**Literature Review**

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| **Student Name** | **Vaishnavi Tumuluri** |
| **Project Topic Title** | **ATTENTION U-NET BASED MULTI-VIEW CLUSTERING MODEL FOR PREDICTING ALZHEIMER’S DISEASE PROGRESSION** |

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| **Week 1** | | | | | | | |
| **1** |
| **Reference in APA format** | | Zhang, X., Yang, Y., Li, T., Zhang, Y., Wang, H., & Fujita, H. (2021). CMC: A consensus multi-view clustering model for predicting Alzheimer's disease progression. Computer Methods and Programs in Biomedicine, 199, 105895. <https://doi.org/10.1016/j.cmpb.2020.105895> | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| <https://doi.org/10.1016/j.cmpb.2020.105895> | | Xiaobo Zhang, Yan Yang, Tianrui Li, Yiling Zhang, Hao Wang, Hamido Fujita | | | | Consensus representation, Multi-view clustering, Alzheimer's disease progression, Non-negative matrix factorization, MRI data. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Consensus Multi-view Clustering (CMC) Model​. | | The CMC model aims to predict multiple stages of Alzheimer’s disease progression. It addresses limitations in single-view data analysis, manual parameter setting, and two-class classification issues by leveraging multi-view clustering. | | | | Consensus Fusion Mechanism: Integrates multiple views.  Non-negative Matrix Factorization (NMF): Generates a consensus representation.  MRI-based Multi-view Dataset: Twelve views constructed from MRI data to predict AD progression. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| The CMC model utilizes multi-view clustering combined with non-negative matrix factorization (NMF) to predict Alzheimer’s disease (AD) progression stages   |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Feature Extraction - The model creates multiple views (twelve in total) from MRI data using techniques such as SIFT, KAZE, and Gabor filters. | This expands feature representation, enhancing the model's robustness. | Computation is intensive, which may limit application speed. | | **2** | Data Preprocessing with PCA and Normalization - To ensure consistency across views, the data undergoes principal component analysis (PCA) and normalization to reduce dimensionality and minimize noise. | Helps improve model performance by reducing data redundancy. | Potential loss of data nuances due to compression. | | **3** | Consensus Representation via Non-negative Matrix Factorization (NMF) - NMF is applied to extract shared and complementary features across all views. This fusion creates a "consensus" view representing the key information in a unified matrix. | Allows effective data integration across views without manual parameter setting. | The optimization process can be computationally demanding. | | **4** | Clustering and Prediction - Finally, the consensus matrix is used in a clustering approach to predict multiple AD stages. | Enables the model to accurately predict AD stages by leveraging multiple data perspectives. | High computational requirements, especially during optimization. | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| The paper proposes a multi-view clustering model to predict Alzheimer’s disease stages by integrating data from multiple MRI views, enhancing prediction accuracy.   |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Prediction of Alzheimer's disease stages, based on the consensus of multi-view data. | Multi-view MRI inputs, processed and combined to enhance feature diversity. | Image quality and the number of views, affecting the reliability of the consensus model. | Data normalization and feature reduction techniques like PCA, helping manage data consistency across views. | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | The CMC model uses multi-view MRI inputs (Independent Variable) to predict the Alzheimer’s stage (Dependent Variable) by generating a consensus representation from multiple views. This process is affected by image resolution and the number of views (Moderating Variables), which influence the quality and detail of data representation. Data preprocessing techniques like PCA and normalization (Mediating Variables) help standardize and compress data across views, facilitating effective integration and enhancing the clustering model’s prediction accuracy. The interplay among these variables allows the model to produce a unified, accurate diagnosis by balancing data consistency and computational efficiency. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | MRI data (multiple views) | Predicted stages of Alzheimer’s progression across multiple phases. | | | | Integrates data from twelve MRI views, enhancing feature representation for Alzheimer’s disease (AD) progression. Generates a consensus representation to unify multiple views, reducing noise and redundancy. Combines views automatically without manual parameter setting, improving ease of implementation. Facilitates multi-stage AD prediction using diverse MRI data, providing a refined clustering solution. | | | | This paper presents a robust, unsupervised multi-view clustering model that improves AD stage prediction by effectively merging information from various MRI data views. The model’s novelty lies in using NMF for automatic parameter-free data fusion. The CMC model contributes to the field of neuroimaging by enhancing early diagnosis of Alzheimer’s disease stages, potentially aiding in timely intervention and improving patient outcomes. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| By improving prediction accuracy, this model offers a significant tool for clinicians, reducing diagnostic load and enhancing treatment decisions in AD care. | | | | | The reliance on high computational power and extensive MRI data can be a limitation, particularly in under-resourced healthcare settings. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| Utilizes non-negative matrix factorization for effective multi-view learning, enhancing robustness and predictive performance. The structured approach of integrating views is efficient but requires optimization to manage the computational burden effectively. | | | | Non-negative Matrix Factorization (NMF)  Principal Component Analysis (PCA)  Feature Extraction Algorithms | | | 1. Abstract 2. Introduction 3. Related Work 4. Methodology 5. Optimization Algorithm 6. Experiments 7. Conclusion 8. References |
| **Diagram/Flowchart** | | | | | | | |
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| **2** |
| **Reference in APA format** | | Nazir, I., Haq, I., AlQahtani, S. A., Jadoon, M. M., & Dahshan, M. (2023). Machine Learning-Based Lung Cancer Detection Using Multiview Image Registration and Fusion. *Journal of Sensors*, 2023, 6683438. <https://doi.org/10.1155/2023/6683438> | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://doi.org/10.1155/2023/6683438 | | Imran Nazir, Ihsan ul Haq, Salman A. AlQahtani, Muhammad Mohsin Jadoon, Mostafa Dahshan | | | | Lung cancer detection, Image registration, Multi-view image fusion, CT scans, ResNet-18, Machine learning. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Machine Learning-Based Lung Cancer Detection Using Multiview Image Registration and Fusion | | This model aims to enhance lung cancer detection accuracy by using multi-view image registration and fusion methods. The primary problem addressed is the limited information from single-view images, which hinders effective identification and staging of lung cancer. | | | | Image Registration and Fusion: Aligns and combines images from multiple views.  Deep Learning Classifier (ResNet-18): For tumor detection and stage classification.  Data Preprocessing Techniques: Includes wavelet transform and principal component averaging. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| This model employs multi-view image registration and fusion to improve the detection and staging of lung cancer from CT scans. The process involves the following steps:   |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Image Alignment with Multiresolution Rigid Registration (MRR) - The model uses MRR to align images at different resolutions, ensuring that different views are spatially synchronized. | Ensures high precision in image alignment, enhancing diagnostic reliability. | High-resolution images are needed for optimal performance, requiring significant computational resources. | | **2** | Feature Extraction using Discrete Wavelet Transform (DWT) and Principal Component Averaging (PCA) - DWT and PCA are applied to reduce image redundancy and enhance feature quality by merging information across multiple views. | Improves the quality and relevance of features used for classification. | The preprocessing is resource-intensive, limiting speed and requiring powerful hardware. | | **3** | Classification with ResNet-18 for Cancer Detection and Stage Classification - The ResNet-18 classifier detects lung cancer and classifies it into stages (STG-1 through STG-4) based on the combined image views. | High detection accuracy and reliable staging due to deep learning. | Overfitting may occur if the dataset is small, and large computational resources are needed. | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| The paper introduces a fusion-based model for accurate lung cancer detection and staging, utilizing multi-view CT images to improve diagnostic precision.   |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Accurate detection and staging of lung cancer. | Multiview CT scan images, providing comprehensive perspectives for diagnosis. | Image quality and the network architecture (ResNet-18), both crucial for achieving high accuracy. | Image fusion and feature extraction methods like DWT and PCA, enhancing data quality and model robustness. | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | In this model, multiview CT scan images (Independent Variable) are used to detect and stage lung cancer (Dependent Variable) by fusing different views to create a comprehensive diagnostic image. The image quality and the network architecture (ResNet-18) (Moderating Variables) influence the classification accuracy, as higher-quality images and a robust network improve the model’s precision. Image fusion and feature extraction techniques like DWT and PCA (Mediating Variables) enhance the data by removing redundancies and capturing relevant features, improving diagnostic accuracy and reliability. These variables work together to optimize the model’s ability to detect lung cancer accurately and minimize false positives. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution in This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multiview CT images. | Cancer detection with stages (STG-1 to STG-4). | | | | Precisely aligns multiple CT scan views to maintain spatial consistency. Enhances data quality by fusing relevant features and removing redundancy, resulting in more accurate classifications. Uses a deep learning classifier to identify and stage lung cancer, improving detection accuracy. Combines multiple images to create a comprehensive diagnostic view, improving the detail and reliability of cancer detection. | | | | The paper introduces a multi-view image registration and fusion approach, leveraging advanced feature extraction and deep learning for improved lung cancer detection and staging accuracy. This model provides a practical diagnostic tool with potential applications in clinical settings, reducing false positives in lung cancer screening and enhancing early-stage detection. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| Reduces the likelihood of false positives, thereby decreasing unnecessary medical interventions and enhancing clinical efficiency. | | | | | High computational requirements and a need for high-quality CT images may restrict the model’s deployment in low-resource settings. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The study leverages advanced ML and DL techniques to achieve high detection accuracy. However, dependence on high-quality imaging and sophisticated hardware limits its scalability for broader implementation in diverse clinical environments. | | | | Multiresolution Rigid Registration (MRR)  Discrete Wavelet Transform (DWT) & PCA  ResNet-18 | | | 1. Abstract 2. Introduction 3. Related Work 4. Methodology 5. Dataset and Preprocessing 6. Experimental Results 7. Conclusion 8. References |
| **Diagram/Flowchart** | | | | | | | |
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| **3** |
| **Reference in APA format** | | Al-Shoukry, S., Rassem, T. H., & Makbol, N. M. (2020). Alzheimer’s Disease Detection by Using Deep Learning Algorithms: A Mini-Review. *IEEE Access*, *8*, 77130-77139. https://doi.org/10.1109/ACCESS.2020.2989396 | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://ieeexplore.ieee.org/document/9075205 | | Suhad Al-Shoukry, Taha H. Rassem ([tahahussein@ump.edu.my](mailto:tahahussein@ump.edu.my)), Nasrin M. Makbol | | | | Alzheimer’s Disease, Deep Learning, Early Stage Detection, Diagnosis, MRI Imaging, Neuroimaging, Machine Learning. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Alzheimer’s Diseases Detection by Using Deep Learning Algorithms | | To utilize deep learning algorithms to improve early detection of Alzheimer’s Disease (AD) through automated analysis of neuroimaging data. Existing diagnostic approaches struggle with early AD detection, often relying on manual feature extraction, which limits scalability and accuracy. The paper reviews deep learning's potential to address these issues by automating feature extraction and providing higher diagnostic precision. | | | | MRI Imaging: MRI data is used to identify structural brain abnormalities linked to AD.  Deep Learning Models: Convolutional Neural Networks (CNNs) are applied to automatically extract features relevant to AD, bypassing traditional manual methods.  Data Augmentation: Utilizes data transformation techniques to expand datasets and enhance model robustness. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
