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Multimodal Feature Learning Module for Prostate Cancer Prediction

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Abstract

In worldwide, prostate cancer is one of the frequently identified cancer. Now a days, It is very common in male with above 40 years. The accurate prediction of risk, progression and response to treatment remains challenging issues. Traditional model of predictions primarily depending on individual data such as prostate specific antigen (PSA), biopsy or medical imaging characteristics. The advances of Artificial Intelligence (AI) potentially improved cancer prediction by integrating heterogeneous healthcare information. Effective fusion of multimodal data remains a challenging problem due to the differences in data values, dimensionality and biological significance. This research proposes a Multimodal Feature Learning Module (MFLM) for the prediction of prostate cancer. This Multimodal module integrates deep feature learning from clinical, magnetic resonance imaging (MRI) and genomic data. It employs modality specific feature extraction with an attention based fusion mechanism to learn corresponding relationships from different data modalities. The proposed framework uses deep learning model, including convolutional neural networks (CNNs), transformer based encoders and fully connected system to extract useful patterns from heterogeneous patient information.

Keywords: Prostate cancer prediction; Multimodal learning; Deep learning; MRI; Genomic feature extraction.

1. Introduction

Prostate cancer is considered as a biggest challenge for healthcare industry due to its high rate of incidence, biological complexity and difference of disease progression individuals. Advancements in screening, imaging and therapeutic interventions improved patient outcomes [1][2]. Even though, accurate prediction of progression and treatment planning remains difficult. Clinical behaviour of prostate cancer may be influenced by demographics, biochemical biomarkers, tumour morphology, genetic alterations and environmental conditions [3]. Therefore, single information source may not provide sufficient information about disease mechanisms [4].

Now a days, diagnosis of prostate cancer and assessment of its risk are made using clinical indicators like prostate specific antigen (PSA), digital rectal examination (DRE), Gleason grading and histopathological scrutiny [5][6][7]. Widely adopted initial screening method is PSA. But PSA levels are not always explicit to malignant settings and so it may lead to needless biopsies [8]. Biopsy assessment normally provides important pathological info but, tumour regions may not uniformly appear throughout prostate gland [9]. These limitations encouraged researchers to implement computational approaches for integrating multiple information about the patients.

Multiparametric magnetic resonance imaging (mpMRI) has a vital role in prostate cancer diagnosis and monitoring [10]. MRI is used to provide a clear anatomical and functional evidence about the location, size, texture and vascular characteristics of tumour. The deep learning models like convolutional neural networks (CNNs) effectively extracting discriminative imaging features [11] [12]. However, imaging models alone may not suitable to identify molecular and clinical variations of cancer progression [13].

Application of Artificial Intelligence (AI) allows to analyse complex biomedical dataset through machine learning and deep learning. Deep neural networks learn hierarchical feature patterns from large scale dataset [14]. CNN based models achieved remarkable results in cancer imaging by learning spatial patterns related with tumour [15][16][17]. These models focus on a single modality and do not exploit the complementary data that are available in other healthcare data sources. Machine learning models like Random Forest, Support Vector Machine (SVM) and gradient boosting are extensively applied for clinical data predictions. It uses manually selected features and may not work with complex nonlinear relationships [18].

The emergence of multimodal learning promises a solution by integrating various patient information into a framework. It to identify effective representations from multiple data sources and learn their interactions.

In prostate cancer prediction, the multimodal learning combines clinical variables, MRI features, pathological information and genomic characteristics for a comprehensive understanding about disease behaviour [19].

Genomic information highly influences prostate cancer research due to the strongly influence of genetic alterations in tumour development and response to treatment [20][21]. Gene profiles, mutations and molecular biomarkers give knowledge about tumour aggressiveness and therapeutic response [22]. Thousands of characters with limited patient samples in genomic dataset creates challenges on feature selection and dimensionality reduction [23]. Deep learning potentially extracting meaningful patterns of data from high dimensional genomic samples [24].

The integration of clinical, imaging and genomic information has different technical challenges. Each modality differs in case of data characteristics, scale and its format of representation [25]. Clinical information is normally low dimensional and structured, MRI contain high dimensional spatial information, while genomic data is extremely high dimensional with molecular properties [26] [27]. Direct combination of these heterogeneous data may consist of redundant information and may reduce efficiency [28] [29]. Therefore, advanced feature learning technique and fusion models are needed to extract modality relevant information.

