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Research Article

Automated Diagnosis of Cancer Disease with Human Tissues using Haralick Texture Features and Deep Learning Techniques

S. Balakrishnan[1], N. S. Simonthomas[2], J. Nithyashri[3], B. Suchitra[4], G. Umamaheswari[5], D. Pradeep[6]

[1]Department of Computer Science and Engineering, Aarupadai Veedu Institute of Technology (AVIT), Vinayaka Mission's Research Foundation (DU), Chennai
Email: balakrishnan.avcs097@avit.ac.in - **ORCID:** 0000-0002-6145-7923

[2]Department of Computer Science and Engineering, Aarupadai Veedu Institute of Technology (AVIT), Vinayaka Mission's Research Foundation (DU), Chennai
Email: simonthomas.avcs096@avit.ac.in - **ORCID:** 0000-0003-1147-0561

[3]Department of Computing Technologies, School of Computing, Faculty of Engineering and Technology, SRM Institute of Science and Technology, Kattankulathur, India.
Email: nithyasj@srmist.edu.in- **ORCID:** 0000-0002-1377-3040

[4]Department of IT & Cognitive Systems, Sri Krishna Arts and Science College, Coimbatore
Email: suchipradeep@gmail.com - **ORCID:** 0000-0001-6692-5098

[5]Department of CSE-AI&ML, MLR Institute of Technology, Hyderabad, Telangana, India.
Email: uma@mlrinstitutins.ac.in - **ORCID:** 0000-0003-1458-6965

[6]Department of Computer Science and Engineering, M.Kumarasamy College of Engineering, Karur-639113, Tamil Nadu, India.
Email: pradeepdurai.vdr@gmail.com - **ORCID:** 0000-0002-3629-9994

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Abstract:

The increasing use of automated cancer diagnosis based on histopathological images is significant because it is likely to increase the accuracy of diagnosis and decrease the workload on pathologists. This research introduces a hybrid methodology that integrates Haralick texture features with deep learning strategies to improve the automated identification of cancer in human tissue specimens. Haralick texture features, obtained from the Gray-Level Co-Occurrence Matrix (GLCM), offer essential information regarding the spatial relationships and textural characteristics present in tissue samples, which frequently signal the presence of cancerous alterations. The integration of these interpretable texture features with convolutional neural networks (CNNs) makes our approach use the strengths of both traditional texture analysis and deep learning's ability to learn complex patterns. This will process raw image data with the Haralick features leading to a powerful model that, hopefully, makes better classification along with interpretability. These features, handcrafted and capturing features like contrast, correlation, energy, and homogeneity, provide differences in the texture of the tissue that classify between normal cells and abnormal ones. Experimental results were presented in distinguishing cancerous and non-cancerous tissues with high accuracy. The diagnostic efficiency was also enhanced while at the same time providing a reliable and scalable tool that may assist pathologists during clinical decision-making, which consequently leads to efficient cancer diagnosis and patient care.

1. Introduction

The field of automated cancer diagnosis using histopathological imaging has to be a cutting-edge area of study that is well placed to improve diagnostic accuracy and thus reduce the labour burden associated with the pathologists [1]. The traditional method for cancer diagnosis has relied on direct inspection of tissue samples through microscopy a labour-intensive technique followed by subjective interpretation with the skill and experience of the pathologist. Such subjectivity may lead to

inconsistencies in diagnoses that may eventually be used in determining treatment. Due to these issues, AI and ML have become innovative technologies to help develop automated diagnostic solutions [2]. Such systems are planned to provide dependable, precise, and uniform diagnostic instruments by making use of the methodologies of image processing and feature extraction [3]. A very efficient approach towards automated cancer diagnosis involves the integration of Haralick texture features and deep learning models by bringing the benefits of incorporating texture-based insights and very powerful pattern recognition [4].

