

## DAFTAR PUSTAKA

- [1] J. Xiong, *Essential bioinformatics*. Cambridge University Press, 2006.
- [2] S. F. Altschul, W. Gish, W. Miller, E. W. Myers, and D. J. Lipman, “Basic local alignment search tool,” *J. Mol. Biol.*, vol. 215, no. 3, pp. 403–410, 1990, doi: 10.1016/S0022-2836(05)80360-2.
- [3] Z. M. Zhou and Z. W. Chen, “Dynamic programming for protein sequence alignment,” *Int. J. Bio-Science Bio-Technology*, vol. 5, no. 2, pp. 141–150, 2013.
- [4] C. Kemeny and C. Notredame, “Upcoming challenges for multiple sequence alignment methods in the high-throughput era,” *Bioinformatics*, vol. 25, no. 19, pp. 2455–2465, 2009, doi: 10.1093/bioinformatics/btp452.
- [5] T. F. Smith and M. S. Waterman, “Identification of common molecular subsequences,” *J. Mol. Biol.*, vol. 147, no. 1, pp. 195–197, 1981, doi: 10.1016/0022-2836(81)90087-5.
- [6] K. Arumugam, Y. S. Tan, B. S. Lee, and R. Kanagasabai, “Cloud-enabling sequence alignment with hadoop mapreduce: A performance analysis,” 2012.
- [7] P. Chou and G. D. Fasman, “Amino acid sequence,” *Adv. Enzym. Relat. Areas Molec. Biol.*, vol. 47, p. 45, 2009.
- [8] P. Stothard, “The Sequence Manipulation Suite: JavaScript Programs for Analyzing and Formatting Protein and DNA Sequences,” *Biotechniques*, vol. 28, p. 1102,1104, Jul. 2000, doi: 10.2144/00286ir01.
- [9] V. O. Polyanovsky, M. A. Roytberg, and V. G. Tumanyan, “Comparative analysis of the quality of a global algorithm and a local algorithm for alignment of two sequences,” *Algorithms Mol. Biol.*, vol. 6, no. 1, pp. 1–12, 2011, doi: 10.1186/1748-7188-6-25.
- [10] S. B. Needleman and C. D. Wunsch, “A general method applicable to the search for similarities in the amino acid sequence of two proteins,” *J. Mol. Biol.*, vol. 48, no. 3, pp. 443–453, Mar. 1970, doi: 10.1016/0022-2836(70)90057-4.
- [11] A. O’Driscoll *et al.*, “HBLAST: Parallelised sequence similarity - A Hadoop MapReducable basic local alignment search tool,” *J. Biomed. Inform.*, vol. 54, pp. 58–64, 2015, doi: 10.1016/j.jbi.2015.01.008.
- [12] S. Leo, F. Santoni, and G. Zanetti, “Biodoop: Bioinformatics on hadoop,” *Proc. Int. Conf. Parallel Process. Work.*, no. September, pp. 415–422, 2009, doi: 10.1109/ICPPW.2009.37.
- [13] M. Schatz, “BlastReduce: high performance short read mapping with MapReduce,” *Univ. Maryland*, [http://cgis.cs.umd.edu/Grad/ ...](http://cgis.cs.umd.edu/Grad/), 2008, doi: citeulike-article-id:6496105.
- [14] A. Pertsemlidis and J. W. Fondon, “Having a BLAST with bioinformatics (and avoiding BLAST phemy),” *Genome Biol.*, vol. 2, no. 10, 2001, doi:

- 10.1186/gb-2001-2-10-reviews2002.
- [15] Apache Software Foundation, “Hadoop.” <https://hadoop.apache.org> (accessed Dec. 19, 2020).
  - [16] H. Alshammari, H. Bajwa, and J. Lee, “Hadoop based enhanced cloud architecture for bioinformatic algorithms,” *2014 IEEE Long Isl. Syst. Appl. Technol. Conf. LISAT 2014*, no. May, 2014, doi: 10.1109/LISAT.2014.6845204.
  - [17] D. Borthakur, “HDFS architecture guide. Hadoop Apache Project,” pp. 1–14, 2008, [Online]. Available: <http://hadoop.apache.org/hdfs/>.
  - [18] J. Zhang, G. Wu, X. Hu, and X. Wu, “A Distributed Cache for Hadoop Distributed File System in Real-Time Cloud Services,” in *2012 ACM/IEEE 13th International Conference on Grid Computing*, 2012, pp. 12–21, doi: 10.1109/Grid.2012.17.
  - [19] D. L. Eager, J. Zahorjan, and E. D. Lozowska, “Speedup Versus Efficiency in Parallel Systems,” *IEEE Trans. Comput.*, vol. 38, no. 3, pp. 408–423, Mar. 1989, doi: 10.1109/12.21127.