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- [1] World Health Organization (WHO). (2022) Cancer. Accessed: 2025-01-28. [Online]. Available: <https://www.who.int/news-room/fact-sheets/detail/cancer>
- [2] R. D. Nindrea, I. Dwiprahasto, L. Lazuardi, and T. Aryandono, “Development of a breast cancer risk screening tool for women in indonesia,” *Clinical Epidemiology and Global Health*, vol. 24, p. 101446, 2023. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S2213398423002336>
- [3] S. Sarina, R. M. Thaha, and S. Nasir, “faktor yang berhubungan dengan perilaku sadari sebagai deteksi dini kanker payudara pada mahasiswa fkm unhas,” *Hasanuddin Journal of Public Health*, vol. 1, no. 1, pp. 61–70, 2020.
- [4] M. Andika and F. Febriyanti, “Faktor keterlambatan diagnosis kanker payudara pada penderita kanker payudara di poli bedah rsup dr. m. djamil padang mira andika1, febriyanti2,” *Menara Ilmu: Jurnal Penelitian dan Kajian Ilmiah*, vol. 18, no. 2, 2024.
- [5] M. Dieterich, J. Stubert, T. Reimer, N. Erickson, and A. Berling, “Influence of lifestyle factors on breast cancer risk,” *Breast care*, vol. 9, no. 6, pp. 407–414, 2014.
- [6] A. Tsapatsaris, K. Babagbemi, and M. B. Reichman, “Barriers to breast cancer screening are worsened amidst covid-19 pandemic: A review,” *Clinical Imaging*, vol. 82, pp. 224–227, 2022. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S0899707121004563>
- [7] A. Mootz, F. Arjmandi, B. E. Dogan, and W. P. Evans, “Health care disparities in breast cancer: the economics of access to screening, diagnosis, and treatment,” *Journal of Breast Imaging*, vol. 2, no. 6, pp. 524–529, 2020.
- [8] T. D. Ellington, S. J. Henley, R. J. Wilson, J. W. Miller, M. Wu, and L. C. Richardson, “Trends in breast cancer mortality by race/ethnicity, age, and us census region, united states 1999-2020,” *Cancer*, vol. 129, no. 1, pp. 32–38, 2023.
- [9] J. G. Elmore, K. Armstrong, C. D. Lehman, and S. W. Fletcher, “Screening for breast cancer,” *Jama*, vol. 293, no. 10, pp. 1245–1256, 2005.
- [10] H. T. Salem, E. A. S. Sabek, and J. M. Saleh, “Pros and cons of pre mammography examination technique description on pain in mammography and re-attending screening programme,” *Egyptian Journal of Radiation Sciences and Applications*, vol. 36, no. 1, pp. 91–97, 2023.

- [11] S. Alonso Roca, A. Delgado Laguna, J. Arantzeta Lexarreta, B. Cajal Campo, and S. Santamaría Jareño, “Screening in patients with increased risk of breast cancer (part 1): Pros and cons of mri screening,” *Radiología (English Edition)*, vol. 62, no. 4, pp. 252–265, 2020. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S2173510720300422>
- [12] G. Franceschini, A. Di Leone, D. Terribile, M. A. Sanchez, and R. Masetti, “Bilateral prophylactic mastectomy in brca mutation carriers: what surgeons need to know,” *Annali italiani di chirurgia*, vol. 90, no. 1, pp. 1–2, 2019.
- [13] M. RINDE, “Broader ngs use hinges on payers, access, and education,” *Broader NGS Use Hinges on Payers, Access, and Education*, p. 24.
- [14] 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 *et al.*, “Exploring biomarkers in breast cancer: Hallmarks of diagnosis, treatment, and follow-up in clinical practice,” *Medicina*, vol. 60, no. 1, p. 168, 2024.
- [15] T. S. Kalinina, V. V. Kononchuk, A. K. Yakovleva, E. Y. Alekseenok, S. V. Sidorov, and L. F. Gulyaeva, “Association between lymph node status and expression levels of androgen receptor, mir-185, mir-205, and mir-21 in breast cancer subtypes,” *International journal of breast cancer*, vol. 2020, no. 1, p. 3259393, 2020.
- [16] H. Schwarzenbach, N. Nishida, G. A. Calin, and K. Pantel, “Clinical relevance of circulating cell-free micrornas in cancer,” *Nature reviews Clinical oncology*, vol. 11, no. 3, pp. 145–156, 2014.
- [17] H. Wu, “A deep learning-based hybrid feature selection approach for cancer diagnosis,” in *Journal of Physics: Conference Series*, vol. 1848, no. 1. IOP Publishing, 2021, p. 012019.
