

## Proseminar

# Proseminar Bioinformatik

Sommersemester 2017  
Prof. Dr. Caroline Friedel

### Termine und Themen

0. Einführungsveranstaltung [24.4.2017]
1. String Matching: Knuth-Morris-Pratt and Boyer-Moore [8.5.2017] (Sabine Hefele)
  - [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 [8.5.2017] (Marcus Wagner)
  - [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 [22.5.2017] (Natalia Voronova)
  - [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 [22.5.2017] (Konstantin Schütze)
  - [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.
5. Suffix Arrays and BWT [29.5.2017] (Chris Eichhorn)
  - [7] B. Smyth: Computing Pattern in Strings, Pearson & Addison Wesley, 2003, Abschnitt 5.3.2
  - [8] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, CRC Press, 2009, Abschnitte 3.5–3.6.
6. Paarweises Sequenz-Alignment [29.5.2017] (Johannes Kersting)
  - [9] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 3.1, 3.2, 3.3.

- [10] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, CRC Press, 2009, Abschnitte 2.1–2.5.
7. Hidden-Markov-Modelle [12.6.2017] (Quirin Manz)
- [11] R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological Sequence Analysis, Cambridge University Press, 1998; Kapitel 3, Abschnitte 3.1–3.4.
- [12] N.C. Jones, P.P. Pevzner: An Introduction to Bioinformatics Algorithms, The MIT Press, 2004; Kapitel 11.
8. Algorithmen zur Suche in biologischen Datenbanken [12.6.2017] (Jens-Justus Kolbe)
- [13] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 3.1, 3.5.
- [14] D. Gusfield: Algorithms on Strings, Trees, and Sequences — Computer Science and Computational Biology, Cambridge University Press, 1997; Kapitel 15.
- [15] D.W. Mount: Bioinformatics — Sequence and Genome Analysis, Cold Spring Harbor Laboratory Press, 2001, Kapitel 7.
9. Evolutionary Trees (Character-Based Methods) [19.6.2017] (Sijing Li)
- [16] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 6.1, 6.2 sowie Errata zu Lemma 6.1.
- [17] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, Abschnitt, 7.1, 7.2, CRC Press, 2010
10. Evolutionary Trees (Distance-Based Methods) [19.6.2017] (Stefan Irlbauer)
- [18] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 6.1, 6.5.1
- [19] P. Clote, R. Backofen: Computational Molecular Biology — An Introduction, Wiley 2000; Abschnitte 4.3.0 und 4.3.1.
- [20] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, Abschnitt, 7.1, 7.3, CRC Press, 2010
11. Multiples Sequenz-Alignment [3.7.2017] (Kim-Anh Le)
- [21] R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological Sequence Analysis, Cambridge University Press, 1998; Kapitel 6.
- [22] D. Gusfield: Algorithms on Strings, Trees, and Sequences — Computer Science and Computational Biology, Cambridge University Press, 1997; Kapitel 14, Abschnitte 14.1, 14.2, 14.5, 14.6, 14.10.1.
12. Sequence Assembly [3.7.2017] (Kyra Erckert)
- [23] P. Compeau, P. Pevzner: Bioinformatics Algorithms — An Active Learning Approach, AL Active Learning Publishers, 2014, Kapitel 4.
- [24] J. Setubal, J. Meidanis: Introduction to Computational Molecular Biology, PWS, 1997; Abschnitte 4.1, 4.2, 4.3.

- [25] R.C. Deonier, S. Tavaré, M.S. Waterman: Computational Genome Analysis — An Introduction, Springer, 2005, Kapitel 8.
13. Genome Rearrangements [10.7.2017] (Rahel Caspar)
- [26] H.-J. Böckenhauer, D. Bongartz: Algorithmische Grundlagen der Bioinformatik — Modelle, Methoden und Komplexität, B.G. Teubner Verlag, 2003, Abschnitt 10.1 und 10.2.
- [27] W.-K. Sung: Algorithms in Bioinformatics — A Practical Introduction, CRC Press, 2009, Kapitel 9.
- [28] P. Pevzner: Computational Molecular Biology — An Algorithmic Approach, MIT Press, 2000, Abschnitt 10.1.
14. RNA Structure Prediction [10.7.2017] (Daniel Kogan)
- [29] V. Sperschneider: Bioinformatics — Problem Solving Paradigms, Springer-Verlag, 2008, Abschnitte 1.7, 2.9, 3.1, 3.6.
- [30] H.-J. Böckenhauer, D. Bongartz: Algorithmische Grundlagen der Bioinformatik — Modelle, Methoden und Komplexität, Teubner-Verlag, 2003, Abschnitt 12.1.