A computer vision approach for molecular subtyping of breast cancer using MRI

Unmet Need

Breast cancer is the second leading cause of cancer-related deaths in American women and the fourth most common cause of all cancer-related deaths in the U.S. While early screening for cancer using magnetic resonance imaging (MRI) has increased by over 50% in the last decade, breast cancer diagnosis is often complicated by the number of subtypes present. Breast cancer is generally classified into luminal A, luminal B, human epidermal growth factor 2 (HER2)-enriched, and basal-like. These molecular subtypes are highly significant in cancer therapy because encoded within them are characterized progressions and response rates to particular treatments. For example, HER2-enriched breast cancer is highly proliferative and responds best to chemotherapy and HER2-targeting therapies, while luminal A patients benefit from endocrine therapy more than chemotherapy, and vice versa with luminal B. The risk of recurrence also correlates with subtype, where HER2-positive and basal are around five times more likely to recur either locally or distally than either luminal subtype. However, methods to classify subtypes such as standard immunohistochemical analyses do not robustly predict true molecular subtype and require invasive surgery to extract tumor tissue for analysis. Thus, it is necessary to develop methods that can more accurately detect molecular subtype and ease the burden on both breast cancer patients and hospitals.

Technology

Duke inventors have developed a software that can analyze MR images of breast tumors and determine key features of prognosis. This is intended to be used by technicians, radiologists, and oncologists in pre-

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operative settings after non-invasive MRI-based screening has taken place. Specifically, technicians upload the previously-acquired MR images, and an oncologist/radiologist indicates the tumor location. Subsequently, the software segments the tumor into lesion and surrounding parenchyme and extracts key features such as the ratio of tumor enhancement to the surrounding tissue at two frames of the sequence of contrast images (F1 score). The peak location is also another metric measured which refers to the sequence number at which peak tumor enhancement occurs. Both the F1 score and peak location were shown to predict the molecular subtype and consequent recurrence risk. Since this is an algorithmic prediction based on imaging from routine screening, this technology could preclude the need for invasive tumor biopsies and expensive biomarker processing. This technology has been demonstrated using labelled patient data to train a statistical model on these image features and their corresponding prediction of molecular subtype. The inventors identified key features that can distinguish luminal A and luminal B breast cancer subtypes and this technology likely has the potential to be expanded to HER2-enriched and basal subtypes with additional datasets.

Advantages

- Bypasses the need for invasive biopsies required for immunohistochemical analysis
- Accurately predicts molecular subtype of luminal A/B breast cancer
- Significantly faster diagnosis than through conventional pathologist assessment (hours versus weeks, respectively)