

## DAFTAR PUSTAKA

- [1] F. Bray, M. Laversanne, H. Sung, J. Ferlay, R. L. Siegel, I. Soerjomataram, and A. Jemal, “Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries,” *CA: A Cancer Journal for Clinicians*, vol. 74, no. 3, pp. 229–263, 2024, eprint: <https://onlinelibrary.wiley.com/doi/pdf/10.3322/caac.21834>. [Online]. Available: <https://onlinelibrary.wiley.com/doi/abs/10.3322/caac.21834>
- [2] Y. Alashban, “Breast cancer detection and classification with digital breast tomosynthesis: a two-stage deep learning approach,” *Diagnostic and Interventional Radiology*, Dec. 2024. [Online]. Available: <http://dx.doi.org/10.4274/dir.2024.242923>
- [3] R. L. Siegel, T. B. Kratzer, A. N. Giaquinto, H. Sung, and A. Jemal, “Cancer statistics, 2025,” *CA: A Cancer Journal for Clinicians*, vol. 75, no. 1, p. 10–45, Jan. 2025. [Online]. Available: <http://dx.doi.org/10.3322/caac.21871>
- [4] A. H. Saka, A. N. Giaquinto, L. E. McCullough, K. Y. Tossas, J. Star, A. Jemal, and R. L. Siegel, “Cancer statistics for african american and black people, 2025,” *CA: A Cancer Journal for Clinicians*, vol. 75, no. 2, p. 111–140, Feb. 2025. [Online]. Available: <http://dx.doi.org/10.3322/caac.21874>
- [5] C. G. Yedjou, J. N. Sims, L. Miele, F. Noubissi, L. Lowe, D. D. Fonseca, R. A. Alo, M. Payton, and P. B. Tchounwou, *Health and Racial Disparity in Breast Cancer*. Springer International Publishing, 2019, p. 31–49. [Online]. Available: [http://dx.doi.org/10.1007/978-3-030-20301-6\\_3](http://dx.doi.org/10.1007/978-3-030-20301-6_3)
- [6] G. I. Balali, D. D. Yar, V. G. A. Dela, E. Effah-Yeboah, P. Asumang, J. D. Akoto, and F. Abdallah, “Breast cancer: A review of mammography and clinical breast examination for early detection of cancer,” *OALib*, vol. 07, no. 10, p. 1–19, 2020. [Online]. Available: <http://dx.doi.org/10.4236/oalib.1106866>
- [7] C. E. Wulandari, “Skrining mamografi dan mortalitas kanker payudara,” *Cermin Dunia Kedokteran*, vol. 51, no. 12, p. 722–725, Dec. 2024. [Online]. Available: <http://dx.doi.org/10.55175/cdk.v51i12.1139>
- [8] R. M. Mann, A. Athanasiou, P. A. T. Baltzer, J. Camps-Herrero, P. Clauser, E. M. Fallenberg, G. Forrai, M. H. Fuchsänger, T. H. Helbich, F. Killburn-Toppin, M. Lesaru, P. Panizza, F. Pediconi, R. M. Pijnappel, K. Pinker, F. Sardanelli, T. Sella, I. Thomassin-Naggara, S. Zackrisson, F. J. Gilbert, and C. K. Kuhl, “Breast cancer screening in women with extremely dense breasts recommendations of the european society of breast imaging (eusobi),” *European Radiology*, vol. 32, no. 6, p. 4036–4045, Mar. 2022. [Online]. Available: <http://dx.doi.org/10.1007/s00330-022-08617-6>

