

I. INTRODUCTION

Over the past few years, the phenomenon of cancer has become a serious issue. Breast cancer (BRCA) is a type of cancer that poses a significant threat to women's global health which accounts for 11.7% of the total cases followed by lung and colorectal cancer (Zhao et al., 2022; Sung et al., 2021).

Unfortunately, the high survival and mortality rate of BRCA are mainly due to the lack of effective treatments (Wilkinson et al., 2022). Treatments that are commonly used to treat BRCA are surgery, radiotherapy, as well as chemotherapy (Akram et al., 2017). However, studies have identified certain harmful side effects caused by the treatments, contributing to their ineffectiveness against various malignant tumors and resulting in unsatisfactory outcomes (Yahya and Alqadhi et al., 2021). The increasing number of researchers is motivated by the desire to address the limitations and challenges of conventional cancer therapy through the application of gene therapy.

Gene therapy refers to a technique that modified the gene of an individual to treat or cure disease such as cancer (Drew and Martin, 2023). In order to perform an effective gene therapy, it is crucial to identify prognostic gene biomarkers associated with BRCA. Despite having sets of identified genes that are associated with BRCA, lack of accurate prognostic gene biomarkers still remains a crucial issue that influences women's quality of life, physical and emotional health (Li et al., 2023). Moreover, several biomarkers have been shown to fail clinical evaluation while having successfully passed the discovery and validation stages, with reliable and consistent findings across studies (Diamandis., 2012). Therefore, investigation of novel biomarkers with potential prognostic value has enabled medical professionals to ascertain more effective therapy options (Alves et al., 2023).

In line with this, the identification of novel prognostic gene biomarkers can be performed through *in-silico* studies which uses various bioinformatics tools. The use of *in-silico* analysis is very beneficial for identifying novel prognostic gene biomarkers, characterized by its cost-effectiveness and ease of accessing patient data and databases (Moradi et al., 2022). Furthermore, bioinformatics research provides various databases of possible BRCA genes that serve as the foundation of analysis for further validation (Pereira et al., 2020). Therefore, this research aims to identify novel prognostic gene biomarkers that are associated with BRCA in order to further enhance therapeutic approaches. Additionally, it is hypothesized that the novel prognostic gene biomarker that associates with BRCA can be identified through a data mining process employing several bioinformatics tools.