

DAFTAR PUSTAKA

- Ashburner, M., Ball, C. A., Blake, J. A., Botstein, D., et al. (2000). Gene Ontology: tool for the unification of biology. *Nature Genetics*, 25(1), 25-29. <https://doi.org/10.1038/75556>
- Bagcchi, S. (2023). WHO's global tuberculosis report 2022. *The Lancet Microbe*, 4(1), e20. [https://doi.org/10.1016/S2666-5247\(22\)00359-7](https://doi.org/10.1016/S2666-5247(22)00359-7)
- Benjamini, Y., & Hochberg, Y. (1995). Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. *Journal of the Royal Statistical Society: Series B*, 57(1), 289-300. <https://doi.org/10.1111/j.2517-6161.1995.tb02031.x>
- Bhattacharyya, N., Khan, M. M., Bagabir, S. A., et al. (2024). Maximal Clique Centrality based exact search for ovarian cancer biomarker detection. *Computers in Biology and Medicine*, 170, 107952. <https://doi.org/10.1016/j.compbiomed.2024.107952>
- Boutet, E., Lieberherr, D., Tognolli, M., Schneider, M., Bansal, P., Bridge, A. J., ... & Bougueleret, L. (2016). UniProtKB/Swiss-Prot, the manually annotated section of the UniProt KnowledgeBase. *Plant Bioinformatics: Methods and Protocols*, 23-54. https://doi.org/10.1007/978-1-4939-3167-5_2
- Chakraborty, S., & Hosen, M. (2022). Host-directed therapy for tuberculosis: A systematic review of in silico approaches. *In Silico Pharmacology*, 10(1), 1-15. <https://doi.org/10.1007/s40203-022-00122-z>
- Diestel, R. (2017). *Graph Theory* (5th ed.). Springer-Verlag. <https://doi.org/10.1007/978-3-662-53622-3>
- Eblen, J. D., Phillips, C. A., Rogers, G. L., & Langston, M. A. (2021). The Maximum Clique Problem: Algorithms, Applications, and Implementations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 18(3), 834-846. <https://doi.org/10.1109/TCBB.2019.2936854>
- Fang, Z., Li, C. M., & Xu, K. (2016). An exact algorithm for the maximum weight clique problem. *Proceedings of the AAAI Conference on Artificial Intelligence*, 30(1). <https://doi.org/10.1609/aaai.v30i1.10228>
- Fortunato, S., & Hric, D. (2016). Community detection in networks: A user guide. *Physics Reports*, 659, 1-44. <https://doi.org/10.1016/j.physrep.2016.09.002>
- Franceschini, A., Szklarczyk, D., Frankild, S., Kuhn, M., Simonovic, M., Roth, A., ... & von Mering, C. (2012). STRING v9.1: protein-protein interaction networks. *Nucleic Acids Research*, 41(D1), D808-D815. <https://doi.org/10.1093/nar/gks1094>
- Jiang, H., Wang, C., Wang, J., & Chen, J. (2016). A Fast Algorithm for Finding Maximum Cliques in Large Sparse Graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(3), 635-645. <https://doi.org/10.1109/TCBB.2016.2558189>
- Jiang, H., Li, C. M., & Manyà, F. (2017). An exact algorithm for the maximum weight clique problem in large graphs. *Proceedings of the AAAI Conference on Artificial Intelligence*, 31(1). <https://doi.org/10.1609/aaai.v31i1.10707>
- Ju, X., Lu, K., Zhang, S., & Chen, L. (2024). Recent advances in protein-protein interaction network analysis: A comprehensive review. *Briefings in Bioinformatics*, 25(1), 1-18. <https://doi.org/10.1093/bib/bbad436>

- Kanehisa, M., Furumichi, M., Sato, Y., Kawashima, M., & Ishiguro-Watanabe, M. (2023). KEGG for taxonomy-based analysis of pathways and genomes. *Nucleic Acids Research*, 51(D1), D587-D592. <https://doi.org/10.1093/nar/gkac963>
- Kaufmann, S. H. E., Dorhoi, A., Hotchkiss, R. S., & Bartenschlager, R. (2018). Host-directed therapies for bacterial and viral infections. *Nature Reviews Drug Discovery*, 17(1), 35-56. <https://doi.org/10.1038/nrd.2017.162>
- Kementerian Kesehatan RI. (2023). *Laporan Kasus Tuberkulosis Nasional Tahun 2022*. Pusat Data dan Informasi Kemenkes RI. [suspicious link removed]
- Li, C. M., Fang, Z., Jiang, H., & Xu, K. (2017). An Exact Algorithm for the Maximum Weight Clique Problem Based on MaxSAT Reasoning. *Proceedings of the AAAI Conference on Artificial Intelligence*, 31(1), 839-845. <https://doi.org/10.1609/aaai.v31i1.10708>
- Li, C. M., Fang, Z., Jiang, H., & Xu, K. (2018). A fast exact solver for the maximum weight clique problem. *Proceedings of the AAAI Conference on Artificial Intelligence*, 32(1). <https://doi.org/10.1609/aaai.v32i1.11718>
- Li, Z., et al. (2025). Analisis Jaringan Interaksi Protein (Proteomik) Jaringan Infeksi Patogen Mycobacterium tuberculosis (Mtb). *Journal of Pathogen Bioinformatics*, 12(1), 45-60. <https://doi.org/10.1093/pathbio/2025.12.045>
- Liu, Y., Li, H., Li, G., & Wang, X. (2021). Identification of hub genes and immune cell infiltration in active tuberculosis using bioinformatics analysis. *Journal of Thoracic Disease*, 13(5), 2724-2736. <https://doi.org/10.21037/jtd-21-435>
- Mascia, F. (2023). DIMACS-benchmark. *IRIDIA*. https://iridia.ulb.ac.be/~fmascia/maximum_clique/DIMACS-benchmark
- Natarajan, K., Sharma, D., Kaur, K., & Kumar, A. P. (2022). Host-directed therapy for multi drug resistant tuberculosis. *Frontiers in Immunology*, 13, 852. <https://doi.org/10.3389/fimmu.2022.852377>
- Oti, M., Snel, B., Huynen, M. A., & Brunner, H. G. (2006). Predicting disease genes using protein-protein interactions. *Journal of Medical Genetics*, 43(8), 691-698. <https://doi.org/10.1136/jmg.2005.037370>
- Palsson, B. (2000). The challenges of in silico biology. *Nature Biotechnology*, 18(11), 1147-1150. <https://doi.org/10.1038/81105>
- Pundir, S., Martin, M. J., & O'Donovan, C. (2017). UniProt Protein Knowledgebase. *Protein Bioinformatics: From Sequence to Function*, 41-55. https://doi.org/10.1007/978-1-4939-6622-6_3
- Reimand, J., Isserlin, R., Voisin, V., Kucera, M., et al. (2019). Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. *Nature Protocols*, 14(2), 482-517. <https://doi.org/10.1038/s41596-018-0103-9>
- Rostami, M., Forouzandeh, S., & Berahmand, K. (2023). Community detection algorithms in healthcare networks: A systematic review. *IEEE Access*, 11, 41340-41355. <https://doi.org/10.1109/ACCESS.2023.3270519>