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| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Data Collection & Preprocessing | Prepares MRI data, enabling the model to detect AD-specific patterns with minimal manual intervention | Limited by the quality and diversity of MRI datasets | | **2** | Deep Learning Model (CNN) | Automates feature extraction, identifying subtle changes in brain images that may indicate AD | High computational requirements, especially for 3D brain imaging data | | **3** | Data Augmentation | Improves model robustness, allowing for better performance on varied data samples | Augmentation methods may introduce noise, potentially impacting accuracy | | **4** | **Classification** | Accurately differentiates AD from healthy samples, aiding early-stage diagnosis | Can misclassify cases in datasets with overlapping AD and non-AD features | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Diagnostic Accuracy (ability to correctly identify AD) | Neuroimaging Data (MRI) | MRI Data Augmentation Techniques | Deep Learning Model (CNN) Architecture and Parameter Settings | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | The deep learning model (mediating variable) processes neuroimaging data (independent variable) to output diagnostic predictions (dependent variable), with data augmentation techniques (moderating variable) enhancing accuracy by providing more diverse training data. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | MRI neuroimaging data | AD diagnostic prediction based on extracted features | | | | CNNs automate feature extraction and classification, removing the need for manual processing. | | | | The work contributes to advancing early AD detection by using CNNs to automate diagnosis, improving clinical outcomes through early intervention capabilities. This approach is significant in the neuroimaging field, offering a scalable solution for AD prediction. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The system allows for early diagnosis of AD with high accuracy, potentially enabling preventive care before severe cognitive decline. | | | | | High computational costs limit accessibility, and there are potential biases if MRI datasets are not sufficiently diverse. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The paper effectively demonstrates how deep learning can improve early-stage Alzheimer's Disease (AD) detection by automating feature extraction from MRI data, reducing dependency on manual processes. However, its reliance on computationally intensive CNN models may limit accessibility, especially in clinical settings with limited resources. Additionally, accuracy can be affected by the diversity and quality of MRI datasets, potentially introducing biases if the data is not sufficiently representative. | | | | Convolutional Neural Networks (CNNs)  Data Augmentation  Statistical Metrics | | | 1. Abstract 2. Introduction 3. Literature Survey 4. Methods 5. Data Analysis 6. Conclusion 7. References |
| **Diagram/Flowchart** | | | | | | | |
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| **4** |
| **Reference in APA format** | | Khan, H. N., Shahid, A. R., Raza, B., Dar, A. H., & Alquhayz, H. (2019). Multi-view feature fusion based four views model for mammogram classification using convolutional neural network. *IEEE Access*, 7, 165724-165731. doi:10.1109/ACCESS.2019.2953318 | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://ieeexplore.ieee.org/document/8897609 | | H.N. Khan, A.R. Shahid, B. Raza, A.H. Dar, H. Alquhayz Emails: Basit Raza ([basit.raza@comsats.edu.pk](mailto:basit.raza@comsats.edu.pk)) | | | | Breast cancer, classification, computer-aided diagnosis (CADx), multi-view feature fusion, convolutional neural network (CNN), mammogram, deep learning. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Multi-view feature fusion based four views model for mammogram classification using convolutional neural network. | | The objective of the MVFF-based CADx system is to enhance the classification accuracy of mammograms in identifying normal vs. abnormal tissue, mass vs. calcification, and benign vs. malignant cases. The key problem addressed is the limitation of single-view mammography in effectively diagnosing breast cancer, where integrating four mammographic views could lead to better diagnostic accuracy and sensitivity. | | | | Multi-view feature fusion model: Combines four mammographic views (L-CC, L-MLO, R-CC, R-MLO) to improve accuracy in classifications.  CNN architectures: Applies CNN-based feature extraction and augmentation with models like VGGNet, GoogLeNet, and ResNet.  Data augmentation and transfer learning: Uses augmentation techniques and pre-trained models to enhance learning on limited datasets. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | CNN-based feature extraction | Extracts rich, detailed features from each view of the mammogram | High computational cost due to CNN depth and multi-view processing | | **2** | Early feature fusion | Fuses features from all views to enhance classification performance | May face overfitting on smaller datasets despite data augmentation efforts | | **3** | Multi-stage CADx classification | Provides classification at multiple levels: abnormality, type, pathology | Complexity increases with each classification stage, affecting performance | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | CADx classification accuracy across three stages | Multi-view mammograms from CBIS-DDSM dataset | Quality of mammogram images | Augmentation and data preprocessing | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | Multi-view fusion (independent) affects CADx classification accuracy (dependent) with dataset quality as a moderator, while data preprocessing and augmentation techniques mitigate limitations from image quality and dataset size, improving model robustness. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Mammogram images in four views per patient (L-CC, L-MLO, R-CC, R-MLO) | Predicted classification: normal vs. abnormal, mass vs. calcification, benign vs. malignant | | | | Multi-View Fusion: Combines four mammogram views (L-CC, L-MLO, R-CC, R-MLO) to enhance classification accuracy by integrating different perspectives of breast tissue.  CNN-Based Feature Extraction: Uses deep learning models (e.g., VGGNet) for detailed feature extraction from each mammogram view, optimizing for classification tasks.  Three-Stage CADx Classification: Classifies mammograms into normal vs. abnormal, mass vs. calcification, and benign vs. malignant, allowing for granular diagnostics.  Data Augmentation & Transfer Learning: Increases robustness with data augmentation and fine-tunes pre-trained models for handling limited medical imaging data.  Efficient Architecture: Achieves high classification performance with a simpler network structure, reducing computational complexity compared to traditional methods. | | | | The MVFF-based CADx system contributes significantly to improving breast cancer detection by utilizing multi-view mammograms, thereby addressing the limitations of single-view analysis. Its robustness across multiple classification stages shows promise in early cancer diagnosis and computer-aided diagnostics. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| Enhanced diagnostic accuracy: The multi-view fusion approach provides radiologists with a more comprehensive tool for identifying breast cancer.  Cost-effectiveness: As a CADx solution, this system may reduce diagnostic time and associated costs in clinical settings. | | | | | Overfitting potential: Limited by the dataset size, data augmentation is crucial but may not entirely eliminate overfitting risks.  Higher computational demands: Requires advanced hardware due to CNN model depth and feature fusion techniques. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The MVFF CADx system represents a step forward in multi-view mammogram analysis for breast cancer diagnosis. However, the computational overhead and the need for large, high-quality datasets remain challenges. The feature fusion approach shows considerable improvement over single-view models but would benefit from further optimization to reduce hardware demands and overfitting risks. | | | | VGGNet, GoogLeNet, ResNet (Deep learning frameworks for CNN architectures)  CBIS-DDSM and mini-MIAS datasets (for data source and validation)  Transfer learning with ImageNet pre-trained weights (for enhanced feature extraction and learning transfer) | | | 1. Abstract 2. Introduction 3. Literature Review 4. Methodology 5. Results and Discussion 6. Conclusion and Future Work |
| **Diagram/Flowchart** | | | | | | | |
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| **5** |
| **Reference in APA format** | | Liu, W., Zhu, J., Wang, H., & Zhang, Y. (2024). Robust multi-view clustering via graph-oriented high-order correlations learning. *IEEE Transactions on Network Science and Engineering*. https://doi.org/10.1109/TNSE.2024.3485646 | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://ieeexplore.ieee.org/document/10740343 | | Wenzhe Liu, Jiongcheng Zhu, Huibing Wang, Yong Zhang | | | | Multi-view clustering, Tensor, Tucker decomposition, Graph learning, High-order correlations. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Robust multi-view clustering via graph-oriented high-order correlations learning. | | The GHCL model addresses the limitations of existing multi-view clustering methods that inadequately fuse multi-view information and often disregard higher-order correlations between data views, leading to reduced clustering performance. | | | | Third-order Tensor Representation: Stacks low-dimensional embeddings of each view.  Tucker Decomposition: Captures higher-order correlations among views.  Adaptive Confidence Mechanism: Integrates similarity matrix and consensus representation, enhancing multi-view fusion.  Graph Learning: Produces high-quality affinity matrices for more robust clustering. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Low-dimensional Embeddings - The model generates latent embeddings for each view. | Provides a robust basis by reducing data dimensionality. | Initial embeddings may lose some information. | | **2** | Third-order Tensor Formation - Embeddings are stacked into a tensor. | Maintains structural information across views. | Higher computational demand. | | **3** | Tucker Decomposition and Regularization - Applies decomposition to manage data noise and retain key patterns. | Removes redundant information effectively. | Computational intensity increases with large data volumes. | | **4** | Clustering via Fusion Graph - A consensus graph is generated to achieve accurate clustering results. | Ensures a refined final clustering output by leveraging multiple perspectives. | Requires tuning of hyperparameters for optimal performance. | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Clustering accuracy and robustness. | Multi-view data input from various perspectives. | Number of views and quality of embeddings. | Tucker decomposition and confidence weighting. | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | In the GHCL model, multi-view data inputs (Independent Variable) are processed to achieve high clustering accuracy and robustness (Dependent Variable). The number of views and embedding quality (Moderating Variables) directly influence the clustering outcome by determining the richness and relevance of data representations across views. Meanwhile, Tucker decomposition and confidence weighting (Mediating Variables) act to standardize and refine the fused data, enhancing the final clustering performance by capturing essential patterns and reducing noise. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multi-view data. | High-quality clustering results with refined, denoised embeddings. | | | | High-order Correlation Learning: Utilizes third-order tensors and Tucker decomposition to capture complex relationships between multiple views.  Adaptive Confidence Mechanism: Assigns confidence scores based on each view's contribution, improving information integration.  Graph Learning with Robust Affinity Matrices: Ensures a denoised, high-quality similarity matrix that enhances clustering accuracy.  Multi-view Fusion: Combines diverse perspectives for comprehensive clustering, effectively handling noise and inconsistencies across data views. | | | | GHCL introduces a tensor-based clustering framework that captures high-order relationships, enhancing the reliability and precision of clustering in multi-view datasets. This model is valuable in fields requiring robust clustering of complex data, such as multimedia and bioinformatics, enabling improved analysis from multiple data perspectives. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| Enhances clustering performance by integrating comprehensive information from diverse data views, with practical implications for more accurate analyses. | | | | | High computational demands may limit scalability to very large datasets or low-resource environments. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| GHCL’s multi-layered approach in integrating higher-order correlations and adaptive confidence mechanisms creates a robust solution for clustering complex, multi-view data.  The reliance on high-quality, multi-view data and complex parameter tuning may limit its practical application in real-time clustering tasks. | | | | Tensor Formation and Tucker Decomposition  Graph Learning and Confidence Mechanism  Low-dimensional Embedding Techniques | | | 1. Abstract 2. Introduction 3. Related Work 4. Methodology 5. Experiments 6. Conclusion 7. References |
| **Diagram/Flowchart** | | | | | | | |
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**Work Evaluation Table**