- [18] 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, 12 2024. [Online]. Available: <https://doi.org/10.1093/bib/bbae628>
- [19] A. Kishore, L. Venkataramana, D. V. V. Prasad, A. Mohan, and B. Jha, “Enhancing the prediction of idc breast cancer staging from gene expression profiles using hybrid feature selection methods and deep learning architecture,” *Medical & Biological Engineering & Computing*, vol. 61, no. 11, pp. 2895–2919, 2023.
- [20] R. D. Rosen and A. Sapra, *TNM Classification*. Treasure Island (FL): StatPearls Publishing, 2020, available from: <https://www.ncbi.nlm.nih.gov/books/NBK553187/>.

- [21] E. L. Davies, “Breast cancer,” *Medicine*, vol. 44, no. 1, pp. 42–46, 2016, oncology. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S1357303915002674>
- [22] J. Koh and M. J. Kim, “Introduction of a new staging system of breast cancer for radiologists: an emphasis on the prognostic stage,” *Korean journal of radiology*, vol. 20, no. 1, pp. 69–82, 2019.
- [23] A. E. Giuliano, J. L. Connolly, S. B. Edge, E. A. Mittendorf, H. S. Rugo, L. J. Solin, D. L. Weaver, D. J. Winchester, and G. N. Hortobagyi, “Breast cancer—major changes in the american joint committee on cancer eighth edition cancer staging manual,” *CA: a cancer journal for clinicians*, vol. 67, no. 4, pp. 290–303, 2017.
- [24] D. Ramsköld, E. Kavak, and R. Sandberg, “How to analyze gene expression using rna-sequencing data,” *Next Generation Microarray Bioinformatics: Methods and Protocols*, pp. 259–274, 2012.
- [25] A. P. Heath, V. Ferretti, S. Agrawal *et al.*, “The nci genomic data commons,” *Nature Genetics*, vol. 53, pp. 257–262, 2021. [Online]. Available: <https://doi.org/10.1038/s41588-021-00791-5>
- [26] Z. Akond, M. Alam, and M. N. H. Mollah, “Biomarker identification from rna-seq data using a robust statistical approach,” *Bioinformation*, vol. 14, no. 4, p. 153, 2018.
- [27] S. D. Fiedler, M. Z. Carletti, and L. K. Christenson, “Quantitative rt-pcr methods for mature microrna expression analysis,” *RT-PCR Protocols: Second Edition*, pp. 49–64, 2010.
- [28] S. Tam, R. De Borja, M.-S. Tsao, and J. D. McPherson, “Robust global microrna expression profiling using next-generation sequencing technologies,” *Laboratory investigation*, vol. 94, no. 3, pp. 350–358, 2014.
- [29] J. Y. Jang, Y. S. Kim, K. N. Kang, K. H. Kim, Y. J. Park, and C. W. Kim, “Multiple micrornas as biomarkers for early breast cancer diagnosis,” *Molecular and clinical oncology*, vol. 14, no. 2, p. 31, 2021.
- [30] 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, pp. 1154–1168, 2024. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S2001037024000424>
- [31] 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, pp. e47–e47, 01 2015. [Online]. Available: <https://doi.org/10.1093/nar/gkv007>
- [32] R. Gentleman, V. Carey, W. Huber, R. Irizarry, and S. Dudoit, *Bioinformatics and computational biology solutions using R and Bioconductor*. Springer Science & Business Media, 2005.
- [33] J. Labory, E. Njomgue-Fotso, and S. Bottini, “Benchmarking feature selection and feature extraction methods to improve the performances of machine-learning algorithms for patient classification using metabolomics biomedical data,” *Computational and Structural Biotechnology Journal*, vol. 23, pp. 1274–1287, 2024. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S2001037024000692>
- [34] J. Qin and Y. Lou, “L1-2 regularized logistic regression,” in *2019 53rd Asilomar Conference on Signals, Systems, and Computers*. Pacific Grove, CA, USA: IEEE, 2019, pp. 779–783.
- [35] D. Jurafsky and J. H. Martin, *Speech and Language Processing: An Introduction to Natural Language Processing, Computational Linguistics, and Speech Recognition*, ser. Prentice Hall Series in Artificial Intelligence. Upper Saddle River, NJ, USA: Pearson Prentice Hall, 2009. [Online]. Available: <https://books.google.co.id/books?id=fZmj5UNK8AQC>
- [36] S.-I. Lee, H. Lee, P. Abbeel, and A. Y. Ng, “Efficient ℓ^1 regularized logistic regression,” in *Aaaai*, vol. 6, 2006, pp. 401–408.
