Building a Predictive Breast Cancer Risk Model

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Abstract. The poster outlines the development of a breast cancer risk assessment tool for the World-Wide-Web based on well-established epidemiological, clinical, and genetic risk factors.

Introduction. In the U.S. breast cancer is the most common incident cancer and second most common cause of cancer death in women [1]. Breast cancer accounts for approximately 26% of all new cancer cases. In addition, less than 10% of breast cancer cases are considered inherited. Thus, the majority of breast cancer cases are attributable to lifestyle and hormonal factors. Mortality due to breast cancer can be decreased by identifying and treating cases at an earlier stage. Therefore, in addition to screening, disease risk models are important to provide specific disease probabilities based on epidemiological, clinical, biological, and/or genetic factors for a particular disease. Predictive models are useful in terms of disease prevention for determining an individual’s risk of developing a chronic disease such as cancer. We are building a breast cancer risk prediction model based on published evidence of epidemiologic, genetic, and clinical factors to be hosted on the Internet for use by healthcare consumers and potentially clinicians.

Methods: The model is being built through a meta-analysis of the estimated risks abstracted from a systematic review of the literature. Cohort studies, nested case-control studies, population-based case control studies, and clinical trials that use breast cancer incidence as the endpoint are included in the analysis. Segmented case-weighted least squares regression was employed to estimate the parameters and change-points of each risk factor model. Two levels of adjustments are being made to the published results. To permit combining the published results, we represented the different category ranges with averages from USA national survey data such as the National Health Interview Survey. Additionally, we adjusted each model for the prevalence of the risk factor within the general population. Our long term goal is to provide ten-year and lifetime age-conditional probabilities of developing breast cancer using SEER cancer incident rates and the risk factor models.

Results: We have identified 30 potential risk factors for breast cancer. Of these we have developed models for 8 of the factors including age at menarche, menopause and first full-term birth, parity, years of oral contraceptive use, months of breastfeeding, use of hormone replacement therapy and use of selective estrogen receptor modulators (SERMs). A total of 230 studies with 269, 224 breast cancer cases are included in the different models. As expected, hormone replacement therapy and a later age at menopause and first full-term birth increased breast cancer risk (RR=1.47, 1.70, and 1.60, respectively). Parity, breastfeeding, delayed age at menarche, and the use of SERMs contributed to a reduction in risk (RR=0.70, 0.27, 0.64, and 0.50, respectively). There was no association between oral contraceptive use and breast cancer risk.

Discussion. Informatics tools such as disease risk calculators, which host disease predictive models on the Internet need to be constructed using evidence-based medicine, authored by credible sources, and approved by content experts. Tools such as these are useful for physicians, genetic counselors, and healthcare consumers in making informed decisions regarding early screening and lifestyle changes in chronic diseases such as cancer.

References