



LUDWIG-
MAXIMILIANS-
UNIVERSITÄT
MÜNCHEN

FAKULTÄT FÜR MATHEMATIK, INFORMATIK UND STATISTIK
INSTITUT FÜR INFORMATIK



Skriptum zur Vorlesung Algorithmen auf Sequenzen

gehalten im Wintersemester 2024/25

am Lehrstuhl für Bioinformatik

Volker Heun



3. August 2024

Version 10.00

Vorwort

Dieses Skript entstand parallel zur Vorlesung *Algorithmen auf Sequenzen* im Wintersemester 24/25 und baut auf dem vorherigen Skripten der Vorlesungen des Wintersemesters 03/04, des Wintersemesters 04/05, des Wintersemesters 06/07, des Wintersemesters 07/08, des Wintersemesters 09/10, des Sommersemesters 13, des Wintersemesters 15/16, des Wintersemesters 17/18, des Wintersemesters 18/19, des Wintersemesters 20/21 und des Wintersemesters 23/24 auf. Diese Vorlesung wurde an der Ludwig-Maximilians-Universität speziell für Studierende der Bioinformatik, aber auch für Studierende der Informatik, im Rahmen des gemeinsam von der Ludwig-Maximilians-Universität München und der Technischen Universität München veranstalteten Studiengangs Bioinformatik gehalten.

Das vorliegende Skript gibt den Inhalt aller Vorlesungen wieder, die sich jedoch inhaltlich ein wenig unterscheiden. Die Teile, die im Wintersemester 2024/25 nur teilweise behandelt wurden, sind mit einem + markiert und die Teile, die nicht Teil der Vorlesung waren, sind mit einem * markiert.

Diese Fassung ist weitestgehend überarbeitet worden, allerdings kann das Skript immer noch einige (Tipp)Fehler enthalten. Daher bin ich für jeden Hinweis darauf (an Volker.Heun@bio.ifi.lmu.de) dankbar.

An dieser Stelle möchte ich Sabine Spreer, die an der Erstellung des ersten Kapitels in $\text{\LaTeX} 2_{\epsilon}$ maßgeblich beteiligt war, sowie Alois Huber und Hermann Klann, die an der Erstellung des zweiten mit sechsten Kapitels in $\text{\LaTeX} 2_{\epsilon}$ maßgeblich beteiligt waren, danken. Außerdem bin ich folgenden Personen für Hinweise auf Tippfehler und Verbesserungsmöglichkeiten dankbar: Herrn Martin Bickeböller, Herrn Samuel Klein, Herrn Nick Lehner, Herrn Sebastian Stempel, Herrn Vladimir Viro, Herrn Stefan Weber und Herrn Jeremias Weihmann.

Weiterhin möchte ich insbesondere meinen Mitarbeitern Johannes Fischer, Simon W. Ginzinger, Benjamin Albrecht sowie Caroline Friedel und Marie-Sophie Friedl für Ihre Unterstützung bei den Veranstaltungen danken, die somit das vorliegende Skript erst möglich gemacht haben.

München, im Wintersemester 2024/25

Volker Heun

Inhaltsverzeichnis

A	Literaturhinweise	1
A.1	Lehrbücher zur Vorlesung	1
A.2	Skripten anderer Universitäten	1
A.3	Originalarbeiten	2
A.3.1	Optimal Scoring Subsequences	2
A.3.2	Suffix-Trees	3
A.3.3	Repeats	3
A.3.4	Lowest Common Ancestors and Range Minimum Queries . . .	4
A.3.5	Construction of Suffix-Arrays	5
A.3.6	Applications of Suffix-Arrays	6
A.3.7	Sorting by Reversals	7
A.3.8	Sorting by Oriented Reversals	8
A.3.9	Sorting by Transpositions	9
A.3.10	Sorting by Transversals	9
A.3.11	Erweiterungen zu Genome Rearrangements	10

