

REFERENCES

- [ACL⁺ 02] Althaus, E., Caprara, A., Lenhof, H-P., and Reinert, K. 2002. Multiple sequence alignment with arbitrary gap costs: Computing an optimal solution using polyhedral combinatorics. *Bioinformatics*, vol 18, pp S4-S16.
- [Isa 06] Isaev, A. *Introduction to Mathematical Methods in Bioinformatics*. Springer. 2006.
- [LG 91] Li, W-H., and Graur, D. *Fundamentals of Molecular Evolution*. 1st ed. Sinauer Associates. 1991.
- [MDW 96] Morgenstern, B., Dress, A., and Werner, T. 1996. Multiple DNA and protein sequence alignment based on segment-to-segment comparison. *Proc. Natl Acad. Sci. USA*, vol 93, pp 12098-12103.
- [Mor 98] Morgenstern, B. 1998. DIALIGN 2: Improvement of The Segment-to-segment Approach to Multiple Sequence Alignment. *Bioinformatics*, vol 15, no 1999, pp 211-218.
- [Mor 04] Morgenstern, B. 2004. DIALIGN: Multiple DNA and Protein Sequence Alignment at BiBiServ. *Nucleic Acids Research*, vol 32, web server issue.
- [Xia 07] Xia, X. *Bioinformatics and The Cell: Modern Computational Approaches in Genomics, Proteomics and Transcriptomics*. Springer. 2007.