

DAFTAR PUSTAKA

- [1] M. B. Cook *et al.*, “Testosterone Therapy in Relation to Prostate Cancer in a U.S. Commercial Insurance Claims Database,” *Cancer Epidemiology, Biomarkers & Prevention*, vol. 29, no. 1, pp. 236–245, Jan. 2020, doi: 10.1158/1055-9965.EPI-19-0619.
- [2] M. Wang *et al.*, “Temporal and spatial trends and determinants of aggressive prostate cancer among Black and White men with prostate cancer,” *Cancer Causes & Control*, vol. 31, no. 1, pp. 63–71, Jan. 2020, doi: 10.1007/s10552-019-01249-0.
- [3] H. Sung *et al.*, “Global Cancer Statistics 2020: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries,” *CA Cancer J Clin*, vol. 71, no. 3, pp. 209–249, May 2021, doi: 10.3322/caac.21660.
- [4] S. Iqbal *et al.*, “Prostate Cancer Detection Using Deep Learning and Traditional Techniques,” *IEEE Access*, vol. 9, pp. 27085–27100, 2021, doi: 10.1109/ACCESS.2021.3057654.
- [5] P. C. Albertsen, “Competing Risk Analysis of Men Aged 55 to 74 Years at Diagnosis Managed Conservatively for Clinically Localized Prostate Cancer,” *JAMA*, vol. 280, no. 11, p. 975, Sep. 1998, doi: 10.1001/jama.280.11.975.
- [6] M. Atiq, E. Chandran, F. Karzai, R. A. Madan, and J. B. Aragon-Ching, “Emerging treatment options for prostate cancer,” *Expert Rev Anticancer Ther*, vol. 23, no. 6, pp. 625–631, Jun. 2023, doi: 10.1080/14737140.2023.2208352.
- [7] A. Bernal, A. Bechler, K. Mohan, A. Rizzino, and G. Mathew, “The Current Therapeutic Landscape for Metastatic Prostate Cancer,” *Pharmaceuticals*, vol. 17, no. 3, p. 351, Mar. 2024, doi: 10.3390/ph17030351.
- [8] A. Yaqoob, M. A. Mir, G. V. V. Jagannadha Rao, and G. G. Tejani, “Transforming Cancer Classification: The Role of Advanced Gene Selection,” *Diagnostics*, vol. 14, no. 23, p. 2632, Nov. 2024, doi: 10.3390/diagnostics14232632.
- [9] J. Gao *et al.*, “Research progress and applications of epigenetic biomarkers in cancer,” *Front Pharmacol*, vol. 15, Apr. 2024, doi: 10.3389/fphar.2024.1308309.

