MONDAY 1/21/80
BE BACK 12:15 - 12:30

Dove H.
(quality maternal mortality

$\mu_1 = \mu_{\text{base}, 1}$, $\Sigma_1 \sim N(\mu_{\text{base}, 1}, \Sigma)$

region

$\mu_{\text{base}} \sim N(\mu_0, \Sigma)$

$\mu_1 \sim N(\mu_{\text{base}}, \Sigma)$

$\mu_1 \sim N(\mu_{\text{base}}, \Sigma)$

$K = R = 10$

$E_0 \sim \text{Cat}(p_1, \ldots, p_K)$ allocation

$p_k \sim \text{Dir}(\alpha)$

$\alpha \sim \text{Unif}(0.9, 10)$
Utility of White Blood Cell Global and Lone-1 Methylation as Biomarkers for Breast Cancer

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INTRODUCTION

Main focus: DNA methylation addition of cytosine to CGG site

DNA in breast tumors is often frequently found to be hypomethylated, which aids to genetic instability. Since DNA hypomethylation is among the most commonly observed abnormalities in breast cancer cases, the use of DNA methylation as a breast cancer diagnostic tool is of great interest, especially for low-cost and non-invasive detection methods.

METHODS

- Literature search conducted on PubMed and Google Scholar through the use of the term “DNA methylation” in breast cancer.
- Analysis of published studies involving DNA methylation in breast cancer patients.
- Logistic regression analysis to determine the association between DNA methylation and breast cancer risk.
- Receiver operating characteristic (ROC) curve analysis to evaluate the diagnostic accuracy of DNA methylation as a biomarker for breast cancer.