Purpose: To identify computer-extracted mammographic features and develop prediction methods which relate these features to breast cancer risk.

Materials and Methods: Mammograms from 15 BRCA1/BRCA2-mutation carriers and 143 "low risk" women were digitized at 10-bit quantization and a pixel size of 0.1 mm. Regions of interest of size 256x256 were manually selected from the central part of breast region. Various algorithms were developed to automatically extract features to characterize mammographic parenchymal patterns. These features include the skewness, balance, contrast and coarseness, and RMS variation and first moment of power spectrum from Fourier analysis. Linear discriminant analysis and an artificial neural network were employed to merge multiple features in order to classify subjects as mutation carriers or "low risk". The prediction accuracy of these models were evaluated in terms of their ability to differentiate between the "low risk" women and mutation carriers. To rule out possible bias due to the difference in age distribution between the two groups, ROC analysis was also performed on the 15 mutation carriers and 30 "low risk" women who were randomly selected and age-matched with the 15 mutation carriers.

Results: The multivariate methods yielded A_z values, in the task of distinguishing between the mutation carriers and "low risk" women, of 0.90 and 0.89 for the entire database and
age-matched database, respectively.

Conclusion: Noninvasive computerized radiographic analysis has the potential to aid in identification of BRCA1/BRCA2-mutation carriers.

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