Ludwig-Maximilians-Universität München
Institut für Informatik
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Proseminar
Proseminar Bioinformatik
Sommersemester 2016
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Themenliste

1. String Matching: Knuth-Morris-Pratt and Boyer-Moore

   [1] D. Gusfield: Algorithms on Strings, Trees, and Sequences — Computer Science and Computational Biology, Cambridge University Press, 1997; Kapitel 1-3.

   [2] V. Heun: Grundlegende Algorithmen, Vieweg-Verlag, 2003, Abschnitt 6.1-6.3

2. String Matching: Shift-And and Karp-Rabin

   [3] D. Gusfield: Algorithms on Strings, Trees, and Sequences — Computer Science and Computational Biology, Cambridge University Press, 1997; Kapitel 4.

3. Suffix Trees: Simple Algorithm and Applications

   [4] D. Gusfield: Algorithms on Strings, Trees, and Sequences — Computer Science and Computational Biology, Cambridge University Press, 1997; Kapitel 5, Abschnitt 6.4, Abschnitte 7.1 und 7.3-7.6.

4. Textcompression: Burrows-Wheeler-Transformation

   [5] M. Burrows, D.J. Wheeler: A Block-Sorting Lossless Data Compression Algorithm, Digital SRC Research Report No. 124, 1994.

   [6] V. Heun: Grundlegende Algorithmen, Vieweg-Verlag, 2003, Abschnitt 6.5.

   [7] B. Langmead, C. Trapnell, M. Pop, S.L. Salzberg: Ultrafast and Memory-Efficient Alignment of Short DNA Sequences to the Human Genome, Genome Biology 10:R25, 2009.

5. Suffix Arrays and BWT

   [8] B. Smyth: Computing Pattern in Strings, Pearsen & Addison Wesley, 2003, Abschnitt 5.3.2

   [9] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, CRC Press, 2009, Abschnitte 3.5–3.6.

   [10] G. Navarro, V. Mäkinen: Compressed Full-Text Indexes, ACM Computing Surveys, Vol. 39, No. 1, 2007, Abschnitte 1–5.

6. Algorithmic Concepts for Pairwise Sequence Alignment

   [11] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 3.1, 3.2, 3.3.

   [12] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, CRC Press, 2009, Abschnitte 2.1–2.5.

7. Sequence Assembly

   [13] P. Compeau, P. Pevzner: Bioinformatics Algorithms — An Active Learning Approach, AL Active Learning Publishers, 2014, Kapitel 4.

   [14] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 4.1, 4.2, 4.3.

   [15] R.C. Deonier, S. Tavaré, M.S. Waterman: Computational Genome Analysis — An Introduction, Springer, 2005, Kapitel 8.

8. Genome Rearrangements

   [16] H.-J. Böckenhauer, D. Bongartz: Algorithmische Grundlagen der Bioinformatik — Modelle, Methoden und Komplexität, B.G. Teubner Verlag, 2003, Abschnitt 10.1 und 10.2.

   [17] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, CRC Press, 2009, Kapitel 9.

   [18] P. Pevzner: Computational Molecular Biology — An Algorithmic Approach, MIT Press, 2000, Abschnitt 10.1.

9. Evolutionary Trees (Character-Based Methods)

   [19] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 6.1, 6.2 sowie Errata zu Lemma 6.1.

   [20] W.-K: Sung: Algorithms in Bioinformatics — A Practical Introduction, Abschnitt, 7.1, 7.2, CRC Press, 2010

10. Evolutionary Trees (Distance-Based Methods)

   [21] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 6.1, 6.5.1

   [22] P. Clote, R. Backofen: Computational Molecular Biology — An Introduction, Wiley 2000; Abschnitte 4.3.0 und 4.3.1.

   [23] W.-K: Sung: Algorithms in Bioinformatics — A Practical Introduction, Abschnitt, 7.1, 7.3, CRC Press, 2010

11. RNA Structure Prediction

   [24] V. Sperschneider: Bioinformatics — Problem Solving Paradigms, Springer-Verlag, 2008, Abschnitte 1.7, 2.9, 3.1, 3.6.

   [25] H.-J. Böckenhauer, D. Bongartz: Algorithmische Grundlagen der Bioinformatik — Modelle, Methoden und Komplexität, Teubner-Verlag, 2003, Abschnitt 12.1.