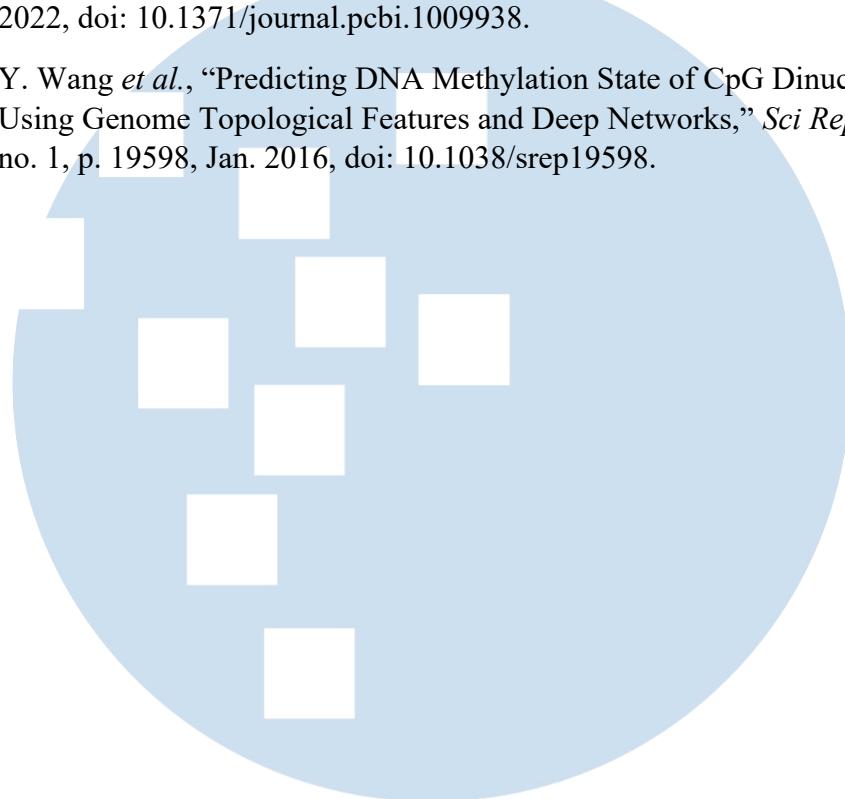
- [10] Z. A. Sherif, O. O. Ogunwobi, and H. W. Ressom, “Mechanisms and technologies in cancer epigenetics,” *Front Oncol*, vol. 14, Jan. 2025, doi: 10.3389/fonc.2024.1513654.
- [11] M. Li, Z. Xia, R. Wang, M. Xi, and M. Hou, “Unveiling DNA methylation: early diagnosis, risk assessment, and therapy for endometrial cancer,” *Front Oncol*, vol. 14, Jan. 2025, doi: 10.3389/fonc.2024.1455255.
- [12] S.-J. Lee *et al.*, “A dimension-reduction based multilayer perception method for supporting the medical decision making,” *Pattern Recognit Lett*, vol. 131, pp. 15–22, Mar. 2020, doi: 10.1016/j.patrec.2019.11.026.
- [13] Z. Wang *et al.*, “Optimized multilayer perceptrons for molecular classification and diagnosis using genomic data,” *Bioinformatics*, vol. 22, no. 6, pp. 755–761, Mar. 2006, doi: 10.1093/bioinformatics/btk036.
- [14] Z. Wang, X. Yuan, Y. Nie, J. Wang, G. Jiang, and K. Chen, “Next-Generation Sequencing vs. Clinical-Pathological Assessment in Diagnosis of Multiple Lung Cancers: A Systematic Review and Meta-Analysis,” *Thorac Cancer*, vol. 16, no. 6, Mar. 2025, doi: 10.1111/1759-7714.70039.
- [15] M. Desai and M. Shah, “An anatomization on breast cancer detection and diagnosis employing multi-layer perceptron neural network (MLP) and Convolutional neural network (CNN),” *Clinical eHealth*, vol. 4, pp. 1–11, 2021, doi: 10.1016/j.ceh.2020.11.002.
- [16] I. Lorencin, N. Andelić, J. Španjol, and Z. Car, “Using multi-layer perceptron with Laplacian edge detector for bladder cancer diagnosis,” *Artif Intell Med*, vol. 102, p. 101746, Jan. 2020, doi: 10.1016/j.artmed.2019.101746.
- [17] S. A. Mojarrad, S. S. Dlay, W. L. Woo, and G. V. Sherbet, “Breast cancer prediction and cross validation using multilayer perceptron neural networks,” in *2010 7th International Symposium on Communication Systems, Networks & Digital Signal Processing (CSNDSP 2010)*, IEEE, Jul. 2010, pp. 760–764. doi: 10.1109/CSNDSP16145.2010.5580318.
- [18] S. Gupta and M. Kumar, “Prostate Cancer Prognosis Using Multi-Layer Perceptron and Class Balancing Techniques,” in *2021 Thirteenth International Conference on Contemporary Computing (IC3-2021)*, New York, NY, USA: ACM, Aug. 2021, pp. 1–6. doi: 10.1145/3474124.3474125.
- [19] C. Zheng and R. Xu, “Predicting cancer origins with a DNA methylation-based deep neural network model,” *PLoS One*, vol. 15, no. 5, p. e0226461, May 2020, doi: 10.1371/journal.pone.0226461.