**<Use the same factors you have used in "Work Evaluation Table" to build your own "Proposed and Previous comparison table ">**

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|  | **Work Goal** | **System's Components** | **System's Mechanism** | **Features /Characteristics** | **Cost** | **Speed** | **Security** | **Performance** | **Advantages** | **Limitations /Disadvantages** | **Platform** | **Results** |
| **Xiaobo Zhang et al.** | Predict Alzheimer’s disease stages with multi-view clustering | CMC model, NMF, MRI views | Multi-view MRI feature fusion | Robust feature representation, comprehensive disease stage prediction | High | |  | | --- | | Moderate |  |  | | --- | |  | | - | Moderate | Enhanced AD progression prediction accuracy | Computationally intensive, potential data compression losses | Not specified | Improved accuracy in AD stage prediction |
| **Imran Nazir et al.** | Enhance lung cancer detection via image registration and fusion | MRR, DWT, PCA, ResNet-18 | Multi-view CT scan registration and feature extraction | High accuracy and staging reliability | High, requires powerful hardware | Moderate | - | High | Precise detection, reliable staging | Overfitting on small datasets, high resource needs | Not specified | Accurate lung cancer detection and staging |
| **Suhad Al-Shoukry et al.** | Early Alzheimer’s detection through deep learning automation | CNNs, Data Augmentation | Automated MRI feature extraction for AD diagnosis | Scalable model, early detection | High for initial setup | Moderate | - | High | Automated, accurate early AD detection | High computational costs, dataset diversity needed | Not specified | Effective deep learning-based AD detection |
| **Hasan Nasir Khan et al.** | Improve mammogram classification accuracy | MVFF CADx, CNN architectures | Multi-view mammogram fusion and CNN feature extraction | Cost-effective CADx solution, reduces diagnostic time | Moderate | Moderate | - | High | Reduces diagnostic time and costs in clinical settings | Risk of overfitting, high computational demand | Not specified | Enhanced multi-view mammogram classification accuracy |
| **Wenzhe Liu et al.** | Improve multi-view clustering with graph-based high-order correlations | Tensor representation, Tucker Decomposition, Graph Learning | Graph-oriented multi-view clustering | Robust clustering, high-order correlation learning | High | Moderate | - | High | High clustering precision | High computational demand, complex parameter tuning | Not specified | High-quality clustering results with robust view fusion |

**Literature Review**

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| **Student Name** | **E V Sai Vindhya** |
| **Project Topic Title** | **ATTENTION U-NET BASED MULTI-VIEW CLUSTERING MODEL FOR PREDICTING ALZHEIMER’S DISEASE PROGRESSION** |

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Week 1** | | | | | | | |
| **6** |
| **Reference in APA format** | | Thanh, V. D., Le, T. T., Tuan, P. M., Trung, N. L., Abed-Meraim, K., Adel, M., Dung, N. V., Trung, N. T., Long, D. D., & Chén, O. Y. (2024). Tensor kernel learning for classification of Alzheimer’s conditions using multimodal data. bioRxiv. | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://www.biorxiv.org/content/10.1101/2024.07.17.603875v1 | | Vu Duy Thanh1,2, Thanh Trung Le1, Pham Minh Tuan1,3, Nguyen Linh Trung1, Karim Abed-Meraim4,  Mouloud Adel3, Nguyen Viet Dung1, Nguyen Thanh Trung5, Dinh Doan Long6, and Oliver Y. Ch´en2 | | | | Alzheimer's Disease (AD), Tensor Kernel Learning (TKL), Multimodal Data, Machine Learning, Data Fusion, MRI (Magnetic Resonance Imaging), PET (Positron Emission Tomography), Biomarkers, Kernel Support Vector Machine (SVM), Tensor Decomposition | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| **Tensor Kernel Learning (TKL).** | | The goal of **Tensor Kernel Learning (TKL)** is to improve the early and accurate classification of **Alzheimer’s disease (AD)**, especially in the early **Mild Cognitive Impairment (MCI)** stage. It aims to solve the challenge of analyzing complex, multimodal data (MRI, PET, CSF, SNPs) by integrating these diverse sources to enhance diagnostic accuracy and identify relevant biomarkers | | | | In the first part, **similarity matrices** are generated from each data modality (MRI, PET, CSF, SNPs) using a **Random Forest classifier**.  In the second part, these similarity matrices are integrated into a common feature space through **Tensor Kernel Learning (TKL)**, and a **Kernel SVM** classifier predicts the classification of Alzheimer's conditions. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| The authors propose a Tensor Kernel Learning (TKL) approach to enhance the classification of Alzheimer’s disease (AD) conditions using multimodal data from MRI, PET, cerebrospinal fluid (CSF), and genetic SNP information. The mechanism aims to integrate these diverse data sources to improve the accuracy of AD diagnosis and to provide insights into underlying biomarkers.   |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | **Data preprocessing**: | MRI, PET, CSF, and SNP data are aligned, normalized, and segmented to ensure uniformity. | Preprocessing ensures data consistency and allows for reliable cross-modal comparisons, enhancing the accuracy of the fusion model. | | **2** | **Random Forest Classifier** | is used for each modality to generate a similarity matrix that represents subject relationships. | This step creates a structured basis for each modality, capturing unique data features from each source. | | **3** | **Tensor Decomposition (CP/PARAFAC)** | **Tensor Decomposition (CP/PARAFAC)** on similarity matrices consolidates data into a unified three-way tensor, enabling multi-source integration. | This technique reduces dimensionality while preserving essential information, facilitating efficient data fusion. | | **4** | **Nonlinear Graph Fusion (NGF)** | Uses diffusion processes to refine the tensor by sharing information across modalities, capturing nonlinear interactions. | Enhances classification by capturing complex relationships between modalities, which improves the robustness of the final similarity matrix. | | **5** | Kernel Support Vector Machine (SVM) | Facilitates learning from various data views, which improves model interpretability and prediction. | May require substantial memory and computation time, especially with high-dimensional data. | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| The paper proposes a Tensor Kernel Learning approach to enhance the classification of Alzheimer's conditions using multimodal data. This method allows for better integration of diverse data types and more accurate diagnosis.   |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Class of activity predicted (e.g., CN, MCI, AD) based on multimodal data | Features computed from MRI, PET, CSF, and SNP data | Imaging modalities (e.g., MRI quality, PET resolution) | Age, genetic predisposition | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | Multimodal features derived from MRI, PET, CSF, and SNP data (independent variables) are used to predict Alzheimer’s conditions, including classifications like cognitively normal (CN), mild cognitive impairment (MCI), and Alzheimer’s disease (AD) (dependent variable). The quality of imaging modalities, such as MRI resolution, acts as a moderating variable that can impact the accuracy of these features. Additionally, age and genetic predisposition serve as mediating variables, influencing the relationship between multimodal features and disease classification by affecting the manifestation of disease biomarkers. Together, these variables enhance the model's predictive capability by integrating diverse sources and controlling for critical individual differences. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multimodal data from various sources, including MRI, PET, CSF, and SNP data. Features from each modality are extracted and processed individually to represent different biomarkers of Alzheimer’s disease. | A classifier leverages the fused multimodal data to predict the classification of subjects as cognitively normal (CN), Mild Cognitive Impairment (MCI), or Alzheimer's disease (AD). | | | | The solution integrates heterogeneous data types (imaging, fluid biomarkers, genetic information) to provide a comprehensive analysis. This fusion of multimodal data enables the model to recognize patterns that may be overlooked when using single modalities, thereby improving classification accuracy. | | | | This work provides a valuable contribution to Alzheimer’s research by proposing a novel, multimodal approach that enhances diagnostic accuracy. Through Tensor Kernel Learning (TKL), the solution allows for better early-stage detection of Alzheimer’s and contributes to our understanding of AD-related biomarkers, which may aid in developing targeted interventions. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The integration of multimodal data (MRI, PET, CSF, SNP) enables a more comprehensive and accurate classification of Alzheimer’s stages, improving early detection. This approach may enhance patient outcomes by identifying cognitive decline sooner and potentially slowing disease progression through early intervention. | | | | | The complexity of integrating diverse data types could lead to issues such as computational overhead and longer processing times. Additionally, there is a possibility that certain modality-specific noise or missing data might reduce classification accuracy, potentially leading to misdiagnosis. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| This work is valuable for advancing Alzheimer’s research by integrating multimodal data to improve classification accuracy. The use of Tensor Kernel Learning (TKL) offers a robust approach for combining MRI, PET, CSF, and genetic data, capturing intricate disease patterns and improving early detection. However, the complexity of the method could make it challenging to implement in real-world clinical settings, and the reliance on high-dimensional data may require careful management of computational resources. | | | | Random Forest Classifier, Tensor Kernel Learning (TKL), Nonlinear Graph Fusion (NGF), Kernel Support Vector Machine (SVM) | | | Abstract   1. Introduction 2. LITERATURESURVEY 3. System Overview 4. Conclusion and future work 5. References |
| **Diagram/Flowchart** | | | | | | | |
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**---End of Paper 6-**