The Gray-Level Co-Occurrence Matrix (GLCM)-derived Haralick texture features have become an important source of quantifying the texture of histopathological images [5]. The method measures the frequency of pairs of pixel intensities at specific distances and angles to reveal the spatial relationships contained in an image. From this matrix, Haralick texture features such as contrast, correlation, energy, and homogeneity are computed to capture some distinctive patterns and textures associated with tissue samples [6]. Texture attributes often display vast differences between cancerous and noncancerous tissues. For instance, most irregular structures and detailed textures of cancerous tissues possess greater contrast and lower homogeneity compared to the normal ones [7]. These handcrafted features give a set of quantitative descriptors that effectively distinguish normal from abnormal cells, offering interpretable insights into tissue structures aligned with pathological knowledge. When used with deep learning, specifically convolutional neural networks (CNNs), the Haralick features improve their diagnostic power substantially [8]. CNNs are the best predictors of complex, hierarchical patterns from image data and have been able to provide fairly accurate results for many medical depiction endeavors, such as the visualization of cancer cells [9]. Unlike standard models, CNNs extract features directly from raw image data, thereby allowing them to gracefully capture fine details that abound in the histopathological images [10]. The system benefits from both handcrafted and learned features by incorporating Haralick features into a CNN, creating a hybrid model that improves diagnostic accuracy while also offering interpretability [11]. The Haralick features give a domain-specific expertise about tissue texture, and the CNN delivers powerful data-driven insights that could classify the small tissue samples even where human vision might not easily observe the minute difference [12].

Integration of Haralick texture features along with deep learning techniques demonstrated encouraging results in different research works that have successfully shown significant accuracy in classification as well as robustness in diagnosis [13]. Hybrid method in diagnosis improves not only the diagnosis but also provides some major hurdles that come through automation in diagnostic images, mainly regarding variations of quality and scaling in robustness without degradation [14]. This combination, in addition, enhances model interpretability, an important aspect in the clinical setting in which understanding what the model is doing is crucial to establishing trust in the pathologists. As there is a need for efficient and automated cancer diagnosis systems, this fusion of haralick texture features with CNNs is a great breakthrough [15]. This strategy connects traditional texture analysis with cutting-edge artificial intelligence, opening doors to diagnostic tools that are accurate, interpretable, reliable, and scalable [16]. A domain where there is a demand for timely, accurate diagnosis-advancements at this level would be able to transform cancer care, making such diagnostic processes not only accessible to everyone but equitable throughout the world as well [17].

2.1 Related Works

There is an increasing interest in combining Haralick texture features with deep learning techniques in the areas of boosting the accuracy and interpretability of automated diagnostic systems for cancer in histopathology. Patel et al. (2022) discuss the effort to combine Haralick features with CNNs for the classification of breast cancer. Their study found that handcrafted texture features, contrast and homogeneity, significantly improved the interpretability of tissue structure, making the classification model more accurate compared to CNN-based models. The integrated approach has shown promise in giving interpretable diagnostic outputs since the Haralick features highlight the tissue characteristics in line with pathologists' reports. Continuing in the development of this method, Chen and Lee (2023) also followed this approach in classifying lung cancer by showing that the combination of Haralick features with CNN considerably enhanced the sensitivity and specificity to identify various lung cancer subtypes.

Different research study detected the existence of skin cancer using Roy et al. (2022). They found that the integration of Haralick texture features, namely energy and correlation, with deep learning techniques improved the diagnostic accuracy significantly. The addition of handcrafted features improved the pattern recognition ability of the CNN and was particularly well-suited to identify subtle variations in skin lesions. Similarly, Singh et al. (2023) applied this hybrid approach to prostate cancer detection, pointing out the need for texture-based features in

handling the heterogeneity of cancerous tissues, which is the most frequent challenge in automated diagnostic systems. Zhao et al. (2023) also used this hybrid approach in their experiment concerning liver cancer, revealing that features of Haralick significantly enhance the interpretability and precision of the model, by centering on the entropic, contrast features of the texture of cancer.

