Abstract

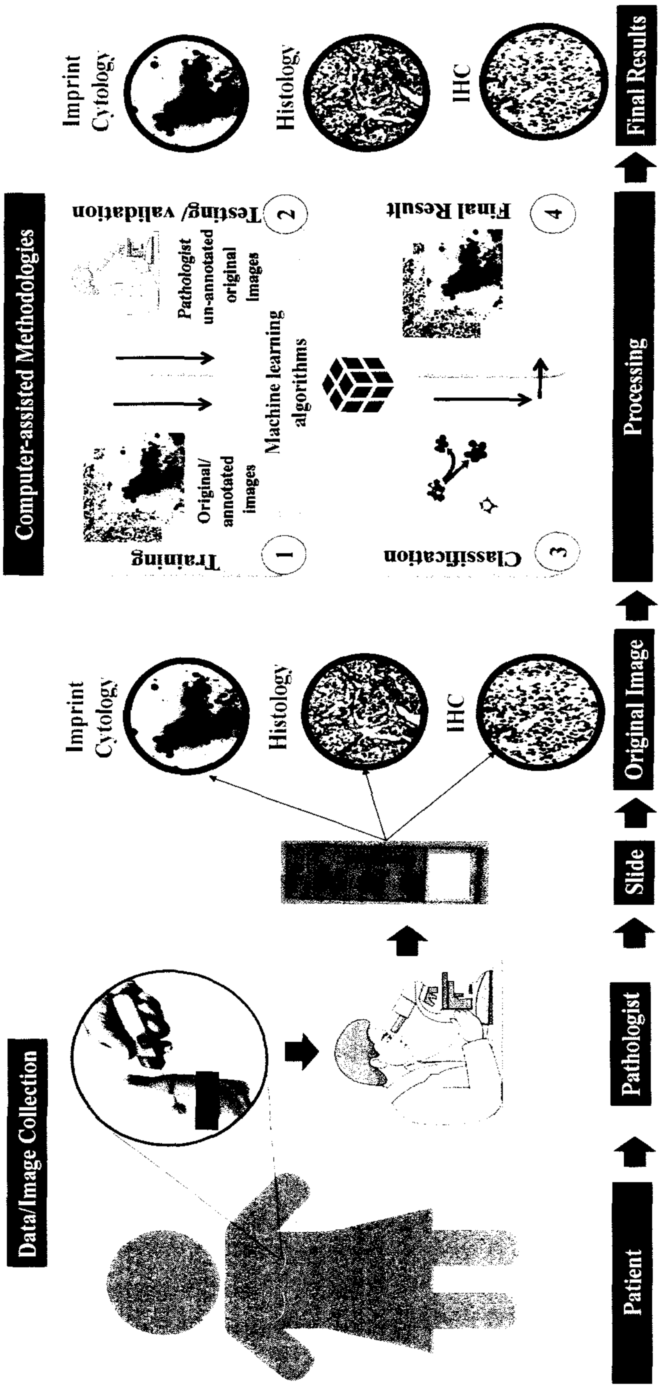
Breast cancer (BC) is the second most common carcinoma among women worldwide. This cancer is not only affecting women but sometimes men also get affected. In diagnostics, pathologists collect a small quantity of tissue components from the suspicious region(s) of the breast by biopsy or through aspiration. Next, the obtained tissue components are further processed for cyto-/immuno-/histological processing and interpretation by an experienced pathologist. Visual inspection of microscopic images of cytology or tissue slides by experienced pathologists involves subjectivity and intra-observer variability even that leads to the error-prone decision. The scarcity of real expert pathologists in rural as well as in urban area-based hospitals/clinics is well known. To improve diagnostic accuracy in the cyto-/immuno-/histological slide/image evaluation, there is an urgent need for semi/fully automated computer-assisted tools for diagnosis and prognosis of cancer.

This thesis focuses on the computer-assisted BC detection and grade evaluation using imprint cytology (IC), histopathology and immunohistology (IHC) images. We developed an efficient algorithm for overlapped and non-overlapped nuclei segmentation using Lagrange's interpolation and superpixels, followed by classification into healthy and malignant cases using breast IC images. The proposed algorithm achieved 98% segmentation and 99% classification accuracies respectively. For mitosis and non-mitosis detection and classification, a deep learning framework comprising of handcrafted features was proposed using breast histopathology images. This methodology achieved 92.95% precision, 87.93% recall and 90.37% F-score. For mucinous region segmentation, Fuzzy C-means with Gap statistic based algorithm was developed here. Our proposed algorithm showed 97.74% segmentation accuracy, 82.85% correlation coefficient, and 74.29% dice coefficient leading to BC screening using IC images.

A deep learning framework consisting of decision layer was proposed for hotspots (immunopositive and immunonegative nuclei) detection and proliferation rate scoring using Ki-67 stained breast IHC images. The proposed methodology achieved 98.52% precision and 98.45% classification accuracy. A deep learning framework (*HscoreNet*) consisting of an encoder, decoder, and scoring layer was proposed for automated scoring of estrogen receptor (ER) and progesterone receptor(PR) using ER and PR stained breast IHC images. This methodology achieved 95.87% precision, 95.64% recall and 96.49% F-score. A deep framework (*Her2Net*) consisting of convolution and deconvolution parts was proposed for semantic segmentation and classification of the cell membrane and nuclei followed by computation of HER2 scoring using HER2 stained breast IHC images. This methodology uses additional trapezoidal long short-term memory. The proposed methodology achieved 96.64% precision, 96.79% recall, and 98.33% classification accuracy. The proposed methodologies showed better performance in comparison with the state-of-art. The research carried out in this thesis yields scope for extension and application of the ideas in the field of IC, histopathology and IHC image analysis for BC grading/evaluation.

Keywords: Breast cancer, imprint cytology, histopathology, immunohistology, digital pathology, molecular markers, mitosis, deep learning, estrogen, progesterone, human epidermal growth factor receptor-2, performance evaluation.

Graphical Abstract



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