIG/HiTSeq: 2009 (co-chair), 2010 (co-chair), 2011 (co-chair), 2017
LATA: 2011, 2012, 2017
ACM-BCB: 2011, 2012, 2013
RECOMB-Seq: 2012, 2013, 2016
ESA: 2012
RECOMB-AB: 2012
Others: CompLife 2005, ISBB 2006, ICCABS 2010, ITMAB 2011, FAW-AAIM 2013, BSB 2013

Member of conference organizing committees:

GCB: 2000, 2004, 2014 (chair)

Best paper award:

CPM 2008: HP Distance via Double Cut and Join (A. Bergeron, J. Mixtacki, J. Stoye)

Invited speaker:

JOBIM 2006: Index Structures in Biological Sequence Analysis: From Simplicity to Complexity and Back
JOBIM 2009: Computational Short Read Metagenomics
BSB 2012: Genome Rearrangement by Double Cut and Join
ALGO 2012: Algorithms for Genome Rearrangement by Double Cut and Join
MAGE 2013: The potential of family-free genome comparison
SocBiN 2014: Family-free genome comparison

Administration:

2002-2014 Vice-Speaker of the Board of Directors, German Bioinformatics Society (GI-Fachgruppe BIOINF)
2002-2014 Member of the Faculty Assembly of the Faculty of Technology, Bielefeld University
2002-2015 Speaker of the Institute for Bioinformatics, Center for Biotechnology (CeBiTec), Bielefeld University
since 2004 Member of the Board of Directors, Center for Biotechnology (CeBiTec), Bielefeld University
2002-2007 Head of Examination Board, Diploma program *Informatics in the Natural Sciences*, Bielefeld Univ.
2007-2012 Head of Examination Board, Master program *Informatics in the Natural Sciences*, Bielefeld Univ.
2007-2009 Dean of the Faculty of Technology, Bielefeld University
2009-2010 Vice-dean of the Faculty of Technology, Bielefeld University
2010-2013 Dean of the Faculty of Technology, Bielefeld University
since 2013 Speaker of the International DFG Research Training Group *Computational Methods for the Analysis of the Diversity and Dynamics of Genomes*, Faculty of Technology, Bielefeld University
since 2014 Member of the DAAD Selection Committee for Postdoc Fellowships
since 2015 Special Visiting Researcher, UFF Niterói, Brazil
since 2015 Speaker of the Research Area *Large Scale Genomics and Big Data Bioinformatics*, Center for Biotechnology (CeBiTec), Bielefeld University
since 2017 Member of the Board of Directors, Center for Interdisciplinary Studies (ZiF), Bielefeld University

Major research grants:

2002-2010 "GK Bioinformatik", DFG Research Training Group, GRK 635. Co-PI, vice-speaker 2003-2010
2002-2009 "Bioinformatics and Genome Research", NRW International Graduate School. Co-PI
2007-2012 "Cognitive Interaction Technology", DFG Cluster of Excellence, EXC 277. Responsible investigator

- 2009-present "Cluster Industrial Biotechnology", NRW Graduate Cluster. Participating researcher
 2009-2010 "Ausbau der Rechner-Infrastruktur am CeBiTec", DFG Major Research Instrumentation Programme. Co-PI (with Bernd Weisshaar, Bielefeld)
 2010-2014 "Algorithmen zur Analyse Approximativer Gen-Cluster", DFG Research Grant. Co-PI (with Sebastian Böcker)
 2013-present "IGK Computational Methods for the Analysis of the Diversity and Dynamics of Genomes", International DFG Research Training Group, GRK 1906. Co-PI, speaker
 2014 German Network for Bioinformatics Infrastructure (de.NBI) – Konzipierungsphase – BiGi
 2015-2016 DAAD Programm des Projektbezogenen Personenaustauschs (PPP) with QUT, Brisbane, Australia, Co-PI
 2015-present German Network for Bioinformatics Infrastructure (de.NBI) – Etablierungsphase – Leistungszentrum BiGi, PI
 2016 ZIF Cooperation Group "Multiscale Modeling of Tumor Initiation, Growth and Progression". Co-PI (with Niko Beerenwinkel, Haralambos Hatzikirou, Barbara Klink, Tyll Krüger)
 2016 DFG grant for conference organization at ZIF, PI

Publications:

2018

Family-Free Genome Comparison

D. Doerr, P. Feijão, J. Stoye

In: J. C. Setubal, P. Stadler, J. Stoye (eds.): *Methods in Molecular Biology*, vol. 1704: *Comparative Genomics: Methods and Protocols*. Chapter 12, pp. 331-342. Springer Verlag, 2018.

