

REFERENCIAS

- (1) Sedaghat, N.; Fathy, M.; Modarressi, M. H.; Shojaie, A. Combining Supervised and Unsupervised Learning for Improved MiRNA Target Prediction. *IEEE/ACM Trans. Comput. Biol. and Bioinf.* **2018**, 1–1. <https://doi.org/10.1109/TCBB.2017.2727042>.
- (2) Ghoshal, A.; Zhang, J.; Roth, M. A.; Xia, K. M.; Grama, A. Y.; Chaterji, S. A Distributed Classifier for MicroRNA Target Prediction with Validation Through TCGA Expression Data. *IEEE/ACM Trans. Comput. Biol. and Bioinf.* **2018**, 15 (4), 1037–1051. <https://doi.org/10.1109/TCBB.2018.2828305>.
- (3) Le, D.-H.; Pham, V.-H.; Nguyen, T. T. An Ensemble Learning-Based Method for Prediction of Novel Disease-MicroRNA Associations. In *2017 9th International Conference on Knowledge and Systems Engineering (KSE)*; IEEE: Hue, 2017; pp 7–12. <https://doi.org/10.1109/KSE.2017.8119426>.
- (4) Mehejabin, T.; Rahman, F.; Yeasmin, S.; Sarkar, M. Identification of Most Relevant Breast Cancer MiRNA Using Machine Learning Algorithms. In *2020 11th International Conference on Computing, Communication and Networking Technologies (ICCCNT)*; IEEE: Kharagpur, India, 2020; pp 1–6. <https://doi.org/10.1109/ICCCNT49239.2020.9225624>.
- (5) Razak, E.; Yusof, F.; Raus, R. A. Classification of MiRNA Expression Data Using Random Forests for Cancer Diagnosis. In *2016 International Conference on Computer and Communication Engineering (ICCCE)*; IEEE: Kuala Lumpur, Malaysia, 2016; pp 187–190. <https://doi.org/10.1109/ICCCE.2016.49>.
- (6) Ibrahim, R.; Yousri, N. A.; Ismail, M. A.; El-Makky, N. M. MiRNA and Gene Expression Based Cancer Classification Using Self-Learning and Co-Training Approaches. In *2013 IEEE International Conference on Bioinformatics and Biomedicine*; IEEE: Shanghai, China, 2013; pp 495–498. <https://doi.org/10.1109/BIBM.2013.6732544>.
- (7) Laplante, J.-F.; Akhloufi, M. A. Predicting Cancer Types From MiRNA Stem-Loops Using Deep Learning. In *2020 42nd Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC)*; IEEE: Montreal, QC, Canada, 2020; pp 5312–5315. <https://doi.org/10.1109/EMBC44109.2020.9176345>.
- (8) Bayrak, T.; Ogul, H. Data Integration for Gene Expression Prediction. In *2018 International Conference on Artificial Intelligence and Data Processing (IDAP)*; IEEE: Malatya, Turkey, 2018; pp 1–6. <https://doi.org/10.1109/IDAP.2018.8620915>.
- (9) Sarkar, J. P.; Saha, I.; Sarkar, A.; Maulik, U. Machine Learning Integrated Ensemble of Feature Selection Methods Followed by Survival Analysis for Predicting Breast Cancer Subtype Specific MiRNA Biomarkers. *Computers in Biology and Medicine* **2021**, 131, 104244. <https://doi.org/10.1016/j.compbiomed.2021.104244>.
- (10) Zhao, C.; Cheng, Q.; Xie, W.; Xu, J.; Xu, S.; Wang, Y.; Feng, W. Methods for Predicting Single-Cell MiRNA in Breast Cancer. *Genomics* **2022**, 114 (3), 110353. <https://doi.org/10.1016/j.ygeno.2022.110353>.

