Assessing a Bayesian Risk Prediction Model in a High-Risk Breast Cancer Population

Jennifer Chun, MPH ¹, Freya Schnabel, MD ², Omolola Ogunyemi, PhD ³
¹ Department of Surgery, Columbia University Comprehensive Breast Center, Women At Risk, New York Presbyterian Hospital, Columbia University Medical Center, New York, NY; ² Department of Surgery, New York University Clinical Cancer Center, New York, NY; ³ Decision Systems Group, Brigham and Woman's Hospital, Harvard Medical School, Boston, MA

Abstract: The purpose of this study was to utilize a Bayesian risk prediction model to predict the incidence of breast cancer in a high risk population. 10-fold cross-validation was performed using a Naïve Bayes classifier. The area under the ROC curve (AUC) was used to measure prediction accuracy. These results were then compared to the ROC curve (AUC) results of the Gail Model Risk Assessment Tool.

Background and Significance: There are a number of models that currently exist for predicting breast cancer risk in various populations¹. Of these, the Gail Model is the most widely utilized; however, there are significant limitations to this model¹,². Bayesian networks are a novel technique for developing risk prediction models by incorporating expert opinion and empirical evidence along with established risk factors.

Objectives: Our aim was to develop a computer-based individualized 5-year breast cancer risk prediction model by using Bayesian networks. In addition, we also sought to evaluate the Bayesian model by assessing its predictive value in a select group of women known to be at high-risk for developing breast cancer and by comparing the results of our Bayesian model to the Gail model.

Methods: The Women At Risk (WAR) Registry at Columbia University was established in 1991 as a database for longitudinal study of women at high risk to develop breast cancer. Women were defined as high-risk if they had one or more of the following: a strong family history of breast cancer (FHBC), a biopsy-proven history of atypical ductal hyperplasia (ADH), atypical lobular hyperplasia (ALH), or lobular carcinoma in situ (LCIS). The WAR Registry was queried for women ages 23-69 at time of entry. Using features that included risk factors such as race, age, age at menarche, age at first live birth, and BMI², a 10-fold cross-validation was performed using a Naïve Bayes classifier to evaluate the predictive ability of the model. To measure prediction accuracy, we measured the Receiver Operating Characteristic (ROC) and estimated the area under the ROC curve (AUC). The data was then split into a 2/3 training and 1/3 test sets. These results were then compared to the area under the ROC curve (AUC) for the Gail model risk scores. All analyses were performed using the Weka data mining tool.

Results: The total data set included 210 high-risk women with a median follow up of 7 years. 10 women had developed breast cancer (5%) during the study period. Using the Naïve Bayes classifier for the 10-fold cross validation, the ROC curve (AUC) was 0.675. The data was split into a 2/3 training (140 cases) and 1/3 test sets (70 cases). The ROC curve (AUC) for the test set was 0.530. In contrast, the ROC curve (AUC) for the 5-year Gail model was 0.561.

Conclusion: At present, there is no single model that accurately predicts the risk of developing breast cancer for an individual woman. Our results indicate that the predictive ability of the Naïve Bayes model is comparable to that of other established breast cancer risk models. It is possible that small sample size and the small number of breast cancer cases reduced the predictive value of our model. Interestingly, in our study, the Bayesian model appeared to better predict breast cancer risk than the Gail model. Recent studies have demonstrated an improvement in predictive power of multivariate risk models when additional risk factors are incorporated, including BRCA status, body mass index (BMI), and mammographic density¹,³. Bayesian models represent an advance in risk prediction modeling by allowing continual modification of the model as new risk factors are identified. Further studies utilizing this model are warranted.

References