Pan-genome Storage and Analysis Techniques

T. Zekic, G. Holley, J. Stoye

In: J. C. Setubal, P. Stadler, J. Stoye (eds.): *Methods in Molecular Biology*, vol. 1704: *Comparative Genomics: Methods and Protocols*. Chapter 2, pp. 29-53. Springer Verlag, 2018.

Comparative Genomics: Methods and Protocols

J. C. Setubal, P. Stadler, J. Stoye (eds.)

Methods in Molecular Biology, Springer Verlag, 2018.

2017

Finding Teams in Graphs and its Application to Spatial Gene Cluster Discovery

T. Schulz, J. Stoye, D. Doerr

Proceedings of RECOMB-CG 2017, Springer Verlag, LNBI 10562, 197-212, 2017.

Algorithms for Computing the Family-Free Genomic Similarity under DCJ

D. P. Rubert, G. L. Medeiros, E. A. Hoshino, M. D. V. Braga, J. Stoye, F. V. Martinez

Proceedings of RECOMB-CG 2017, Springer Verlag, LNBI 10562, 76-100, 2017.

Bioinformatics for NGS-based Metagenomics and the Application to Biogas Research

S. Jünemann, N. Kleinbölting, S. Jaenicke, C. Henke, J. Hassa, J. Nelkner, Y. Stolze, S. P. Albaum, A. Schlüter, A. Goesmann, A. Sczyrba, J. Stoye

J. Biotechnol. 261, 10-23, 2017.

Fast and Simple Jumbled Indexing for Binary Run-Length Encoded Strings

L. Cunha, S. Dantas, T. Gagie, R. Wittler, L. Kowada, J. Stoye

Proceedings of CPM 2017, LIPIcs 78, 19:1-19:9, 2017.

New Genome Similarity Measures based on Conserved Gene Adjacencies

D. Doerr, L. A. B. Kowada, E. Araujo, S. Deshpande, S. Dantas, B. M. E. Moret, J. Stoye

J. Comp. Biol. 24(6): 616-634, 2017.

Dynamic Alignment-Free and Reference-Free Read Compression

G. Holley, R. Wittler, J. Stoye, F. Hach

Proceedings of RECOMB 2017, Springer Verlag, LNBI 10229, 50-65, 2017.

Approximating the DCJ distance of balanced genomes in linear time

D. Rubert, P. Feijão, M. D. V. Braga, J. Stoye, F. H. V. Martinez
Algorithms Mol. Biol. 12:3, 2017.

2016

Finding Approximate Gene Clusters with GECKO 3

S. Winter, K. Jahn, S. Wehner, L. Kuchenbecker, M. Marz, J. Stoye, S. Böcker
Nucleic Acids Res. 44(20): 9600-9610, 2016.

A Linear Time Approximation Algorithm for the DCJ Distance for Genomes with Bounded Number of Duplicates

D. P. Rubert, P. Feijão, M. D. V. Braga, J. Stoye, F. V. Martinez
Proceedings of WABI 2016, Springer Verlag, LNBI 9838, 293-306, 2016.

New Genome Similarity Measures based on Conserved Gene Adjacencies

L. A. B. Kowada, D. Doerr, S. Dantas, J. Stoye
Proceedings of RECOMB 2016, Springer Verlag, LNBI 9649, 204-224, 2016.

Bloom Filter Trie: an alignment-free and reference-free data structure for pan-genome storage

G. Holley, R. Wittler, J. Stoye
Algorithms Mol. Biol. 11:3, 2016.

Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma

L. Krause, K. Nones, K. A. Loffler, D. Nancarrow, H. Oey, Y. H. Tang, N. J. Wayte, A. M. Patch, K. Patel, S. Brosda, S. Manning, G. Lampe, A. Clouston, J. Thomas, J. Stoye, D. J. Hussey, D. I. Watson, R. V. Lord, W. A Phillips, D. Gotley, B. M. Smithers, D. C. Whiteman, N. K. Hayward, S. M. Grimmond, N. Waddell, A. P. Barbour
Carcinogenesis 37(4): 356-365, 2016.