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| **7** |
| **Reference in APA format** | |  | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| [https://ieeexplore.ieee.org/document/9885410](https://doi.org/10.1016/j.cmpb.2020.105895) | | Hariharan S; J Daniel Pushparaj; Muthukumaran Malarvel | | | | Covid-19,Global Pandemic,Virtual World,Video Conferencing Applications, Student Engagement  ,Interaction,Face Identification,Face Spoofing  ,CNN (Convolutional Neural Network),Gaze Tracking  Head Positioning,Eye Tracking | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Multiview Deep Forest (MVDF) for Overall Survival Prediction in Cancer | | The goal of this solution is to improve the accuracy and reliability of overall survival (OS) prediction for cancer patients. The problem it addresses is the complexity of high-dimensional, multiview clinical data, which makes it challenging to model OS effectively and avoid overfitting. | | | | Divides patient data into views (e.g., patient info, pathology, treatment) and trains random forests for each view.  Compresses data to retain only essential, predictive features, helping to avoid overfitting.  Prunes trees to reduce noise and optimize accuracy.  Integrates features from different views to improve prediction robustness.  Enhances information density of features and mitigates overfitting risk. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| The proposed system, MVDF, addresses the challenge of predicting overall survival (OS) in cancer patients by integrating multiview data through a structured deep learning approach. MVDF utilizes multiple kernel learning to process each data view, compresses data with Information Bottleneck (IB) theory to reduce redundancy, and applies a pruning strategy to enhance accuracy by filtering out noisy data.   |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Multiview Feature Extraction | Enables the integration of diverse clinical data for improved survival prediction. | Risk of overfitting if features are not well-selected; requires careful view partitioning. | | **2** | Information Bottleneck (IB) Theory | Reduces data redundancy and enhances generalization, lowering the chance of overfitting. | Potential data loss, which may affect accuracy if too much information is compressed. | | **3** | Pruning Strategy | Enhances prediction reliability by eliminating low-quality or noisy data. | Reduces model diversity, which may lead to overfitting if too many trees are pruned. | | **4** | Cascade Forest | Ensures a structured learning process, where each forest level refines predictions iteratively. | Increases computational complexity, making it more resource-intensive to run. | | **5** | Random Forest and Kernel Learning | Facilitates learning from various data views, which improves model interpretability and prediction. | May require substantial memory and computation time, especially with high-dimensional data. | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | OS Prediction Accuracy  Model Generalization & Overfitting  Model Interpretability | Quality of multiview clinical data  Use of IB theory for data compression Multiview feature selection and engineering | Data preprocessing methods   |  | | --- | | Hyperparameter tuning |  |  | | --- | |  |   Clinical expert knowledge quality | Feature extraction based on IB theory  Effectiveness of pruning strategy  Integration of multiview data | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | In the MVDF model for OS prediction, accuracy depends on achieving effective model generalization and minimizing overfitting. This is influenced by multiview feature extraction and multiple kernel learning, which separate and integrate distinct clinical data views. The quality of these data moderates the model’s success, while the Information Bottleneck (IB) theory and pruning strategy act as mediating variables, helping to filter noise and reduce redundancy. Together, these factors enable MVDF to make accurate and interpretable predictions, balancing complexity and reliability in OS prediction. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution in This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multiview clinical data (e.g., patient demographics, pathology reports, treatment details) | Accurate overall survival (OS) predictions for cancer patients, aiding in treatment planning and patient counseling | | | | The MVDF model uses a multiview feature extraction process that separates clinical data into distinct views and trains random forests for each view. With Information Bottleneck theory, it reduces redundant data, and a pruning strategy filters out noisy data for better accuracy and generalization. | | | | The proposed MVDF model enhances accuracy in overall survival (OS) prediction for cancer patients by handling complex, high-dimensional clinical data effectively, providing clinicians with reliable survival predictions that can inform personalized treatment planning and decision-making. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The MVDF model improves accuracy in predicting cancer patient survival by handling complex, multiview data effectively. It provides valuable guidance for treatment planning and patient counseling. | | | | | The model's complexity may limit interpretability for clinicians, and the need for high-quality, multiview data can make it challenging to apply broadly across varied datasets. | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| Logically, the MVDF approach is an innovative step in OS prediction, integrating multiview data to improve prediction accuracy and reduce overfitting. The use of information bottleneck and pruning enhances the model's generalization and relevance in clinical applications. | | | | Random Forest, Information Bottleneck (IB) Theory, Multigrained Cascade Forest (gcForest), Gradient Boosting, Gini Score | | | 1. Abstract 2. Introduction 3. Related Work 4. Experiment Results 5. Conclusion |
| **Diagram/Flowchart** | | | | | | | |
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**--End of Paper 7--**

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| **8** |
| **Reference in APA format** | | Strijbis, V. I. J., de Bloeme, C. M., Jansen, R. W., Kebiri, H., Nguyen, H.-G., de Jong, M. C., Moll, A. C., Bach-Cuadra, M., de Graaf, P., & Steenwijk, M. D. (2021). Multi-view convolutional neural networks for automated ocular structure and tumor segmentation in retinoblastoma. Scientific Reports, 11(1), 14590. | | | | | |
| **URL of the Reference** | | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://doi.org/10.1038/s41598-021-93905-2 | | Victor I. J. Strijbis - v.strijbis@amsterdamumc.nl, Christiaan M. de Bloeme, Robin W. Jansen, Hamza Kebiri, Huu-Giao Nguyen, Marcus C. de Jong, Annette C. Moll, Merixtell Bach-Cuadra, Pim de Graaf, Martijn D. Steenwijk | | | | Surveillance Systems,Anomalous Behavioral Patterns,False Detection (False Alarm) Errors,Performance,Semi-Supervised Techniques,Supervised Techniques,Accuracy  Minimizing False Detection Errors,Crowded Environments,Convolutional Neural Network (CNN)  Long Short-Term Memory (LSTM)  Image Features | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Multi-view Convolutional Neural Network (MV-CNN) Model | | The goal of the MV-CNN model is to automate the segmentation of ocular structures and tumors in retinoblastoma patients using MRI. The main problem is the time-consuming and subjective nature of manual segmentation, which limits the use of radiomics in clinical and research applications for retinoblastoma. | | | | The MV-CNN model consists of multiple MRI sequence inputs (FIESTA, T2, and T1-weighted with contrast), a multi-scale pyramid structure for contextual information, and a branched architecture that handles multiple anatomical planes for comprehensive segmentation. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Multi-view image input (FIESTA, T2, T1-weighted with contrast) | Allows integration of multiple MRI sequences, capturing diverse anatomical details for more accurate segmentation. | Requires high-quality MRI data and consistency across sequences, which may limit generalizability. | | **2** | Multi-scale pyramid structure | Enhances contextual understanding by integrating information at multiple scales, improving segmentation of fine details. | May introduce additional complexity and computational requirements, especially for larger datasets. | | **3** | MV-CNN architecture with branched network for each imaging plane | Enables simultaneous analysis across anatomical planes, capturing details for each ocular structure and tumor. | The model's complexity can lead to over-segmentation, especially in boundaries like the sclera, requiring refinement. | | **4** | Data augmentation with left-right mirroring | Expands training data to improve robustness and generalization of the model across different patient cases | Augmentation may introduce artifacts that impact model performance if not carefully controlled. | | **5.** | Single-step segmentation of ocular structures and tumors | Reduces time and manual effort, providing efficient and accurate segmentations for clinical use. | May struggle with very small tumors, leading to missed detections in some cases. | | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Segmentation accuracy of ocular structures and tumors | Quality and type of MRI sequences (FIESTA, T2, T1-weighted with contrast) | Multi-scale pyramid structure for contextual information | Multi-view CNN architecture for comprehensive segmentation | | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | The segmentation accuracy (dependent variable) is driven by the quality and type of MRI inputs (independent variable), which influence the model’s ability to differentiate ocular structures accurately. This relationship is moderated by the multi-scale pyramid structure, which provides additional contextual detail across scales. The MV-CNN architecture serves as the mediating variable, integrating multi-view data and enabling the model to handle complex ocular anatomy in a single step, resulting in enhanced segmentation accuracy. | | | | | | | | |
| **Input and Output** | | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | The input for the proposed MV-CNN model consists of MRI image frames of the eye, specifically taken from retinoblastoma and healthy patients. These images include multiple MRI sequences (FIESTA, T2-weighted, and contrast-enhanced T1-weighted) and are processed through multi-scale convolutional layers to extract features from different views and anatomical planes. The multi-view approach combines these different perspectives into fully connected layers for classification. | The output of the MV-CNN model is the segmentation of ocular structures and tumor regions within the eye MRI images. The model accurately identifies and delineates structures such as the sclera, vitreous humor, lens, retinal detachment, and tumor. It provides high volumetric and spatial performance metrics, including a Dice similarity coefficient (DSC) and intra-class correlation (ICC), to assess segmentation accuracy. Additionally, it outputs performance statistics in the form of comparison metrics, such as confusion matrices, indicating correctly and incorrectly segmented regions across various classes. | | | | The MV-CNN model leverages multiple MRI sequences (FIESTA, T2-weighted, and contrast-enhanced T1-weighted) and incorporates a multi-scale, multi-view approach to capture detailed anatomical features for segmentation of ocular structures and tumors. By utilizing a 2.5D convolutional approach, it efficiently processes data without the computational overhead of full 3D networks, while still incorporating spatial context for improved accuracy. | | | | Contribution of the Work:  This study presents a performance analysis of MV-CNN in segmenting ocular structures and tumors within MRI scans for retinoblastoma patients. The model's one-step approach achieves high accuracy in both spatial and volumetric performance, outperforming traditional methods (such as ASM and U-Net models) by reducing the need for manual feature engineering and performing multi-class segmentation in a single step. It also offers potential for integration into radiomics pipelines, enabling more precise treatment planning for retinoblastoma. Value of the Work:  This research addresses the challenge of time-consuming and subjective manual segmentation in MRI-based retinoblastoma treatment. By automating segmentation with high accuracy, the MV-CNN model offers a valuable solution for clinical and research applications, potentially enhancing the precision of tumor delineation and supporting the development of personalized treatment plans. It also sets a foundation for more adaptable segmentation models that could handle data from various imaging sources and scanners, advancing the field of automated medical imaging. |
| **Positive Impact of this Solution in This Project Domain** | | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The multi-view convolutional neural network (MV-CNN) used in this project significantly improves the accuracy and efficiency of ocular structure and tumor segmentation in retinoblastoma cases. This model provides a one-step solution for accurately segmenting critical ocular regions, including the sclera, vitreous humour, lens, retinal detachment, and tumors. Its high intra-class correlation (ICC > 0.99) and Dice similarity coefficient (DSC > 0.8) for both tumor and eye volumes demonstrate its reliability for clinical application. The MV-CNN also eliminates the need for feature engineering and ASM-based pre-segmentation, making it well-suited for use in a radiomics pipeline, where it can enhance personalized treatment plans by providing detailed quantitative information about tumor morphology and spread | | | | | One limitation of the MV-CNN solution is its dependency on high-quality, single-center imaging data, which restricts its generalizability to data from other MRI machines or centers. This dependency could limit the model's practicality in real-world applications involving diverse scanner settings and image quality. Additionally, the current approach shows reduced accuracy in segmenting smaller tumors, sometimes missing those under 0.1 mL in volume entirely. Finally, the tendency of the model to slightly overestimate total eye volume, especially in the sclera region, indicates a need for further refinement to enhance accuracy in boundary detection | | |
| **Analyse This Work By Critical Thinking** | | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| This study demonstrates a novel application of MV-CNNs in retinoblastoma segmentation, outperforming traditional methods by handling multiple classes simultaneously without manual feature engineering. However, the reliance on data from a single MRI source raises concerns about the model's robustness in real-world applications, where diverse imaging conditions are common. The research highlights the model’s potential but also points to the need for further validation on multi-center datasets and optimization for varied scanner outputs to ensure widespread clinical utility. | | | |  Dice Similarity Coefficient (DSC) for measuring spatial segmentation accuracy.   Intra-Class Correlation (ICC) for volumetric performance assessment.   3D Slicer for manual reference segmentation.   TensorFlow and NVIDIA GeForce GTX 1080 TI for model training and implementation. | | |  Abstract   I. Introduction   II. Related Work   III. Materials and Methods   IV. Results   V. Discussion   VI. Conclusion and Future Work |
| **Diagram/Flowchart** | | | | | | | |
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**--End of Paper 8--**