- [37] Deepali, N. Goel, and Padmavati, “Optimized prognostic models for oral cancer survival using feature selection methods,” *Procedia Computer Science*, vol. 235, pp. 1832–1840, 2024, international Conference on Machine Learning and Data Engineering (ICMLDE 2023). [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S1877050924008500>
- [38] A. Bustamam, A. Bachtiar, and D. Sarwinda, “Selecting features subsets based on support vector machine-recursive features elimination and one dimensional-naïve bayes classifier using support vector machines for classification of prostate and breast cancer,” *Procedia Computer Science*, vol. 157, pp. 450–458, 2019, the 4th International Conference on Computer Science and Computational Intelligence (ICCSCI 2019) : Enabling Collaboration to Escalate Impact of Research Results for Society. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S1877050919311573>
- [39] M.-W. Huang, C.-W. Chen, W.-C. Lin, S.-W. Ke, and C.-F. Tsai, “Svm and svm ensembles in breast cancer prediction,” *PloS one*, vol. 12, no. 1, p. e0161501, 2017.

- [40] S. Ray, “A quick review of machine learning algorithms,” in *2019 International conference on machine learning, big data, cloud and parallel computing (COMITCon)*. IEEE, 2019, pp. 35–39.
- [41] Y. Hamasuna, Y. Endo, and S. Miyamoto, “Support vector machine for data with tolerance based on hard-margin and soft-margin,” in *2008 IEEE International Conference on Fuzzy Systems (IEEE World Congress on Computational Intelligence)*. IEEE, 2008, pp. 750–755.
- [42] M. L. Dantas Dias and A. R. Rocha Neto, “Training soft margin support vector machines by simulated annealing: A dual approach,” *Expert Systems with Applications*, vol. 87, pp. 157–169, 2017. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S0957417417304347>
- [43] H. Yu and S. Kim, *SVM Tutorial — Classification, Regression and Ranking*. Berlin, Heidelberg: Springer Berlin Heidelberg, 2012, pp. 479–506. [Online]. Available: https://doi.org/10.1007/978-3-540-92910-9_15
- [44] T. M. Manik, P. Gultom, and E. Nababan, “Analisis karakteristik fungsi lagrange dalam menyelesaikan permasalahan optimasi berkendala,” in *Talenta Conference Series: Science and Technology (ST)*, vol. 1, no. 1, 2018, pp. 037–043.
- [45] A. S. Nugroho, A. B. Witarto, and D. Handoko, “Support vector machine,” *Proceeding Indones. Sci. Meeiting Cent. Japan*, 2003.
- [46] I. Roman, R. Santana, A. Mendiburu, and J. A. Lozano, “In-depth analysis of svm kernel learning and its components,” *Neural Computing and Applications*, vol. 33, no. 12, pp. 6575–6594, 2021.
- [47] R. Guido, S. Ferrisi, D. Lofaro, and D. Conforti, “An overview on the advancements of support vector machine models in healthcare applications: a review,” *Information*, vol. 15, no. 4, p. 235, 2024.
- [48] M. A. Shaik, G. Rakshitha, K. Saipriya, T. Thrisha, M. Varshini, and J. G. Sai, “Machine learning for detecting the phishing threats,” in *2025 6th International Conference on Mobile Computing and Sustainable Informatics (ICMCSI)*. IEEE, 2025, pp. 1221–1226.
- [49] V. Jackins, S. Vimal, M. Kaliappan, and M. Y. Lee, “Ai-based smart prediction of clinical disease using random forest classifier and naive bayes,” *The Journal of Supercomputing*, vol. 77, no. 5, pp. 5198–5219, 2021.
- [50] Y. Tian, B. Wu, X. Su, Y. Qi, Y. Chen, and Z. Min, “A crown contour envelope model of chinese fir based on random forest and mathematical modeling,” *Forests*, vol. 12, no. 1, p. 48, 2020.

- [51] N. Huang, G. Lu, G. Cai, D. Xu, J. Xu, F. Li, and L. Zhang, “Feature selection of power quality disturbance signals with an entropy-importance-based random forest,” *Entropy*, vol. 18, no. 2, p. 44, 2016.
- [52] M. I. Prasetyowati, N. U. Maulidevi, and K. Surendro, “Determining threshold value on information gain feature selection to increase speed and prediction accuracy of random forest,” *Journal of Big Data*, vol. 8, no. 1, p. 84, 2021.