Literaturhinweise

A

A.1 Lehrbücher zur Vorlesung

- D. Adjeroh, T. Bell, A. Mukherjee: *The Burrows-Wheeler Transform*, Springer, 2008
- S. Aluru (Ed.): *Handbook of Computational Molecular Biology*; Chapman and Hall/CRC, 2006.
- H.-J. Böckenhauer, D. Bongartz: *Algorithmische Grundlagen der Bioinformatik: Modelle, Methoden und Komplexität*; Teubner, 2003.
- G. Fertin, A. Labarre, I. Rusu, E. Tannier, S. Vialette: *Combinatorics of Genome Rearrangements*; MIT Press, 2009.
- D. Gusfield: *Algorithms on Strings, Trees, and Sequences — Computer Science and Computational Biology*; Cambridge University Press, 1997.
- M. Lothaire: *Applied Combinatorics on Words*, Encyclopedia of Mathematics and Its Applications, Cambridge University Press, 2005.
- V. Mäkinen, D. Belazzougui, F. Cunial, A.I. Tomescu: *Genome-Scale Algorithm Design: Biological Sequence Analysis in the Era of High-Throughput Sequencing*, Cambridge University Press, 2015.
- E. Ohlebusch: *Bioinformatics Algorithms: Sequence Analysis, Genome Rearrangements, and Phylogenetic Reconstruction*, Oldenbusch Verlag, 2013.
- P.A. Pevzner: *Computational Molecular Biology — An Algorithmic Approach*; MIT Press, 2000.
- J.C. Setubal, J. Meidanis: *Introduction to Computational Molecular Biology*; PWS Publishing Company, 1997.

A.2 Skripten anderer Universitäten

- J. Fischer: *Text-Indexierung und Information Retrieval*, Technische Universität Dortmund, 2015.
ls11-www.cs.tu-dortmund.de/_media/fischer/teaching/tir-ws2014/script-tir-ws14.pdf

S. Kurtz: *Lecture Notes for Foundations of Sequence Analysis*, Universität Bielefeld, 2001.
citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.23.7142&rep=rep1&type=pdf

A.3 Originalarbeiten

A.3.1 Optimal Scoring Subsequences

K.-M. Chung, H.-I. Lu: An Optimal Algorithm for the Maximum-Density Segment Problem, *SIAM Journal on Computing*, Vol. 34, No. 2, 373–387, 2004.
DOI: [10.1137/S0097539704440430](https://doi.org/10.1137/S0097539704440430)

M. Csürös: Maximum-Scoring Segment Sets, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Vol. 1, No. 4, 139–150, 2004.
DOI: [10.1109/TCBB.2004.43](https://doi.org/10.1109/TCBB.2004.43)

P. Fariselli, M. Finelli, D. Marchignoli, P.L. Martelli, I. Rossi, R. Casadio: MaxSubSeq: An Algorithm for Segment-Length Optimization. The Case Study of the Transmembrane Spanning Segments, *Bioinformatics*, Vol. 19, 500–505, 2003.
DOI: [10.1093/bioinformatics/btg023](https://doi.org/10.1093/bioinformatics/btg023)

M.H. Goldwasser, M.-Y. Kao, H.-I. Lu: Linear-Time Algorithms for Computing Maximum-Density Sequence Segments with Bioinformatics Applications, *Journal of Computer and System Sciences*, Vol.70, No. 2, 128–144, 2005.
DOI: [10.1016/j.jcss.2004.08.001](https://doi.org/10.1016/j.jcss.2004.08.001)

S.K. Kim: Linear-Time Algorithm for Finding a Maximum-Density Segment of a Sequence, *Information Processing Letter*, Vol. 86, 339–342, 2003.
DOI: [10.1016/S0020-0190\(03\)00225-4](https://doi.org/10.1016/S0020-0190(03)00225-4)

Y.-L. Lin, T. Jiang, K.-M. Chao: Efficient Algorithms for Locating the Length-Constrained Heaviest Segments with Applications to Biomolecular Sequence Analysis, *Journal of Computer and System Sciences*, Vol. 65, 570–586, 2002.
DOI: [10.1016/S0022-0000\(02\)00010-7](https://doi.org/10.1016/S0022-0000(02)00010-7)

W.L. Ruzzo, M. Tompa: A Linear Time Algorithm for Finding All Maximal Scoring Subsequences, *Proceedings of the 7th International Conference on Intelligent Systems for Molecular Biology (ISMB'99)*, 234–241, 1999.

