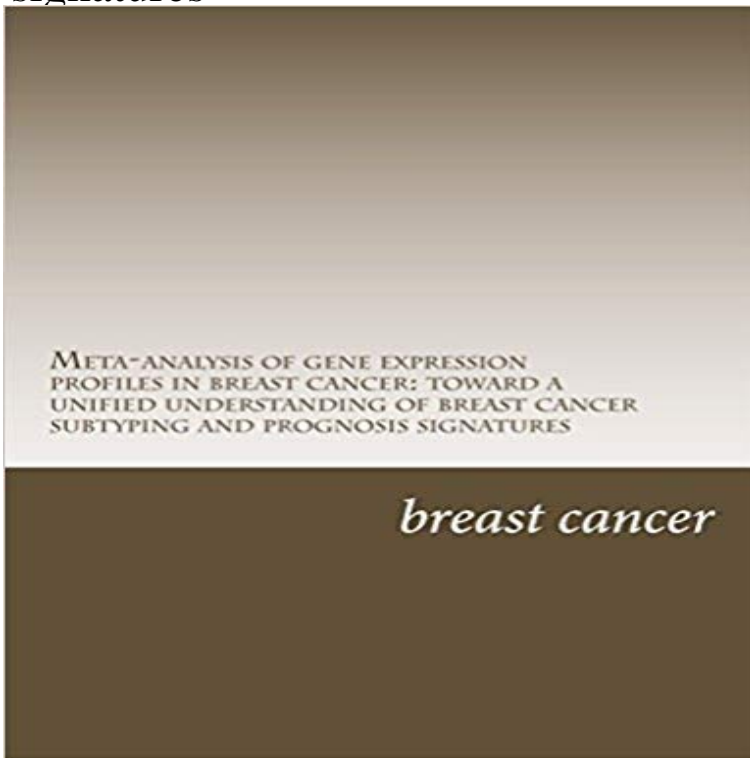


Meta-analysis of gene expression profiles in breast cancer: toward a unified understanding of breast cancer subtyping and prognosis signatures



Breast cancer subtyping and prognosis have been studied extensively by gene expression profiling, resulting in disparate signatures with little overlap in their constituent genes. Although a previous study demonstrated a prognostic concordance among gene expression signatures, it was limited to only one dataset and did not fully elucidate how the different genes were related to one another nor did it examine the contribution of well-known biological processes of breast cancer tumorigenesis to their prognostic performance.

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