**Work Evaluation Table**

**<Use the same factors you have used in "Work Evaluation Table" to build your own "Proposed and Previous comparison table ">**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Work Goal** | **System's Components** | **System's Mechanism** | **Features /Characteristics** | **Cost** | **Speed** | **Security** | **Performance** | **Advantages** | **Limitations /Disadvantages** | **Platform** | **Results** |
| **Vu Duy Thanh1,2, Thanh Trung Le1, Pham Minh Tuan1,3, Nguyen Linh Trung1, Karim Abed-Meraim4,**  **Mouloud Adel3, Nguyen Viet Dung1, Nguyen Thanh Trung5, Dinh Doan Long6, and Oliver Y. Ch´en2** | **To classify Alzheimer’s disease stages using multimodal data integration (MRI, PET, CSF, SNP).** | **Features computed from video frames, Classifier for prediction** | **TKL combines kernel learning and tensor decomposition to integrate multimodal data for classification.** | **High accuracy in identifying Alzheimer’s stages; integrates diverse data types.** | **High** | **Moderate** | **Not explicitly addressed.** | **Achieves 91.31% accuracy in classifying CN vs AD, 81.45% for CN vs MCI, and 78.27% for AD vs MCI.** | **Captures relationships across data types, improves AD detection accuracy, and provides interpretable results.** | **High computational cost, challenging to handle data heterogeneity.** | **MATLAB (LibSVM and Tensor Toolbox).** | **Effective for identifying Alzheimer’s stages and interpreting multimodal data relationships.** |
| **Victor I. J. Strijbis - v.strijbis@amsterdamumc.nl, Christiaan M. de Bloeme, Robin W. Jansen, Hamza Kebiri, Huu-Giao Nguyen, Marcus C. de Jong, Annette C. Moll, Merixtell Bach-Cuadra, Pim de Graaf, Martijn D. Steenwijk** | **To segment ocular structures and tumors in MRI scans of retinoblastoma patients.** | **FIESTA, T2, T1c MRI sequences; MV-CNN model with multi-scale and multi-view architecture.** | **MV-CNN uses a multi-view, multi-scale approach to process images from multiple MRI sequences for precise segmentation.** | **Real-time, single-step segmentation of eye and tumor structures; high spatial accuracy.** | **High** | **Fast** | **Ensures privacy** | **High volumetric and spatial performance with ICC > 0.99 and DSC > 0.8 for tumor segmentation.** | **Provides precise tumor segmentation, operates in a single step, and requires no feature engineering.** | **Overestimates certain structures; requires high-quality images from a single scanner for optimal performance.** | **Python (TensorFlow with Cuda for GPU processing).** | **Accurate and reliable for segmenting ocular structures in retinoblastoma, achieving superior results over baseline models.** |
| **Hariharan S; J Daniel Pushparaj; Muthukumaran Malarvel** | **Improve accuracy in cancer overall survival prediction by handling multiview data and overfitting** | **Multiview feature extraction module, Information Bottleneck (IB) compression, Cascade pruning strategy, Deep forest with random forests** | **Extracts and integrates features from multiview clinical data using random forests, minimizes redundancy and overfitting through IB compression, and reduces impact of low-quality data with pruning strategy** | **Handles high-dimensional multiview data, incorporates ensemble learning for robustness, and uses IB theory for overfitting control** | **Not specified** | **Not specified** | **Privacy maintained for patient data, though security not explicitly detailed** | **Higher classification accuracy (75.42% on the GCOS dataset)** | **Enhanced feature integration, generalization, reduced overfitting, interpretable prediction** | **Limited performance in imbalanced datasets and when secondary indicators have low information density** | **Tested on medical datasets: GCOS, PSP, and PST** | **MVDF outperformed other methods (Random Forest, SVM, etc.), showing improved prediction accuracy and recall on cancer survival data** |

**Literature Review**

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| --- | --- |
| **Student Name** | **P.Mahitha** |
| **Project Topic Title** | **Attention U-Net based Multi-view clustering model for predicting Alzheimer’s disease progression.** |

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| **Week 1** | | | | | | |
| **9** | | | | | | |
| **Reference in APA format** |  | | | | | |
| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| **https://doi.org/10.1093/bib/bbad282** | Wenlan Chen, Hong Wang and Cheng Liang | | | | Cancer subtype identification, Multi-view learning, Contrastive learing, Clustering, Self-supervised learning, Deep learning, Latent representation, Autoencoders, Kullback-Leibler(KL) divergence. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Deep Multi-view Contrastive Learning for Cancer Subtype Identification. | The aim of this research is to propose self-supervised learning model for identifying cancer subtypes called Deep Multi-view Contrastive Learning(DMCL). The goal is to improve the cancer subtype identification by integrating multi-omics data within a unified deep learning framework that optimizes feature extraction, contrastive learning and clustering. | | | | Autoencoders, Contrastive learning, Clustering with Kullback-Leibler(KL) Divergence. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Latent Representation Extraction via Autoencoders | Captures essential information within each omic type, preserving unique data characteristics. | Features may not inherently carry discriminative clustering information for the final analysis. | | **2** | Cross-View Alignment through Contrastive Learning | Reinforces connections among views, making representations more robust by aligning latent representations across different omics data. | Requires careful sample pair construction; runtime increases significantly with large datasets. | | **3** | Cluster Structure Refinement using Kullback-Leibler Divergence | Directly optimizes cluster quality, leading to well-separated subtypes for practical clinical insights. | Sensitive to initial cluster centroids; clustering quality may vary with input characteristics. | | **4** | Unified Training Framework with Composite Loss Optimization | Holistic training improves final clustering accuracy and subtype identification precision. | Performance affected by equal weighting of loss components across datasets; requires adjustment for optimal accuracy. | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| The paper proposes a self-supervised deep learning model called Deep Multi-view Contrastive Learning (DMCL) for identifying cancer subtypes using multi-omics data. The approach integrates reconstruction, contrastive, and clustering losses in a unified framework to improve the clustering accuracy and biological significance of cancer subtype identification.   |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Cancer subtype identification (classification) | Features learned from multi-omics data | Data Quality Types of omics data used  Data integration methods | Latent representations from autoencoders  Contrastive Learning outcome  Clustering structure(via KL divergence) | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | Cancer subtype identification (Dependent Variable) relies on features derived from multi-omics data (Independent Variable). The quality and type of omics data (Moderating Variable) influence classification accuracy by affecting data integration. Autoencoder-generated latent representations (Mediating Variable) align diverse omics types, enabling consistent data integration. Together, these variables improve clustering structure (e.g., via KL divergence) and refine cancer subtype classification. This approach advances precision oncology and supports targeted treatments. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | The model first extracts features from each type of omics data using autoencoders, followed by contrastive learning for enhanced discriminability. | Cancer subtypes are identified based on the learned latent representations and refined cluster structures. | | | To improve the secqurity for the community so that everyone can be safe and the rate of crimes would be decreased | | | | The work significantly contributes to the field of cancer research by offering a novel method for precise cancer subtype identification. The proposed DMCL framework integrates multi-omics data, enhancing the understanding of cancer heterogeneity and improving patient stratification for targeted therapies. |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The DMCL framework improves cancer subtype identification by integrating multi-omics data, enabling more accurate patient stratification and targeted therapies, which can enhance treatment outcomes and reduce the cancer burden. | | | | The model may struggle with varying data quality across different omics types, potentially leading to inaccurate cancer subtype identification. This could result in misclassification, affecting treatment decisions. | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The work is valuable as it introduces a novel approach for cancer subtype identification by integrating multi-omics data using deep learning. The unified DMCL framework enhances clustering accuracy and provides insights into cancer heterogeneity, which can improve targeted therapies and precision medicine. | | | Multi-omics data analysis, contrastive learning, clustering techniques, and evaluation metrics such as clustering accuracy, Adjusted Rand Index (ARI), and Normalized Mutual Information (NMI). | | | Abstract   1. Introduction 2. Materials and Methods 3. Results 4. Case Study 5. Conclusion 6. References |
| **Diagram/Flowchart** | | | | | | |
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**---End of Paper 9-**

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| **10** | | | | | | |
| **Reference in APA format** |  | | | | | |
| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://doi.org/10.1016/j.jbi.2023.104406 | Bastian Pfeifer , Marcus D. Bloice, Michael G. Schimek | | | | Multi-view clustering, Ensemble clustering, Hierarchical clustering, Multi-omics, Disease subtyping, Parea, Pyrea, Genetic algorithm, Affinity matrix. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| *Parea*: Multi-view ensemble clustering for cancer subtype discovery | The goal of this solution is to identify cancer subtypes by clustering multi-omics data (e.g., gene expression, DNA methylation, micro-RNA) through a multi-view hierarchical ensemble clustering approach, enabling personalized treatment strategies for patients.  The problem that needs to be solved is the difficulty of accurately stratifying cancer patients into subgroups with similar molecular characteristics due to the diversity and complexity of multi-omics data. Traditional single-view clustering methods struggle to capture this complexity, resulting in less accurate subtype identification and impacting the effectiveness of targeted treatments in precision medicine. | | | | Multi-view Data Integration, Parea clustering Method, Hierarchical clustering and Affinity Matrix, Genetic Algorithm, Pyrea Software package, Parea1 and Parea2 configuration. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Multi-view Clustering on Each Data View | Allows handling heterogeneous data from different omics views, such as gene expression and DNA methylation, enabling detailed patient stratification. | Increased complexity in managing data diversity, as views may have differing distributions and dimensions, complicating integration. | | **2** | Fusion of Clustering Results Using Genetic Algorithms | Genetic algorithms optimize clustering parameters (e.g., Ward’s minimum variance), ensuring high-quality clustering across cancer types. | Computationally intensive and requires substantial processing power, especially with large datasets. | | **3** | Hierarchical Clustering Techniques (Ward, UPGMA, etc.) | Enhanced adaptability to multiple data sources with varying cluster structures, producing consensus clusters that reflect disease subtypes accurately. | Can introduce bias if certain clustering methods dominate, potentially leading to overfitting in smaller datasets. | | **4** | Final Consensus Cluster Selection | Provides a final output that maximizes clustering stability and aligns well with known cancer subtypes, aiding precision medicine. | Minor discrepancies may occur if clustering methods differ significantly, occasionally requiring additional consensus algorithms. | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Clustering Accuracy  Computational efficiency  cluster Stability | Data Views  GPU and CPU Performance  Clustering Methods | Data Quality  Data Volume  View Variability | Data Fusion Technique  Genetic Algorithm Parameters  Consensus Method | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | Clustering Accuracy (Dependent Variable) depends on the computational efficiency and cluster stability achieved during the data analysis process (Independent Variable). The performance of GPU and CPU hardware, along with chosen clustering methods (Moderating Variable), influences how efficiently and effectively clustering can be executed, impacting overall accuracy and stability. Data fusion techniques, such as genetic algorithm parameters and consensus methods (Mediating Variable), facilitate the integration of diverse data views and quality levels, enhancing the cohesiveness and robustness of clusters. Together, these variables improve clustering outcomes, supporting more reliable insights and decision-making. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution in This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multi-omics data | Clustering results for cancer subtypes | | | This method offers a flexible and robust solution for identifying cancer subtypes, improving diagnostic and treatment precision in precision medicine applications. By integrating multiple data views, it addresses the challenges posed by data heterogeneity and complexity in cancer subtype discovery | | | | The system uses a multi-view ensemble clustering approach, Parea, to cluster each type of input data separately and then combines these results using hierarchical clustering methods (e.g., Ward’s method, UPGMA). Genetic algorithms optimize the selection of clustering parameters, enhancing the precision and adaptability of the clustering results. |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The Parea system enhances cancer subtype discovery by integrating diverse molecular data, allowing precise and personalized treatment. Its flexible design adapts to various datasets, making it a valuable tool for precision medicine and broader medical research applications. | | | | The Parea clustering system may face privacy concerns due to handling sensitive multi-omics data. Additionally, its high computational demands could restrict access for institutions with limited resources, potentially widening research disparities. | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| Parea is an advanced ensemble clustering approach for cancer subtype discovery, integrating diverse molecular data to improve patient classification in precision medicine. While effective in clustering accuracy and stability, it requires substantial computational resources and optimized algorithms for handling complex multi-view datasets. | | | Pyrea  Genetic Algorithm | | | 1. Abstract 2. Introduction 3. Related Work 4. Ensemble Architecture 5. Proposed Approach 6. Comparative Analysis 7. Results and Discussion 8. Conclusion |
| **Diagram/Flowchart** | | | | | | |
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**--End of Paper 10--**