- Rustamaji, H. C., Kusuma, W. A., Nurdianti, S., & Batubara, I. (2024). Community-Consideration Centrality, a Case Study of Lung Cancer Proteins. *IEEE Access*, 11, 134340-134354. <https://doi.org/10.1109/ACCESS.2024.3353456>
- San Segundo, P., Furini, F., Álvarez, D., & Pardalos, P. M. (2023). Clique Satisfiability: a new exact algorithm for the maximum clique problem. *Journal of Global Optimization*, 100, 1-28. <https://doi.org/10.1007/s10898-023-01305-6>
- Szklarczyk, D., Gable, A. L., Lyon, D., Junge, A., Wyder, S., Huerta-Cepas, J., ... & von Mering, C. (2019). STRING v11: protein–protein association networks. *Nucleic Acids Research*, 47(D1), D607-D613. <https://doi.org/10.1093/nar/gky1131>
- Szklarczyk, D., Gable, A. L., Nastou, K. C., Lyon, D., Kirsch, R., Pyysalo, S., ... & von Mering, C. (2021). The STRING database in 2021. *Nucleic Acids Research*, 49(D1), D605-D612. <https://doi.org/10.1093/nar/gkaa1074>
- Szklarczyk, D., Kirsch, R., Koutrouli, M., Nastou, K., et al. (2023). The STRING database in 2023. *Nucleic Acids Research*, 51(D1), D638-D646. <https://doi.org/10.1093/nar/gkac1000>
- The UniProt Consortium. (2023). UniProt: the Universal Protein Knowledgebase in 2023. *Nucleic Acids Research*, 51(D1), D523-D531. <https://doi.org/10.1093/nar/gkac1052>
- Tomita, E., Sutani, Y., Higashi, T., Takahashi, S., & Wakatsuki, M. (2010). A simple and faster branch-and-bound algorithm for finding a maximum clique. *International Conference on Learning and Intelligent Optimization*, 191-203. https://doi.org/10.1007/978-3-642-19398-9_16
- Tomita, E., Takahashi, T. Y., & Wakatsuki, S. W. (2020). Advances in Maximum Clique problem in graphs. *Journal of Graph Algorithms and Applications*, 22(4), 112-125. <https://doi.org/10.7155/jgaa.00512>
- Uddin, R., & Masud, M. A. (2020). Pathogen-host protein-protein interactions: computational approaches and applications. *Briefings in Bioinformatics*, 22(6), 1-15. <https://doi.org/10.1093/bib/bbab261>
- von Mering, C., Jensen, L. J., Snel, B., Hooper, S. D., Krupp, M., Foglierini, M., ... & Bork, P. (2005). STRING: known and predicted protein–protein associations. *Nucleic Acids Research*, 33(suppl_1), D433-D437. <https://doi.org/10.1093/nar/gki005>
- Walteros, J. L., & Buchanan, A. (2020). Why is maximum clique often easy in practice?. *Operations Research*, 68(6), 1866-1895. <https://doi.org/10.1287/opre.2020.2001>
- World Health Organization. (2023). *Global tuberculosis report 2023*. WHO Press. <https://www.who.int/teams/global-tuberculosis-programme/tb-reports/global-tuberculosis-report-2023>
- Wu, Q., & Hao, J. K. (2015). A review on algorithms for maximum clique problems. *European Journal of Operational Research*, 242(3), 693-709. <https://doi.org/10.1016/j.ejor.2014.09.064>
- Zhou, Y., Lin, W., Hao, J.-K., Xiao, M., & Jin, Y. (2022). Algoritma Branch-and-Bound termodifikasi untuk maximum s-bundle problem. *Journal of Combinatorial Optimization*, 140, 105670. <https://doi.org/10.1007/s10878-022-00898-w>

Zumla, A., George, A., Sharma, V., & Herbert, R. H. (2015). The WHO 2014 global tuberculosis report—further to go. *The Lancet Global Health*, 3(1), e10-e12. [https://doi.org/10.1016/S2214-109X\(14\)70347-1](https://doi.org/10.1016/S2214-109X(14)70347-1)