

DAFTAR PUSTAKA

- Breiman, L., 1996. Bagging predictors. *Mechine Learn.* 24, 1–26.
- Charlton, J., Jung, E.J., Mattei, A.L., Bailly, N., Liao, J., Martin, E.J., Giesselmann, P., Brändl, B., Stamenova, E.K., Müller, F.-J., Kiskinis, E., Gnirke, A., Smith, Z.D., Meissner, A., 2020. TETs compete with DNMT3 activity in pluripotent cells at thousands of methylated somatic enhancers. *Nat. Genet.* 52, 819–827.
- Chen, K., Zhou, F., Yin, L., Wang, S., Wang, Y., Wan, F., 2018. A hybrid particle swarm optimizer with sine cosine acceleration coefficients. *Inf. Sci. (Ny).* 422, 218–241.
- Chen, Y., Li, L., Xiao, J., Yang, Y., Liang, J., Li, T., 2018. Particle swarm optimizer with crossover operation. *Eng. Appl. Artif. Intell.* 70, 159–169.
- Chuang, L.-Y., Yang, Cheng-Huei, Wu, K.-C., Yang, Cheng-Hong, 2011. A hybrid feature selection method for DNA microarray data. *Comput. Biol. Med.* 41, 228–237.
- Cortes, C., Vapnik, V., 1995. Support-vector networks. *Mach. Learn.* 20, 273–297.
- Douillet, D., Sze, C.C., Ryan, C., Piunti, A., Shah, A.P., Ugarenko, M., Marshall, S.A., Rendleman, E.J., Zha, D., Helmin, K.A., Zhao, Z., Cao, K., Morgan, M.A., Singer, B.D., Bartom, E.T., Smith, E.R., Shilatifard, A., 2020. Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. *Nat. Genet.* 52, 615–625.
- Esteller, M., 2007. Cancer epigenomics: DNA methylomes and histone-modification maps 8.
- Friedman, J., 2001. Greedy Function Approximation: A Gradient Boosting Machine Author (s): Jerome H . Friedman Source : The Annals of Statistics , Vol . 29 , No . 5 (Oct . , 2001), pp . 1189-1232 Published by : Institute of Mathematical Statistics Stable URL : <http://www.ann-stat.org/> Ann. Stat. 29, 1189–1232.
- Frommer, M., McDonald, L.E., Millar, D.S., Collis, C.M., Watt, F., Grigg, G.W., Molloy, P.L., Paul, C.L., 1992. A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in individual DNA strands. *Proc. Natl. Acad. Sci. U. S. A.* 89, 1827–1831.
- Ghosh, J., Coutifaris, C., Sapienza, C., Mainigi, M., 2017. Global DNA methylation levels are altered by modifiable clinical manipulations in assisted reproductive technologies. *Clin. Epigenetics* 9, 1–10.
- Huang, H., Liu, R., Niu, Q., Tang, K., Zhang, B., Zhang, H., Chen, K., Zhu, J.-K., Lang, Z., 2019. Global increase in DNA methylation during orange fruit development and ripening. *Proc. Natl. Acad. Sci.* 116, 1430–1436.
- Jones, P.A., Baylin, S.B., 2002. The fundamental role of epigenetic events in cancer. *Nat. Rev. Genet.* 3, 415–428.
- Jones, P.A., Ohtani, H., Chakravarthy, A., De Carvalho, D.D., 2019. Epigenetic therapy in immune-oncology. *Nat. Rev. Cancer* 19, 151–161.
- Josephine, J.A., Maharana, S.K., Walid, M.A.A., T, T., Alam, M.S., Tiwari, M., 2022. Hybrid *Particle Swarm Optimization* with Deep Learning Driven Sarcasm Detection on Social Media. In: 2022 International Conference on

- Automation, Computing and Renewable Systems (ICACRS). IEEE, pp. 687–693.
- Kalabarige, L.R., Rao, R.S., Abraham, A., Gabralla, L.A., 2022. Multilayer Stacked Ensemble Learning Model to Detect Phishing Websites. *IEEE Access* 10, 79543–79552.
- Kennedy, J., Eberhart, R., 1995. *Particle Swarm Optimization* 1942–1948.
- LeCun, Y., Bengio, Y., Hinton, G., 2015. Deep learning. *Nature* 521, 436–444.
- Li, E., Bestor, T.H., Jaenisch, R., 1992. Targeted mutation of the DNA methyltransferase gene results in embryonic lethality. *Cell* 69, 915–926.
- Mafarja, M.M., Mirjalili, S., 2017. Hybrid Whale Optimization Algorithm with simulated annealing for feature selection. *Neurocomputing* 260, 302–312.
- Moazen, H., Molaei, S., Farzinvas, L., Sabaei, M., 2023. PSO-ELPM: PSO with elite learning, enhanced parameter updating, and exponential mutation operator. *Inf. Sci. (Ny)*. 628, 70–91.
- Opitz, D., Maclin, R., 1999. Popular Ensemble Methods: An Empirical Study. *J. Artif. Intelligence* 1.
- Poli, R., Kennedy, J., Blackwell, T., 2007. Quantification & Assessment of the chemical form of residual gadolinium in the brain.pdf. *Swarm Intell* 1, 33–57.
- Reik, W., Dean, W., Walter, J., 2001. Epigenetic Reprogramming in Mammalian Development. *Science* (80-.). 293, 1089–1093.
- Saha, S., Halder, R.K., Uddin, M.N., 2023. *Particle Swarm Optimization* -Assisted Multilayer Ensemble Model to predict DNA 4mC sites. *Informatics Med. Unlocked* 42, 9–10.
- Sharma, A., Heuck, C.J., Fazzari, M.J., Mehta, J., Singhal, S., Grealley, J.M., Verma, A., 2010. DNA methylation alterations in multiple myeloma as a model for epigenetic changes in cancer. *Wiley Interdiscip. Rev. Syst. Biol. Med.* 2, 654–669.
- Wojdacz, T.K., Lotte Hansen, L., 2006. Reversal of PCR Bias for Improved Sensitivity of the DNA Methylation Melting Curve Assay. *Biotechniques* 41, 274–278.
- Xiong, Z., Laird, P.W., 1997. COBRA: a sensitive and quantitative DNA methylation assay. *Nucleic Acids Res.* 25, 2532–2534.
- Zong, T., Li, J., Lu, G., 2024. Parameter estimation of multivariable Wiener nonlinear systems by the improved *Particle Swarm Optimization* and coupling identification. *Inf. Sci. (Ny)*. 661, 120192.
- Zhou, Z.-H., & Feng, J. (2017). Deep Forest. *Proceedings of the 26th International Joint Conference on Artificial Intelligence (IJCAI)*, 3552–3558. <https://doi.org/10.24963/ijcai.2017/497>