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| **11** | | | | | | |
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| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://academic.oup.com/nar/article/46/20/10546/5123392 | Nimrod Rappoport and Ron Shamir | | | | Multi-omic, Data integration, Multi-view clustering, Cancer, Machine Learning, Bioinformatics. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Multi-omic and multi-view clustering algorithms:  review and cancer benchmark | The goal of the solution is to review and benchmark algorithms for multi-omics clustering using cancer data from TCGA, aiming to enhance the understanding of multi-omics methods in computational biology. The main problem addressed is the difficulty in integrating multi-omics data to uncover biological insights and identify cancer subtypes, which are not apparent with single-omic approaches. | | | | Similarity- based methods, Dimension Reduction methods, Matrix factorization methods, Statistical models, Deep Learning algorithms. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
|  | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Early Integration: Concatenate all omic data matrices, apply clustering algorithms. | Utilizes existing clustering techniques, simplifying the process. | Can lead to biases if omics are not normalized; high data dimension increases computational complexity. | | **2** | Late Integration: Cluster each omic separately, then integrate clustering solutions. | Allows using specialized algorithms for each omic. | May miss weak signals not present in individual omics. | | **3** | Dimension Reduction: Reduce data to essential features before clustering. | Improves interpretation by highlighting dominant features. | Assumes linear transformations, limiting applicability for non-linear data. | | **4** | Similarity-Based Methods: Use sample similarities across omics for integration. | Supports diverse omic types and is computationally efficient. | Difficult to interpret results in terms of original features | | **5.** | Deep Learning: Employ neural networks for feature learning and clustering. | Can capture complex relationships within the data. | Requires large datasets and is prone to overfitting with few samples. | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Cancer subtype identification using clustering techniques | Multi-omics data inputs (e.g., gene expression, DNA methylation) | Data type or quality differences | Omic-specific data transformations | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | Cancer subtype identification (Dependent Variable) depends on clustering techniques applied to multi-omics data inputs, like gene expression and DNA methylation (Independent Variable). The quality and type of data (Moderating Variable) affect the precision of subtype identification, either clarifying or limiting clustering outcomes. Omic-specific data transformations (Mediating Variable) help align diverse omics data, enhancing integration and strengthening cluster reliability. These variables collectively deepen insights into cancer subtypes, supporting precision medicine and targeted treatment approaches. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multi-omics data | Identified cancer subtypes through multi-omics clustering | | | Uses diverse clustering algorithms to integrate different omics data  Highlights various algorithms such as matrix factorization, statistical models, and deep learning approaches | | | | Contribution of the Work:  Provides a comprehensive review and benchmark of multi-omics clustering methods, aiding in understanding their strengths and weaknesses for cancer subtype identification  Value of the Work:  The work facilitates advancements in precision medicine by improving the detection of cancer subtypes, thus potentially guiding treatment decisions. Addresses challenges in integrating heterogeneous multi-omics data​ |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| Multi-omic clustering enhances cancer research by integrating diverse data for better subtype identification, improves survival-based patient grouping for personalized treatment, and reduces noise for more accurate results​ | | | | 1. High computational demands due to large data dimensions. 2. Increased noise susceptibility across diverse omics data types. 3. Potential biases if omics data are unevenly normalized​ | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| This document reviews and benchmarks multi-omic and multi-view clustering algorithms for cancer research. It explores the complexity of integrating varied omics data (e.g., genomics, transcriptomics) to uncover cancer insights, focusing on challenges like computational scalability, noise management, and ensuring consistent clustering across diverse data types. | | | Early integration  Similarity-based methods  Dimension reduction techniques  Statistical modeling  Deep Learning | | | Abstract   1. Introduction 2. Review of Multi-Omics Clustering Methods 3. Benchmark: Datasets and Methods 4. Results and Analysis 5. Discussion on Key Issues and Future Directions 6. Conclusion |
| **Diagram/Flowchart** | | | | | | |
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**--End of Paper 11--**

**Work Evaluation Table**

**<Use the same factors you have used in "Work Evaluation Table" to build your own "Proposed and Previous comparison table ">**

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|  | **Work Goal** | **System's Components** | **System's Mechanism** | **Features /Characteristics** | **Cost** | **Speed** | **Security** | **Performance** | **Advantages** | **Limitations /Disadvantages** | **Platform** | **Results** |
| **Wenlan Chen, Hong Wang and Cheng Liang** | **Cancer subtype identification using self-supervised multi-view learning** | **Autoencoders, Contrastive Learning, KL Divergence, Multi-omics Data** | **Contrastive learning, clustering** | **Improves clustering accuracy, Enhances subtype discovery** | **High** | **Moderate** | **-** | **High** | **Enhanced clustering with distinct subtypes** | **Sensitive to initial clustering, large datasets increase runtime** | **Not Specified** | **Offers precise cancer subtype identification contributing to patient stratification.** |
| **Bastian Pfeifer , Marcus D. Bloice, Michael G. Schimek** | **Multi-view hierarchical clustering for identifying cancer subtypes** | **Multi-view integration, Genetic Algorithm, Hierarchical Clustering** | **Ensemble clustering with genetic algorithm** | **High clustering stability, adaptable to multi-omics data** | **High** | **Moderate to High** | **-** | **High** | **Accurately reflects disease subtypes, handles heterogeneity** | **Requires high computational power, privacy concerns with sensitive data** | **Pyrea** | **Supports personalized treatment strategies through clustering in precision medicine applications.** |
| **Nimrod Rappoport and Ron Shamir** | **Benchmarking multi-omics clustering algorithms** | **Dimension reduction, Similarity-based methods, Deep learning** | **Uses statistical models, clustering based on omics similarity** | **High interpretability, Utilizes multiple integration strategies** | **High** | **Variable** | **-** | **Moderate to High** | **Supports diverse data types, improves subtype identification** | **High computational demands, susceptible to noise, data normalization needed** | **Not specified** | **Provides comprehensive benchmark for precision medicine, guiding clustering methods selection.** |

**Literature Review**

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| **Student Name** | **G. Shivani** |
| **Project Topic Title** | **ATTENTION U-NET BASED MULTI-VIEW CLUSTERING MODEL FOR PREDICTING ALZHEIMER’S DISEASE PROGRESSION** |

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| **Week 1** | | | | | | |
| **12** | | | | | | |
| **Reference in APA format** |  | | | | | |
| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2024.1363896/full | Yanjio Ren; Yimeng Gao; Wei Du; Weibo Qiao; Wei Li; Qianqian Yang; Yanchun Liang; Gaoyang Li | | | | Multi-view graph neural network, multi-omics data, attention mechanism, feature selection, cancer differentiation, cancer sub-types. | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Multi-View Graph Neural Network (MVGNN). | Aimsto enhance precisionin cancer prognosis and treatment selection. To improve breast cancer classification by combining multiple omics data types like mRNA,DNA methylation,CNV using multi-view graph neural network. The problem it marks is the limitation of single-omics and traditional machine learning methods by predicting cancer differences and subtypes. | | | | It comprises Graph Convolutional Network(GCN) for feature learning and an attention module for integrating multi-omics data. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
| The model uses GCN to learn features from omics data and an attention module to integrate them, enhancing prediction accuracy GCN effectively uses correlations, while attention improves classification but adds computational complexity.   |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Feature Learning with Graph Convolutional Network (GCN) | GCN captures relationships within omics data by building patient similarity networks, preserving the biological and geometric structures crucial for cancer subtype predictions. | It is important to note that deep learning models require a large amount of data for training and may not generalize well to new data. | | **2** | Data Integration with Attention Module | The attention module assigns varying importance to features, highlighting key data points and boosting classification accuracy for cancer differentiation and subtypes. | [Adding attention layers increases computational complexity, requiring more processing power and time, especially with large, multi-omics datasets.](https://doi.org/10.1016/j.cmpb.2020.105895) | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| The major impact factors include multi-omics data integration, use of GCN for capturing complex relationships, and the attention mechanism for improved classification accuracy in cancer subtyping.   |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Breast cancer classification outcome, specifically the differentiation level and subtype of cancer. | Features from multi-omics data: mRNA expression, DNA methylation, and CNV (copy number variation) data. | The moderating variable is the type of omics data (mRNA, DNA methylation, CNV), affecting model accuracy. | Feature integration process through GCN and attention modules, which links omics data to improved cancer classification. | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | Breast cancer classification outcomes, such as differentiation level and subtype, are influenced by features from multi-omics data (mRNA, DNA methylation, CNV), with the type of omics data moderating model accuracy. The integration process using GCN and attention modules mediates this relationship by improving classification accuracy. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multi-omics data, including mRNA expression, DNA methylation, and CNV, used for cancer classification. | Predicted breast cancer differentiation level and subtype classification. | | | This solution integrates multi-omics data using GCN and attention mechanisms for precise cancer subtype classification, enhancing prediction accuracy. | | | | This work contributes by providing a robust model for cancer classification through multi-omics data integration, improving accuracy in breast cancer subtyping, valuable for personalized medicine. |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The solution enhances precision in breast cancer diagnosis and subtyping, supporting personalized treatment plans and advancing research in cancer genomics | | | | Multi-view graph neural network (MVGNN) solution in cancer classification include increased data complexity, risk of overfitting, and high computational demands. | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The study proposes a multi-view graph neural network (MVGNN) for cancer classification, effectively integrating multi-omics data to improve predictive accuracy while addressing challenges like overfitting and computational demands. | | | Graph Convolutional Network (GCN):  Used for learning features from different omics data.  Attention Mechanism: Employed to integrate multi-omics data effectively.  Feature Selection Methods: Techniques like the chi-square test and minimum redundancy maximum relevance (mRMR) were utilized for selecting relevant features from the omics data. | | | Abstract   1. Introduction 2. Methods 3. Results 4. Discussion 5. Conclusion |
| **Diagram/Flowchart** | | | | | | |
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**---End of Paper 12-**

