DAFTAR PUSTAKA

Bishop, C. M. (2006) *Pattern Recognition and Machine Learning*, *The Ecstatic and the Archaic: An Analytical Psychological Inquiry*. Springer.

Gregory, S. G. (2005) 'Contig Assembly', *Encyclopedia of Life Sciences*, pp. 1–4. doi: 10.1038/npg.els.0005365.

Handelsman, J. (2004) 'Metagenomics: Application of Genomics to Uncultured Microorganisms', *Microbiology and Molecular Biology Reviews*, 68(4), pp. 669–685. doi: 10.1128/mmbr.69.1.195.2005.

Kaufman, L. and Rousseeuw, P. J. (1990) *Finding Groups in Data: An Introduction to Cluster Analysis*. 99th edn. Hoboken: John Wiley & Sons, Inc.

Liu, J. *et al.* (2020) 'Capped norm linear discriminant analysis and its applications', (1), pp. 1–11. Available at: http://arxiv.org/abs/2011.02147.

Margulies, M. *et al.* (2005) 'Genome sequencing in microfabricated high-density picolitre reactors', *Nature*, 437(7057), pp. 376–380. doi: 10.1038/nature03959.

Overbeek, M. V., Kusuma, W. A. and Buono, A. (2013) 'Clustering metagenome fragments using growing self organizing map', *2013 International Conference on Advanced Computer Science and Information Systems, ICACSIS 2013*, pp. 285–289. doi: 10.1109/ICACSIS.2013.6761590.

Pedregosa, F. *et al.* (2011) 'Scikit-learn: Machine Learning in Python', *Journal of Machine Learning Research*, 12, pp. 2825–2830. Available at: http://scikit-learn.sourceforge.net. (Accessed: 3 June 2021).

Raschka, S. and Mirjalili, V. (2019) *Python Machine Learning*. Third. Birmingham: Packt Publishing Ltd.

Richter, D. C. *et al.* (2008) 'MetaSim - A sequencing simulator for genomics and metagenomics', *PLoS ONE*, 3(10). doi: 10.1371/journal.pone.0003373.

Rosen, G. *et al.* (2008) 'Metagenome Fragment Classification Using -Mer Frequency Profiles', *Advances in Bioinformatics*, 2008, pp. 1–12. doi: 10.1155/2008/205969.

SAS Institute Inc. (2009) *SAS/STAT(R) 9.2 User's Guide, Second Edition*. 2nd edn. Edited by A. Jones and E. Huddleston. Cary, NC: SAS Institute Inc.

Scholz, M. *et al.* (2020) 'Large scale genome reconstructions illuminate Wolbachia evolution', *Nature Communications*, 11(1). doi: 10.1038/s41467-020-19016-0.

Simangunsong, V. F. R. (2015) 'Klasifikasi Fragmen Metagenom Menggunakan

Principal Component Analysis Dan K-Nearest Neighbor', pp. 1–34.

Sultana, S. I. (2020) *How The Hierarchical Clustering Algorithm Works*. Available at: https://dataaspirant.com/hierarchical-clustering-algorithm/ (Accessed: 22 December 2020).

Tharwat, A. *et al.* (2017) 'Linear discriminant analysis: A detailed tutorial', *AI Communications*, 30(2), pp. 169–190. doi: 10.3233/AIC-170729.

What is DNA?: MedlinePlus Genetics (2021). Available at: https://medlineplus.gov/genetics/understanding/basics/dna/ (Accessed: 28 June 2021).

Wu, L. *et al.* (2012) 'Learning Bregman Distance Functions for Semi-Supervised Clustering', *IEEE Trans. Knowl. Data Eng.*, 24, pp. 478–491. doi: 10.1109/TKDE.2010.215.

Yan, C. *et al.* (2020) 'Self-Weighted Robust LDA for Multiclass Classification with Edge Classes'. Available at: http://arxiv.org/abs/2009.12362.