- [20] X. Xu, Y. Guo, M. Liu, Y. Hu, and S. Li, “Advancements in the clinical application of gene methylation for early cancer detection,” *Frontiers in Epigenetics and Epigenomics*, vol. 2, Jul. 2024, doi: 10.3389/freae.2024.1430294.
- [21] M. Liu *et al.*, “A multilayer perceptron-based model applied to histopathology image classification of lung adenocarcinoma subtypes,” *Front Oncol*, vol. 13, May 2023, doi: 10.3389/fonc.2023.1172234.
- [22] Y. Fujiwara, S. Kato, and R. Kurzrock, “Evolution of Precision Oncology, Personalized Medicine, and Molecular Tumor Boards,” *Surg Oncol Clin N Am*, vol. 33, no. 2, pp. 197–216, Apr. 2024, doi: 10.1016/j.soc.2023.12.004.
- [23] G. Wang, D. Zhao, D. J. Spring, and R. A. DePinho, “Genetics and biology of prostate cancer,” *Genes Dev*, vol. 32, no. 17–18, pp. 1105–1140, Sep. 2018, doi: 10.1101/gad.315739.118.
- [24] W. Ou *et al.*, “Integrated proteogenomic characterization of localized prostate cancer identifies biological insights and subtype-specific therapeutic strategies,” *Nat Commun*, vol. 16, no. 1, p. 3189, Apr. 2025, doi: 10.1038/s41467-025-58569-w.
- [25] K. H. Stopsack *et al.*, “Transcriptomes of Prostate Cancer with TMPRSS2:ERG and Other ETS Fusions,” *Molecular Cancer Research*, vol. 21, no. 1, pp. 14–23, Jan. 2023, doi: 10.1158/1541-7786.MCR-22-0446.
- [26] W.-A. Kwon and J. Y. Joung, “Precision Targeting in Metastatic Prostate Cancer: Molecular Insights to Therapeutic Frontiers,” *Biomolecules*, vol. 15, no. 5, p. 625, Apr. 2025, doi: 10.3390/biom15050625.
- [27] L. Brady *et al.*, “Inter- and intra-tumor heterogeneity of metastatic prostate cancer determined by digital spatial gene expression profiling,” *Nat Commun*, vol. 12, no. 1, p. 1426, Mar. 2021, doi: 10.1038/s41467-021-21615-4.
- [28] L. Wu *et al.*, “Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants,” *Cancer Res*, vol. 79, no. 13, pp. 3192–3204, Jul. 2019, doi: 10.1158/0008-5472.CAN-18-3536.
- [29] T. Hu, N. Chitnis, D. Monos, and A. Dinh, “Next-generation sequencing technologies: An overview,” *Hum Immunol*, vol. 82, no. 11, pp. 801–811, Nov. 2021, doi: 10.1016/j.humimm.2021.02.012.
- [30] Y. Zhong, F. Xu, J. Wu, J. Schubert, and M. M. Li, “Application of Next Generation Sequencing in Laboratory Medicine,” *Ann Lab Med*, vol. 41, no. 1, pp. 25–43, Jan. 2021, doi: 10.3343/alm.2021.41.1.25.

- [31] S. Li and T. O. Tollefsbol, “DNA methylation methods: Global DNA methylation and methylomic analyses,” *Methods*, vol. 187, pp. 28–43, Mar. 2021, doi: 10.1016/j.ymeth.2020.10.002.
- [32] M. Ehrlich, “Dna Hypomethylation In Cancer Cells,” *Epigenomics*, vol. 1, no. 2, pp. 239–259, Dec. 2009, doi: 10.2217/epi.09.33.
- [33] S. G. Zhao *et al.*, “The DNA methylation landscape of advanced prostate cancer,” *Nat Genet*, vol. 52, no. 8, pp. 778–789, Aug. 2020, doi: 10.1038/s41588-020-0648-8.
- [34] M. P. Campagna *et al.*, “Epigenome-wide association studies: current knowledge, strategies and recommendations,” *Clin Epigenetics*, vol. 13, no. 1, p. 214, Dec. 2021, doi: 10.1186/s13148-021-01200-8.
- [35] R. Sun *et al.*, “Systematic Investigation of DNA Methylation Associated With Platinum Chemotherapy Resistance Across 13 Cancer Types,” *Front Pharmacol*, vol. 12, Apr. 2021, doi: 10.3389/fphar.2021.616529.
- [36] B. F. Darst, K. C. Malecki, and C. D. Engelman, “Using recursive feature elimination in random forest to account for correlated variables in high dimensional data,” *BMC Genet*, vol. 19, no. S1, p. 65, Sep. 2018, doi: 10.1186/s12863-018-0633-8.
- [37] J. Sheng, M. Shao, Q. Zhang, R. Zhou, L. Wang, and Y. Xin, “Alzheimer’s disease, mild cognitive impairment, and normal aging distinguished by multi-modal parcellation and machine learning,” *Sci Rep*, vol. 10, no. 1, p. 5475, Mar. 2020, doi: 10.1038/s41598-020-62378-0.
- [38] O. Bulut, B. Tan, E. Mazzullo, and A. Syed, “Benchmarking Variants of Recursive Feature Elimination: Insights from Predictive Tasks in Education and Healthcare,” *Information*, vol. 16, no. 6, p. 476, Jun. 2025, doi: 10.3390/info16060476.
- [39] M. Desai and M. Shah, “An anatomization on breast cancer detection and diagnosis employing multi-layer perceptron neural network (MLP) and Convolutional neural network (CNN),” *Clinical eHealth*, vol. 4, pp. 1–11, 2021, doi: 10.1016/j.ceh.2020.11.002.
- [40] H. Ramchoun, M. Amine, J. Idrissi, Y. Ghanou, and M. Ettaouil, “Multilayer Perceptron: Architecture Optimization and Training,” *International Journal of Interactive Multimedia and Artificial Intelligence*, vol. 4, no. 1, p. 26, 2016, doi: 10.9781/ijimai.2016.415.
- [41] P. A. Jones, “Functions of DNA methylation: islands, start sites, gene bodies and beyond,” *Nat Rev Genet*, vol. 13, no. 7, pp. 484–492, Jul. 2012, doi: 10.1038/nrg3230.