- [9] A. F. Flemban, “Overdiagnosis due to screening mammography for breast cancer among women aged 40 years and over: A systematic review and meta-analysis,” *Journal of Personalized Medicine*, vol. 13, no. 3, p. 523, Mar. 2023. [Online]. Available: <http://dx.doi.org/10.3390/jpm13030523>
- [10] L. Lopez-Gonzalez, A. Sanchez Cendra, C. Sanchez Cendra, E. D. Roberts Cervantes, J. C. Espinosa, T. Pekarek, O. Fraile-Martinez, C. García-Montero, A. M. Rodriguez-Slocker, L. Jiménez-Álvarez, L. G. Guijarro, S. Aguado-Henche, J. Monserrat, M. Alvarez-Mon, L. Pekarek, M. A. Ortega, and R. Diaz-Pedrero, “Exploring biomarkers in breast cancer: Hallmarks of diagnosis, treatment, and follow-up in clinical practice,” *Medicina*, vol. 60, no. 1, p. 168, Jan. 2024. [Online]. Available: <http://dx.doi.org/10.3390/medicina60010168>
- [11] H. Satam, K. Joshi, U. Mangrolia, S. Waghoo, G. Zaidi, S. Rawool, R. P. Thakare, S. Banday, A. K. Mishra, G. Das, and S. K. Malonia, “Next-generation sequencing technology: Current trends and advancements,” *Biology*, vol. 12, no. 7, p. 997, Jul. 2023. [Online]. Available: <http://dx.doi.org/10.3390/biology12070997>
- [12] S. C. Das, W. Tasnim, H. K. Rana, U. K. Acharjee, M. M. Islam, and R. Khatun, “Comprehensive bioinformatics and machine learning analyses for breast cancer staging using TCGA dataset,” *Briefings in Bioinformatics*, vol. 26, no. 1, p. bbae628, Jan. 2025. [Online]. Available: <https://doi.org/10.1093/bib/bbae628>
- [13] Y. Wu, “Diagnosis of breast cancer based on support vector machine and random forest methods,” in *2020 International Conference on Computing and Data Science (CDS)*. IEEE, Aug. 2020, p. 147–151. [Online]. Available: <http://dx.doi.org/10.1109/CDS49703.2020.00036>
- [14] M. A. Naji, S. E. Filali, K. Aarika, E. H. Benlahmar, R. A. Abdelouhahid, and O. Debauche, “Machine learning algorithms for breast cancer prediction and diagnosis,” *Procedia Computer Science*, vol. 191, p. 487–492, 2021. [Online]. Available: <http://dx.doi.org/10.1016/j.procs.2021.07.062>
- [15] S. Yerukala Sathipati and S.-Y. Ho, “Identifying a mirna signature for predicting the stage of breast cancer,” *Scientific Reports*, vol. 8, no. 1, Oct. 2018. [Online]. Available: <http://dx.doi.org/10.1038/s41598-018-34604-3>
- [16] M. B. Amin, S. B. Edge, F. L. Greene, D. R. Byrd, R. K. Brookland, M. K. Washington, and L. R. Meyer, Eds., *AJCC Cancer Staging Manual*, 8th ed. Springer Cham, 2018, copyright American College of Surgeons 2017. [Online]. Available: <http://www.breastsurgeonsweb.com/wp-content/uploads/downloads/2020/10/AJCC-Breast-Cancer-Staging-System.pdf>

- [17] N. Budhbhatti and R. Saini, “Breast cancer progression to other organs,” *International journal of health sciences*, p. 13945–13958, Jun. 2022. [Online]. Available: <http://dx.doi.org/10.53730/ijhs.v6nS2.8658>
- [18] T. P. Padera, E. F. Meijer, and L. L. Munn, “The lymphatic system in disease processes and cancer progression,” *Annual Review of Biomedical Engineering*, vol. 18, no. 1, p. 125–158, Jul. 2016. [Online]. Available: <http://dx.doi.org/10.1146/annurev-bioeng-112315-031200>
- [19] C. Pulido, I. Vendrell, A. R. Ferreira, S. Casimiro, A. Mansinho, I. Alho, and L. Costa, “Bone metastasis risk factors in breast cancer,” *ecancermedicalscience*, vol. 11, Jan. 2017. [Online]. Available: <http://dx.doi.org/10.3332/ecancer.2017.715>
- [20] “Breast Cancer Statistics | How Common Is Breast Cancer?” [Online]. Available: <https://www.cancer.org/cancer/types/breast-cancer/about/how-common-is-breast-cancer.html>
- [21] Z. He, Z. Chen, M. Tan, S. Elingarami, Y. Liu, T. Li, Y. Deng, N. He, S. Li, J. Fu, and W. Li, “A review on methods for diagnosis of breast cancer cells and tissues,” *Cell Proliferation*, vol. 53, no. 7, Jun. 2020. [Online]. Available: <http://dx.doi.org/10.1111/cpr.12822>
- [22] R. D. Rosen and A. Sapra, “TNM Classification,” in *StatPearls*. Treasure Island (FL): StatPearls Publishing, 2025. [Online]. Available: <http://www.ncbi.nlm.nih.gov/books/NBK553187/>
- [23] F. Finotello and B. Di Camillo, “Measuring differential gene expression with rna-seq: challenges and strategies for data analysis,” *Briefings in Functional Genomics*, vol. 14, no. 2, p. 130–142, Sep. 2014. [Online]. Available: <http://dx.doi.org/10.1093/bfgp/elu035>
- [24] Y. Zhao, M.-C. Li, M. M. Konaté, L. Chen, B. Das, C. Karlovich, P. M. Williams, Y. A. Evrard, J. H. Doroshow, and L. M. McShane, “Tpm, fpkm, or normalized counts? a comparative study of quantification measures for the analysis of rna-seq data from the nci patient-derived models repository,” *Journal of Translational Medicine*, vol. 19, no. 1, Jun. 2021. [Online]. Available: <http://dx.doi.org/10.1186/s12967-021-02936-w>
- [25] C. Backes, B. Meder, M. Hart, N. Ludwig, P. Leidinger, B. Vogel, V. Galata, P. Roth, J. Menegatti, F. Grässer, K. Ruprecht, M. Kahraman, T. Grossmann, J. Haas, E. Meese, and A. Keller, “Prioritizing and selecting likely novel mirnas from ngs data,” *Nucleic Acids Research*, vol. 44, no. 6, p. e53–e53, Dec. 2015. [Online]. Available: <http://dx.doi.org/10.1093/nar/gkv1335>
- [26] D. Rosati, M. Palmieri, G. Brunelli, A. Morrione, F. Iannelli, E. Frullanti, and A. Giordano, “Differential gene expression analysis pipelines and