2015

Proceedings of the 13th Annual Research in Computational Molecular Biology (RECOMB) Satellite Workshop on Comparative Genomics: Genomics

J. Meidanis, J. Stoye (eds.)
BMC Genomics, 16(Suppl. 10), 2015.

Proceedings of the 13th Annual Research in Computational Molecular Biology (RECOMB) Satellite Workshop on Comparative Genomics: Bioinformatics

J. Meidanis, J. Stoye (eds.)
BMC Bioinformatics, 16(Suppl. 14), 2015.

Bloom Filter Trie - a data structure for pan-genome storage

G. Holley, R. Wittler, J. Stoye
Proceedings of WABI 2015, Springer Verlag, LNBI 9289, 217-230, 2015.

Sorting linear genomes with rearrangements and indels

M. D. V. Braga, J. Stoye
IEEE/ACM Trans. Comput. Biol. Bioinf. 12(3): 500-506, 2015.

On the family-free DCJ distance and similarity

F. V. Martinez, P. Feijão, M. D. V. Braga, J. Stoye
Algorithms Mol. Biol. 10:13, 2015.

2014

Improving the genome annotation of the acarbose producer *Actinoplanes* sp. SE50/110 by sequencing enriched 5'-ends of primary transcripts

P. Schwientek, A. Neshat, J. Kalinowski, A. Klein, C. Rückert, S. Schneiker-Bekel, S. Wendler, J. Stoye, A. Pühler
J. Biotechnol. 190: 85-95, 2014.

Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing

T. Jakobi, K. Brinkrolf, A. Tauch, T. Noll, J. Stoye, A. Pühler, A. Goesmann
J. Biotechnol. 190: 64-75, 2014.

Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework

N. Luhmann, C. Chauve, J. Stoye, R. Wittler
Proceedings of BSB 2014, Springer Verlag, LNBI 8826, 135-143, 2014.

Identifying Gene Clusters by Discovering Common Intervals in Indeterminate Strings

D. Doerr, J. Stoye, S. Böcker, K. Jahn
BMC Genomics 15(Suppl. 6): S2, 2014. (Proceedings of RECOMB-CG 2014)

Suffix Tree Construction

J. Stoye
In: M.-Y. Kao (ed.): Encyclopedia of Algorithms. Springer Verlag, 2014.

GABenchToB: A Genome Assembly Benchmark Tuned on Bacteria and Benchtop Sequencers

S. Jünemann, K. Prior, A. Albersmeier, S. Albaum, J. Kalinowski, A. Goesmann, J. Stoye, D. Harmsen
PLOS ONE 9(9): e107014, 2014.

Metatranskriptomik der Mikrobiota der menschlichen Achselhöhle (invited article, in German)

E. Fredrich, C. Ander, J. Stoye, I. Brune, A. Tauch
BIOSpektrum 20(5): 294-296, 2014.

Orthology Detection Combining Clustering and Synteny for Very Large Datasets

M. Lechner, M. Hernandez-Rosales, D. Doerr, N. Wieseke, A. Thévenin, J. Stoye, R. K. Hartmann, S. J. Prohaska, P. F. Stadler
PLOS ONE 9(8): e105015, 2014.

On the family-free DCJ distance

F. V. Martinez, P. Feijão, M. D. V. Braga, J. Stoye
Proceedings of WABI 2014, Springer Verlag, LNBI 8701, 174-186, 2014.

ReadXplorer - Visualization and Analysis of Mapped Sequences

R. Hilker, K. B. Stadermann, D. Doppmeier, J. Kalinowski, J. Stoye, J. Straube, J. Winnebald, A. Goesmann
Bioinformatics 30(16): 2247-2254, 2014.

Mycoplasma salivarium as a dominant coloniser of Fanconi anaemia associated oral carcinoma

B. Henrich, M. Rummig, A. Sczyrba, E. Velleuer, R. Dietrich, W. Gerlach, M. Gombert, S. Rahn, J. Stoye, A. Borkhardt, U. Fischer
PLOS ONE 9(3): e92297, 2014.

