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Clustering MRI Scans Using Deep Clustering Algorithm

BTP-1 Presentation by:

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Introduction

Clinical Statistics of Brain Tumor

Brain tumors affect approximately **5–10 people per 100,000 globally per year**. They account for around **3% of all cancers**, with 3,00,000 new cases each year, but with a high mortality rate due to late diagnosis. Overall **survival rate is 35%,** which varies by the type and region. Even after successful treatment the **recurrence rate is around 30-40%.**

The Challenge

Modern medical imaging faces significant obstacles:

- **Data Labels:** Medical data is large and often unlabeled, making automated analysis difficult.
- **Noise and artifacts:** Technical variations affect image quality and interpretation

Motivation and Goal

Early detection and accurate categorization can greatly improve survival chances. Use deep clustering on available unlabeled data to extract meaningful patterns from MRI scans for improved diagnosis and prediction

Objective

Objective 1 : July 25’ – Nov 25’

Develop an unsupervised deep clustering pipeline to extract meaningful features from MRI brain scans for tumor pattern discovery

Objective 2 : Jan 26’ – Apr 26’

Build a predictive model using extracted features to classify and diagnose brain tumour.

Why This Matters: Accurate clustering of MRI scans can reduce diagnostic time from hours to minutes, reveal hidden disease patterns, and enable precision medicine approaches tailored to individual patient characteristics.

Literature Survey

Supervised Methods

Paper	Main Algorithm	Accuracy or Main Metric
[1]	CNN + SVM(Transfer learning)	99.35% accuracy
[2]	Clustering + classifier(ELM)	98.56% accuracy
[3]	CNN(Grad-CAM interpretability)	98% accuracy

Unsupervised Methods

Paper / Method	Technique	Dataset	Accuracy / Metric	Remarks
[4]	CNN + K-Means clustering	ImageNet / MRI (adapted)	~87–90% (MRI adaptation)	Introduced iterative pseudo-label learning. No explicit tumor separation.
[5]	Autoencoder + Soft Assignment	BraTS MRI	89.2%	Unsupervised clustering, suffers from cluster collapse on imbalanced MRI data.
[6]	VAE + K-Means + U-Net hybrid	BraTS 2020	91.1% Dice Score	Focused on segmentation, not classification; required heavy post-processing.
Proposed (This Work)	ResNet18 Encoder + K-Means + GMM Refinement + Joint Loss	Kaggle Brain MRI	**93.5% Accuracy**	Efficient, interpretable, semi-supervised learning with limited labeled data.

Deep Clustering Pipeline Stages

Data Preparation

Gathering and preparing MRI scans for model output

Feature Extraction

Use a deep autoencoder to learn robust features

Clustering Initialization

Establishing initial cluster centers from the extracted features.

Joint Training and Optimization

Simultaneously refining features and clustering assignments.