Instead of giving equal importance to all features, attention based methods dynamically learn modality specific weights [30]. This is useful in medical applications where, few biomarkers or genomic data may contribute more to the prediction [31] [32].

In recent researches, integration of multimodal feature learning with latest technologies like Digital Twins, Generative AI and Explainable AI shows remarkable results [33][34]. A patient specific Digital Twin needs complete representation of clinical, biological and imaging info to simulate disease progression more accurately. Multimodal serves as a foundation for constructing individualized patient information. Similarly, explainable AI identify important features that contribute to the prediction [35].

In this article, a Multimodal Feature Learning Module (MFLM) is developed for prostate cancer prediction by participating clinical, MRI and genomic data. This framework consists of three major components like modality specific feature extraction, adaptive multimodal fusion and prediction optimization. it employs deep learning encoders to learn independent values from each modality and attention based fusion is utilized to generate patient feature vector.

2. Dataset Preparation

The proposed model requires clinical, radiological and molecular characteristics of the patient The clinical component includes age, PSA level, Gleason score, TNM stage and prostate volume. The radiological - MRI includes T2-weighted, diffusion-weighted and apparent diffusion coefficient. molecular or genomic component includes gene expression, mutation information and copy number alterations. The corresponding preprocessed dataset from TCGA-PRAD and PROSTATEx collection are used in this research to train and test the model.

3. Multimodal Feature Learning Module

The Multimodal Feature Learning Module (MFLM) is to learn complementary information from multiple healthcare data. In prostate cancer, the major data modalities are clinical records, medical imaging and genomic profiles. However, direct integration of these heterogeneous data is challenging due to the differences in its dimensions, distribution characteristics and semantic representation. Hence, the proposed MFLM uses hierarchical learning of modality-specific feature extraction, feature transformation, adaptive attention-based fusion and classification optimization. The diagrammatic representation of the proposed model is given in figure 1.

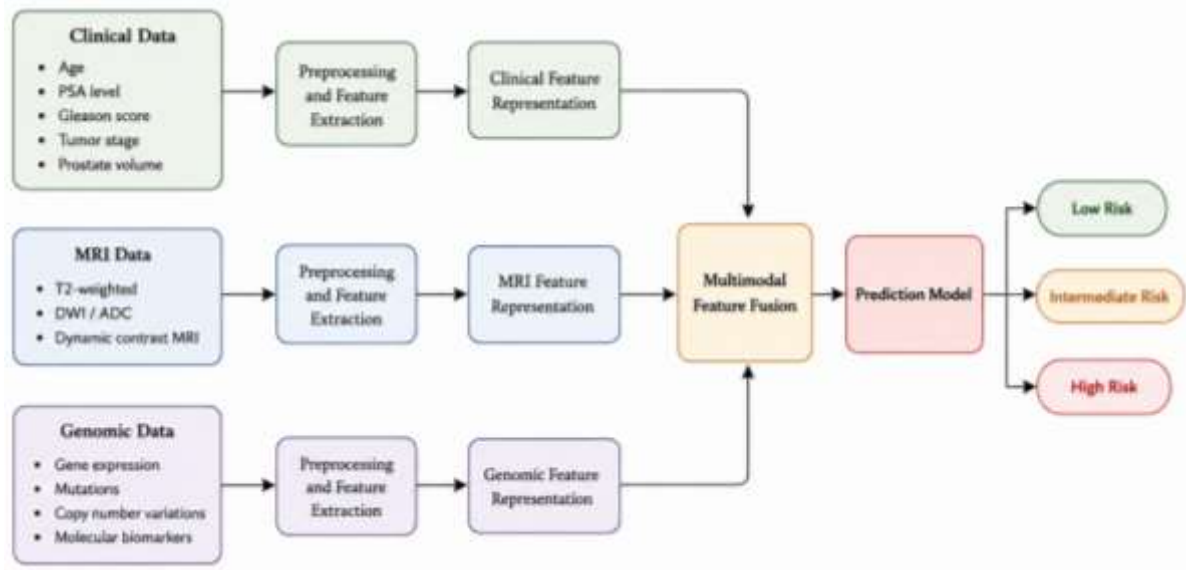


Fig.1: Multimodal Feature Learning Module

Let a patient is represented by a multimodal input vector,

$$X = \{X_c, X_m, X_g\}$$

where,

X_c represents clinical information,

X_m represents MRI-based imaging information,

X_g represents genomic information.