BiPACE 2D - Graph-based multiple alignment for comprehensive two-dimensional gas chromatography-mass spectrometry

N. Hoffmann, M. Wilhelm, A. Doebbe, K. Niehaus, J. Stoye
Bioinformatics 30(7): 988-995, 2014.

2013

Restricted DCJ-Indel Model Revisited

M. D. V. Braga, J. Stoye
Proceedings of BSB 2013, Springer Verlag, LNBI 8213, 36-46, 2013.

Statistics for approximate gene clusters

K. Jahn, S. Winter, J. Stoye, S. Böcker
BMC Bioinformatics 14(Suppl. 15): S14, 2013. (Proceedings of RECOMB-CG 2013)

On the Inversion-Indel Distance

E. Willing, S. Zaccaria, M. D. V. Braga, J. Stoye

BMC Bioinformatics 14(Suppl. 15): S3, 2013. (Proceedings of RECOMB-CG 2013)

The Potential of Family-Free Genome Comparison

M. D. V. Braga, C. Chauve, D. Doerr, K. Jahn, J. Stoye, A. Thévenin, R. Wittler

In: C. Chauve, N. El-Mabrouk, E. Tannier (eds.): Models and Algorithms for Genome Evolution, Springer Verlag, Computational Biology Series, Vol. 19, 287-307, 2013.

The Genesis of the DCJ Formula

A. Bergeron, J. Stoye

In: C. Chauve, N. El-Mabrouk, E. Tannier (eds.): Models and Algorithms for Genome Evolution, Springer Verlag, Computational Biology Series, Vol. 19, 63-81, 2013.

Next-generation-sequencing-spectratyping reveals public T-cell receptor repertoires in pediatric very severe aplastic anemia and identifies a beta chain CDR3 sequence associated with hepatitis-induced pathogenesis

P. F. I. Krell, S. Reuther, U. Fischer, T. Keller, S. Weber, M. Gombert, F. R. Schuster, C. Asang, P. Stepensky, B. Strahm, R. Meisel, J. Stoye, A. Borkhardt

Haematologica 98(9): 1388-1396, 2013.

Proceedings of the 13th International Workshop on Algorithms in Bioinformatics, WABI 2013

A. Darling, J. Stoye (eds.)

Lecture Notes in Bioinformatics 8126, Springer Verlag, Heidelberg, 2013.

Comparative RNA-sequencing of the acarbose producer *Actinoplanes* sp. SE50/110 cultivated in different growth media

P. Schwientek, S. Wendler, A. Neshat, C. Eirich, C. Rückert, A. Klein, U. F. Wehmeier, J. Kalinowski, J. Stoye, A. Pühler

J. Biotechnol. 167(2): 166-177, 2013.

MetaSAMS - A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets

M. Zakrzewski, T. Bekel, C. Ander, A. Pühler, O. Rupp, J. Stoye, A. Schlüter, A. Goesmann

J. Biotechnol. 167(2): 156-165, 2013.

Taxonomic classification of metagenomic shotgun sequences with CARMA3

W. Gerlach, J. Stoye

In: K. E. Nelson (ed.): Encyclopedia of Metagenomics. Springer Verlag, 2013.

metaBEETL: high-throughput analysis of heterogeneous microbial populations from shotgun DNA sequences

C. Ander, O. B. Schulz-Trieglaff, J. Stoye, A. J. Cox

BMC Bioinformatics 14(Suppl. 5): S2, 2013. (Proceedings of RECOMB-Seq 2013)

Updating benchtop sequencing performance comparison

S. Jünemann, F. J. Sedlazeck, K. Prior, A. Albersmeier, U. John, J. Kalinowski, A. Mellmann, A. Goesmann, A. v. Haeseler, J. Stoye, D. Harmsen

Nat. Biotechnol. 31(4): 294-296, 2013. (Corrigendum: Nat. Biotechnology 31(12): 1148, 2013)

2012

Multiple genome comparison based on overlap regions of pairwise local alignments

K. Jahn, H. Sudek, J. Stoye

BMC Bioinformatics 13(Suppl. 19): S7, 2012. (Proceedings of RECOMB-CG 2012)

Gene Family Assignment-Free Comparative Genomics

D. Doerr, A. Thévenin, J. Stoye

BMC Bioinformatics 13(Suppl. 19): S3, 2012. (Proceedings of RECOMB-CG 2012)

UniMoG - A unifying framework for genomic distance calculation and sorting based on DCJ

R. Hilker, C. Sickinger, C. N. S. Pedersen, J. Stoye
Bioinformatics 28(9): 2509-2511, 2012.

Combining peak- and chromatogram-based retention time alignment algorithms for multiple chromatography-mass spectrometry datasets

N. Hoffmann, M. Keck, H. Neuweger, M. Wilhelm, P. Högy, K. Niehaus, J. Stoye
BMC Bioinformatics 13: 214, 2012.

Bacterial Community Shift in Treated Periodontitis Patients Revealed by Ion Torrent 16S rRNA Gene Amplicon Sequencing

S. Jünemann, K. Prior, R. Szczepanowski, I. Harks, B. Ehmke, A. Goesmann, J. Stoye, D. Harmsen
PLOS ONE 7(8): e41606, 2012.