A.3.2 Suffix-Trees

- R. Giegerich, S. Kurtz, J. Stoye: Efficient Implementation of Lazy Suffix Trees, *Software — Practice and Experience*, Vol. 33, 1035–1049, 2003.
DOI: [10.1002/spe.535](https://doi.org/10.1002/spe.535)
- M. Maaß: *Suffix Trees and Their Applications*, Ausarbeitung von der Ferienakademie, Kurs 2, Bäume: Algorithmik und Kombinatorik, 1999.
www14.in.tum.de/konferenzen/Ferienakademie99/
- E.M. McCreight: A Space-Economical Suffix Tree Construction Algorithm; *Journal of the ACM*, Vol. 23, 262–272, 1976.
DOI: [10.1145/321941.321946](https://doi.org/10.1145/321941.321946)
- E. Ukkonen: On-Line Construction of Suffix Trees, *Algorithmica*, Vol. 14, 149–260, 1995.
DOI: [10.1007/BF01206331](https://doi.org/10.1007/BF01206331)

A.3.3 Repeats

- A.S. Fraenkel, J. Simpson: How Many Squares Can a String Contain?, *Journal of Combinatorial Theory, Series A*, Vol. 82, 112–120, 1998.
DOI: [10.1006/jcta.1997.2843](https://doi.org/10.1006/jcta.1997.2843)
- D. Gusfield, J. Stoye: Linear Time Algorithm for Finding and Representing All the Tandem Repeats in a String, *Journal of Computer and System Sciences*, Vol. 69, 525–546, 2004; see also *Technical Report CSE-98-4*, Computer Science Department, UC Davis, 1998.
DOI: [10.1016/j.jcss.2004.03.004](https://doi.org/10.1016/j.jcss.2004.03.004)
- R. Kolpakov, G. Kucherov: Finding Maximal Repetitions in a Word in Linear Time, *Proceedings of the 40th Annual IEEE Symposium on Foundations of Computer Science (FOCS'99)*, 596–604, 1999.
DOI: [10.1109/SFFCS.1999.814634](https://doi.org/10.1109/SFFCS.1999.814634)
- R. Kolpakov, G. Kucherov: On Maximal Repetitions in Words, *Proceedings of the 12th International Symposium on Fundamentals of Computation Theory (FCT'99)*, Lecture Notes in Computer Science, Vol. 1684, 374–385, 1999.
DOI: [10.1007/3-540-48321-7_31](https://doi.org/10.1007/3-540-48321-7_31)
- R. Kolpakov, G. Kucherov: Finding Approximate Repetitions Under Hamming Distance, *Theoretical Computer Science*, Vol. 303, 135–156, 2003.
DOI: [10.1016/S0304-3975\(02\)00448-6](https://doi.org/10.1016/S0304-3975(02)00448-6)

- G.M. Landau, J.P. Schmidt: An Algorithm for Approximate Tandem Repeats, *Proceedings of the 4th Symposium on Combinatorial Pattern Matching (CPM'93)*, Lecture Notes in Computer Science, Vol. 684, 120–133, 1993.
DOI: [10.1007/BFb0029801](https://doi.org/10.1007/BFb0029801)
- G.M. Landau, J.P. Schmidt, D. Sokol: An Algorithm for Approximate Tandem Repeats, *Journal of Computational Biology*, Vol. 8, No. 1, 1–18, 2001.
DOI: [10.1089/106652701300099038](https://doi.org/10.1089/106652701300099038)
- M.G. Main, R.J. Lorentz: An $O(n \log n)$ Algorithm for Finding All Repetitions in a String, *Journal of Algorithms*, Vol. 5, No. 3, 422–432, 1984.
DOI: [10.1016/0196-6774\(84\)90021-X](https://doi.org/10.1016/0196-6774(84)90021-X)
- J. Stoye, D. Gusfield: Simple and Flexible Detection of Contiguous Repeats Using a Suffix Tree, *Theoretical Computer Science*, Vol. 270, 843–856, January 2002.
DOI: [10.1016/S0304-3975\(01\)00121-9](https://doi.org/10.1016/S0304-3975(01)00121-9)

