

- [15] Oladipo, H. J.; Tajudeen, Y. A.; Oladunjoye, I. O.; Yusuff, S. I.; Yusuf, R. O.; Oluwaseyi, E. M.; AbdulBasit, M. O.; Adebisi, Y. A.; El-Sherbini, M. S. (2022): Increasing challenges of malaria control in sub-Saharan Africa: Priorities for public health research and policymakers. *Annals of Medicine and Surgery*, **81**, pp. 1-6. Available at: <https://doi.org/10.1016/j.amsu.2022.104366>
- [16] Salanti, A.; Clausen, T. M.; Agerbæk, M. Ø.; Al Nakouzi, N.; Dahlbäck, M.; Oo, H. Z.; Lee, S.; Gustavsson, T.; Rich, J. R.; Hedberg, B. J.; Mao, Y.; Barington, L.; Pereira, M. A.; LoBello, J.; Endo, M.; Fazli, L.; Soden, J.; Wang, C. K.; ... ; Daugaard, M. (2015): Targeting human cancer by a glycosaminoglycan binding malaria protein. *cancer cell*, **28**(4), pp. 500–514. Available at: <https://doi.org/10.1016/j.ccell.2015.09.003>
- [17] Scardoni, G.; Tosadori, G.; Faizan, M.; Spoto, F.; Fabbri, F.; Laudanna, C. (2014): Biological network analysis with CentiScaPe: centralities and experimental dataset integration. *F1000Research* 2015, **3**, pp. 139. Available at: <https://doi.org/10.12688/f1000research.4477.2>
- [18] Szklarczyk, D.; Gable, A. L.; Lyon, D.; Junge, A.; Wyder, S.; Huerta-Cepas, J.; Simonovic, M.; Doncheva, N. T.; Morris, J. H.; Bork, P.; Jensen, L. J.; Mering, C. V. (2019): STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic acids research*, **47**(D1), pp. D607–D613. Available at: <https://doi.org/10.1093/nar/gky1131>
- [19] Szklarczyk, D.; Gable, A. L.; Nastou, K. C.; Lyon, D.; Kirsch, R.; Pyysalo, S.; Doncheva, N. T.; Legeay, M.; Fang, T.; Bork, P.; Jensen, L. J.; von Mering, C. (2021): The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. *Nucleic acids research*, **49**(D1), pp. D605–D612. Available at: <https://doi.org/10.1093/nar/gkaa1074>
- [20] Szklarczyk, D.; Kirsch, R.; Koutrouli, M.; Nastou, K.; Mehryary, F.; Hachilif, R.; Gable, A. L.; Fang, T.; Doncheva, N. T.; Pyysalo, S.; Bork, P.; Jensen, L. J.; von Mering, C. (2023): The STRING database in 2023: protein-protein association networks and functional enrichment analyses for any sequenced genome of interest. *Nucleic acids research*, **51**(D1), pp. D638–D646. Available at: <https://doi.org/10.1093/nar/gkac1000>
- [21] Talapko, J.; Škrlec, I.; Alebić, T.; Jukić, M.; Včev, A. (2019): Malaria: The past and the present. *Microorganisms*, **7**(6), p. 179. Available at: <https://doi.org/10.3390/microorganisms7060179>
- [22] Tang, Y.; Li, M.; Wang, J.; Pan, Y.; Wu, F. X. (2015): CytoNCA: a Cytoscape plugin for centrality analysis and evaluation of protein interaction networks. *Biosystems*, **127**, pp. 67–72. Available at: <https://doi.org/10.1016/j.biosystems.2014.11.005>
- [23] Thomas, P.D. (2017): The Gene Ontology and the Meaning of Biological Function. *The Gene Ontology Handbook*, **1446**, pp. 15-24. Available at: <https://doi.org/10.1007/978-1-4939-3743-1>
- [24] White, N. J.; Pukrittayakamee, S.; Hien, T. T.; Faiz, M. A.; Mokuolu, O. A.; Dondorp, A. M. (2014): Malaria. *Lancet* (London, England), **383**(9918), pp. 723–735. Available at: [https://doi.org/10.1016/S0140-6736\(13\)60024-0](https://doi.org/10.1016/S0140-6736(13)60024-0)
- [25] World Health Organization. (2022): *World Malaria Report 2022*. Geneva, Switzerland: Author.
- [26] Wu, C.; Buyya, R. (2015): Data Center Networks. In *Cloud Data Centers and Cost Modeling*. Elsevier Inc, Amsterdam. Available at: <https://doi.org/10.1016/b978-0-12-801413-4.00013-1>
- [27] Yi, Y.; Fang, Y.; Wu, K.; Liu, Y.; Zhang, W. (2020): Comprehensive gene and pathway analysis of cervical cancer progression. *Oncology Letters*, **19**(4), pp. 3316–3332. Available at: <https://doi.org/10.3892/ol.2020.11439>

Authors Profile



Nana Oktaviana is a final-year student majoring in Statistics and Data Science at the Department of Mathematics and Natural Sciences, IPB University. She has completed an internship in the field of bioinformatics at the Tropical Biofarmaka Research Center. Nana is passionate about applying statistical methods to solve real-world problems with a focus on data-driven research. She is currently exploring the intersection of statistics and life sciences to contribute to advancements in data-analysis methodologies.



Ananda Herlina Lutfitasari is a final-year student of Statistics and Data Science, at the Faculty of Mathematics and Natural Science, IPB University. Ananda has completed the bioinformatics internship at the Tropical Biofarmaka Research Center, IPB University. Ananda has applied statistical analysis to solve real problems. She is a data scientist who uses and processes raw data to discover interesting insights that help researchers make more informed decisions through visualization.



Wisnu Ananta Kusuma received his bachelor's and master's degrees from Bandung Institute of Technology, as well as his Ph.D. from Tokyo Institute of Technology, in 2012. He is currently an Associate Professor at the Department of Computer Science, IPB University. He also serves as Executive Secretary of Institute for International Research on Advanced Technology, IPB University, coordinator of Bioinformatics Working Group, Faculty of Mathematics and Natural Sciences, IPB University, and coordinator of Bioinformatics and High Performance Computing Research Group, Advanced Research Laboratory, IPB University. He has been the author of more than 60 articles and has reviewed for international journals. His current research interests include machine learning, high-performance computing, and bioinformatics research.