Visualization

Assessing cluster separability in a lower-dimensional space

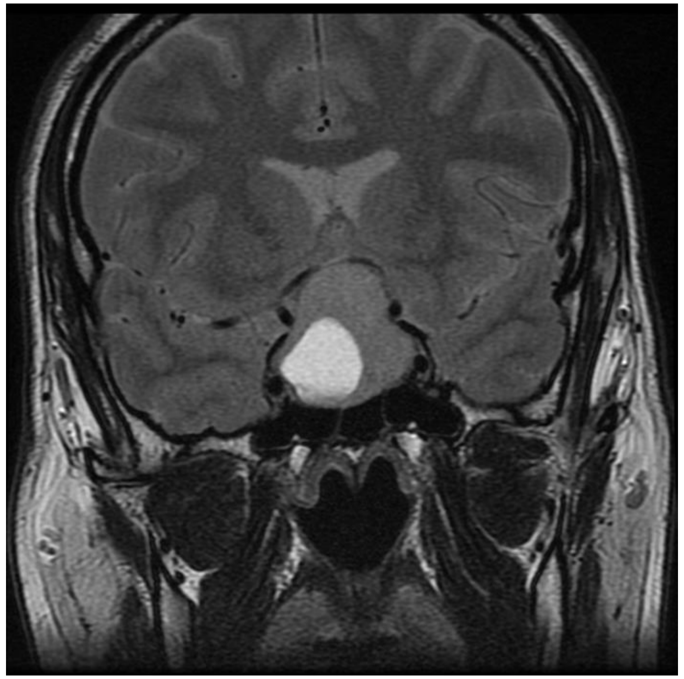
1. Data Pipeline

Data Acquisition

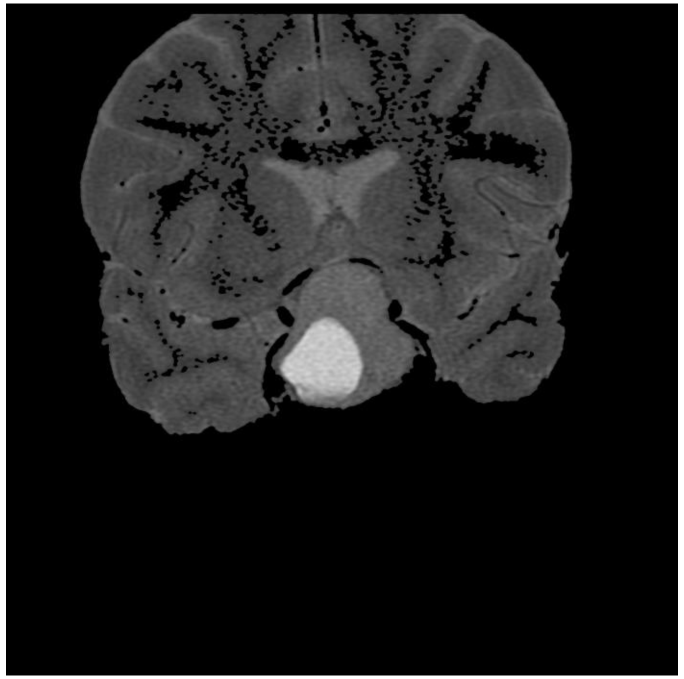
- A total of 5712 MRI brain images were obtained from Kaggle brain tumor MRI dataset [7]
- The dataset includes 1,321 Meningioma, 1,339 Glioma, 1,596 No Tumour, and 1,457 Pituitary Tumour images
- Dataset split: 20% labeled for supervision and 80% unlabeled for clustering-based learning.

Data Preprocessing Steps

- Skull stripping[8] performed to isolate brain tissue from bone and non brain areas.
- Normalization and resizing ensured uniform input dimensions for the model.
- Augmentation(rotation, contrast adjustment) for improved generalization and avoiding clustering based on orientation of brain in MRI scan



After Preprocessing



2. Feature Extraction

MRI Input

Raw MRI brain scans are provided as input after preprocessing

Encoder

CNN compresses the input, extracting key spatial and textural tumor features.

Latent Space

Compact Numerical representation of MRI-captures essential tumor structures

Decoder

Reconstruct the original MRI from latent space to ensure all features are preserved

3. Clustering Initialization

Latent Space Features

Features from pre-trained autoencoder

K-Means Pre-initialization

Initial cluster centroids derived from k means on latent space

GMM Integration

Clustering component formulated with Gaussian Mixture Model for probabilistic assignments

4. Joint Training and Optimization

Pseudo-Labels
Temporary labels from GMM used to guide learning of unlabelled MRIs

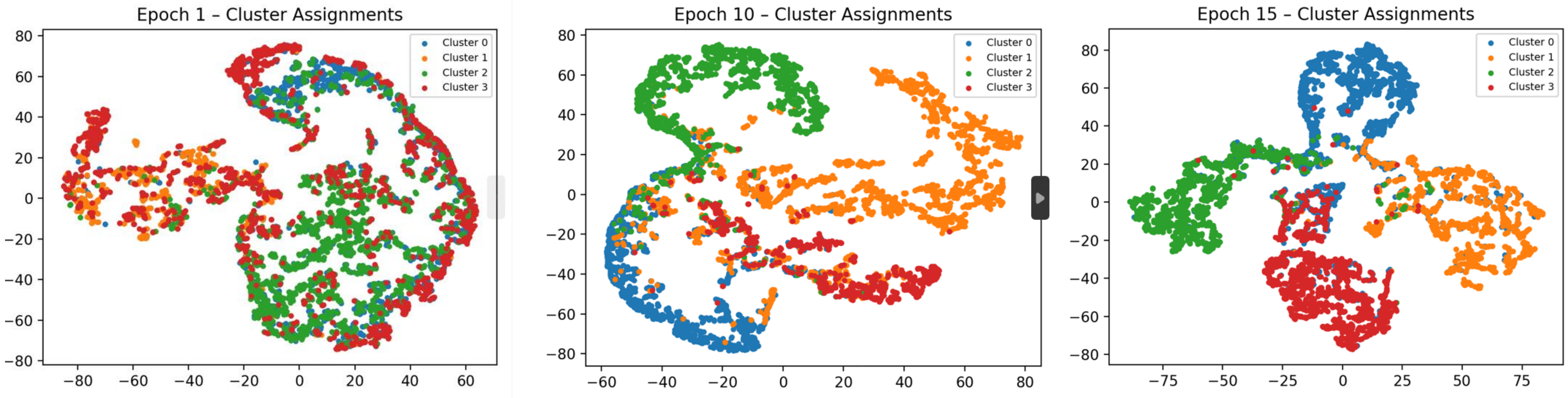
Joint Loss
Cross entropy(labelled) + Clustering loss(unlabelled)