To learn a nonlinear mapping function,

$$F: \{X_c, X_m, X_g\} \rightarrow Y$$

where,

Y represents the predicted prostate cancer outcome (cancer risk category, tumour aggressiveness, disease progression probability or treatment response).

The complete multimodal learning fusion is,

$$Y = f \left(F_{fusion} \left(F_{cf}(X_{cf}), F_{mf}(X_{mf}), F_{gf}(X_{gf}) \right) \right)$$

where,

F_{cf} represents clinical feature extraction

F_{mf} represents imaging feature extraction

F_{gf} represents genomic feature extraction

F_{fusion} represents multimodal feature fusion.

3.1 Clinical Feature Representation Model

Clinical data represents important characteristics of prostate cancer progression. It generally includes PSA concentration, prostate volume, age, family history, Gleason score, tumour stage, hormonal status and previous treatment information. Therefore, the clinical input vector is,

$$X_c = [x_1, x_2, x_3, \dots, x_n]$$

where,

x_i represents individual clinical parameters.

The clinical values are in different scales and so normalization is applied before feature learning,

$$X'_c = \frac{X_c - \mu_c}{\sigma_c}$$

where,

μ_c represents mean value of clinical features

σ_c represents standard deviation

The normalized clinical vector is passed through a fully connected neural network to learn high level clinical characters

$$F_c = \sigma(W_c X'_c + b_c)$$

where:

W_c represents the learnable weight matrix

b_c represents bias

σ represents activation function

Rectified Linear Unit (ReLU) activation is applied for nonlinear feature learning,

$$ReLU(x) = \max(0, x)$$

Created clinical embedding is,

$$F_c \in R^{d_c}$$

where,

d_c represents the learned feature dimension.

The clinical encoder is to learn complex relationships between patient characteristics and create compact representation for multimodal fusion.

3.2 MRI based Imaging Feature Learning Model

Medical images show spatial and structural information of prostate tumour. The MRI is represented as,

$$X_m \in R^{H \times W \times C}$$

where,

H represents height (ie. 224)

W represents width (ie. 224)

C represents the number of imaging channels (ie. 3)

A convolution operation is applied to extract spatial features,

$$F_m^{(l)} = \phi(W_m^{(l)} * X_m^{(l-1)} + b_m^{(l)})$$

where,

$F_m^{(l)}$ represents feature maps at layer l

$W_m^{(l)}$ represents convolution kernels

$b_m^{(l)}$ represents bias

$*$ represents convolution operation

ϕ represents nonlinear activation function

The convolution layer extract low level characteristics like edges, intensity variations and texture patterns. But deeper layer learns high level characteristics like tumour boundaries, lesion morphology, tissue heterogeneity and vascular patterns.

Therefore, the final MRI feature representation is,

$$F_m = Flatten(F_m^{(L)})$$

where, L represents the final feature extraction layer. The imaging embedding is,

$$F_m \in R^{d_m}$$

where, d_i is the dimensionality of MRI features.

3.3 Genomic Feature Learning

Genomic information offers molecular level information of prostate cancer development and its progression stages. It contains gene expression values, mutation patterns, copy number variations and molecular biomarkers.

The genomic input vector is

$$X_g = [g_1, g_2, g_3, \dots, g_m]$$

where, g_1 to g_m represents genomic attributes.

Due to the high dimensionality of genomic data, dimensionality reduction is applied. Here, an autoencoder genomic encoder is used.

Therefore, encoder transformation is,

$$F_g = \sigma(W_g X_g + b_g)$$

where,

W_g represents genomic encoder weights

b_g represents bias parameters

The compressed genomic representation is,

$$F_g \in R^{d_g}$$

where, d_g is the learned genomic feature dimension.

The genomic encoder took important molecular patterns like tumour aggressiveness, cancer subtype, therapy response and recurrence probability.

3.4 Multimodal Feature Alignment

The three types of modalities generate feature vectors with different dimensions like $F_c \in R^{d_c}$, $F_m \in R^{d_i}$ and $F_g \in R^{d_g}$. The concatenation of these features may lead to feature imbalance. Therefore, the transformation of all modalities into a common feature is made with feature projection.

$$Z_{mo} = W_{mo}F_{mo} + b_{mo}$$

where,

$$m \in \{c, i, g\}$$

Z_{mo} represents aligned modality features.