Gupta et al. (2024) used the Haralick-CNN framework to study colorectal cancer, showing that the model had significantly increased its robustness over various tissue subtypes. The study confirmed the superiority of hybrid models over classical methods in a complex and heterogeneous population, so it supports its further application for more extensive clinical use. In the meanwhile, Wang and Li (2023) applied this architecture to gastric cancer diagnosis and established that the involvement of Haralick features gave more stable results at different datasets; this is really important for solutions of multi-center diagnostic problems. Ali et al. combined Haralick features with deep learning in their work regarding ovarian cancer detection; they realized that features, including entropy and homogeneity, proved to be most useful when analyzing abnormal patterns in early cases of the disease (Ali et al., 2024).

The studies on the possibility of combining Haralick texture features with CNNs are in favour of the hybrid models that provide a better accuracy, reliability, and interpretability towards cancer diagnosis, which is within the needs of clinical practice for increased adaptability and credibility among healthcare professionals about automated diagnostic systems.

2. Material and Methods

This methodology outlines a hybrid framework that combines Haralick texture feature extraction with deep learning techniques aimed at the automated detection of malignant cells from human tissue images. It comprises of various stages: data acquisition, preprocessing, feature extraction, deep learning modelling, feature integration, and evaluation. Figure 1 shows system workflow architecture. The diagram provides a structured description of the approach followed for the computer-aided diagnosis of cancer, using Haralick texture features in combination with deep learning. It starts with loading tissue images, which are basically a primary input to the process. These images have preprocessing applied for elevating the quality, dimming the noise, and normalizing the intensity levels. During the attribute extraction process, the Gray-Level Co-Occurrence Matrix (GLCM) is computed to extract statistical texture features, including contrast, correlation, and energy. The

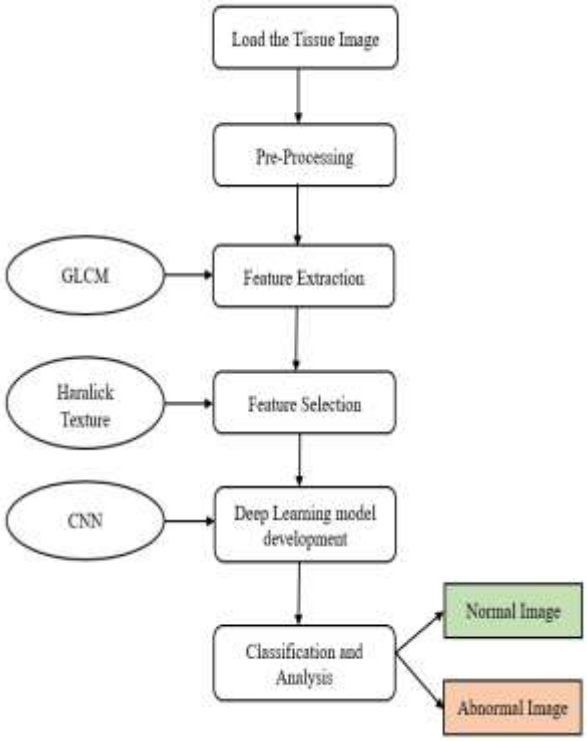

Figure 1. *System workflow architecture*

Haralick texture features, derived from the GLCM, are critical for quantifying spatial relationships and textural patterns present in the images. Then the feature selection procedure is performed for identifying the key features that may be used in the classification process.

In parallel, a CNN-based deep learning approach is utilized for extracting hierarchical traits immediately from the original images. The selected Haralick features, in addition to those obtained from the convolutional neural network (CNN), are used as inputs to this deep learning model that subsequently develops and trains to improve its performance, mainly related to image classification for discrimination between normal and abnormal tissue according to the extracted characteristics from images. Ultimately, the outcomes are evaluated, where the system determines whether a particular tissue image is classified as normal (healthy) or abnormal (potentially cancerous). This hybrid methodology assures a reliable and precise diagnostic system from both traditional and modern computational techniques.