A.3.4 Lowest Common Ancestors and Range Minimum Queries

- S. Alstrup, C. Gavoille, H. Kaplan, T. Rauhe: Nearest Common Ancestors: A Survey and a New Distributed Algorithm, *Theory of Computing Systems*, Vol. 37, No. 3, 441–456, 2004.
DOI: [10.1007/s00224-004-1155-5](https://doi.org/10.1007/s00224-004-1155-5)
- M.A. Bender, M. Farach-Colton: The LCA Problem Revisited, *Proceedings of the 4th Latin American Symposium on Theoretical Informatics (LATIN'00)*, Lecture Notes in Computer Science, Vol. 1776, 88–94, 2000.
DOI: [10.1007/10719839_9](https://doi.org/10.1007/10719839_9)
- O. Berkman, U. Vishkin: Recursive Star-Tree Parallel Data Structure, *SIAM Journal on Computing*, Vol. 22, 221–242, 1993.
DOI: [10.1137/0222017](https://doi.org/10.1137/0222017)
- J. Fischer, V. Heun. Space-Efficient Preprocessing Schemes for Range Minimum Queries on Static Arrays, *SIAM Journal on Computing*, Vol. 40, No. 2, 465–492, 2011.
DOI: [10.1137/090779759](https://doi.org/10.1137/090779759)
- B. Schieber, U. Vishkin: On Finding Lowest Common Ancestors: Simplification and Parallelization, *SIAM Journal on Computing*, Vol. 17, 1253–1262, 1988.
DOI: [10.1137/0217079](https://doi.org/10.1137/0217079)

A.3.5 Construction of Suffix-Arrays

- S. Burkhardt, J. Kärkkäinen: Fast Lightweight Suffix Array Construction and Checking, *Proceedings of the 14th Symposium on Combinatorial Pattern Matching (CPM'03)*, Lecture Notes in Computer Science, Vol. 2676, 55–69, 2003.
DOI: [10.1007/3-540-44888-8_5](https://doi.org/10.1007/3-540-44888-8_5)
- S. Gog, T. Beller, A. Moffat, M. Petri: From Theory to Practice: Plug and Play with Succinct Data Structures, *Proceedings of the 13th International Symposium on Experimental Algorithms (SEA 2014)*, Lecture Notes in Computer Science, Vol. 8504, 326–337, 2014.
DOI: [10.1007/978-3-319-07959-2_28](https://doi.org/10.1007/978-3-319-07959-2_28)
SDSL Homepage: algo2.iti.kit.edu/gog/docs/html/index.html
- D.K. Kim, J.S. Sim, H. Park, K. Park: Linear-Time Construction of Suffix Arrays, *Proceedings of the 14th Symposium on Combinatorial Pattern Matching (CPM'03)*, Lecture Notes in Computer Science, Vol. 2676, 186–199, 2003.
DOI: [10.1007/3-540-44888-8_14](https://doi.org/10.1007/3-540-44888-8_14)
- P. Ko, A. Aluru: Space Efficient Linear Time Construction of Suffix Arrays, *Proceedings of the 14th Symposium on Combinatorial Pattern Matching (CPM'03)*, Lecture Notes in Computer Science, Vol. 2676, 200–210, 2003.
DOI: [10.1007/3-540-44888-8_15](https://doi.org/10.1007/3-540-44888-8_15)
- J. Kärkkäinen, P. Sanders: Simple Linear Work Suffix Array Construction, *Proceedings of the 30th International Colloquium on Automata, Languages and Programming (ICALP'03)*, Lecture Notes in Computer Science, Vol. 2719, 943–955, 2003.
DOI: [10.1007/3-540-45061-0_73](https://doi.org/10.1007/3-540-45061-0_73)
- G. Nong, S. Zhang, W.H. Chan: Two Efficient Algorithms for Linear Time Suffix Array Construction, *IEEE Transaction on Computers*, Vol 60, No. 10, 1471–1484, 2011.
DOI: [10.1109/TC.2010.188](https://doi.org/10.1109/TC.2010.188)
- U. Manber, G. Myers: Suffix Arrays: A New Method for On-Line String Searches, *SIAM Journal on Computing*, Vol. 22, 935–948, 1993.
DOI: [10.1137/0222058](https://doi.org/10.1137/0222058)
- Y. Mori: Implementation of SAIS in Different Programming Languages (C/C++, C#, Java). Web: sites.google.com/site/yuta256/sais vom 15.12.2017, zuletzt zugegriffen am 08.01.2018 (momentan nicht verfügbar).