- [53] M. I. Jauhari, M. P. Wirakusuma, A. Sidqi, I. G. N. R. Putra, I. Wijayanto, A. Rizal, and S. Hadiyoso, “Implementation of ensemble machine learning with voting classifier for reliable tuberculosis detection using chest x-ray images with imbalance dataset,” *Journal of Electronics, Electromedical Engineering, and Medical Informatics*, vol. 6, no. 4, pp. 543–548, 2024.
- [54] A. Manconi, G. Armano, M. Gnocchi, and L. Milanesi, “A soft-voting ensemble classifier for detecting patients affected by covid-19,” *Applied Sciences*, vol. 12, no. 15, p. 7554, 2022.
- [55] K. Shah, H. Patel, D. Sanghvi, and M. Shah, “A comparative analysis of logistic regression, random forest and knn models for the text classification. augment hum res 5 (1): 12,” 2020.
- [56] M. J. Goldman, B. Craft, M. Hastie, K. Repečka, F. McDade, A. Kamath, A. Banerjee, Y. Luo, D. Rogers, A. N. Brooks *et al.*, “Visualizing and interpreting cancer genomics data via the xena platform,” *Nature biotechnology*, vol. 38, no. 6, pp. 675–678, 2020.
- [57] J. Luengo, D. García-Gil, S. Ramírez-Gallego, S. García, and F. Herrera, “Big data preprocessing,” *Cham: Springer*, vol. 1, pp. 1–186, 2020.
- [58] S. Vinay, “Standardization in machine learning,” ResearchGate. [Online]. Available: https://www.researchgate.net/publication/349869617_STANDARDIZATION_IN_MACHINE_LEARNING, 2021.
- [59] 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, pp. 119–125, 2019. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S0378111919300137>
- [60] A. Louw, “The functional characterisation of human rmnd5 proteins in normal physiology and prostate cancer,” Ph.D. dissertation, University of Western Australia, 2013.
- [61] J. Li, Z. Yan, J. Ma, Z. Chu, H. Li, J. Guo, Q. Zhang, H. Zhao, Y. Li, and T. Wang, “Zkscan5 activates vegfc expression by recruiting setd7 to promote

the lymphangiogenesis, tumour growth, and metastasis of breast cancer,” *Frontiers in Oncology*, vol. 12, p. 875033, 2022.

- [62] Y. Yang, B. Ma, M. Djamshidi, Q. Zhang, A. Sarkar, A. Chanda, U. Tran, J. Soh, C. Sandall, H.-M. Chen, J. A. MacDonald, S. Bonni, C. W. Senzen, J. Zheng, and K. Riabowol, “Ing1 inhibits twist1 expression to block emt and is antagonized by the hdac inhibitor vorinostat,” *European Journal of Cell Biology*, vol. 102, no. 3, p. 151341, 2023. [Online]. Available: <https://www.sciencedirect.com/science/article/pii/S0171933523000560>
- [63] J. P. C. Da Cunha, P. A. F. Galante, J. E. S. De Souza, M. Pieprzyk, D. M. Carraro, L. J. Old, A. A. Camargo, and S. J. De Souza, “The human cell surfaceome of breast tumors,” *BioMed research international*, vol. 2013, no. 1, p. 976816, 2013.
- [64] H. Zhang, X. Qu, and L. Han, “Identification of death-associated protein-like 1 (dapl1) as a novel prognostic biomarker of breast cancer,” 2020.
- [65] S. Wang, J. Jin, J. Chen, and W. Lou, “Muc14-related ncRNA-mRNA network in breast cancer,” *Genes*, vol. 12, no. 11, p. 1677, 2021.
- [66] P. L. Farré, G. D. Scalise, R. B. Duca, G. N. Dalton, C. Massillo, J. Porretti, K. Graña, K. Gardner, P. De Luca, and A. De Siervi, “Ctbp1 and metabolic syndrome induce an mRNA and miRNA expression profile critical for breast cancer progression and metastasis,” *Oncotarget*, vol. 9, no. 17, p. 13848, 2018.
- [67] J. Jung and S. Yoo, “Identification of breast cancer metastasis markers from gene expression profiles using machine learning approaches,” *Genes*, vol. 14, no. 9, p. 1820, 2023.
- [68] B. Zhang, Y. Gu, and G. Jiang, “28p expression and prognosis characteristics of m6a RNA methylation regulators in breast cancer,” *Annals of Oncology*, vol. 31, p. S1225, 2020.
- [69] H. Wang, L. Shu, N. Niu, C. Zhao, S. Lu, Y. Li, H. Wang, Y. Liu, T. Zou, J. Zou *et al.*, “Novel lncRNAs with diagnostic or prognostic value screened out from breast cancer via bioinformatics analyses,” *PeerJ*, vol. 10, p. e13641, 2022.