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- [1] World Health Organization, "Breast cancer," 2025. [Online]. Available: <https://www.who.int/news-room/fact-sheets/detail/breast-cancer>
- [2] E. I. Obeagu and G. U. Obeagu, "Breast cancer: A review of risk factors and diagnosis," *Medicine*, vol. 103, p. e36905, 1 2024. [Online]. Available: <https://journals.lww.com/10.1097/MD.00000000000036905>
- [3] U. Naseem, J. Rashid, L. Ali, J. Kim, Q. E. U. Haq, M. J. Awan, and M. Imran, "An automatic detection of breast cancer diagnosis and prognosis based on machine learning using ensemble of classifiers," *IEEE Access*, vol. 10, pp. 78 242–78 252, 2022. [Online]. Available: <https://doi.org/10.1109/ACCESS.2022.3174599>
- [4] V. Chaurasia and S. Pal, "Applications of machine learning techniques to predict diagnostic breast cancer," *SN Computer Science*, vol. 1, p. 270, 9 2020. [Online]. Available: <https://doi.org/10.1007/s42979-020-00296-8>
- [5] M. E. Mayerhoefer, A. Materka, G. Langs, I. Häggström, P. Szczypiński, P. Gibbs, and G. Cook, "Introduction to radiomics," *Journal of Nuclear Medicine*, vol. 61, pp. 488–495, 4 2020. [Online]. Available: <https://jnm.snmjournals.org/content/61/4/488>
- [6] T. Honjo, D. Ueda, Y. Katayama, A. Shimazaki, A. Jogo, K. Kageyama, K. Murai, H. Tatekawa, S. Fukumoto, A. Yamamoto *et al.*, "Visual and quantitative evaluation of microcalcifications in mammograms with deep learning-based super-resolution," *European Journal of Radiology*, vol. 154, p. 110433, 2022. [Online]. Available: <https://doi.org/10.1016/j.ejrad.2022.110433>
- [7] W. Rogers, T. Seetha, S. Refaee, T. I. Y. Lieveise, R. W. Y. Granzier, and R. Ibrahim, "Radiomics: from qualitative to quantitative imaging," 2020. [Online]. Available: <https://doi.org/10.1259/bjr.20190948>
- [8] J. Wu and C. Hicks, "Breast cancer type classification using machine learning," pp. 1–12, 2 2021. [Online]. Available: <https://doi.org/10.3390/jpm11020061>
- [9] L. Macías-García, M. Martínez-Ballesteros, J. M. Luna-Romera, J. M. García-Heredia, J. García-Gutiérrez, and J. C. Riquelme-Santos, "Autoencoded dna methylation data to predict breast cancer recurrence: Machine learning models and gene-weight significance," *Artificial Intelligence in Medicine*, vol. 110, p. 101976, 2020. [Online]. Available: <https://doi.org/10.1016/j.artmed.2020.101976>
- [10] 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>
- [11] R. Alvarez-Gonzalez, D. Glez-Pena, F. Diaz, and F. Fdez-Riverola, "Discriminant fuzzy pattern to filter differentially expressed genes," 2010.
