International Journal of Scientific Research in Engineering and Management (IJSREM)
Volume: 08 Issue: 05 | May - 2024 SJIF Rating: 8.448 ISSN: 2582-3930

PATHOMIC FUSION: CANCER DIAGNOSIS AND PROGNOSIS INTEGRATION

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Abstract:

This paper proposes a novel approach to cancer diagnosis and prognosis, integrating pathology and molecular data. A machine learning algorithm is developed, trained, and validated on extensive datasets. A clinical software tool will facilitate clinicians in delivering accurate, personalized diagnoses and prognoses, potentially revolutionizing cancer care.

Introduction:

Integrating pathology images and genetic data holds promise in enhancing cancer prognosis by offering a holistic view of the disease. Pathomics, a novel approach, facilitates this integration without relying on labeled data. This research bridges pathology and molecular realms, aiming to enhance diagnostic precision. Through machine learning, it seeks to empower clinicians with a versatile tool for personalized cancer care, potentially revolutionizing treatment outcomes.

Literature Review:

Previous studies like MultiCoFusion and Radiopathomics model integration of radiomics and pathomics data for cancer prognosis. Challenges include small cohorts and time-consuming processes. MSF-Model addresses domain adaptation issues but faces limitations in contrast enhancement.

Methodology:

Our approach consists of several key steps:

1. **Data Visualization:** Bar plot using Seaborn visualizes the distribution of data across different categories.
2. **Data Loading and Preprocessing:** Involves resizing and converting images into arrays, while categorical data is encoded using Scikit-learn's LabelEncoder, preparing both image and categorical variables for analysis or model training.
3. **Data augmentation :** Utilizing Keras' ImageDataGenerator, enriches the dataset by applying diverse transformations such as zooming, rotation, and brightness adjustment, alongside a custom contrast stretching function, enhancing dataset variability and model robustness for improved generalization.
4. **Model training :** It encompasses selecting and customizing a pre-trained base model for image classification, freezing its layers, compiling with a loss function and optimizer, training with augmented data flow, and evaluating various machine learning classifiers with specific parameters for accuracy and error metrics on the test set.
5. **Fusion Module:** A fusion module is introduced to combine the outputs from the histopathology and genomic models. The module concatenates the outputs and passes them through additional fully connected layers with dropout regularization to prevent overfitting.

6. **Final Prediction:** The fusion module outputs a final prediction that incorporates information from both the histopathology images and genomic data, aiming to improve the overall diagnostic and prognostic capabilities of the system .
7. **Grade classification :** It involves categorizing tumors based on their microscopic appearance and growth potential, assessing characteristics like architecture, cellularity, nuclear features, and mitotic rate to assign grades ranging from 1 to 3, aiding in treatment planning and prognosis estimation by providing insights into tumor aggressiveness and behavior.
8. **Survival Analysis:** The model incorporates survival analysis techniques to predict survival outcomes based on the integrated histology and genomic features.

Results:

The study showed that the multimodal fusion approach outperformed unimodal deep networks trained solely on histology or genomic data. By combining information from both modalities, the model achieved better predictive performance, highlighting the importance of leveraging multiple data sources for comprehensive analysis .

Discussion:

Pathomic Fusion integrates histology and genomic data, enhancing predictive accuracy and providing insights into feature importance and localization. Its interpretive capability aids in understanding disease mechanisms, improving prognostic determinations beyond traditional methods.

Conclusion:

In conclusion, the fusion of pathology and molecular data through advanced machine learning offers a transformative approach to cancer care, addressing diagnostic inaccuracies and treatment limitations. Integrating these data sources enables more informed decisions, potentially leading to earlier diagnoses, tailored treatments, and improved patient outcomes, heralding a promising future for personalized cancer care.

References:

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