

Steffen Heber

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Education

GERMAN CANCER RESEARCH CENTER (DKFZ), GERMANY
UNIVERSITY OF HEIDELBERG, GERMANY

2001 Ph.D. in Mathematics.

Thesis title: *Algorithms for Physical Mapping*.

Thesis advisers: Professor M. Vingron, Dr. J. Hoheisel.

UNIVERSITY OF HEIDELBERG, GERMANY

1998 Staatsexamen in Mathematics and Biology.

UNIVERSITY OF HEIDELBERG, GERMANY

1995 Diploma in Mathematics (graduated with honors).

Thesis title: *Additive Periodizität bei Nim-Spielen*.

Thesis adviser: Professor A. Brandis.

Research Interests

Algorithmic and statistical problems in bioinformatics, especially in the fields of gene order comparison, protein interaction, physical mapping, EST assembly, and alternative splicing.

Professional Experience

UNIVERSITY OF CALIFORNIA, SAN DIEGO, USA
BIOINFORMATICS LABORATORY, CSE

2001–present Postdoctoral Research Associate with Professor P. Pevzner.

HEIDELBERG LIFE SCIENCE LAB, GERMANY

2000–2001 Bioinformatics lecturer.

GERMAN CANCER RESEARCH CENTER (DKFZ), GERMANY

1997–2001 Research fellow.

UNIVERSITY OF HEIDELBERG, GERMANY

1994–1996 Research assistant.

ROBERT BOSCH GMBH, GERMANY

1992 (summer), 1993 (summer) Research assistant.

- Teaching Experience**
- AKADEMIE FÜR WEITERBILDUNG, GERMANY
2001 (spring) Bioinformatics lecturer.
- HEIDELBERG LIFE SCIENCE LAB, GERMANY
2000–2001 Bioinformatics lecturer.
- UNIVERSITY OF HEIDELBERG, GERMANY
1994–1996 Teaching assistant.
- Awards**
- 2000 Best poster at the DKFZ poster presentation.
- 1995 Diploma passed with distinction.
- 1987 School-leaving exam passed with distinction.
- 1986 First place in the Baden-Württemberg mathematics contest.
- 1984–1987 Member of the Robert Bosch foundation.
- Professional Activities**
- Refereeing for RECOMB 2001, RECOMB 2002, ISMB 2001, GCB 2000, Bioinformatics, and Journal of Computational Biology.
- iSCB member.
- Publications**
1. S. Heber, J. Stoye. “The European Conference on Computational Biology (ECCB 2002),” *BioSilico*, to appear.
 2. A. Bergeron, S. Heber, J. Stoye, 2002. “Common Intervals and Sorting by Reversals: A Marriage of Necessity,” *European Conference on Computational Biology 2002 (ECCB 2002)*, *Bioinformatics*, Suppl. 2, 54–61.
 3. S. Heber, M. Alekseyev, S.-H. Sze, H. Tang, P. Pevzner, 2002. “Splicing Graphs and EST Assembly Problem,” *The 10th International Conference on Intelligent Systems for Molecular Biology (ISMB 2002)*, *Bioinformatics*, Suppl. 1, 181–188.
 4. S. Heber, J. Stoye, M. Frohme, J. Hoheisel, M. Vingron, 2002. “Resampling Methods in Physical Mapping,” In: W. Gaul, G. Ritter (Eds.): *Classification, Automation, and New Media: Proc. 24th Annual Conference of the GfKl, 2000*. Volume 20 of *Studies in Classification, Data Analysis, and Knowledge Organization*, 437–444.
 5. S. Heber, J. Stoye, 2001. “Algorithms for finding gene clusters,” In: O. Gascuel, B. Moret (Eds.): *Algorithms in Bioinformatics, Lecture Notes in Computer Science 2149*, 254–265.
 6. S. Heber, J. Stoye, 2001. “Finding all Common Intervals of k Permutations,” In: A. Amir, G. Landau (Eds.): *Combinatorial Pattern Matching, Lecture Notes in Computer Science 2089*, 207–218.

7. S. Heber, 2001. "Algorithms for Physical Mapping," Ph.D. thesis, Rupprecht-Karls-Universität Heidelberg, IWR/SFB-Preprints.
8. R. Wambutt, G. Murphy, G. Volckaert, et al., 2000. "Progress in *Arabidopsis* genome sequencing and functional genomics," J. Biotechnology, 281–292.
9. S. Heber, J. Hoheisel, M. Vingron, 2000. "Applications of Bootstrap Techniques to Physical Mapping," GENOMICS, 69(2), 235–241.
10. M. Frohme, A. Camargo, S. Heber, C. Czink, A. Simpson, J. Hoheisel, A. de Souza, 2000. "Mapping analysis of the *Xylella fastidiosa* genome," Nucleic Acids Res., 28(16), 3100–3104.
11. S. Heber, J. Stoye, M. Frohme, J. Hoheisel, M. Vingron, 2000. "Contig Selection in Physical Mapping," J. Comp. Bio., 7(3/4), 395–408.
12. S. Heber, J. Stoye, J. Hoheisel, M. Vingron, 2000. "Contig Selection in Physical Mapping," Proc. of the Fourth Annual International Conference on Computational Molecular Biology (RECOMB 2000), 155–164.
13. K. Mayer, C. Schuller, R. Wambutt, et al., 1999. "Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*," Nature 402, 769–777.
14. P. Scholler, S. Heber, J. Hoheisel, 1998. "Optimization and automation of fluorescence-based DNA hybridization for high-throughput clone mapping," Electrophoresis 19, 504–508.

Patent

1. "Splicing graph assembler," U.S. provisional patent application: (PR2179) 51293/276515.

Selected Presentations

1. "Common Intervals and Sorting by Reversals: A Marriage of Necessity," talk, ECCB 2002, Saarbrücken, Germany 2002.
2. "Splicing graphs and EST assembly problem," talk, ISMB 2002, Edmonton, Canada, 2002.
3. "Splicing graphs and EST assemblies," talk, RECOMB Satellite Meeting on DNA Sequencing and Characterization, Stanford University, 2002.
4. "Finding all Common Intervals of k Permutations," talk, CPM 2001, Jerusalem, Israel, 2001.
5. "Contig Selection in Physical Mapping," talk, RECOMB 2000, Tokyo, Japan, 2000.
6. "Bootstrap Methods in Physical Mapping," talk, 24th Annual Conference of the GfKI, Passau, Germany, 2000.
7. "Reliability in Physical Mapping," talk, Exploratory Workshop "Functional Genomics", Paris, France, 1999.