- bioinformatic tools for the identification of specific biomarkers: A review,” *Computational and Structural Biotechnology Journal*, vol. 23, p. 1154–1168, Dec. 2024. [Online]. Available: <http://dx.doi.org/10.1016/j.csbj.2024.02.018>
- [27] M. E. Ritchie, B. Phipson, D. Wu, Y. Hu, C. W. Law, W. Shi, and G. K. Smyth, “limma powers differential expression analyses for rna-sequencing and microarray studies,” *Nucleic Acids Research*, vol. 43, no. 7, p. e47–e47, Jan. 2015. [Online]. Available: <http://dx.doi.org/10.1093/nar/gkv007>
- [28] G. K. Smyth, M. Ritchie, N. Thorne, J. Wettenhall, W. Shi, and Y. Hu, “bioconductor.org,” <https://www.bioconductor.org/packages-devel/bioc/vignettes/limma/inst/doc/usersguide.pdf>, p. 70, 2002.
- [29] A. Bommert, T. Welchowski, M. Schmid, and J. Rahnenführer, “Benchmark of filter methods for feature selection in high-dimensional gene expression survival data,” *Briefings in Bioinformatics*, vol. 23, no. 1, Sep. 2021. [Online]. Available: <http://dx.doi.org/10.1093/bib/bbab354>
- [30] M. BÜYÜKKEundefinedECİ and M. C. OKUR, “A comprehensive review of feature selection and feature selection stability in machine learning,” *Gazi University Journal of Science*, vol. 36, no. 4, p. 1506–1520, Dec. 2023. [Online]. Available: <http://dx.doi.org/10.35378/gujs.993763>
- [31] M. M. Ali, M. S. Islam, M. N. Uddin, and M. A. Uddin, “A conceptual iot framework based on anova-f feature selection for chronic kidney disease detection using deep learning approach,” *Intelligence-Based Medicine*, vol. 10, p. 100170, 2024. [Online]. Available: <http://dx.doi.org/10.1016/j.ibmed.2024.100170>
- [32] A. C. R. and V. M. A. Bai, “Optimizing breast cancer recurrence forecasting using anova feature selection and gru models,” *International Journal of Electronics and Communication Engineering*, vol. 11, no. 11, p. 213–227, Nov. 2024. [Online]. Available: <http://dx.doi.org/10.14445/23488549/IJECE-V11I11P118>
- [33] A. M. Priyatno and T. Widyaningtyas, “A systematic literature review: Recursive feature elimination algorithms,” *JITK (Jurnal Ilmu Pengetahuan dan Teknologi Komputer)*, vol. 9, no. 2, p. 196–207, Feb. 2024. [Online]. Available: <http://dx.doi.org/10.33480/jitk.v9i2.5015>
- [34] E. S. Septiany, H. H. Handayani, T. A. Mudzakir, and A. F. N. Masruriyah, “Optimasi metode support vector machine menggunakan seleksi fitur recursive feature elimination dan forward selection untuk klasifikasi kanker payudara,” *TIN: Terapan Informatika Nusantara*, vol. 5, no. 2, p. 144–154, Jul. 2024. [Online]. Available: <http://dx.doi.org/10.47065/tin.v5i2.5324>