A.3.6 Applications of Suffix-Arrays

- M.I. Abouelhoda, S. Kurtz, E. Ohlebusch: The Enhanced Suffix Array and Its Applications to Genome Analysis, *Proceedings of the 2nd Workshop on Algorithms in Bioinformatics (WABI'02)*, Lecture Notes in Computer Science, Vol. 2452, 449–463, 2002.
DOI: [10.1007/3-540-45784-4_35](https://doi.org/10.1007/3-540-45784-4_35)
- M.I. Abouelhoda, E. Ohlebusch, S. Kurtz: Optimal Exact String Matching Based on Suffix Arrays, *Proceedings of the 9th International Symposium on String Processing and Information Retrieval (SPIRE'02)*, Lecture Notes in Computer Science, Vol. 2476, 31–43, 2002.
DOI: [10.1007/3-540-45735-6_4](https://doi.org/10.1007/3-540-45735-6_4)
- M.I. Abouelhoda, S. Kurtz, E. Ohlebusch: Replacing Suffix Trees with Enhanced Suffix Arrays, *Journal of Discrete Algorithms*, Vol. 2, 53–86, 2004.
DOI: [10.1016/S1570-8667\(03\)00065-0](https://doi.org/10.1016/S1570-8667(03)00065-0)
- M. Burrows, D.J. Wheeler: A Block-Sorting Lossless data Compression Algorithm; *Research Report*, Digital Research Center, SRC-Report 124, 1994.
<https://www.hpl.hp.com/techreports/Compaq-DEC/SRC-RR-124.html>
- P. Ferragina, G. Manzini: Indexing Compressed Text; *Journal of the ACM*, Vol. 52, Issue 4, 552–581, 2005
DOI: [10.1145/1082036.1082039](https://doi.org/10.1145/1082036.1082039)
- J. Fischer: Combined Data Structure for Previous- and Next-Smaller-Values; *Theoretical Computer Science*, Vol. 412, Issue 22, 2451–2456, 2011.
DOI: [10.1016/j.tcs.2011.01.036](https://doi.org/10.1016/j.tcs.2011.01.036)
- J. Fischer, V. Heun: A New Succinct Representation of RMQ-Information and Improvements in the Enhanced Suffix Array, *Proceedings of the International Symposium on Combinatorics, Algorithms, Probabilistic and Experimental Methodologies (ESCAPE'07)*, Lecture Notes in Computer Science, Vol. 4614, 459–470, Springer, 2007.
DOI: [10.1007/978-3-540-74450-4_41](https://doi.org/10.1007/978-3-540-74450-4_41)
- T. Kasai, G. Lee, H. Arimura, S. Arikawa, K. Park: Linear-Time Longest-Common-Prefix Computation in Suffix Arrays and Its Applications, *Proceedings of the 12th Symposium on Combinatorial Pattern Matching (CPM'01)*, Lecture Notes in Computer Science, Vol. 2089, 181–192, 2001.
DOI: [10.1007/3-540-48194-X_17](https://doi.org/10.1007/3-540-48194-X_17)

- G. Manzini: Two Space Saving Tricks for Linear Time LCP Array Computation, *Proceedings of the 9th Scandinavian Workshop on Algorithm Theory (SWAT'04)*, Lecture Notes in Computer Science, Vol. 3111, 372–383, 2004.
DOI: [10.1007/b98413](https://doi.org/10.1007/b98413)
- G. Navarro, V. Mäkinen: Compressed Full-Text Indexes, *ACM Computing Surveys*, Vol. 39, No. 1, 2007.
DOI: [10.1145/1216370.1216372](https://doi.org/10.1145/1216370.1216372)
- K. Sadakane: Succinct Representations of LCP Information and Improvements in the Compressed Suffix Arrays, *Proceedings of the 13th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA'02)*, 225-232, 2002.
- K. Sadakane: Compressed Suffix Trees with Full Functionality, *Theory of Computing Systems*, Vol. 41, No. 4, 589–607, 2007.
DOI: [10.1007/s00224-006-1198-x](https://doi.org/10.1007/s00224-006-1198-x)

A.3.7 Sorting by Reversals

- V. Bafna, P.A. Pevzner: Genome Rearrangements and Sorting by Reversals, *SIAM Journal on Computing*, Vol. 25, 272–289, 1996.
DOI: [10.1137/S0097539793250627](https://doi.org/10.1137/S0097539793250627)
- P. Berman, S. Hannenhalli, M. Karpinski: A 1.375-Approximation Algorithm for Sorting by Reversals, *Proceedings of the 10th Annual European Symposium on Algorithms (ESA'02)*, Lecture Notes in Computer Science, Vol. 2461, 200–210, 2002.
DOI: [10.1007/3-540-45749-6_21](https://doi.org/10.1007/3-540-45749-6_21)
- P. Berman, M. Karpinski: On Some Tighter Inapproximability Results, *Proceedings of the 26th International Colloquium on Automata, Languages and Programming (ICALP'99)*, Lecture Notes in Computer Science, Vol. 1644, 200–209, 1999.
DOI: [10.1007/3-540-48523-6_17](https://doi.org/10.1007/3-540-48523-6_17)
- D. Christie: A 3/2-Approximation Algorithms for Sorting by Reversals, *Proceedings of the 9th ACM Symposium on Discrete Algorithms (SODA'98)*, 244–252, 1998.