Proceedings of the 23rd Annual Symposium on Combinatorial Pattern Matching, CPM 2012

J. Kärkkäinen, J. Stoye (eds.)
Lecture Notes in Computer Science 7354, Springer Verlag, Heidelberg, 2012.

The complete genome sequence of the acarbose producer *Actinoplanes* sp. SE50/110

P. Schwientek, R. Szczepanowski, C. Rückert, J. Kalinowski, A. Klein, K. Selber, U. F. Wehmeier, J. Stoye, A. Pühler
BMC Genomics 13: 112, 2012.

Generic Software Frameworks for GC-MS Based Metabolomics

N. Hoffmann, J. Stoye
In: U. Roessner (ed.): Metabolomics. Chapter 4, pp. 73-98. InTech, 2012.

2011

On the weight of indels in genomic distances

M. D. V. Braga, R. Machado, L. C. Ribeiro, J. Stoye
BMC Bioinformatics 12(Suppl. 9): S13, 2011. (Proceedings of RECOMB-CG 2011)

Genomic distance under gene substitutions

M. D. V. Braga, R. Machado, L. C. Ribeiro, J. Stoye
BMC Bioinformatics 12(Suppl. 9): S8, 2011. (Proceedings of RECOMB-CG 2011)

Restricted DCJ Model: Rearrangement Problems with Chromosome Reincorporation

J. Kováč, R. Warren, M. D. V. Braga, J. Stoye
J. Comp. Biol. 18(9), 1231-1241, 2011.

Double Cut and Join with Insertions and Deletions

M. D. V. Braga, E. Willing, J. Stoye
J. Comp. Biol. 18(9), 1167-1184, 2011.

Consistency of Sequence-Based Gene Clusters

R. Wittler, J. Maňuch, M. Patterson, J. Stoye
J. Comp. Biol. 18(9), 1023-1039, 2011.

Sequencing of high G + C microbial genomes using the ultrafast pyrosequencing technology

P. Schwientek, R. Szczepanowski, C. Rückert, J. Stoye, A. Pühler
J. Biotechnol. 155(1), 68-77, 2011.

Taxonomic classification of metagenomic shotgun sequences with CARMA3

W. Gerlach, J. Stoye
Nucleic Acids Res. 39(14), e91, 2011.

Common Intervals of Multiple Permutations

S. Heber, R. Mayr, J. Stoye
Algorithmica 60(2), 175-206, 2011.

Exact and complete short read alignment to microbial genomes using GPU programming

J. Blom, T. Jakobi, D. Doppmeier, S. Jaenicke, J. Kalinowski, J. Stoye, A. Goesmann
Bioinformatics 27(10), 1351-1358, 2011.

Swiftly Computing Center Strings

F. Hufsky, L. Kuchenbecker, K. Jahn, J. Stoye, S. Böcker
BMC Bioinformatics 12:106, 2011.

Balanced Vertices in Trees and a Simpler Algorithm to Compute the Genomic Distance

P. L. Erdős, L. Soukup, J. Stoye
Appl. Math. Lett. 24(1), 82-86, 2011.

2010

The complete genome sequence of *Corynebacterium pseudotuberculosis* FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence

E. Trost, L. Ott, J. Schneider, J. Schröder, S. Jaenicke, A. Goesmann, P. Husemann, J. Stoye, F. Alves Dorella, F. Souza Rocha, S. de Castro Soares, V. D'Afonseca, A. Miyoshi, J. Ruiz, A. Silva, V. Azevedo, A. Burkovski, N. Guiso, O. F. Join-Lambert, S. Kayal, A. Tauch
BMC Genomics 11:728, 2010.