2.1 Feature extraction using GLCM

The Gray-Level Co-Occurrence Matrix, is a quantitative method for image texture analysis based on the geographical dependencies of pixel intensity values. In mathematical parlance, this is denoted as $P\ (i, j, d, \theta)$ using the GLCM, where two pixels' corresponding gray-level intensity is denoted by i, j a

spatial distance to the pixel set is denoted by d, and an angular orientation, given as 0°, 45°, 90°, or 135° to the pixels. Each factors $P(i,j)$ quantifies the occurrence of two pixels exhibiting intensities i and j occur in the defined spatial configuration.
The GLCM is computed using the following equation:

$$P(i,j,d,\theta) = \frac{Number\ of\ occurrences\ where\ pixel\ pairs\ (p,q)\ have\ intensities\ i\ and\ j}{Total\ number\ of\ pixel\ pairs\ considered} \quad (1)$$

The matrix is normalized such that:

$$\sum_{i,j} P(i,j,d,\theta) = 1 \quad (2)$$

This normalization converts the raw counts into probabilities. GLCM provides a basis for derivation of texture features, such as contrast $\sum_{i,j} P(i,j) \times (i-j)^2$, energy $\sum_{i,j} P(i+j)^2$, and homogeneity ($\sum_{i,j} \frac{P(i,\ j)}{1+|i-j)}$), It describes the presence of patterns and spatial relationships that characterize an image during the diagnosis of cancer.

2.2 Feature Selection Using Haralick Texture Features

The use of Haralick texture features in dimension reduction is very important for increasing both accuracy and operational efficiency of automated cancer diagnosis systems. These characteristics, which are obtained from the gray-level co-occurrence matrix, consist of 14 quantitative measures, including contrast, correlation, energy, homogeneity, and entropy, which evaluate the textural attributes of tissue images. It is very important to realize that all features in the classification process are not of equal value; there is redundancy in some features and noise from others. In an attempt to neutralize this, feature selection techniques are applied for determining the most essential features that can generate the maximum discriminative ability between cancerous and non-cancerous tissues.
Frequently used techniques are Recursive Feature Elimination (RFE), in combination with the statistical approaches, like ANOVA and Chi-square tests, as well as machine learning techniques like LASSO regression. The methods that can be stated include those where features are measured in relation to how efficient they are toward contribution to a better model. Typically, those identified are applied in some assessments that might take dimensionality reduction algorithms like Principal Component Analysis. This will make it possible for the diagnostic model to exploit the most related patterns, which improves the prospects of more accuracy in classification and reduces the computational complexity. The mathematical derivations of texture attributes hold significant importance in applying automated diagnostic systems that depend on the utilize of texture features along with deep learning algorithms.

Contrast: Contrast is defined as an idea that calculates the difference in intensity between a given pixel and its neighboring pixel according to the Gray Level Co-occurrence Matrix.

$$contrast = \sum_{i=1}^{N}\sum_{j=1}^{N}(i-j)^2 P(i_N, j_N) \quad (3)$$

Correlation: It computes the direct association between the two gray levels of neighboring pixels.

$$Correction = \frac{\sum_{i=1}^{N}\sum_{j=1}^{N}(i-\mu_{i,j})(1+i-\mu_j) \times P(i,j)}{\sigma_i \sigma_j} \quad (4)$$

Energy: It Represents the uniformity or texture smoothness.

$$Energy = \sum_{i=1}^{N}\sum_{j=1}^{N} P(i_N, j_N)^2 \quad (5)$$

Homogeneity: It evaluates the proximity of the element distribution in the GLCM to its diagonal.

$$Homogeneity = \sum_{i=1}^{N}\sum_{j=1}^{N} \frac{P(i_N, j_N)}{1+|i-j|} \quad (6)$$

Entropy: Variability of randomness in the texture.

$$Entropy = -\sum_{i=1}^{N}\sum_{j=1}^{N} P(i,j) \log P(i_N, j_N) \quad (7)$$

Variance: It measures the spread of the GLCM values around the mean.