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| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://www.iieta.org/journals/ts/paper/10.18280/ts.380613 | Devanshu Tiwari; Manish Dixit; Kamlesh Gupta | | | | Thermal infrared images, multi-view, breast cancer, VGG16, VGG19, ResNet50, Inception Net, augmentation | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| Deep Multi-view Breast Cancer Detection based on deep transfer learning. | The goal of the "Deep Multi-view Breast Cancer Detection" solution is to enhance the accuracy of breast cancer detection by automating the classification of thermal images into normal or abnormal categories, addressing the challenge of early detection in a non-invasive manner. | | | | Deep Learning Model: Utilizes the VGG16 architecture for classification.  Image Datasets: Comprises both static and dynamic breast thermal images, including multi-view images (left, frontal, right).  Image Processing Techniques: Involves concatenation of thermal images to enhance information capture.  Comparison Models: Includes VGG19, ResNet50V2, and InceptionV3 for performance benchmarking.  Performance Metrics: Evaluates accuracy in training, validation, and testing phases. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
| The "Deep Multi-view Breast Cancer Detection" system uses deep transfer learning with VGG16 to classify breast thermal images as normal or abnormal, achieving a testing accuracy of 99% by integrating multi-view thermal data.   |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Data Acquisition:  Collects static and dynamic breast thermal images from multiple views (left, frontal, right). | Provides a comprehensive dataset that captures variations in breast temperature for better anomaly detection. | Requires high-quality imaging equipment and can be time-consuming to gather sufficient data. | | **2** | Image Preprocessing:  Concatenates multi-view images to create a more informative thermal map. | Enhances the model's ability to identify abnormalities by utilizing richer data inputs. | Increased complexity in data handling and potential for overfitting if not managed properly. | | **3** | Model Selection and Training:  Employs the VGG16 architecture along with comparisons to VGG19, ResNet50V2, and InceptionV3 for classification tasks. | Achieves high accuracy (99% on testing dataset) through effective transfer learning techniques. | Requires significant computational resources and may take considerable time to train. | | **4** | Evaluation and Comparison:  Assesses model performance using metrics such as accuracy on validation and testing datasets. | Identifies the most effective model for breast cancer detection, ensuring reliability in clinical settings. | May not generalize well to unseen data if validation is insufficient or biased. | | **5** | Implementation of Results:  Deploys the trained model for real-time detection in clinical environments. | Facilitates early detection of breast cancer, potentially improving patient outcomes through timely intervention. | Relies on accurate image acquisition and proper patient compliance for effective screening results. | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Classification of breast thermal images into either normal or abnormal  categories based on the input data processed by the deep learning model. | Multi-view Breast Thermal Images  Image Acquisition Protocols  Deep Learning Model Parameters | Patient Demographics  Image Quality  Thermal Imaging Protocols | Feature Extraction Quality | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | The classification of breast thermal images as normal or abnormal is influenced by multi-view images and deep learning model parameters, with patient demographics and image quality moderating this relationship. Feature extraction quality mediates the effect of these variables on classification accuracy. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution in This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | Multi-view breast thermal images | Classification results of breast thermal images | | | The "Deep Multi-view Breast Cancer Detection" solution features a fully automated system utilizing the VGG16 deep learning model to classify breast thermal images into normal or abnormal categories. It enhances detection accuracy by integrating multi-view thermal images from multiple angles, achieving a remarkable testing accuracy of 99% on dynamic images. | | | | The contribution of this work lies in presenting a fully automated breast cancer detection system utilizing the VGG16 deep transfer learning model, which effectively classifies breast thermal images into normal or abnormal categories. Additionally, it introduces the novel approach of using multi-view thermal images by concatenating left, frontal, and right views, resulting in improved accuracy compared to traditional single-view methods. |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The positive impact of this solution in the project domain is its ability to significantly enhance early breast cancer detection accuracy through a fully automated system that utilizes multi-view thermal imaging, achieving up to 99% accuracy. | | | | The negative impact of this solution in the project domain may include potential over-reliance on automated systems, which could lead to misdiagnosis if the model encounters unusual cases or if the training data is not sufficiently diverse. | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The critical analysis of the "Deep Multi-view Breast Cancer Detection" work highlights its innovative use of deep learning for enhanced diagnostic accuracy while also addressing potential limitations related to data quality and model generalization in clinical applications. | | | Deep Learning Models  Thermal Imaging Techniques  Data Augmentation  Performance Metrics | | | 1. Abstract 2. Introduction 3. Literature Review 4. Methodology 5. Results and Discussion 6. Conclusion |
| **Diagram/Flowchart** | | | | | | |
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**--End of Paper 13--**

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| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://ieeexplore.ieee.org/abstract/document/8723315 | XIN HONG; RONGJIE LIN; CHENHUI YANG; NIANYIN ZENG ; CHUNTING CAI; IN GOU; JANE YANG | | | | Alzheimer’s Disease (AD)  Prediction  LSTM (Long Short-Term Memory)  Time Sequence  Magnetic Resonance Imaging (MRI) | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| The current solution proposed in the reference "Predicting Alzheimer’s Disease Using LSTM" is based on the Long Short-Term Memory (LSTM) network. This model is specifically designed to predict the progression of Alzheimer's Disease by utilizing temporal data from patients, effectively connecting previous information to forecast future stages of the disease. The LSTM network incorporates fully connected layers and activation layers to encode the temporal relationships between features and the subsequent stages of Alzheimer's Disease | The goal of the solution presented in "Predicting Alzheimer’s Disease Using LSTM" is to predict the progression of Alzheimer’s Disease (AD) by utilizing temporal data from patients. The objective is to develop a model that can forecast the transition between different stages of AD, such as from Mild Cognitive Impairment (MCI) to Alzheimer's, rather than merely classifying the current state of the disease.  The problem that needs to be solved is the lack of effective predictive models for Alzheimer's Disease progression. Current studies primarily focus on classifying existing stages of AD, which does not provide insights into future developments. | | | | The research paper "Predicting Alzheimer’s Disease Using LSTM" focuses on utilizing Long Short-Term Memory (LSTM) networks to forecast the progression of Alzheimer’s Disease (AD). The objective is to improve early diagnosis and intervention by predicting future stages of the disease based on temporal data, rather than merely classifying current states. By employing a robust data preprocessing pipeline and LSTM architecture, the model aims to capture the intricate temporal relationships in patient data, ultimately outperforming existing predictive models in its accuracy. | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
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| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | Data Preprocessing: This initial step includes image preprocessing (skull stripping, normalization, and segmentation) and handling missing data through techniques like linear interpolation. | Ensures high-quality input data, enabling the model to learn effectively from relevant features. | Time-consuming and may introduce biases if missing data is not handled appropriately. | | **2** | LSTM Model Construction: The core mechanism involves building an LSTM network with layers designed to capture long-term dependencies in the data, including forget gates, input gates, update gates, and output gates. | Capable of learning complex temporal relationships, which is crucial for predicting disease progression. | Requires substantial computational resources and may be prone to overfitting if not properly regularized. | | **3** | Model Training and Evaluation: The model is trained on the preprocessed data and evaluated against existing models to assess its predictive accuracy. | Provides a benchmark for performance comparison and helps refine the model. | Depending on the dataset size and quality, results may vary significantly, impacting the generalizability of the model. | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Normal Control  Mild Cognitive Impairment  Alzheimer’s Disease | MRI Biomarkers: Cortical Thickness,Volume of White Matter and Gray Matter  Time Series Data  Demographic and Clinical Features | Age  Genetic factors  Comorbid Conditions | NA | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | The classification of cognitive states—Normal Control, Mild Cognitive Impairment, and Alzheimer’s Disease—is influenced by MRI biomarkers such as cortical thickness and brain volume. Demographic and clinical features, including age and genetic factors, moderate this relationship, while the integration of time series data enhances the accuracy of classification. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | The input for the study "Predicting Alzheimer’s Disease Using LSTM" consists of various neuroimaging and clinical data, primarily sourced from MRI scans and cognitive assessments. Key inputs include MRI biomarkers such as cortical thickness, white matter volume, and other relevant features collected over time to create a longitudinal dataset for patients.. | The output of the study "Predicting Alzheimer’s Disease Using LSTM" consists of predicted stages of Alzheimer’s Disease for each patient, indicating whether they are likely to transition to Normal Control (NC), Mild Cognitive Impairment (MCI), or Alzheimer's Disease (AD). | | | The output of the study "Predicting Alzheimer’s Disease Using LSTM" is the predicted stage of Alzheimer’s Disease for patients, indicating whether they are likely to transition to Normal Control (NC), Mild Cognitive Impairment (MCI), or Alzheimer's Disease (AD). This prediction is based on historical neuroimaging and clinical data processed through the LSTM model, which demonstrates improved accuracy compared to existing predictive models. | | | | The contribution of the work "Predicting Alzheimer’s Disease Using LSTM" is significant as it introduces a predictive model that utilizes Long Short-Term Memory (LSTM) networks to forecast the progression of Alzheimer’s Disease (AD). This approach shifts the focus from classifying current disease stages to predicting future transitions, which is crucial for early diagnosis and timely intervention.  Value of this work lies in its ability to leverage temporal data from neuroimaging and clinical assessments, enhancing the understanding of disease progression and offering a more effective tool for clinicians. By demonstrating improved accuracy over existing models, this research addresses a critical gap in Alzheimer's studies and has the potential to inform better treatment strategies. |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| The positive impact of the solution "Predicting Alzheimer’s Disease Using LSTM" is significant as it enhances early diagnosis capabilities, allowing for timely interventions that can slow disease progression. | | | | The negative impact of the solution "Predicting Alzheimer’s Disease Using LSTM" may include potential over-reliance on the model's predictions, which could lead to misdiagnosis or inappropriate treatment decisions if the model's accuracy is not thoroughly validated. | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| The work "Predicting Alzheimer’s Disease Using LSTM" introduces a predictive model that utilizes Long Short-Term Memory (LSTM) networks to forecast the progression of Alzheimer’s Disease, emphasizing early diagnosis and intervention. By leveraging temporal data from neuroimaging and clinical assessments, the model outperforms existing methods, providing valuable insights for clinicians in managing patient care. | | | Magnetic Resonance Imaging  Data Preprocessing Techniques  Long Short-Term Memory (LSTM) Networks | | | 1. Abstract 2. Introduction 3. Related Work 4. Data Preprocess 5. AD Prediction Model and Evaluation 6. Experiments and Result 7. Conclusion |
| **Diagram/Flowchart** | | | | | | |
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**--End of Paper 14--**