- [35] X. Zou, Y. Hu, Z. Tian, and K. Shen, “Logistic regression model optimization and case analysis,” in *2019 IEEE 7th International Conference on Computer Science and Network Technology (ICCSNT)*. IEEE, Oct. 2019, p. 135–139. [Online]. Available: <http://dx.doi.org/10.1109/ICCSNT47585.2019.8962457>
- [36] A. Zaidi and A. S. M. Al Luhayb, “Two statistical approaches to justify the use of the logistic function in binary logistic regression,” *Mathematical Problems in Engineering*, vol. 2023, no. 1, Jan. 2023. [Online]. Available: <http://dx.doi.org/10.1155/2023/5525675>
- [37] S. H. Hasanah, “Classification support vector machine in breast cancer patients,” *BAREKENG: Jurnal Ilmu Matematika dan Terapan*, vol. 16, no. 1, p. 129–136, Mar. 2022. [Online]. Available: <http://dx.doi.org/10.30598/barekengvol16iss1pp129-136>
- [38] P. Kartikasari, I. T. Utami, S. Suparti, and S. D. F. Rahman, “Breast cancer classification using support vector machine (svm) and light gradient boosting machine (lightgbm) models,” *MEDIA STATISTIKA*, vol. 16, no. 2, p. 182–193, Feb. 2024. [Online]. Available: <http://dx.doi.org/10.14710/medstat.16.2.182-193>
- [39] Z. Jun, “The development and application of support vector machine,” *Journal of Physics: Conference Series*, vol. 1748, no. 5, p. 052006, Jan. 2021. [Online]. Available: <http://dx.doi.org/10.1088/1742-6596/1748/5/052006>
- [40] Vujovic, “Classification model evaluation metrics,” *International Journal of Advanced Computer Science and Applications*, vol. 12, no. 6, 2021. [Online]. Available: <http://dx.doi.org/10.14569/IJACSA.2021.0120670>
- [41] T. Fawcett, “An introduction to roc analysis,” *Pattern Recognition Letters*, vol. 27, no. 8, p. 861–874, Jun. 2006. [Online]. Available: <http://dx.doi.org/10.1016/j.patrec.2005.10.010>
- [42] K. undefinedorbacıoğlu and G. Aksel, “Receiver operating characteristic curve analysis in diagnostic accuracy studies: A guide to interpreting the area under the curve value,” *Turkish Journal of Emergency Medicine*, vol. 23, no. 4, p. 195–198, Oct. 2023. [Online]. Available: [http://dx.doi.org/10.4103/tjem.tjem\\_182\\_23](http://dx.doi.org/10.4103/tjem.tjem_182_23)
- [43] “STAR Counts - GDC Docs — docs.gdc.cancer.gov,” [https://docs.gdc.cancer.gov/Encyclopedia/pages/STAR\\_Counts/#:~:text=STAR%20%2D%20Counts%20is%20a%20pipeline, and %20generates%20transcriptome%20profiling%20data.,](https://docs.gdc.cancer.gov/Encyclopedia/pages/STAR_Counts/#:~:text=STAR%20%2D%20Counts%20is%20a%20pipeline, and %20generates%20transcriptome%20profiling%20data.,) [Accessed 23-05-2025].
- [44] L. Chen, D. Lu, K. Sun, Y. Xu, P. Hu, X. Li, and F. Xu, “Identification of biomarkers associated with diagnosis and prognosis of colorectal cancer patients based on integrated bioinformatics analysis,”

*Gene*, vol. 692, p. 119–125, Apr. 2019. [Online]. Available: <http://dx.doi.org/10.1016/j.gene.2019.01.001>

