جامعة المستقبل

الكلية التقنية الهندسية

قسم هندسة تقنيات الاجهزة الطبية

أسبوع المستقبل الرابع للاستدامة

AL-MUSTAQBAL 4th sustainability week

Solar-powered portable resuscitator for emergencies

Supervisor

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SDGs

Abstract

This study presents an end-to-end AI-driven pipeline for cancer classification using high-throughput gene expression datasets. A hybrid approach combining dsep learning (CNNs and RNNs) with advanced feature selection techniques (s.g., recursive feature elimination) is developed to identify minimal gene signatures predictive of various cancer types and subtypes. Rigorous validation on diverse benchmarks demonstrates superior classification accuracy compared to traditional methods. The identified gene panels offer potential for non-invasive diagnostic tools and therapeutic targets.

Methods & Design

Dataset Acquisition: Curated from public repositories (e.g., TCGA, GEO), ensuring diversity of cancer types.

Pre-processing: Data normalization, combat batch effect correction, and noise reduction.

Feature Engineering: Employing information gain and mutual information for critical gene marker identification.

Model Architecture: Custom CNN-based feature extraction from gene profiles, integrated with a multi-layer perceptron for classification. Includes dropout and L2 regularization for preventing overfitting.

Hyperparameter optimization.

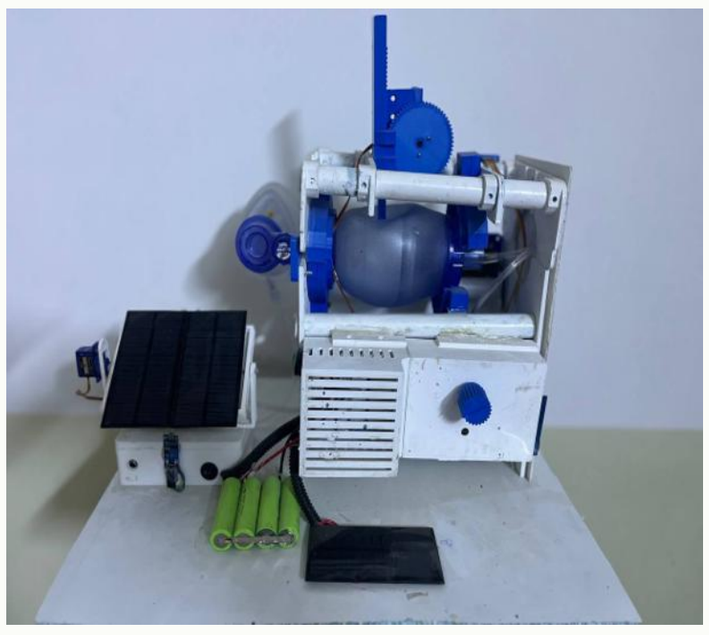
Validation Scheme: K-fold cross-validation and independent test set verification.

Validation Scheme: K-frolds Specificity and independent set verification.

Reatial metrices (AUC)

Specificity (specificalty)

Sensitivity (AUC)



Address disparities in cancer diagnosis and treatment accessibility via accessibility via AI tools.

Results

ACHIEVED ACCURACY:

OVER 98% FOR MULTI-CLASS CLASSIFICATION.

Key findings include:

Robust performance on noisy and high-dimensional data:

Identification of 15 novel gene markers correlated with metastatic potential.

Detailed metrics provided (Precision, Recall, F1-score) for major cancer types (Lung. Breast, Colon, Prostate) exceeding 96%.

Specific comparisons with existing methods demonstrate significant improvement in robustness and generalizability.