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| **Reference in APA format** |  | | | | | |
| **URL of the Reference** | **Authors Names and Emails** | | | | **Keywords in this Reference** | |
| https://arxiv.org/abs/2204.05798 | Eleonora Lopez; Eleonora Grassucci; Martina Valleriani;Danilo Comminiello | | | | Multi-View Learning  Hypercomplex Neural Networks  Hypercomplex Algebra  Breast Cancer Screening | |
| **The Name of the Current Solution (Technique/ Method/ Scheme/ Algorithm/ Model/ Tool/ Framework/ ... etc )** | **The Goal (Objective) of this Solution & What is the problem that need to be solved** | | | | **What are the components of it?** | |
| The current solution is referred to as "Parameterized Hypercomplex Neural Networks" (PHNNs), and specific models developed within this framework include PHResNets, PHYSEnet, and PHYBOnet. | The goal of this solution is to improve breast cancer classification by leveraging the information contained in multiple views of mammograms, specifically ipsilateral and bilateral views. The problem that needs to be solved is the limitation of traditional deep learning methods that perform single-view analysis, which fails to capture the crucial correlations between different mammographic views. By using parameterized hypercomplex neural networks, the proposed approach aims to effectively model and exploit these inter-view correlations, mimicking the reading process performed by clinicians and ultimately enhancing diagnostic accuracy. | | | | Parameterized Hypercomplex Neural Networks (PHNNs)  PHResNets  PHYSEnet  PHYBOnet  Hypercomplex Algebra  Convolutional Layers  Training Pipeline  Loss Functions  Evaluation Metrics | |
| **The Process (Mechanism) of this Work; Means How the Problem has Solved & Advantage & Disadvantage of Each Step in This Process** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | |  | **Process Steps** | **Advantage** | **Disadvantage (Limitation)** | | **1** | 1.Parameterized Hypercomplex Neural Networks (PHNNs) Framework:  This framework generalizes hypercomplex algebra to model interactions between multiple views of mammograms.  2. Model Architectures (PHResNets, PHYSEnet, PHYBOnet):  Different architectures are designed to handle two-view and four-view exams, utilizing specific configurations (e.g., shared encoders, bottleneck layers).  3. Hypercomplex Convolutional Layers (PHC Layers):  These layers process multi-dimensional inputs while preserving the correlations between different views.  4.Training Pipeline:  Mechanism: Involves pretraining on patches of mammograms to learn fine-grained features, followed by training on whole images | 1. It allows for capturing both global properties and local inter-view correlations, enhancing the model's ability to leverage multi-view information. 2. Tailored architectures can optimize performance for specific tasks (e.g., patient-level vs. breast-level analysis).. 3. They reduce the number of parameters needed compared to traditional convolutional layers, which can lead to more efficient training.   4. Pretraining helps the model learn crucial features from limited data, improving performance when transitioning to whole images. | 1. The complexity of hypercomplex algebra may require more computational resources and expertise to implement effectively.  2. Selecting the appropriate architecture may require experimentation and could lead to overfitting if not managed properly.  3. The introduction of hypercomplex layers may complicate the network design and training process.  4.  The need for patch-level annotations may limit the applicability of this approach in datasets without ROI annotations. | | | | | | | |
| **Major Impact Factors in this Work** | | | | | | |
| |  |  |  |  | | --- | --- | --- | --- | | **Dependent Variable** | **Independent Variable** | **Moderating variable** | **Mediating (Intervening ) variable** | | Classification Outcome:Malignant:  Benign/Normal | Mammographic Images:  Multi-View Data  Features Extracted from Images:  Pixel Intensities  Texture Features  Shape Features  Activation Maps  Preprocessing Information:  Augmentation Techniques  Patch-Level Data | Patient Demographics  Image Quality  Type of Lesion  Training Conditions  Clinical Context | Feature Extraction  Model Architecture  Training Process  Pretraining Effects  Data Augmentation  Model Interpretability | | | | | | | |
| |  | | --- | | **Relationship Among The Above 4 Variables in This article** | | The classification outcome of mammographic images as either malignant or benign/normal is influenced by features extracted from multi-view data, including pixel intensities, texture, and shape features. Patient demographics and image quality moderate this relationship, while preprocessing techniques and model factors—such as feature extraction, architecture, and training conditions—mediate the effects on classification accuracy. | | | | | | | |
| **Input and Output** | | **Feature of This Solution** | | | | **Contribution & The Value of This Work** |
| |  |  | | --- | --- | | **Input** | **Output** | | n the breast cancer classification models, the primary input consists of mammographic images, including the Craniocaudal (CC) and Mediolaateral Oblique (MLO) views. These images undergo preprocessing, such as resizing and augmentation, to enhance their quality and variability. Additionally, multi-view architectures utilize concatenated multi-dimensional arrays of these views to leverage correlations for improved classification accuracy. | The output of the breast cancer classification models includes prediction labels indicating whether a mammogram is malignant or benign/normal, along with probability scores that reflect the confidence of these predictions. Additionally, some models generate activation maps to highlight key areas in the images that influenced the decision. Performance metrics like accuracy and Area Under the ROC Curve (AUC) are also reported to evaluate the model's effectiveness, aiding radiologists in their diagnostic processes. | | | The proposed solution for breast cancer classification utilizes multi-view processing and hypercomplex neural networks to effectively capture correlations between different mammogram views. It features a pretraining strategy to enhance learning from limited data while reducing the number of parameters for computational efficiency. Additionally, visualization tools like activation and saliency maps provide insights into the model's decision-making process, aiding radiologists in diagnostics. | | | | This work introduces a novel multi-view learning framework for breast cancer classification that mimics radiologists' diagnostic processes, enhancing accuracy by leveraging correlations between mammogram views. It employs parameterized hypercomplex neural networks, capturing complex relationships while reducing parameters for computational efficiency. The models demonstrate robust generalizability across various datasets, offering a more effective solution for early detection and improved patient outcomes in breast cancer screening. |
| **Positive Impact of this Solution in This Project Domain** | | | | **Negative Impact of this Solution in This Project Domain** | | |
| This solution significantly improves breast cancer screening by enhancing diagnostic accuracy through multi-view learning and hypercomplex neural networks, closely mimicking radiologists' processes. Its generalizability across various datasets ensures effective application in diverse clinical settings, leading to earlier detection and better patient outcomes. | | | | The potential negative impact of this solution may include reliance on the availability of high-quality, annotated datasets for training, which can be limited in some regions. Additionally, the complexity of hypercomplex neural networks might lead to challenges in interpretability, making it harder for clinicians to trust and understand the model's predictions. Lastly, the computational requirements for training and deploying these models could pose barriers in resource-limited healthcare settings. | | |
| **Analyse This Work By Critical Thinking** | | | **The Tools That Assessed this Work** | | | **What is the Structure of this Paper** |
| This work presents an innovative approach to breast cancer screening by employing multi-view hypercomplex neural networks, which effectively address the limitations of traditional single-view deep learning methods. By leveraging hypercomplex algebra, the model captures inter-view correlations, closely mimicking the clinical practices of radiologists who analyze multiple views simultaneously. This alignment could lead to improved diagnostic accuracy and better patient outcomes. However, the reliance on high-quality, annotated datasets raises concerns about data availability and representativeness, potentially hindering the model's effectiveness in diverse populations. Additionally, the complexity of hypercomplex neural networks may challenge interpretability, making it difficult for clinicians to trust and understand the model's predictions. | | | The assessment of this work utilized deep learning frameworks like TensorFlow or PyTorch for model implementation, along with publicly available datasets such as CBIS-DDSM and INbreast for training and testing. Performance metrics, including AUC and classification accuracy, were employed, alongside visualization tools like Grad-CAM to interpret model decisions. Statistical analysis ensured the robustness of results through significance testing. | | | 1. Abstract 2. Index terms 3. Introduction 4. Multi-view approach in Breast Cancer Analysis 5. Quaternion and Hypercomplex Neural Networks 6. Proposed method 7. Experimental Setup 8. Experimental Evaluation 9. Visualizing Multi-View Learning 10. Conclusion 11. References |
| **Diagram/Flowchart** | | | | | | |
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**--End of Paper 15—**

**Work Evaluation Table**

**<Use the same factors you have used in "Work Evaluation Table" to build your own "Proposed and Previous comparison table ">**

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|  | **Work Goal** | **System's Components** | **System's Mechanism** | **Features /Characteristics** | **Cost** | **Speed** | **Security** | **Performance** | **Advantages** | **Limitations /Disadvantages** | **Platform** | **Results** |
| **Eleonora Lopez, Eleonora Grassucci, et al.** | **To improve breast cancer classification accuracy** | **PHResNets, PHYSEnet, PHYBOnet neural networks** | **Uses hypercomplex neural networks to capture multi-view correlations** | **Supports two-view and four-view processing of mammograms** | **High** | **High** | **Moderate** | **Outperforms real-valued baselines** | **Mimics radiologists' multi-view diagnosis process** | **Limited to certain multi-view medical exams** | **Medical imaging** | **Improved multi-view classification accuracy** |
| **Xin Hong, Rongjie Lin, et al.** | **Predict progression of Alzheimer’s Disease** | **LSTM neural network, fully connected layers** | **Encodes temporal relations between features** | **Effective for time-series medical data analysis** | **High** | **Moderate** | **High** | **Good time-series prediction** | **Captures long-term dependencies in temporal data** | **Requires large dataset for accurate predictions** | **MRI data, ADNI** | **Higher accuracy in predicting AD stages** |
| **Yanjiao Ren, Yimeng Gao, et al.** | **Predict breast cancer differentiation and subtypes** | **Multi-omics data fusion, GCN and attention modules** | **Integrates multi-omics data with graph neural network** | **Preserves biological and geometric structure of data** | **-** | **High** | **High** | **Good cancer classification** | **Better cancer subtype accuracy** | **Limited to multi-omics data, high complexity** | **Bioinformatics systems** | **Improved differentiation accuracy** |
| **Devanshu Tiwari, Manish Dixit, Kamlesh Gupta** | **To develop a fully automated breast cancer detection system using deep transfer learning.** | **VGG16 model, Static and Dynamic breast thermal images dataset.** | **Utilizes deep transfer learning to classify breast thermal images into normal or abnormal.** | **Multi-view thermal images, concatenation of left, frontal, and right views.** | **Not specified in the abstract** | **High speed due to deep learning optimization.** | **-** | **Achieved testing accuracy of 99% on dynamic images; 95%, 94%, and 89% for VGG19, ResNet50V2, InceptionV3 respectively.** | **Fully automated, high accuracy, non-invasive method compared to traditional techniques.** | **Limited research on CAD systems using thermal images compared to mammography; requires significant training data for optimal performance.** | **Not specified** | **Best accuracy results compared to other models tested (VGG19, ResNet50V2, InceptionV3).** |