

DAFTAR PUSTAKA

- Ahn, H., Chang, T.-W., 2019. A Similarity-Based Hierarchical Clustering Method for Manufacturing Process Models. *Sustainability* 11, 2560. <https://doi.org/10.3390/su11092560>
- Chenna, R., Sugawara, H., Koike, T., Lopez, R., Gibson, T.J., Higgins, D.G., Thompson, J.D., 2003. Multiple sequence alignment with the Clustal series of programs. *Nucleic Acids Res* 31, 3497–3500.
- Dayhoff, M., Schwartz, R. and Orcutt, B., 1978. 22 A Model of Evolutionary Change in Proteins. *Atlas of Protein Sequence and Structure*, 5, pp.345-352.
- Edgar, R.C., 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 32, 1792–1797. <https://doi.org/10.1093/nar/gkh340>
- Edgar, R., 2018. Taxonomy annotation and *guide tree* errors in 16S rRNA databases. *PeerJ* 6, e5030. <https://doi.org/10.7717/peerj.5030>
- Higgins, D.G., Bleasby, A.J. and Fuchs, R., 1992. CLUSTAL V: improved software for multiple sequence alignment. *Bioinformatics*, 8(2), pp.189-191.
- Higgins, D.G., Sharp, P.M., 1988. CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. *Gene* 73, 237–244. [https://doi.org/10.1016/0378-1119\(88\)90330-7](https://doi.org/10.1016/0378-1119(88)90330-7)
- Jain, A.K., Dubes, R.C., 1988. Algorithms for clustering data, Prentice Hall advanced reference series. Prentice Hall, Englewood Cliffs, N.J.
- Jones, N.C., Pevzner, P.A., 2004. An introduction to bioinformatics algorithms. MIT press.
- Katoh, K., Misawa, K., Kuma, K., Miyata, T., 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Res* 30, 3059–3066.
- Mount, D.W., 2004. Bioinformatics: sequence and genome analysis, 2nd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.
- Nelesen, S., Liu, K., Zhao, D., Linder, C.R. and Warnow, T., 2008. The effect of

- the *guide tree* on multiple sequence alignments and subsequent phylogenetic analyses. In *Biocomputing 2008* (pp. 25-36).
- Notredame, C., Higgins, D.G., Heringa, J., 2000. T-coffee: a novel method for fast and accurate multiple sequence alignment¹¹ Edited by J. Thornton. *Journal of Molecular Biology* 302, 205–217. <https://doi.org/10.1006/jmbi.2000.4042>
- Ouaftouh, S., Sassi, I., Zellou, A., Anter, S., 2019. Flat and hierarchical user profile clustering in an e-commerce recommender system, in: 2019 1st International Conference on Smart Systems and Data Science (ICSSD). Presented at the 2019 1st International Conference on Smart Systems and Data Science (ICSSD), pp. 1–5. <https://doi.org/10.1109/ICSSD47982.2019.9002690>
- Park, S., Park, Y.B., 2018. Photovoltaic power data analysis using hierarchical clustering, in: 2018 International Conference on Information Networking (ICOIN). Presented at the 2018 International Conference on Information Networking (ICOIN), pp. 727–731. <https://doi.org/10.1109/ICOIN.2018.8343214>
- Pevsner, J., 2009. *Bioinformatics and functional genomics*, 2nd ed. ed. Wiley-Blackwell, Hoboken, N.J.
- Rokach, L., Maimon, O., 2005. Clustering Methods, in: Maimon, O., Rokach, L. (Eds.), *Data Mining and Knowledge Discovery Handbook*. Springer-Verlag, New York, pp. 321–352. https://doi.org/10.1007/0-387-25465-X_15
- Roux, M., 2018. A Comparative Study of Divisive and Agglomerative Hierarchical Clustering Algorithms. *J Classif* 35, 345–366. <https://doi.org/10.1007/s00357-018-9259-9>
- Saitou, N., Nei, M., 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* 4, 406–425. <https://doi.org/10.1093/oxfordjournals.molbev.a040454>
- Studier, J.A., Keppler, K.J., 1988. A note on the neighbor-joining algorithm of Saitou and Nei. *Molecular Biology and Evolution* 5, 729–731. <https://doi.org/10.1093/oxfordjournals.molbev.a040527>
- Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F., Higgins, D.G., 1997. The CLUSTAL_X Windows Interface: Flexible Strategies for Multiple

- Sequence Alignment Aided by Quality Analysis Tools. *Nucleic Acids Research* 25, 4876–4882. <https://doi.org/10.1093/nar/25.24.4876>
- Thompson, J.D., Higgins, D.G., Gibson, T.J., 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* 22, 4673–4680. <https://doi.org/10.1093/nar/22.22.4673>
- Thompson, J.D., Plewniak, F., Poch, O., 1999. BALiBASE: a benchmark alignment database for the evaluation of multiple alignment programs. *Bioinformatics* 15, 87–88. <https://doi.org/10.1093/bioinformatics/15.1.87>
- Vijaya, S. Sharma, N. Batra, 2019. Comparative Study of Single Linkage, Complete Linkage, and Ward Method of Agglomerative Clustering, in: 2019 International Conference on Machine Learning, Big Data, Cloud and Parallel Computing (COMITCon). Presented at the 2019 International Conference on Machine Learning, Big Data, Cloud and Parallel Computing (COMITCon), pp. 568–573. <https://doi.org/10.1109/COMITCon.2019.8862232>
- Wang, Y., Qin, K., Chen, Y., Zhao, P., 2018. Detecting Anomalous Trajectories and Behavior Patterns Using Hierarchical Clustering from Taxi GPS Data. *ISPRS International Journal of Geo-Information* 7, 25. <https://doi.org/10.3390/ijgi7010025>