A.3.8 Sorting by Oriented Reversals

- D.A. Bader, N.M.E. Moret, M. Yan: A Linear-Time Algorithm for Computing Inversion Distance Between Signed Permutations With an Experimental Study, *Journal of Computational Biology*, Vol. 8, No. 5, 483–491, 2001.
DOI: [10.1089/106652701753216503](https://doi.org/10.1089/106652701753216503)
- A. Bergeron: A Very Elementary Presentation of the Hannenhalli-Pevzner Theory, *Discrete Applied Mathematics*, Vol. 146, No. 2, 134–145, 2005.
DOI: [10.1016/j.dam.2004.04.010](https://doi.org/10.1016/j.dam.2004.04.010)
- A. Bergeron, J. Mixtacki, J. Stoye: Reversal Distance without Hurdles and Fortresses, *Proceedings of the 15th Symposium on Combinatorial Pattern Matching (CPM'04)*, Lecture Notes in Computer Science, Vol. 3109, 388–399, 2004.
DOI: [10.1007/b98377](https://doi.org/10.1007/b98377)
- P. Berman, S. Hannenhalli: Faster Sorting by Reversals, *Proceedings of the 7th Symposium on Combinatorial Pattern Matching (CPM'96)*, Lecture Notes in Computer Science, Vol. 1075, 168–185, 1996.
DOI: [10.1007/3-540-61258-0_14](https://doi.org/10.1007/3-540-61258-0_14)
- S. Hannenhalli, P. Pevzner: Transforming Cabbage into Turnip: Polynomial Algorithm for Sorting Signed Permutations by Reversals, *Journal of the ACM*, Vol. 46, 1–27, 1999; also in *Proceedings of the 27th Annual ACM Symposium on Computing (STOC'95)*, 178–189, 1995.
DOI: [10.1145/300515.300516](https://doi.org/10.1145/300515.300516)
- S. Hannenhalli, P. Pevzner: To Cut ... or Not to Cut (Applications of Comparative Physical Maps in Molecular Evolution), *Proceedings of the 7th ACM Symposium on Discrete Algorithms (SODA'96)*, 304–313, 1996.
- H. Kaplan, R. Shamir, R. Tarjan: Faster and Simpler Algorithm for Sorting Signed Permutations by Reversals, *SIAM Journal on Computing*, Vol. 29, 880–892, 1999; also in *Proceedings of the 8th ACM-SIAM Symposium on Discrete Algorithms (SODA'97)*, 344–351, 1997.
DOI: [10.1137/S0097539798334207](https://doi.org/10.1137/S0097539798334207)
- A.C. Siepel: An Algorithm to Enumerate all Sorting Reversals, *Journal of Computational Biology*, Vol. 10, 575–597, 2003; also in *Proceedings of the 6th Annual International Conference on Computational Biology (RECOMB'02)*, 281–290, 2002.
DOI: [10.1145/565196.565233](https://doi.org/10.1145/565196.565233)

A.3.9 Sorting by Transpositions

- V. Bafna, P.A. Pevzner: Sorting by Transpositions, *SIAM Journal on Discrete Mathematics*, Vol. 11, No. 2, 224–240, 1998.
DOI: [10.1137/S089548019528280X](https://doi.org/10.1137/S089548019528280X)
- L.F.I. Cunha, L.A.B. Kowada, R. de A. Hausen, C.M.H. de Figueiredo: A faster 1.375-approximation algorithm for sorting by transpositions, *Journal on Computational Biology*, Vol. 22, No. 11, 1044–56, 2015.
DOI: [10.1089/cmb.2014.0298](https://doi.org/10.1089/cmb.2014.0298)
- I. Elias, T. Hartman: A 1.375-Approximation Algorithm for Sorting by Transpositions, *Proceedings of the Fifth Workshop on Algorithms in Bioinformatics (WABI'05)*, Lecture Notes in Computer Science, Vol. 3692, 204–215, 2005. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Vol. 3, No. 4, 369–379, 2006.
DOI: [10.1109/TCBB.2006.44](https://doi.org/10.1109/TCBB.2006.44)
- T. Hartman: A Simpler 1.5-Approximation Algorithms for Sorting by Transpositions, *Proceedings of the 14th Symposium on Combinatorial Pattern Matching (CPM'03)*, Lecture Notes in Computer Science, Vol. 2676, 156–169, 2003.
DOI: [10.1007/3-540-44888-8_12](https://doi.org/10.1007/3-540-44888-8_12)

