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**Lift the veil of breast cancers using 4 or fewer critical genes**

Known genes in the breast cancer study literature could not be confirmed whether they are vital to breast cancer formations due to lack of convincing accuracy, although they may be biologically directly related to breast cancer based on present biological knowledge. It is hoped vital genes can be identified with the highest possible accuracy, e.g., 100% accuracy and convincing causal patterns beyond what has been known in breast cancer. One hope is that finding gene-gene interaction signatures and functional effects may solve the puzzle. This research uses a recently developed competing linear factor analysis method in differentially expressed gene detection to advance the study of breast cancer formation. Surprisingly, three genes are detected to be differentially expressed in TNBC and non-TNBC (Her2, Luminal A, Luminal B) samples with 100% sensitivity and 100% specificity in one study of triple-negative breast cancers (TNBC, with 54675 genes and 265 samples). These three genes show a clear signature pattern of how TNBC patients can be grouped. For another TNBC study (with 54673 genes and 66 samples), four genes bring the same accuracy of 100% sensitivity and 100% specificity. Four genes are found to have the same accuracy of 100% sensitivity and 100% specificity in one breast cancer study (with 54675 genes and 121 samples), and the same four genes bring an accuracy of 100% sensitivity and 96.5% specificity in the fourth breast cancer study (with 60483 genes and 1217 samples.) These results show the four-gene-based classifiers are robust and accurate.

The detected genes naturally classify patients into subtypes, e.g., seven subtypes. these findings demonstrate the clearest gene-gene interaction patterns and functional effects with the smallest numbers of genes and the highest accuracy compared with findings reported in the literature. The four genes are considered to be essential for breast cancer studies and practice. They can provide focused, targeted researches and precision medicine for each subtype of breast cancer. new breast cancer disease types may be detected using the classified subtypes, and hence new effective therapies can be developed.

#### Recent Publications

1. Hongxuan Huang & Zhengjun Zhang (2019) Virtual Standard Currency for Approximating Foreign Exchange Rates, International Journal of Electronic Commerce, 23:1, 33-62,
2. Zhengjun Zhang&Kazuhiko Shinki, Extreme co-movements and extreme impacts in high frequency data in finance (2007) Journal of Banking & Finance, 1399-1415

#### Biography

Zhengjun Zhang writes about a variety of subjects, including fundamental dependence theory, extreme value theory and risk analysis, high-dimensional statistical learning using max-linear regression, zero-inflated protective barrier regression, variable selection based on tail limits, variable screening based on tail dependence and sure explained variability and nonlinear causal inference his collaborators, including my undergraduate/graduate students, and he introduced tail quotient correlation, generalized measures of correlation, competing factor copula, and max-linear computing regressions, amongst others.

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