

Daftar Pustaka

- [1] "Cancer," World Health Organization. [Online]. Available: <https://www.who.int/health-topics/cancer>. [Accessed: 17-Nov-2020].
- [2] H. Ayadenta and Adiwijaya, "A clustering approach for feature selection in microarray data classification using random forest," *Journal of Information Processing Systems*, vol. 14, pp. 1167–1175, Jan. 2018.
- [3] Elvira biomedical Dataset Repository, "Kent Ridge Biomedical Data Set Repository," 2005. [Online]. Available: <http://leo.ugr.es/elvira/DBCRepository/>. [Accessed: 17-Dec-2020].
- [4] H. Omara, M. Lazaar, and Y. Tabii, "Effect of Feature Selection on Gene Expression Datasets Classification Accuracy," *International Journal of Electrical and Computer Engineering (IJECE)*, vol. 8, no. 5, p. 3194, 2018.
- [5] M. Babu and K. Sarkar, "A comparative study of gene selection methods for cancer classification using microarray data," *2016 Second International Conference on Research in Computational Intelligence and Communication Networks (ICRCICN)*, 2016.
- [6] Z. Rustam and S. A. A. Kharis, "Comparison of Support Vector Machine Recursive Feature Elimination and Kernel Function as feature selection using Support Vector Machine for lung cancer classification," *Journal of Physics: Conference Series*, vol. 1442, p. 012027, 2020.
- [7] F. V. Sharbaf, S. Mosafer, and M. H. Moattar, "A hybrid gene selection approach for microarray data classification using cellular learning automata and ant colony optimization," *Genomics*, vol. 107, no. 6, pp. 231–238, 2016.
- [8] R. Nurviarelda., Adiwijaya., and A. A. Rohmawati., "Klasifikasi Data Microarray Menggunakan Discrete Wavelet Transform dan Naives Bayes Classification," *e-Proceeding Eng.*, vol. 5, no. 1, p. 1536, 2018
- [9] I. Guyon, J. Weston, S. Barnhill, and V. Vapnik, "Gene Selection for Cancer Classification using Support Vector Machines," *Machine Learning*, vol. 46, no. 1/3, pp. 389–422, 2002.
- [10] Z. Li, W. Xie, and T. Liu, "Efficient feature selection and classification for microarray data," *Plos One*, vol. 13, no. 8, 2018.
- [11] H. Sanz, C. Valim, E. Vegas, J. M. Oller, and F. Reverter, "SVM-RFE: selection and visualization of the most relevant features through non-linear kernels," *BMC Bioinformatics*, vol. 19, no. 1, p. 432, 2018.
- [12] A. Goel and S. K. Srivastava, "Role of kernel parameters in performance evaluation of SVM," *2016 Second International Conference on Computational Intelligence & Communication Technology (CICT)*, 2016.
- [13] H. Zhang et al., "Informative gene selection and direct classification of tumor based on Chi-square test of pairwise gene interactions," *Biomed Res. Int.*, vol. 2014, p. 589290, 2014.
- [14] C. S. R. Annavarapu, S. Dara, and H. Banka, "Cancer microarray data feature selection using multi-objective binary particle swarm optimization algorithm," *EXCLI J.*, vol. 15, pp. 460–473, 2016.
- [15] R. B. Purnomoputra, A. Adiwijaya, and U. Novia Wisesty, "Sentiment analysis of movie review using Naïve Bayes method with Gini index feature selection," *Journal of Data Science and Its Applications*, vol. 2, no. 2, pp. 85–94. 2019.
- [16] N. Cilia, C. De Stefano, F. Fontanella, S. Raimondo, and A. Scotto di Freca, "An experimental comparison of feature-selection and classification methods for microarray datasets," *Information (Basel)*, vol. 10, no. 3, p. 109, 2019.
- [17] H. A. Gusman, Adiwijaya and W. Astuti, "Microarray Data Classification to Detect Cancer Cells by Using Discrete Wavelet Transform and Combining Classifiers Methods," *2020 International Conference on Data Science and Its Applications (ICoDSA)*, pp. 1-7, 2020.
- [18] R. K. Singh and M. Sivabalakrishnan, "Feature selection of gene expression data for cancer classification: A review," *Procedia Comput. Sci.*, vol. 50, pp. 52–57, 2015.
- [19] A. Manik, A. Adiwijaya, and D. Q. Utama, "Classification of electrocardiogram signals using Principal Component Analysis and Levenberg Marquardt Backpropagation for detection Ventricular Tachyarrhythmia," *J. Data Sci. Appl.*, vol. 2, no. 1, pp. 78–87, 2019.
- [20] Kira, Kenji, and Larry A. Rendell. "The feature selection problem: Traditional methods and a new algorithm." *Aaai*, vol. 2, 1992.

- [21] M. Nuruddin Qaisar Bhuiyan, M. Shamsujjoha, S. H. Ripon, F. H. Proma, and F. Khan, “Transfer learning and supervised classifier based prediction model for breast cancer,” in *Big Data Analytics for Intelligent Healthcare Management*, Elsevier, 2019, pp. 59–86
- [22] B. M. and C. P., “An automated technique using Gaussian naïve Bayes classifier to classify breast cancer,” *Int. J. Comput. Appl.*, vol. 148, no. 6, pp. 16–21, 2016.
- [23] A. Saini, J. Hou, and W. Zhou, “Breast cancer prognosis risk estimation using integrated gene expression and clinical data,” *Biomed Res. Int.*, vol. 2014, p. 459203, 2014.
- [24] L. Ein-Dor, O. Zuk, and E. Domany, “Thousands of samples are needed to generate a robust gene list for predicting outcome in cancer,” *Proc. Natl. Acad. Sci. U. S. A.*, vol. 103, no. 15, pp. 5923–5928, 2006.
- [25] M. Shi and B. Zhang, “Semi-supervised learning improves gene expression-based prediction of cancer recurrence,” *Bioinformatics*, vol. 27, no. 21, pp. 3017–3023, 2011.