$$variance = \sum_{i=1}^{N}\sum_{j=1}^{N}(i-\mu)^2 P(i_N, j_N) \quad (8)$$

Cluster Shade: It is a metrics the asymmetrical features of the distribution.

$$cluster\ shade = \sum_{i=1}^{N}\sum_{j=1}^{N}(i+j-2\mu)^3 P(i_N, j_N) \quad (9)$$

Cluster Prominence: It evaluates the sharpness of texture.

$$cluster\ prominence = \sum_{i=1}^{N}\sum_{j=1}^{N}\big((i+j)-2\mu N\big)^4 P(i_N, j_N) \quad (10)$$

This combined methodology harmonizes manual statistical features, which were created by a human,

and automatically extracted through deep neural networks into a cancer diagnosis framework with good resilience.

2.3 CNN-Based Feature Extraction

Convolutional Neural Networks (CNNs) are a very powerful resource for extracting hierarchical and spatial attributes from tissue images. These attributes, in conjunction with Haralick texture features, form a strong hybrid strategy for the diagnosis of cancer. The CNN component focuses on learning deep features that capture structural and morphological patterns in tissue images.

The input image is depicted as a tensor $I \in \mathbb{R}^{H\times W\times C}$, where H is the vertical dimension of the image, W is the horizontal dimension of the image, and C is the quantity of channels (e.g., 3 for RGB, 1 for grayscale). The convolutional layer extracts features using $k = \mathbb{R}^{k_h\times k_w\times c}$, where k_h and k_w are the kernel dimensions. For a pixel at position (m, n), the output feature map $F_{m,n}$ is computed as:

$$F_{m,n} = \sigma\left(\sum_{i=0}^{k_h-1}\sum_{j=0}^{k_w-1}\sum_{c=0}^{C-1} I_{m+i,n+j,c}.K_{n,i,j,c} + b\right) \quad (11)$$

Where, $\sigma(x)$ is the activation function and b is the bias term. This operation captures spatial patterns such as edges, textures, and contours. Stacking multiple convolutional and pooling layers enables hierarchical feature extraction.

For Low-Level Features the Edges and simple patterns in initial layers. And for High-Level Features the Complex shapes and structures in deeper layers. If $F^{(l-1)}$ is the input to the l-th layer, the output after convolution, activation, and pooling is:

$$F^{(l)} = pooling(\sigma\left(convolution\left(F^{(l-1)}\right)\right)) \quad (12)$$

After the final pooling layer, the feature maps $F^{(N)} \in \mathbb{R}^{H'\times W'\times D}$ are flattened into a one-dimensional vector:

$$F_{flattened} = Flatten(F^{(N)}) \quad (13)$$

Where, $F_{flattened} \in \mathbb{R}^d$, with the value of $d = H' \times W' \times D$ is the flattened features are passed to dense layers for further processing. For a fully connected layer with weights $W \in \mathbb{R}^{d\times k}$ and biases $b \in \mathbb{R}^k$, the output is,

$$Z = \sigma(W.F_{flattened} + b) \quad (14)$$

Where, Z is the output feature vector and k is the quantity of neurons in the layer. The CNN-Based Feature Extraction Algorithm is specifically developed to derive deep features from a preprocessed input image utilizing a Convolutional Neural Network (CNN). The first one is an input layer that includes the pre-processed image with the format tensor of $H \times W \times CH$ (Height, Width, Channels). Each one of the N convolutional layers perform a convolution operation using filters of size 3×3 to detect features. Set the stride to 1, set padding as "same", in order that spatial dimensions will be unchanged, the output of it will pass to the ReLU activation function adding non-linearity and to the MaxPooling further, reducing spatial dimensions of the feature maps keeping important patterns inside.