- [12] 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, 7 2020. [Online]. Available: <https://doi.org/10.1111/cpr.12822>
- [13] G. Natale, M. E. Stouthandel, T. V. Hoof, and G. Bocci, "The lymphatic system in breast cancer: Anatomical and molecular approaches," 11 2021. [Online]. Available: <https://doi.org/10.3390/medicina57111272>

- [14] D. C. Teichgraber, M. S. Guirguis, and G. J. Whitman, "Breast cancer staging: Updates in the ajcc cancer staging manual , 8th edition, and current challenges for radiologists, from the ajr special series on cancer staging," *American Journal of Roentgenology*, vol. 217, pp. 278–290, 8 2021. [Online]. Available: <https://doi.org/10.2214/AJR.20.25223>
- [15] S. S. Badve, P. D. Beitsch, S. Bose, D. R. Byrd, V. W. Chen, I. A. Mayer, B. McCormick, E. A. Mittendorf, A. Recht, J. S. Reis-Filho, F. Hope, S. Rugo, J. F. Simpson, L. J. Solin, F. W. F. Symmans, T. M. Vallerand, D. L. Weaver, and D. J. Winchester, "Members of the breast expert panel," 2017. [Online]. Available: <https://doi.org/10.2214/AJR.20.25223>
- [16] L. A. Corchete, E. A. Rojas, D. Alonso-López, J. D. L. Rivas, N. C. Gutiérrez, and F. J. Burguillo, "Systematic comparison and assessment of rna-seq procedures for gene expression quantitative analysis," *Scientific Reports*, vol. 10, p. 19737, 11 2020. [Online]. Available: <https://doi.org/10.1038/s41598-020-76881-x>
- [17] 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, p. 269, 12 2021. [Online]. Available: <https://doi.org/10.1186/s12967-021-02936-w>
- [18] R. Saatchi, "Fuzzy logic concepts, developments and implementation," *Information (Switzerland)*, vol. 15, 10 2024. [Online]. Available: <https://doi.org/10.3390/info15100656>
- [19] U. M. Khaire and R. Dhanalakshmi, "Stability of feature selection algorithm: A review," *Journal of King Saud University - Computer and Information Sciences*, vol. 34, pp. 1060–1073, 4 2022. [Online]. Available: <https://doi.org/10.1016/j.jksuci.2019.06.012>
- [20] Z. Jun, "The development and application of support vector machine," *Journal of Physics: Conference Series*, vol. 1748, p. 052006, 1 2021. [Online]. Available: <https://doi.org/10.1088/1742-6596/1748/5/052006>
- [21] J. Wang, M. A. Khan, S. Wang, and Y. Zhang, "Snsvm: Squeezenet-guided svm for breast cancer diagnosis," *Computers, Materials Continua*, vol. 76, pp. 2201–2216, 8 2023. [Online]. Available: <https://doi.org/10.32604/cmc.2023.041191>
- [22] G. Varoquaux and O. Colliot, *Evaluating Machine Learning Models and Their Diagnostic Value*. Humana Press Inc., 2023, vol. 197, pp. 601–630. [Online]. Available: https://link.springer.com/10.1007/978-1-0716-3195-9_20
- [23] Şeref Kerem Çorbacıoğlu and G. Aksel, "Receiver operating characteristic curve analysis in diagnostic accuracy studies," *Turkish Journal of Emergency Medicine*, vol. 23, pp. 195–198, 10 2023. [Online]. Available: https://journals.lww.com/10.4103/tjem.tjem_182_23
- [24] N. K. V. Abrar Yaqoob, "Feature selection in breast cancer gene expression data using kao and aoa with svm classification," *Journal of medical systems*, vol. 49, no. 1, 2025. [Online]. Available: <https://doi.org/10.1007/s10916-025-02171-6>
- [25] N. A. Nasarudin, F. Al-Jasmi, N. H. A. Aziz, N. A. A. Aziz, W. Khan, Y. Hendrawan, D. F. A. Riza, A. Manzoor, B. R. Ali, and M. S. Mohamad, "An improved deep learning algorithm for breast cancer survival prediction based on multi-omics data," *F1000Research*, vol. 14, p. 765, 8 2025. [Online]. Available: <https://doi.org/10.12688/f1000research.166682.2>
- [26] A. Abidalkareem, A. K. Ibrahim, M. Abd, O. Rehman, and H. Zhuang, "Identification of gene expression in different stages of breast cancer with machine learning," *Cancers*, vol. 16, 5 2024. [Online]. Available: <https://doi.org/10.3390/cancers16101864>