- [45] X. Ding, F. Yang, and F. Ma, “An efficient model selection for linear discriminant function-based recursive feature elimination,” *Journal of Biomedical Informatics*, vol. 129, p. 104070, May 2022. [Online]. Available: <http://dx.doi.org/10.1016/j.jbi.2022.104070>
- [46] G. Lee and M. Lee, “Classification of genes based on age-related differential expression in breast cancer,” *Genomics & Informatics*, vol. 15, no. 4, p. 156–161, Dec. 2017. [Online]. Available: <http://dx.doi.org/10.5808/GI.2017.15.4.156>
- [47] J. Du, Y. Dong, and Y. Li, “Identification and prognostic value exploration of cyclophosphamide (cytoxan)-centered chemotherapy response-associated genes in breast cancer,” *DNA and Cell Biology*, vol. 40, no. 11, p. 1356–1368, Nov. 2021. [Online]. Available: <http://dx.doi.org/10.1089/dna.2021.0077>
- [48] Y. He, X. Li, Y. Meng, S. Fu, Y. Cui, Y. Shi, and H. Du, “A prognostic 11 long noncoding rna expression signature for breast invasive carcinoma,” *Journal of Cellular Biochemistry*, vol. 120, no. 10, p. 16692–16702, May 2019. [Online]. Available: <http://dx.doi.org/10.1002/jcb.28927>
- [49] Y. Tian, J. Wang, Q. Wen, A. Gao, A. Huang, R. Li, Y. Zhang, G. Su, and Y. Sun, “The significance of tumor microenvironment score for breast cancer patients,” *BioMed Research International*, vol. 2022, no. 1, Jan. 2022. [Online]. Available: <http://dx.doi.org/10.1155/2022/5673810>
- [50] H. Ren, X. Shen, M. Xie, and X. Guo, “Construction of a prognostic score model for breast cancer based on multi-omics analysis of study on bone metastasis,” *Translational Cancer Research*, vol. 13, no. 5, p. 2419–2436, May 2024. [Online]. Available: <http://dx.doi.org/10.21037/tcr-23-1881>
- [51] I. X. Perez-Añorve, C. H. Gonzalez-De la Rosa, E. Soto-Reyes, F. O. Beltran-Anaya, O. Del Moral-Hernandez, M. Salgado-Albaran, O. Angeles-Zaragoza, J. A. Gonzalez-Barrios, D. A. Landero-Huerta, M. Chavez-Saldaña, A. Garcia-Carranca, N. Villegas-Sepulveda, and E. Arechaga-Ocampo, “New insights into radioresistance in breast cancer identify a dual function of mir-122 as a tumor suppressor and oncomir,” *Molecular Oncology*, vol. 13, no. 5, p. 1249–1267, Apr. 2019. [Online]. Available: <http://dx.doi.org/10.1002/1878-0261.12483>
- [52] Y. Pan, Q. Zou, W. Yin, Z. Huang, Y. Zhao, Z. Mo, L. Li, and J. Yang, “Development of lymph node metastasis-related prognostic markers in breast cancer,” *Journal of Proteomics*, vol. 291, p. 105045, Jan. 2024. [Online]. Available: <http://dx.doi.org/10.1016/j.jprot.2023.105045>

- [53] Y. Wang, J. Wu, J. Zhao, T. Xu, M. Zhang, J. Liu, Y. Wang, Q. Wang, and X. Song, “Global characterization of rna editing in genetic regulation of multiple ovarian cancer subtypes,” *Molecular Therapy - Nucleic Acids*, vol. 35, no. 1, p. 102127, Mar. 2024. [Online]. Available: <http://dx.doi.org/10.1016/j.omtn.2024.102127>
- [54] M. Sharma, I. Castro-Piedras, A. D. Rodgers, and K. Pruitt, “Genomic profiling of dvl-1 and its nuclear role as a transcriptional regulator in triple negative breast cancer,” *Genes amp; Cancer*, vol. 12, p. 77–95, Oct. 2021. [Online]. Available: <http://dx.doi.org/10.18632/genesandcancer.217>
- [55] R. Medina-Aguilar, C. Pérez-Plasencia, P. Gariglio, L. A. Marchat, A. Flores-Pérez, C. López-Camarillo, and J. García Mena, “Dna methylation data for identification of epigenetic targets of resveratrol in triple negative breast cancer cells,” *Data in Brief*, vol. 11, p. 169–182, Apr. 2017. [Online]. Available: <http://dx.doi.org/10.1016/j.dib.2017.02.006>