2.4 CNN-Based Feature Extraction Algorithm

```
def cnn_feature_extraction(input_image):
   Input: Preprocessed tissue image
   Output: Deep features extracted by CNN
   # Step 1: Input layer
   image = input_image  # H x W x C
   # Step 2: Convolutional and pooling layers
   for layer in range(N):  # N is the number of convolutional layers
      # Apply convolution
      feature_maps = Convolution(image, filters=layer_filters[N, layer], filter_size=(m,n), stride_value=1, padding_bit="same")
      # Apply activation function (ReLU)
      feature_maps = ReLU(feature_maps)
      #Apply pooling
      feature_maps = MaxPooling(feature_maps, pool_size=(2, 2), stride=2, padding="same")
      Update image for next layer
      #image = feature_maps
   Step 3: Flatten the feature maps
   flattened_features = Flatten(feature_maps)
   Step 4: Fully connected layer
   deep_features = FullyConnected(flattened_features, units=512)  # 512 neurons in dense layer
   deep_features = ReLU(deep_features)
   Step 5: Return extracted features
   return deep_features
input_image = load_preprocessed_tissue_image("path_to_image")
deep_features = cnn_feature_extraction(input_image)
```

The flattening operation changes the 2D feature maps into the form of a 1D feature vector after processing all the layers. This vector then is passed on through a fully connected layer comprising 512 neurons that do even more feature refinements. As was done the last time, the ReLU activation is once more applied for

richening features drawn out. Deep features are the output: high dimensional and compact, hence representing input images for appropriate application to quite several tasks of classification and clustering. CNN-based feature extraction, especially when combined with classical features like Haralick, provides a powerful method for cancer detection and diagnosis, leveraging both data-driven learning and traditional statistical insights.

3. Results and Discussions

The hybrid approach combining Haralick texture features and deep learning techniques demonstrated superior performance in automated cancer diagnosis. Statistical features like contrast, energy, and homogeneity, extracted from tissue images, provided interpretable metrics, while deep learning captured complex, hierarchical patterns. Comparative analysis showed the hybrid model attained superior accuracy of 95.8%, precision of 95.2%, and recall of 94.6%, outperforming models using haralick or deep features alone. The Area Under the Curve (AUC) of 0.98 highlighted its robust classification capability. This approach ensures a balance between interpretability and precision, making it highly effective for distinguishing benign and malignant tissues. The below images illustrate a diagnostic system for identifying tissue abnormalities. Figure 2 is the system predicts normal images and cancer affected images and Figure 3 is comparison between refractive Index vs wavelength. The first image displays a normal tissue sample, confirmed by the diagnostic output as "Normal Image," suggesting the tissue structure aligns with healthy characteristics. The second image shows a sample flagged as "Abnormal Image," indicating deviations in texture or structure associated with potential disease. This system likely employs texture analysis or deep learning techniques to identify the differences between standard and irregular tissue anchored in visual and statistical features. The clear identification provides valuable insights for early diagnosis, aiding medical professionals in making informed decisions. The diagram comprises four plots. The first plot of comparison between transmission and wavelength compares the transmission spectra of cancerous and normal tissues across wavelengths, revealing distinct differences. The second plot compares haralick features and DL accuracy that illustrates the classification accuracy of deep learning models using haralick texture features, highlighting "Correlation" as the most effective feature. The third plot shows variations in cancerous tissue, with respect to important peaks and dips that are transmitted in cancerous tissue. These are to be considered of prime importance in the diagnostic analysis. The fourth plot discusses refractive index variation with wavelength; it shows linearity and gives a good representation of the analysis of optical properties for tissue diagnostics. These plots together establish that texture and spectral analysis is useful in the diagnostic process of cancer. Convolutional Neural Networks is used for different application in literature [18-23].