- [27] M. Dalmolin, K. S. Azevedo, L. C. Souza, C. B. de Farias, M. Lichtenfels, and M. A. Fernandes, "Feature selection in cancer classification: Utilizing explainable artificial intelligence to uncover influential genes in machine learning models," *AI (Switzerland)*, vol. 6, pp. 2–0, 1 2025. [Online]. Available: <https://doi.org/10.3390/ai6010002>

- [28] 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, 1 2025. [Online]. Available: <https://doi.org/10.1093/bib/bbae628>
- [29] V. Murugesan and P. Balamurugan, "Breast cancer classification by gene expression analysis using hybrid feature selection and hyper-heuristic adaptive universum support vector machine," 2023. [Online]. Available: <https://doi.org/10.32985/ijeces.14.3.1>
- [30] W. M. Abdullah, "A comparative analysis of feature selection algorithms for cancer classification using gene expression microarray data," *Revue d'Intelligence Artificielle*, vol. 37, pp. 673–687, 6 2023. [Online]. Available: <https://doi.org/10.18280/ria.370316>
- [31] Q. Jiang and M. Jin, "Feature selection for breast cancer classification by integrating somatic mutation and gene expression," *Frontiers in Genetics*, vol. Volume 12 - 2021, 2021. [Online]. Available: <https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2021.629946>
- [32] S. Ghosh, G. Samanta, and M. D. la Sen, "Feature selection and classification approaches in gene expression of breast cancer," *AIMS Biophysics*, vol. 8, pp. 372–384, 2021. [Online]. Available: <https://doi.org/10.3934/biophy.2021029>
- [33] "Bioinformatics analysis of the human surfaceome reveals new targets for a variety of tumor types," *International Journal of Genomics*, vol. 2016, 2016. [Online]. Available: <http://dx.doi.org/10.1155/2016/8346198>
- [34] C. Oh, H. R. Kim, S. Oh, J. Y. Ko, Y. Kim, K. Kang, Y. Yang, J. Kim, J. H. Park, J. S. Roe, and K. H. Yoo, "Epigenetic upregulation of mage-a isoforms promotes breast cancer cell aggressiveness," *Cancers*, vol. 13, 7 2021. [Online]. Available: <https://doi.org/10.3390/cancers13133176>
- [35] Y. He, D. Yu, L. Zhu, S. Zhong, J. Zhao, and J. Tang, "mir-149 in human cancer: A systemic review," *Journal of Cancer*, vol. 9, pp. 375–388, 2018. [Online]. Available: <https://doi.org/10.7150/jca.21044>
- [36] "Uncovering an adh1c-lncrna regulatory axis linking alcohol metabolism to diagnostic potential in colorectal, breast, and gastric cancers," 11 2025. [Online]. Available: <https://doi.org/10.21203/rs.3.rs-8045579/v1>
- [37] Y. Jia, Y. Jia, Y. Shi, W. Zhao, J. Martin, X. Wang, Z. Tong, and Y. Song, "Integrative analysis of lncrna-mrna signature reveals a functional lincrna in triple-negative breast cancer," *Holistic Integrative Oncology*, vol. 1, 12 2022. [Online]. Available: <https://doi.org/10.1007/s44178-022-00009-6>
- [38] J. Wei, Q. Dou, F. Ba, and G.-Q. Jiang, "Development a prognostic model integrating lncrna/ mrna novel biomarkers identified by bioinformatics analysis and experiments in breast cancer," 3 2021. [Online]. Available: <https://doi.org/10.21203/rs.3.rs-251621/v1>
- [39] J. Mani, "Identification and validation of biomarkers for breast cancer from human white blood cells," Ph.D. dissertation, University of Essex, 2015.
- [40] P. Gao, N. Sun, T. Zhao, Y. Sun, J. Gu, D. Ma, H. Tian, Z. Peng, Y. Zhang, F. Han, and X. Qi, "Identification of prognostic indicators, diagnostic markers, and possible therapeutic targets among lim homeobox transcription factors in breast cancer," *Cancer Innovation*, vol. 1, pp. 252–269, 10 2022. [Online]. Available: <https://doi.org/10.1002/cai2.30>