Predicting Lymph Node Metastasis Status Via Image Analysis of Primary Breast Tumor Histology

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Content:

Despite a variety of new tumor markers resulting from significant progress in the molecular and genetic characterization of breast malignancies, axillary lymph node metastasis status remains one of the most critical prognostic variables for the breast cancer management decision-making process and patient survival. Surgical methods for determining metastasis status of breast carcinoma need improvement because they may lead to unnecessary surgeries and its complications. The objective of our study is to demonstrate that lymph node metastasis status may be predicted via computerized image analysis of primary breast tumor histology.

Technology:

A complete computational pipeline that includes image processing, shape/color analysis and machine learning algorithms has been developed to perform automated metastasis status prediction. The stages in the pipeline include: 1) selection and scanning of stained histology slides, 2) automated segmentation of cancer cells and tumor structures, 3) computing geometric measures from stochastic geometry that transform cancer cell/tumor shapes into shape distributions, 4) creating intensity distributions from the texture variation / nuclear hyperchromasia levels within cancer cells, 5) mapping the high-D shape/color distributions into a lower dimensional feature vector, and 6) stacked Relevance Vector Machines (RVMs) that classify test samples into lymph node metastasis status.

Design:

Pathologist-selected subsections of 100 primary breast carcinoma specimens, stained with a complete prognostic panel, were scanned at a resolution of 6000×6000 pixels. The computational pipeline processed the scanned specimens, producing a metastasis status prediction for each specimen (N0 – no metastasis, N1 – metastasis to axillary lymph nodes).

Results:

Computational results were generated from the 100 carcinoma specimens with known metastasis status. Using Leave-One-Out validation the stacked RVM classifiers were able to correctly classify the metastasis status of 90 specimens. The classification results have a specificity of 100% (all 53 N0 samples correctly classified) and a sensitivity of 79% (37 of 47 N1 samples correctly classified). Thus producing a positive predictive value of 100% and a negative predictive value of 84%. The area under the associated ROC curve is 0.842.

Conclusion:

Our computational image analysis of histology of the primary tumor can predict lymph node metastasis and shows promise as an effective means to determine the absence of nodal metastasis.