A.3.10 Sorting by Transversals

- M. Bader, E. Ohlebusch: Sorting by Weighted Reversals, Transpositions, and Inverted Transpositions, *Proceedings of the 10th Annual International Conference on Research in Computational Molecular Biology (RECOMB'06)*, Lecture Notes in Computer Science, Vol. 3909, 563–577, Springer, 2006.
DOI: [10.1007/11732990_46](https://doi.org/10.1007/11732990_46)
- N. Eriksen: $(1 + \varepsilon)$ -Approximation of Sorting by Reversals and Transpositions, *Theoretical Computer Science*, Vol. 289, 517–529, 2002.
DOI: [10.1016/S0304-3975\(01\)00338-3](https://doi.org/10.1016/S0304-3975(01)00338-3)
- Q.-P. Gu, S. Peng, I.H. Sudborough: A 2-Approximation Algorithm for Genome Rearrangements by Reversals and Transpositions, *Theoretical Computer Science*, Vol. 210, 327–339, 1999.
DOI: [10.1016/S0304-3975\(98\)00092-9](https://doi.org/10.1016/S0304-3975(98)00092-9)

- T. Hartman, R. Sharan: A 1.5-Approximation Algorithm for Sorting by Transpositions and Transreversals, *Proceedings of the 4th Workshop on Algorithms in Bioinformatics (WABI'04)*, Lecture Notes in Computer Science, Vol. 3240, 50–61, Springer, 2004.
DOI: [10.1007/978-3-540-30219-3_5](https://doi.org/10.1007/978-3-540-30219-3_5)
- T. Hartman, R. Sharan: A 1.5-Approximation Algorithm for Sorting by Transpositions and Transreversals. *Journal of Computer and System Sciences*, Vol. 70, No. 3, 300–320, 2005.
DOI: [10.1016/j.jcss.2004.12.006](https://doi.org/10.1016/j.jcss.2004.12.006)
- G-H. Lin, G. Xue: Signed Genome Rearrangements by Reversals and Transpositions: Models and Approximations, *Theoretical Computer Science*, Vol. 259, 513–531, 2001
DOI: [10.1016/S0304-3975\(00\)00038-4](https://doi.org/10.1016/S0304-3975(00)00038-4)
- A. Rahmana, S. Shatabdaa, M. Hasan: An approximation algorithm for sorting by reversals and transpositions; *Journal of Discrete Algorithms*, Vol. 6, No. 3, 449–45, 2008.
DOI: [10.1016/j.jda.2007.09.002](https://doi.org/10.1016/j.jda.2007.09.002)

A.3.11 Erweiterungen zu Genome Rearrangements

- M.A. Bender, D. Ge, S. He, H. Hu, R.Y. Pinter, S. Skiena, F. Swidan: Improved Bounds on Sorting with Length-Weighted Reversals, *Proceedings of the 15th Annual ACM-SIAM Symposium on Discrete Algorithms, SODA'04*, 919–928, 2004.
- A. Bergeron, J. Mixtacki, J. Stoye: On Sorting by Translocations, *Proceedings of the 9th Annual International Conference on Computational Biology (RECOMB'05)*, Lecture Notes in Computer Science, Vol. 3500, 615–629, Springer, 2005.
DOI: [10.1007/11415770_47](https://doi.org/10.1007/11415770_47)
- A. Bergeron, J. Mixtacki, J. Stoye: A Unifying View of Genome Rearrangements, *Proceedings of the 6th International Workshop on Algorithms in Bioinformatics, (WABI'06)*, Lecture Notes in Computer Science, Vol. 4175, 163–173, Springer, 2006.
DOI: [10.1007/11851561_16](https://doi.org/10.1007/11851561_16)
- D. Bryant: A Lower Bound for the Breakpoint Phylogeny Problem, *Proceedings of the 11th Workshop on Combinatorial Pattern Matching, CPM'00*, 235–247, 2000.
DOI: [10.1007/3-540-45123-4_21](https://doi.org/10.1007/3-540-45123-4_21)