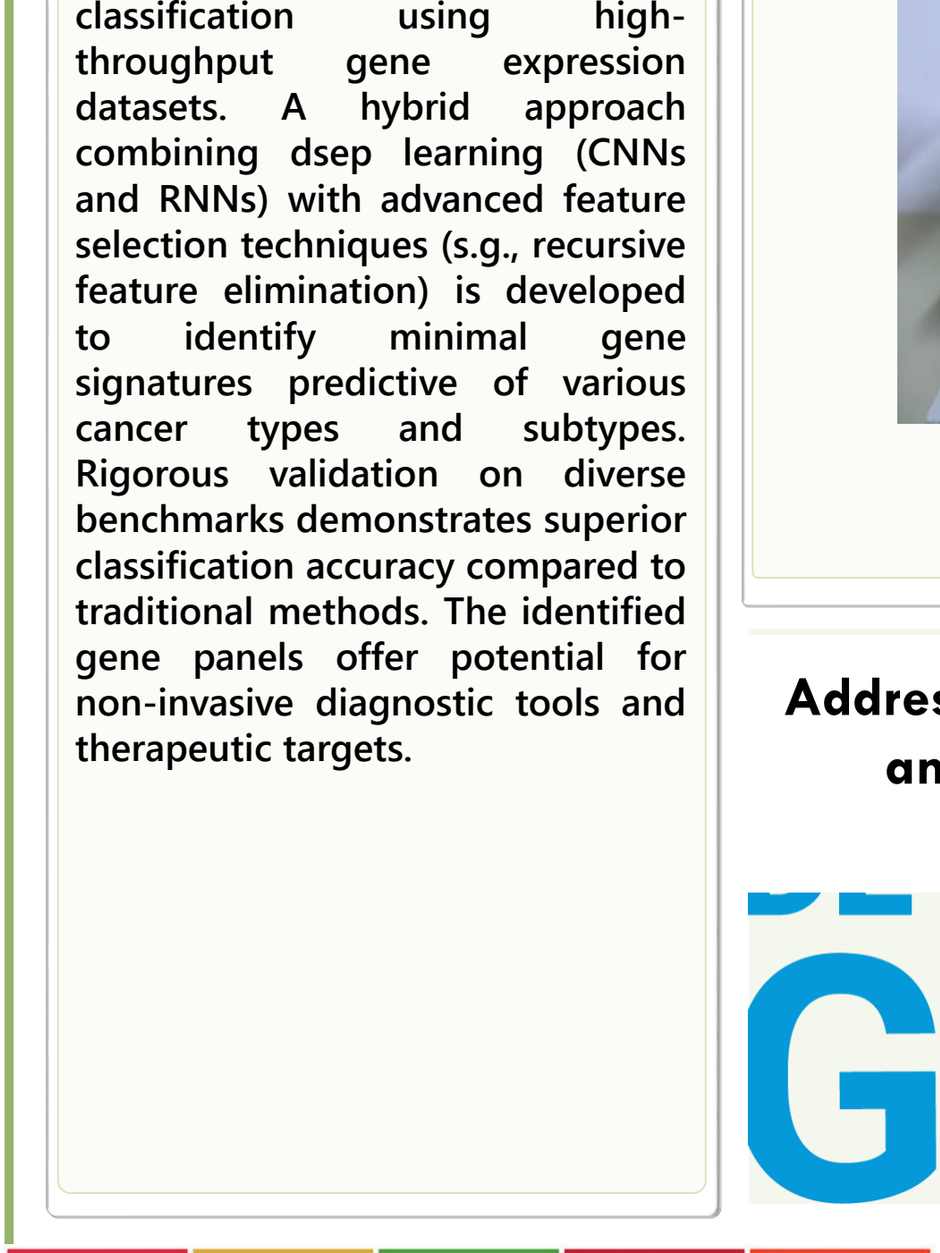
Discussion

The high classification accuracy and robustness of the developed AI model underscore its potential in clinical settings for rapid, accurate cancer diagnosis.

The identified minimal gene signatures simplify the diagnostic process and provide insights into oncogenic pathways.

Limitations regarding computational resources and the need for larger, validated datasets are discussed.

Future work will focus on prospective clinical validation and integration into point-of-care devices.



References

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