Consistency of Sequence-based Gene Clusters

R. Wittler, J. Stoye
Proceedings of RECOMB-CG 2010, Springer Verlag, LNBI 6398, 252-263, 2010.

The Problem of Chromosome Reincorporation in DCJ Sorting and Halving

J. Kováč, M. D. V. Braga, J. Stoye
Proceedings of RECOMB-CG 2010, Springer Verlag, LNBI 6398, 13-24, 2010.

Rearrangement Models and Single-Cut Operations

A. Bergeron, P. Medvedev, J. Stoye
J. Comp. Biol. 17(9), 1213-1225, 2010.

Finding Nested Common Intervals Efficiently

G. Blin, D. Faye, J. Stoye
J. Comp. Biol. 17(9), 1183-1194, 2010.

The Solution Space of Sorting by DCJ

M. D. V. Braga, J. Stoye
J. Comp. Biol. 17(9), 1145-1165, 2010.

Repeat-aware Comparative Genome Assembly

P. Husemann, J. Stoye
Proceedings of GCB 2010, LNI P-173, 61-70, 2010.

Swiftly Computing Center Strings

F. Hufsky, L. Kuchenbecker, K. Jahn, J. Stoye, S. Böcker
Proceedings of WABI 2010, Springer Verlag, LNBI 6293, 325-336, 2010.

Genomic Distance with DCJ and Indels

M. D. V. Braga, E. Willing, J. Stoye
Proceedings of WABI 2010, Springer Verlag, LNBI 6293, 90-101, 2010.

Partitioning Biological Data with Transitivity Clustering

T. Wittkop, D. Emig, S. J. Lange, S. Rahmann, M. Albrecht, J. H. Morris, S. Böcker, J. Stoye, J. Baumbach
Nature Methods 7(6), 419-420, 2010.

r2cat: Synteny Plots and Comparative Assembly

P. Husemann, J. Stoye

Bioinformatics 26(4), 570-571, 2010.

Indexing and Searching a Mass Spectrometry Database

S. Besenbacher, B. Schwikowski, J. Stoye

In: T. Elomaa, H. Mannila, P. Orponen (eds.): Algorithms and Applications: Essays Dedicated to Esko Ukkonen on the Occasion of His 60th Birthday, Springer Verlag, LNCS 6060, 62-76, 2010.

Phylogenetic Comparative Assembly

P. Husemann, J. Stoye

Algorithms Mol. Biol. 5:3, 2010.

2009

WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads

W. Gerlach, S. Jünemann, F. Tille, A. Goesmann, J. Stoye

BMC Bioinformatics 10:430, 2009.

A New Linear Time Algorithm to Compute the Genomic Distance Via the Double Cut and Join Distance

A. Bergeron, J. Mixtacki, J. Stoye

Theor. Comput. Sci. 410(51), 5300-5316, 2009.

A Report on the 2009 SIG on Short Read Sequencing and Algorithms (Short-SIG) (invited report)

M. Brudno, P. Medvedev, J. Stoye, F. De La Vega

Bioinformatics, 25(21), 2863-2864, 2009.

Rearrangement Models and Single-Cut Operations

P. Medvedev, J. Stoye

Proceedings of RECOMB-CG 2009, Springer Verlag, LNBI 5817, 84-97, 2009.

Finding Nested Common Intervals Efficiently

G. Blin, J. Stoye

Proceedings of RECOMB-CG 2009, Springer Verlag, LNBI 5817, 59-69, 2009.

Counting All DCJ Sorting Scenarios

M. D. V. Braga, J. Stoye

Proceedings of RECOMB-CG 2009, Springer Verlag, LNBI 5817, 36-47, 2009.

A Unified Approach for Reconstructing Ancient Gene Clusters

J. Stoye, R. Wittler

IEEE/ACM Trans. Comput. Biol. Bioinf. 6(3), 387-400, 2009.

Phylogenetic Comparative Assembly

P. Husemann, J. Stoye

Proceedings of WABI 2009, Springer Verlag, LNBI 5724, 145-156, 2009.

Computation of Median Gene Clusters

S. Böcker, K. Jahn, J. Mixtacki, J. Stoye

J. Comp. Biol. 16(8), 1085-1099, 2009.

ChromA: Signal Based Retention Time Alignment for Chromatography-Mass Spectrometry Data

N. Hoffmann, J. Stoye

Bioinformatics 25(16), 2080-2081, 2009.

Computational Short Read Metagenomics (invited abstract)

J. Stoye

Proceedings of JOBIM 2009, 3-4, 2009.

Approximative Gencluster und ihre Anwendung in der komparativen Genomik (in German)

K. Jahn, J. Stoye

Informatik-Spektrum 32(4), 288-300, 2009.

The Sequence Analysis and Management System - SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies

T. Bekel, K. Henckel, H. Küster, V. Mittard Runte, H. Neuweger, D. Paarmann, O. Rupp, M. Zakrzewski, A. Pühler, J. Stoye, A. Goesmann

J. Biotechnol. 140(1-2), 3-12, 2009.

2008

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