

DAFTAR PUSTAKA

- [1] J. Simarmata, *Rekayasa Perangkat Lunak*, Yogyakarta: Penerbit ANDI, 2010.
- [2] D. P. A. P. Ernawati, "Implementasi Algoritma Smith-Waterman Pada Local Alignment Dalam Pencarian Kesamaan Pensejajaran Barisan DNA (Studi Kasus : DNA Tumor Wilms)," *Jurnal Pseudocode*, pp. 170-177, 2014.
- [3] D. Agashe, "Large-Effect Beneficial Synonymous Mutations Mediate Rapid and Parallel Adaptation in a Bacterium," *Molecular Biology and Evolution*, vol. 33, no. 6, pp. 1542-1553, 2016.
- [4] W. H. B. R. Alex Aravind, "Pairwise sequence alignment algorithms : a survey," *Association for Computing Machinery Journal*, 2016.
- [5] A. Chan, "Stanford Project," 2004. [Online]. Available: biochem218.stanford.edu/Projects%202004.Chan.pdf.
- [6] S. J. P. J. Z. Shanika Kuruppu, "Optimized Relative Lempel-Ziv Compression of Genomes," vol. XXXIV, pp. 1-8, 2011.
- [7] Z. R. Yang, *Machine Learning Approaches to Bioinformatics*, Singapore: World Scientific Publishing Co. Pte. Ltd., 2010.
- [8] W. S. Susan Elrod, *Schaum's Genetika*, Jakarta: Erlangga, 2007.
- [9] V. Likic, "The Needleman-Wunsch Algorithm for Sequence Alignment," dalam *Bio21 Molecular Science and Biotechnology Institute*, Melbourne, 2008.
- [10] S. J. P. Dominik Kempa, "Lempel-Ziv Factorization: Simple, Fast, Practical," *Algorithm Engineering and Experiments (ALENEX)*, pp. 103-112, 2013.
- [11] J. C. G. C. N. L. J. L. J. F. D. B. S. C. L. Dandan Song, "Parameterized BLOSUM Matrices for Protein Alignment," *Transactions on Computational Biology and Bioinformatics*, vol. 12, no. 3, pp. 686-694, 2015.
- [12] Suyanto, *Algoritma Optimasi Deterministik Atau Probabilitik*, Yogyakarta: Graha Ilmu, 2014.

- [13] S. W. P. M. F. R. Muhamad Reza Firdaus Zen, “Penerapan Algoritma Needleman-Wunsch sebagai Salah Satu Implementasi Program Dinamis Pada Pensejajaran DNA dan Protein,” *Jurnal STMIK*, pp. 1-5, 2006.
- [14] R. S. Harris, *Improved Pairwise Alignment Of Genomic DNA*, Pennsylvania: Pennsylvania State University, 2007.
- [15] A. A. B. R. Waqar Haque, “An Efficient Algorithm for Local Sequence Alignment,” *30th Annual International IEEE EBMS Conference*, p. 1367, 2008.