- (11) Amethiya, Y.; Pipariya, P.; Patel, S.; Shah, M. Comparative Analysis of Breast Cancer Detection Using Machine Learning and Biosensors. *Intelligent Medicine* **2022**, *2* (2), 69–81. <https://doi.org/10.1016/j.imed.2021.08.004>.
- (12) Andreini, P.; Bonechi, S.; Bianchini, M.; Geraci, F. MicroRNA Signature for Interpretable Breast Cancer Classification with Subtype Clue. *Journal of Computational Mathematics and Data Science* **2022**, *3*, 100042. <https://doi.org/10.1016/j.jcmds.2022.100042>.
- (13) Betancur, J. G. por el grado de Maestría Académica en Biología con énfasis en Genética y Biología.
- (14) Wang, D.; Zhang, Y.; Zhao, Y. LightGBM: An Effective MiRNA Classification Method in Breast Cancer Patients. In *Proceedings of the 2017 International Conference on Computational Biology and Bioinformatics*; ACM: Newark NJ USA, 2017; pp 7–11. <https://doi.org/10.1145/3155077.3155079>.
- (15) Yerukala Sathipati, S.; Ho, S.-Y. Identifying a MiRNA Signature for Predicting the Stage of Breast Cancer. *Sci Rep* **2018**, *8* (1), 16138. <https://doi.org/10.1038/s41598-018-34604-3>.
- (16) Rehman, O.; Zhuang, H.; Muhamed Ali, A.; Ibrahim, A.; Li, Z. Validation of MiRNAs as Breast Cancer Biomarkers with a Machine Learning Approach. *Cancers* **2019**, *11* (3), 431. <https://doi.org/10.3390/cancers11030431>.
- (17) Naorem, L. D.; Muthaiyan, M.; Venkatesan, A. Identification of Dysregulated MiRNAs in Triple Negative Breast Cancer: A Meta-analysis Approach. *Journal Cellular Physiology* **2019**, *234* (7), 11768–11779. <https://doi.org/10.1002/jcp.27839>.
- (18) Lan, C.; Peng, H.; McGowan, E. M.; Hutvagner, G.; Li, J. An IsomiR Expression Panel Based Novel Breast Cancer Classification Approach Using Improved Mutual Information. *BMC Med Genomics* **2018**, *11* (S6), 118. <https://doi.org/10.1186/s12920-018-0434-y>.
- (19) Yu, Z.; Wang, Z.; Yu, X.; Zhang, Z. RNA-Seq-Based Breast Cancer Subtypes Classification Using Machine Learning Approaches. *Computational Intelligence and Neuroscience* **2020**, *2020*, 1–13. <https://doi.org/10.1155/2020/4737969>.
- (20) Sherafatian, M. Tree-Based Machine Learning Algorithms Identified Minimal Set of MiRNA Biomarkers for Breast Cancer Diagnosis and Molecular Subtyping. *Gene* **2018**, *677*, 111–118. <https://doi.org/10.1016/j.gene.2018.07.057>.
- (21) Qiu, M.; Fu, Q.; Jiang, C.; Liu, D. Machine Learning Based Network Analysis Determined Clinically Relevant MiRNAs in Breast Cancer. *Front. Genet.* **2020**, *11*, 615864. <https://doi.org/10.3389/fgene.2020.615864>.
- (22) Zhao, J.; Cheng, W.; He, X.; Liu, Y.; Li, J.; Sun, J.; Li, J.; Wang, F.; Gao, Y. Construction of a Specific SVM Classifier and Identification of Molecular Markers for Lung Adenocarcinoma Based on LncRNA-MiRNA-mRNA Network. *OTT* **2018**, *Volume 11*, 3129–3140. <https://doi.org/10.2147/OTT.S151121>.

- (23) Yao, D.; Zhan, X.; Kwoh, C.-K. An Improved Random Forest-Based Computational Model for Predicting Novel MiRNA-Disease Associations. *BMC Bioinformatics* **2019**, *20* (1), 624. <https://doi.org/10.1186/s12859-019-3290-7>.
- (24) Uthayopas, K.; De Sá, A. G. C.; Alavi, A.; Pires, D. E. V.; Ascher, D. B. TSMDA: Target and Symptom-Based Computational Model for MiRNA-Disease-Association Prediction. *Molecular Therapy - Nucleic Acids* **2021**, *26*, 536–546. <https://doi.org/10.1016/j.omtn.2021.08.016>.
- (25) Banu A, B.; Thirumalaikolundusubramanian, P. Comparison of Bayes Classifiers for Breast Cancer Classification. *Asian Pac J Cancer Prev* **2018**, *19* (10). <https://doi.org/10.22034/APJCP.2018.19.10.2917>.
- (26) Alkhadar, H.; Macluskey, M.; White, S.; Ellis, I.; Gardner, A. Comparison of Machine Learning Algorithms for the Prediction of Five-year Survival in Oral Squamous Cell Carcinoma. *J Oral Pathol Med* **2021**, *50* (4), 378–384. <https://doi.org/10.1111/jop.13135>.
- (27) López, N. C.; García-Ordás, M. T.; Vitelli-Storelli, F.; Fernández-Navarro, P.; Palazuelos, C.; Alaiz-Rodríguez, R. Evaluation of Feature Selection Techniques for Breast Cancer Risk Prediction. *IJERPH* **2021**, *18* (20), 10670. <https://doi.org/10.3390/ijerph182010670>.
- (28) Lopez-Rincon, A.; Mendoza-Maldonado, L.; Martinez-Archundia, M.; Schönhuth, A.; Kraneveld, A. D.; Garssen, J.; Tonda, A. Machine Learning-Based Ensemble Recursive Feature Selection of Circulating MiRNAs for Cancer Tumor Classification. *Cancers* **2020**, *12* (7), 1785. <https://doi.org/10.3390/cancers12071785>.
- (29) Arjmand, F. Decision tree-based classifiers for lung cancer diagnosis and subtyping using TCGA miRNA expression data. *Oncology Letters* **2019**, *18* (2), 2125-2131. DOI: 10.3892/ol.2019.10462.