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TABULAR DATA
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REFERENCES

Almazrua, H., & Alshamlan, H. (2022). A comprehensive survey of recent hybrid feature selection methods in cancer microarray gene expression data. *IEEE Access, 10*, 71427–71449. https://doi.org/10.1109/access.2022.3185226

Alon, U., Barkai, N., Notterman, D. A., Gish, K., Ybarra, S., Mack, D., & Levine, A. J. (1999). Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays. *Proceedings of the National Academy of Sciences, 96*(12), 6745–6750. https://doi.org/10.1073/pnas.96.12.6745

Bhattacharjee, A., Richards, W. G., Staunton, J., Li, C., Monti, S., Vasa, P., Ladd, C., Beheshti, J., Bueno, R., Gillette, M., Loda, M., Weber, G., Mark, E. J., Lander, E. S., Wong, W., Johnson, B. E., Golub, T. R., Sugarbaker, D. J., & Meyerson, M. (2001). Classification of human lung carcinomas by mrna expression profiling reveals distinct adenocarcinoma subclasses. *Proceedings of the National Academy of Sciences, 98*(24), 13790–13795. https://doi.org/10.1073/pnas.191502998

Dey, L., & Mukhopadhyay, A. (2022). Compact genetic algorithm-based feature selection for sequence-based prediction of dengue–human protein interactions. *IEEE/ACM Transactions on Computational Biology and Bioinformatics, 19*(4), 2137–2148. https://doi.org/10.1109/tcbb.2021.3066597

Ghosh, M., Adhikary, S., Ghosh, K. K., Sardar, A., Begum, S., & Sarkar, R. (2018). Genetic algorithm based cancerous gene identification from microarray data using ensemble of Filter Methods. *Medical & Biological Engineering & Computing, 57*(1), 159–176. https://doi.org/10.1007/s11517-018-1874-4

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Ghosh, N., Kumar Mridha, S., & Paul, R. (2025). Lasso-mcga: Machine learning and modified compact genetic algorithm-based biomarker selection for breast cancer subtype classification. *IEEE Access, 13*, 17673–17682. https://doi.org/10.1109/access.2025.3532361

Ha, B. V., Mussetta, M., Pirinoli, P., & Zich, R. E. (2016). Modified compact genetic algorithm for thinned array synthesis. *IEEE Antennas and Wireless Propagation Letters, 15*, 1105–1108. https://doi.org/10.1109/lawp.2015.2494839

Harik, G. R., Lobo, F. G., & Goldberg, D. E. (1998). The compact genetic algorithm. *Proceedings of the 1998 IEEE International Conference on Evolutionary Computation*, 523–528. https://doi.org/10.1109/icec.1998.700083

Jansi Rani, M., & Devaraj, D. (2019). Two-stage hybrid gene selection using mutual information and genetic algorithm for Cancer Data Classification. *Journal of Medical Systems, 43*(8). https://doi.org/10.1007/s10916-019-1372-8

Li, S., Zhang, K., Chen, Q., Wang, S., & Zhang, S. (2020). Feature selection for high dimensional data using weighted K-nearest neighbors and genetic algorithm. *IEEE Access, 8*, 139512–139528. https://doi.org/10.1109/access.2020.3012768

Liu, X.-Y., Liang, Y., Wang, S., Yang, Z.-Y., & Ye, H.-S. (2018). A hybrid genetic algorithm with wrapper-embedded approaches for feature selection. *IEEE Access, 6*, 22863–22874. https://doi.org/10.1109/access.2018.2818682

Peng, C., Wu, X., Yuan, W., Zhang, X., Zhang, Y., & Li, Y. (2021). MGRFE: Multilayer recursive feature elimination based on an embedded genetic algorithm for cancer classification. *IEEE/ACM Transactions on Computational Biology and Bioinformatics, 18*(2), 621–632. https://doi.org/10.1109/tcbb.2019.2921961

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Sayed, S., Nassef, M., Badr, A., & Farag, I. (2019). A nested genetic algorithm for feature selection in high-dimensional cancer microarray datasets. *Expert Systems with Applications, 121*, 233–243. https://doi.org/10.1016/j.eswa.2018.12.022

Shipp, M. A., Ross, K. N., Tamayo, P., Weng, A. P., Kutok, J. L., Aguiar, R. C., Gaasenbeek, M., Angelo, M., Reich, M., Pinkus, G. S., Ray, T. S., Koval, M. A., Last, K. W., Norton, A., Lister, T. A., Mesirov, J. P., Neuberg, D. S., Lander, E. S., Golub, T. R., & Aster, J. C. (2002). Diffuse large B-cell lymphoma outcome prediction by gene-expression profiling and supervised machine learning. *Nature Medicine, 8*(1), 68–74. https://doi.org/10.1038/nm0102-68

Shukla, A. K., Singh, P., & Vardhan, M. (2018). A hybrid gene selection method for microarray recognition. *Biocybernetics and Biomedical Engineering, 38*(4), 975–991. https://doi.org/10.1016/j.bbe.2018.08.004

Shukla, A. K., Singh, P., & Vardhan, M. (2019). A new hybrid feature subset selection framework based on binary genetic algorithm and information theory. *International Journal of Computational Intelligence and Applications, 18*(03). https://doi.org/10.1142/s1469026819500202

Singh, D., Febbo, P. G., Ross, K., Jackson, D. G., Manola, J., Ladd, C., Tamayo, P., Renshaw, A. A., D'Amico, A. V., Richie, J. P., Lander, E. S., Loda, M., Kantoff, P. W., Golub, T. R., & Sellers, W. R. (2002). Gene expression correlates of clinical prostate cancer behavior. *Cancer Cell, 1*(2), 203–209. https://doi.org/10.1016/s1535-6108(02)00030-2