- A. Caprara: Formulations and Hardness of Multiple Sorting by Reversals, *Proceedings of the 3rd Annual International Conference on Computational Biology (RECOMB'99)*, 84–93, 1999.
DOI: [10.1145/299432.299461](https://doi.org/10.1145/299432.299461)
- T. Chen, S.S. Skiena: Sorting with Fixed-Length Reversals, *Discrete Applied Mathematics*, Vol. 71, 269–295, 1996.
DOI: [10.1016/S0166-218X\(96\)00069-8](https://doi.org/10.1016/S0166-218X(96)00069-8)
- D.A. Christie, R.W. Irving: Sorting Strings by Reversals and by Transpositions, *SIAM Journal on Discrete Mathematics*, Vol. 14, 193–206, 2001.
DOI: [10.1137/S0895480197331995](https://doi.org/10.1137/S0895480197331995)
- D.A. Christie: Sorting Permutations by Block-Interchanges, *Information Processing Letters*, Vol. 60, 165–169, 1996.
DOI: [10.1016/S0020-0190\(96\)00155-X](https://doi.org/10.1016/S0020-0190(96)00155-X)
- D.S. Cohen, M. Blum: On the Problem of Sorting Burnt Pancakes, *Discrete Applied Mathematics*, Vol. 61, No. 2, 105–120, 1995.
DOI: [10.1016/0166-218X\(94\)00009-3](https://doi.org/10.1016/0166-218X(94)00009-3)
- B. DasGupta, T. Jiang, S. Kannan, M. Li, E. Sweedyk: On the Complexity and Approximation of Syntenic Distance, *Discrete Applied Mathematics*, Vol. 88, 59–82, 1998.
DOI: [10.1016/S0166-218X\(98\)00066-3](https://doi.org/10.1016/S0166-218X(98)00066-3)
- N. El-Mabrouk, D. Sankoff: The Reconstruction of Doubled Genomes, *SIAM Journal on Computing*, Vol. 32, 754–792, 2003.
DOI: [10.1137/S0097539700377177](https://doi.org/10.1137/S0097539700377177)
- W. Gates, C. Papadimitriou: Bounds for Sorting by Prefix Reversal, *Discrete Mathematics*, Vol. 27, 47–57, 1979.
DOI: [10.1016/0012-365X\(79\)90068-2](https://doi.org/10.1016/0012-365X(79)90068-2)
- S. Hannenhalli: Polynomial-Time Algorithm for Computing Translocation Distance Between Genomes, *Discrete Applied Mathematics*, Vol. 71, 137–151, 1996.
DOI: [10.1016/S0166-218X\(96\)00061-3](https://doi.org/10.1016/S0166-218X(96)00061-3)
- S. Hannenhalli, P.A. Pevzner: To cut ... or not to cut (applications of comparative physical maps in molecular evolution) , *Proceedings of the Seventh Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 96)*, 304–313, 1996.
- S. Hannenhalli, P.A. Pevzner: Transforming Men into Mice (Polynomial Algorithm for Genomic Distance), *Proceedings of the 36th Annual IEEE Symposium on Foundations of Computer Science (FOCS'95)*, 581–592, 1995.
DOI: [10.1145/640075.640108](https://doi.org/10.1145/640075.640108)

- L.S. Heath, J.P. Vergara: Sorting by Bounded Block-Moves, *Discrete Applied Mathematics*, Vol. 88, 181–206, 1998.
DOI: [10.1016/S0166-218X\(98\)00072-9](https://doi.org/10.1016/S0166-218X(98)00072-9)
- J. Kleinberg, D. Liben-Nowell: The Syntenic Diameter of the Space of n -Chromosome Genomes, in *Comparative Genomics*, David Sankoff and Joseph H. Nadeau (Eds.), Kluwer Academic Press, 2000.
- J. Meidanis, Z. Dias: Genome Rearrangements Distance by Fusion, Fission, and Transposition is Easy, *Proceedings of the 8th Symposium on String Processing and Information Retrieval, SPIRE'01*, 250–253, 2001
DOI: [10.1109/SPIRE.2001.989776](https://doi.org/10.1109/SPIRE.2001.989776)
- R.Y. Pinter, S. Skiena: Genomic Sorting with Length-Weighted Reversals, *Genome Informatics*, Vol. 13, 103–111, 2002.