

Project Proposal

Computer Vision for Breast Tissue Analysis

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Cancers remain a major global health issue, and the challenge is even greater in regions affected by medical deserts, where access to specialists and diagnostic resources is limited. These constraints often delay early detection, which is crucial across all cancer types.

In this project, we focus specifically on breast cancer, one of the most prevalent and impactful cancers worldwide. To address this need, we aim to develop a computer vision application capable of assisting with the initial screening of breast tissue images. The objective is to predict whether a tumor is benign or malignant, identify its histological subtype for example, a “fibroadenoma”, “papillary carcinoma” and generate a probability matrix. This matrix will help interpret which regions of the image most influenced the prediction, using associated heatmaps. Our goal is to provide a clear, interpretable, and useful tool in settings where specialist support is scarce.

We will primarily use the BreakHis dataset, which provides breast tissue images across multiple magnification levels and histological subtypes, making it suitable for both binary and multi-class classification. For the modelling phase, we will rely on modern convolutional neural networks with transfer learning (ResNet, EfficientNet).

For the classification task, we will focus on recall, as minimizing false negatives is essential in cancer detection. Additional metrics such as accuracy, F1-score, and confusion matrices will be used to obtain a more comprehensive evaluation of model performance.

In addition to supervised learning, we will investigate two complementary strategies that can provide valuable insights, particularly in low-data or unseen-class scenarios. First, we will explore zero-shot classification using vision–language models such as CLIP, which embed images and text into a shared semantic space. By formulating descriptive prompts for each histological subtype, we aim to evaluate whether these models—despite being trained on natural images—can meaningfully distinguish between different tissue morphologies. This analysis will include prompt engineering to assess the sensitivity and robustness of zero-shot predictions.

Second, we will conduct an embedding-similarity study based on self-supervised feature extractors such as DINO. By computing representations for all images and performing k-nearest-neighbour retrieval, we will assess whether histological subtypes naturally cluster in the learned feature space. Complementary techniques, including prototype-based

classification and dimensionality-reduction visualizations (e.g., t-SNE), will be used to further evaluate the discriminative structure of these embeddings and their potential for supporting downstream diagnostic tasks.

Methodology

1. **Preprocessing and Exploratory Data Analysis**
2. **Supervised Model**
3. **Zero-Shot classification**
4. **Embedding-similarity study**