That is,

$$Z_c, Z_m, Z_g \in R^d$$

Now, all modalities are in identical dimensional for effective fusion.

3.5 Attention based Multimodal Feature Fusion

In multimodal learning, contributing factor determination is a tedious task. For an example, some may have stronger clinical attributes, others may have significant imaging or genomic pattern. An adaptive attention system is needed here to address this issue.

The modality feature matrix is,

$$Z = [Z_c, Z_m, Z_g]$$

The attention score is calculated by,

$$A_m = \frac{e^{W_a Z_{mo}}}{\sum_{mo=1}^{MO} e^{W_a Z_{mo}}}$$

where,

A_{mo} represents attention weight

W_a represents attention parameters

MO represents number of modalities

The attention weights is

$$\sum_{mo=1}^{MO} A_{mo} = 1$$

The final fused representation is achieved as,

$$F_{fusion} = A_c Z_c + A_m Z_m + A_g Z_g$$

where,

F_{fusion} represents the final patient representation

A represents adaptive modality importance

3.6 Prediction Layer

The fused multimodal values are given to fully connected layers for the prediction.

Therefore, prediction function is,

$$\hat{Y} = Softmax(W_f F_{fusion} + b_f)$$

where,

W_f represents prediction weights

b_f represents bias

$\hat{Y}$ represents predicted probability as $\hat{Y} = \begin{cases} 0, & \text{Non-aggressive cancer} \\ 1, & \text{Aggressive cancer} \end{cases}$

3.7 Loss Function and Optimization

The proposed model is trained using categorical cross entropy loss.

$$L = - \sum_{i=1}^N y_i \log(\hat{y}_i)$$

where,

y_i represents actual class label

$\hat{y}_i$ represents predicted probability

N represents number of samples

Regularization is applied to improve generalization

$$L_{total} = L + \lambda ||W||_2^2$$

where,

λ represents regularization coefficient

$||W||_2^2$ represents weight penalty

The model parameters are optimized using Adam optimizer,

$$\theta_{t+1} = \theta_t - \eta \frac{\widehat{m}_t}{\sqrt{\widehat{v}_t} + \epsilon}$$

where,

η represents learning rate,

$\widehat{m}_t$ represents first-order moment estimate,

$\widehat{v}_t$ represents second-order moment estimate.

The complete multimodal feature learning process can be summarized as,

$$Y = \text{Softmax}(W(A_c Z_c + A_m Z_m + A_g Z_g) + b)$$

where, adaptive attention weights of clinical, MRI and Genomic representations are A_c , A_m and A_g respectively.

4. Experimental Discussion and Analysis

The performance of the proposed Multimodal Feature Learning Module (MFLM) is mainly focus on the ability of capturing different biological attributes. The proposed framework becomes more efficient by combining three modalities of patient's condition. Traditional prostate cancer predictions generally depend on one primary data. The attention mechanism is having major role in prediction. It allows the module to determine the contributing factors of each modality. It assigns higher priority to most informative feature of each patient.

The performance of the model is evaluated by using its accuracy, precision, recall, F1-score, specificity and Area Under the Receiver Operating Characteristic Curve (AUC-ROC). Since the MFLM combines three types of dataset, the efficiency of each modality and conventional fusions is compared.

Table 1. Comparison of Diverse Feature Learning

Model / Feature Configuration	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Specificity (%)	AUC (%)
Clinical data only	88.6	87.9	86.8	87.3	89.4	90.1
MRI only	91.4	90.8	90.1	90.4	92.2	93.0
Genomic data only	89.8	89.1	88.7	88.9	90.6	91.5
Clinical + MRI	93.2	92.7	92.1	92.4	94.0	94.6
Clinical + Genomic	92.1	91.5	91.2	91.3	93.0	93.8
MRI + Genomic	94.0	93.5	93.1	93.3	94.8	95.2
Simple Feature Concatenation	94.7	94.1	93.8	93.9	95.4	95.8
Proposed MFLM	97.2	96.8	96.4	96.6	97.8	98.1

In table 1, the clinical only model achieved 88.6% of accuracy and it shows that the attributes of this data is having valuable information for prediction. The image feature provides direct information about tumour morphology and therefore, it has given better performance with 91.4% accuracy. The genomic only data performed with molecular characteristics to achieve an accuracy of 89.8%. The combination of two modalities improved the performance of prediction. The MRI and genomic reached upto 94.0% accuracy, while clinical and MRI obtained 93.2%. Simple feature concatenation increased the accuracy of prediction to 94.7%. The proposed MFLM performed with highest accuracy (97.2%), precision (96.8%), recall (96.4%), F1-score (96.6%), specificity (97.8%) and AUC (98.1%).