Encoder Update
back-propagation adjusts CNN weights so features become more discriminative.

Refined Embeddings
updated latent vectors form tighter, more meaningful clusters.

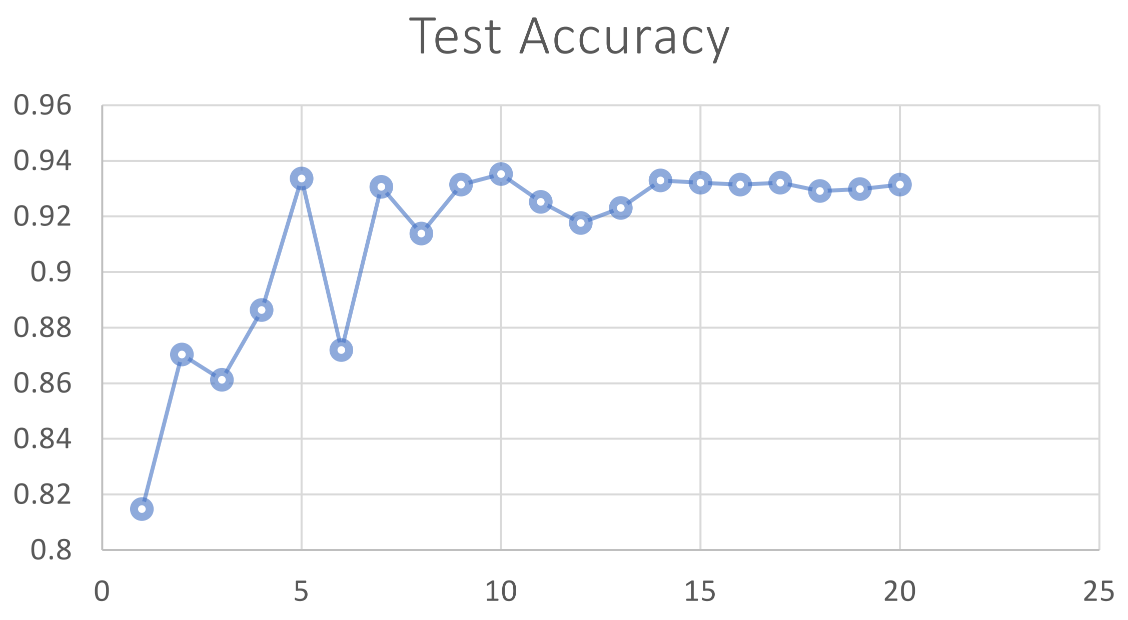
5. Visualization

t-SNE visualization of latent embeddings



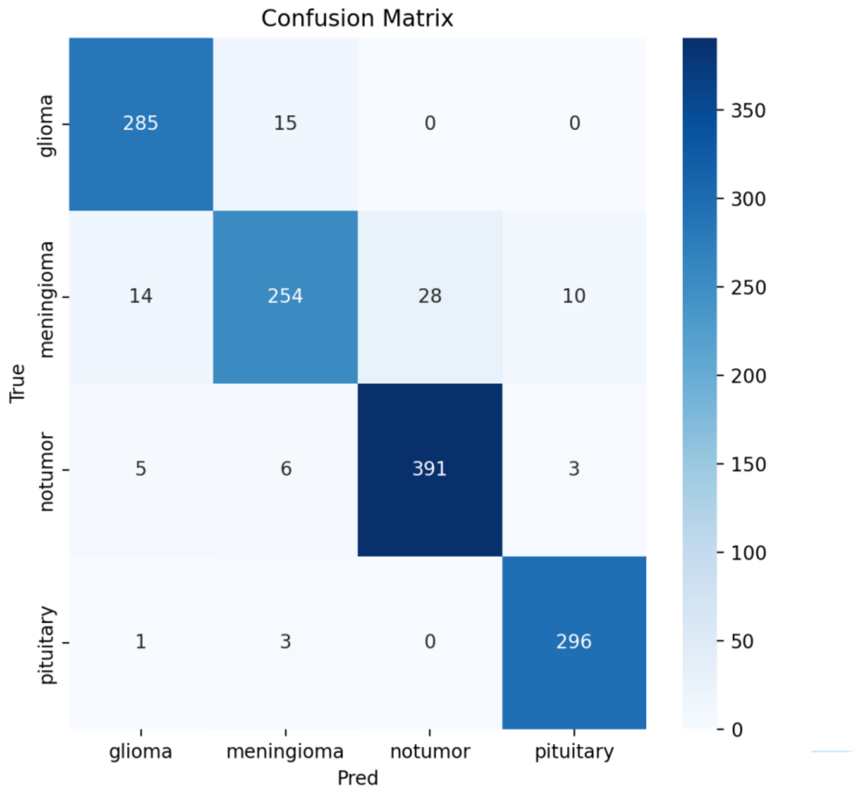
Evolution of Embedding Space During Deep Clustering Optimization.

Results



Accuracy Matrices at epoch 10

Tumour Type	Precision	Recall	F1-Score
Glioma	0.934	0.950	0.942
Meningioma	0.914	0.830	0.870
No Tumor	0.933	0.965	0.949
Pituitary	0.958	0.987	0.972
Overall Accuracy at epoch 10			**0.935**



Observations

1. Achieved **93.5% accuracy** using **deep clustering with semi-supervised joint training (Obtained at Epoch 10)**.
2. Test accuracy stabilizes after epoch 14, training loss is minimum at
3. **High F1-scores** show balanced tumor detection across classes.
4. Model effectively distinguishes tumor and non-tumor regions in MRI scans.
5. Confirms the success of **unsupervised + supervised optimization** in medical imaging classification.

Discussion

Model Interpretation

Deep clustering framework effectively learned discriminative MRI features without full supervision. Stable accuracy after epoch 10 indicates convergence and feature space stabilization. t-SNE plots confirm improved cluster separation.

Observations from Results

- **High Accuracy for Pituitary and No tumor cases, as these classes have clearer structural differences in MRIs.**
- **Meningioma, Glioma overlap suggests similar texture and intensity pattern, leading to mild misclassification.**
- **Precision and recall balance(f1 > 0.87 for all classes) validates model robustness**

Challenges & Future Work

Challenges

Orientation variance : Reduced by transformations like rotation, intensity, flipping etc.