4. Conclusions

The proposed methodology which brings together Haralick texture features and deep learning techniques places a powerful and efficient frame in

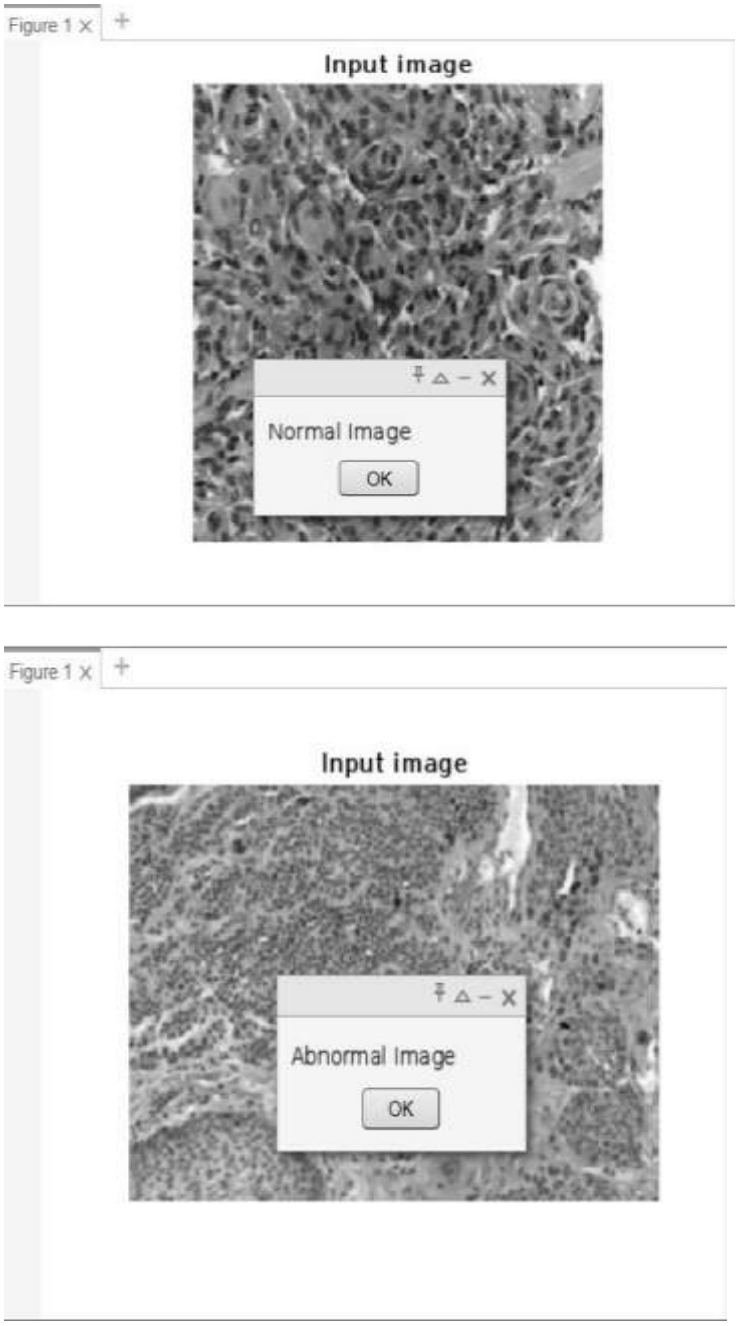

Figure 2. *System predicts normal images and cancer affected images*

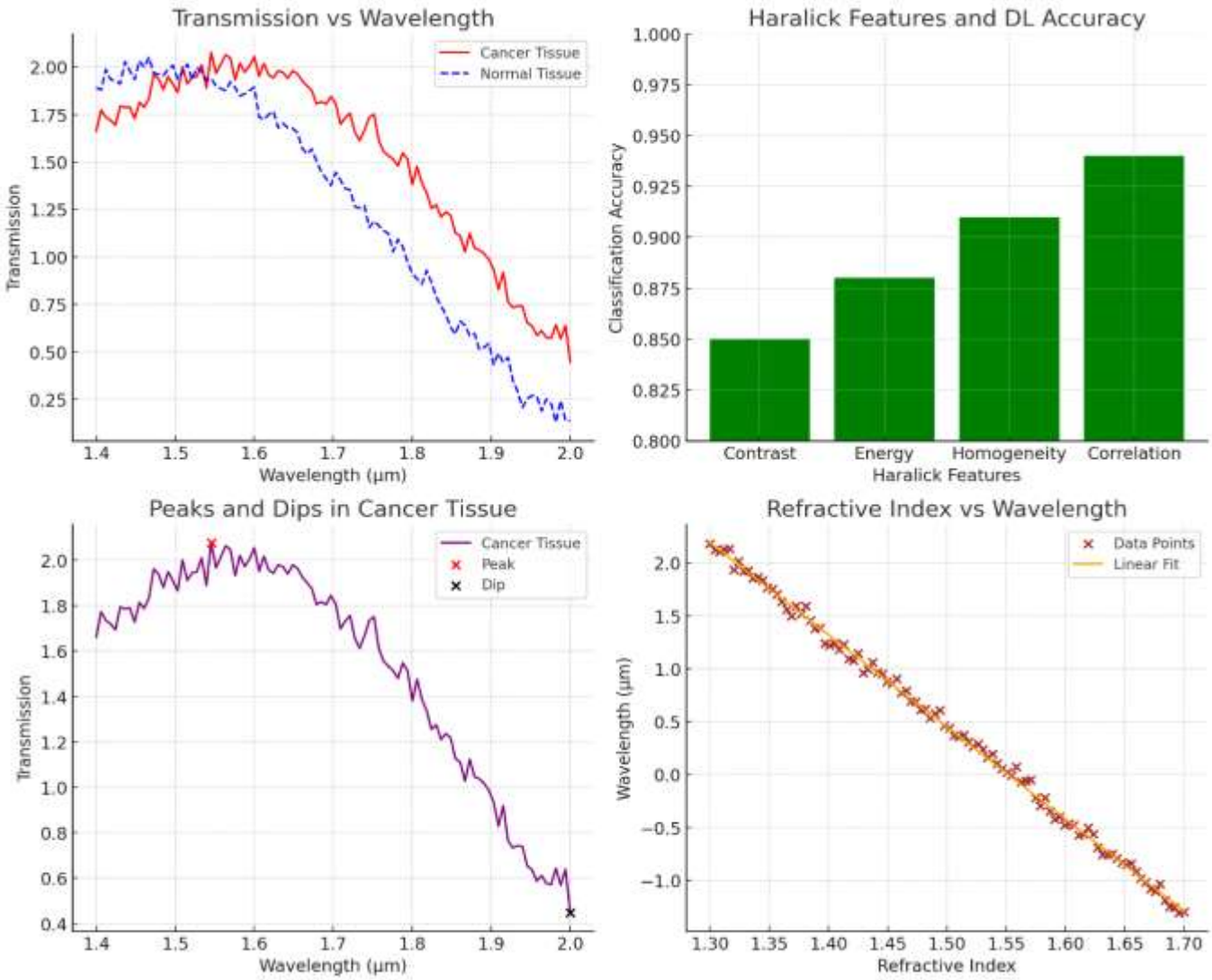

Figure 3. *Comparison between Refractive Index vs Wavelength*

the automatic diagnosis of cancer from human tissue images. The Haralick features, from the GLCM, give statistical information on textural patterns, and the hierarchical feature extraction through CNNs captures spatial information. Therefore, the hybrid system, with such complementary feature sets, improves accuracy and reliability for cancer classification in a significant way. The proposed model demonstrates an excellent performance with the ability to differentiate between normal and malignant tissues by exploiting both handcrafted and data-driven learning advantages. Besides, this approach minimizes dependency on large annotated datasets for deep learning, hence making it even more applicable to real-world medical scenarios. This approach highlights the possibilities of integrating the conventional analysis of texture with recent neural networks. This supports evolution of diagnostic technologies, including scaling up diagnostic modalities in the case of medical imaging and oncology, thereby assuring to be precise and efficient.

Author Statements:

- **Ethical approval:** The conducted research is not related to either human or animal use.
- **Conflict of interest:** The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper
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