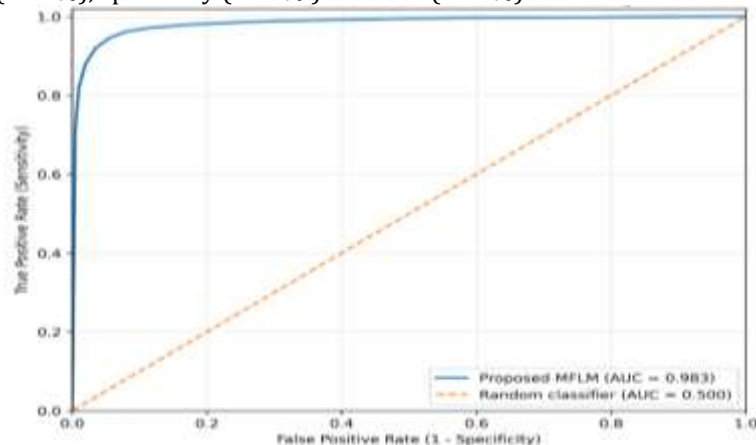


Fig.1: ROC curve of the Multimodal Feature Learning Module

The ROC curve of the proposed Module demonstrates highest classification capability with AUC of 0.983. The curve is placed above the random classification line and reaches to the upper left corner. It shows a reasonable balance between sensitivity and specificity. The AUC showcase that the integration of clinical, MRI and genomic information provides effective discrimination between prostate cancer classes.

5. Advantages of Proposed model

The proposed multimodal feature learning provides several advantages than the conventional cancer prediction models.

- *Comprehensive Patient Representation* - The model combines clinical, imaging and genomic characteristics to create a complete representation of disease behaviour.
- *Adaptive Feature Learning* - The attention mechanism assigns ranking dynamically for influencing features instead of treating all data equally.
- *Improved Prediction* - The integration of multiple features enables the model to read complex disease patterns that may found as hidden in individual modalities.
- *Personalized Healthcare Support* - The framework concentrates on patient specific factors rather than generalized prediction rules.

6. Proposed Applications of the Model

The proposed framework has several possible applications in management of prostate cancer.

6.1 Early Detection

The model can be used to identify high risk patients at the earliest stage by combining PSA values, MRI properties and genomic indicators. The early prediction supports timely clinical intervention and helps to improves treatment results.

6.2 Risk Stratification

The model can provide assistances to classify patients into three different categories such as low risk, intermediate risk and high risk prostate cancer. This classification supports personalized monitoring and reduces unnecessary interventions.

6.3 Personalized Clinical Decision Support

The learned patient characteristics can be integrated to clinical decision support systems. This integration will support oncologists in selecting suitable treatment.

6.4 Digital Twin Integration

The generated multimodal patient representation can be served as a foundation for creating patient specific Digital Twins. It represents current clinical and biological stage of an individual and able to update when a new patient data is available. Digital Twin can use to simulate tumour development and treatment responses in different therapeutic situations.

7. Conclusion

A Multimodal Feature Learning Module is implemented in this research for prostate cancer prediction. The module integrated clinical, MRI and genomic data to addresses the limitations of conventional prediction methods by learning complementary information from heterogeneous patient database. It combines feature extraction, feature alignment, attention based fusion and prediction optimization. The attention model creates an environment of adaptive learning for identifying most relevant patient specific characters from all databases.

The proposed model provides an efficient foundation for intelligent healthcare system for accurate cancer prediction, personalized risk assessment and treatment response analysis. Furthermore, incorporation of Generative AI, Digital Twin technology, Reinforcement Learning and Explainable AI can transform the model into a complete decision making system for personalized management in prostate cancer.

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