Breast cancer is an umbrella term for encompassing multiple different subtypes, with each subtype having a different biological and clinical features, progression pattern, treatment response and prognosis. Stratification of breast cancer is an important objective, which allows clinicians to better evaluate patient risk and select effective therapeutic strategies based on the subtype in question (Dai et al., 2015).

Earlier, breast cancer stratification was conventionally performed using a combination of immunohistochemistry (IHC) detection for cellular markers as well as anatomical features such as tumour node size, number of metastases detected, etc. However, information from gene expression profiling by microarrays became an increasingly important means of breast cancer classification (Dai et al., 2015).

# Bibliography

Dai, X., Li, T., Bai, Z., Yang, Y., Liu, X., Zhan, J., & Shi, B. (2015). Breast cancer intrinsic subtype classification, clinical use and future trends. *American Journal of Cancer Research*, *5*(10), 2929–2943. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4656721/