- [42] P. Di Lena, C. Sala, A. Prodi, and C. Nardini, “Missing value estimation methods for DNA methylation data,” *Bioinformatics*, vol. 35, no. 19, pp. 3786–3793, Oct. 2019, doi: 10.1093/bioinformatics/btz134.
- [43] Stephen B. Edge, David R. Byrd, Carolyn C. Compton, April G. Fritz, and Frederick L. Greene, *AJCC Cancer Staging Manual*, 7th ed. New York: Springer, 2010.
- [44] C. J. Logothetis *et al.*, “Molecular Classification of Prostate Cancer Progression: Foundation for Marker-Driven Treatment of Prostate Cancer,” *Cancer Discov*, vol. 3, no. 8, pp. 849–861, Aug. 2013, doi: 10.1158/2159-8290.CD-12-0460.
- [45] N. Borley and M. R. Feneley, “Prostate cancer: diagnosis and staging,” *Asian J Androl*, vol. 11, no. 1, pp. 74–80, Jan. 2009, doi: 10.1038/aja.2008.19.
- [46] A. Barsouk *et al.*, “Epidemiology, Staging and Management of Prostate Cancer,” *Medical Sciences*, vol. 8, no. 3, p. 28, Jul. 2020, doi: 10.3390/medsci8030028.
- [47] J. G. Tate *et al.*, “COSMIC: the Catalogue Of Somatic Mutations In Cancer,” *Nucleic Acids Res*, vol. 47, no. D1, pp. D941–D947, Jan. 2019, doi: 10.1093/nar/gky1015.
- [48] J. Gao *et al.*, “Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal,” *Sci Signal*, vol. 6, no. 269, Apr. 2013, doi: 10.1126/scisignal.2004088.
- [49] E. Cerami *et al.*, “The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data,” *Cancer Discov*, vol. 2, no. 5, pp. 401–404, May 2012, doi: 10.1158/2159-8290.CD-12-0095.
- [50] S. Suehnholz *et al.*, “Abstract 3208: OncoKB, a precision oncology knowledgebase,” *Cancer Res*, vol. 80, no. 16_Supplement, pp. 3208–3208, Aug. 2020, doi: 10.1158/1538-7445.AM2020-3208.
- [51] A. E. Hassani, K. Shaalan, T. Gaber, A. T. Azar, and M. F. Tolba, Eds., *Proceedings of the International Conference on Advanced Intelligent Systems and Informatics 2016*, vol. 533. Cham: Springer International Publishing, 2017. doi: 10.1007/978-3-319-48308-5.
- [52] H. Meng, E. L. Murrelle, and G. Li, “Identification of a small optimal subset of CpG sites as bio-markers from high-throughput DNA methylation profiles,” *BMC Bioinformatics*, vol. 9, no. 1, p. 457, Dec. 2008, doi: 10.1186/1471-2105-9-457.

- [53] A. Li *et al.*, “Novel feature selection methods for construction of accurate epigenetic clocks,” *PLoS Comput Biol*, vol. 18, no. 8, p. e1009938, Aug. 2022, doi: 10.1371/journal.pcbi.1009938.
- [54] Y. Wang *et al.*, “Predicting DNA Methylation State of CpG Dinucleotide Using Genome Topological Features and Deep Networks,” *Sci Rep*, vol. 6, no. 1, p. 19598, Jan. 2016, doi: 10.1038/srep19598.



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