Data imbalance can cause false cluster centroid formation, Dealt with data augmentation.

Possible Improvement

Skull stripping algorithm can be improved as there are models available for skull stripping for 3d MRI scans. We can use that by making changes for 2d images to improve accuracy. 3D MRI image data will perform better.

The chosen deep clustering approach provides an optimal trade-off between accuracy, efficiency, and interpretability. It demonstrates that meaningful tumor classification can be achieved even with limited labeled data — validating the strength of this framework over heavier, fully-supervised or transformer-based models.

Conclusion

Deep clustering effectively groups MRI scans with clinical relevance

Key Findings Summary

93.5% Accuracy

Outperforms traditional clustering and rivals fully supervised CNNs using only 20% labeled data

Meaningful Feature Clusters

Latent Clusters align with actual tumor type, showing strong feature discrimination

Efficient Semi Supervised Framework

Joint clustering and supervised learning delivers high accuracy with minimal labels

Impact on Medical Imaging Analysis

This research demonstrates that semi-supervised deep clustering can reduce dependence on large labeled MRI datasets while maintaining clinical-level performance. By automatically grouping brain tumors into meaningful subtypes, the model aids radiologists in early diagnosis and improves the scalability of medical imaging AI solutions.

1. **Next Steps**

   Development of predictive model for tumors

2. **Scale Up**

   Train on multi center, larger MRI datasets(BraTs)

3. **Feature Explainability**

   Integrate grad CAM to visualize tumor specific features

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THANK YOU