

SSCLNet : Based Brain MRI Classification

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ABSTRACT

Brain tumor detection using MRI imaging is a critical task in modern medical diagnosis. Traditional deep learning models rely heavily on large annotated datasets, which are often limited in availability due to the time-consuming and costly nature of medical image labeling. This project introduces SSCLNet (Self-Supervised Contrastive Learning Network), a novel framework that reduces reliance on labeled data by learning meaningful features from unlabeled brain MRI scans using contrastive learning techniques. By combining self-supervised pre-training with supervised fine-tuning on a smaller labeled dataset, SSCLNet achieves high classification accuracy and robust performance, demonstrating its effectiveness for real-world medical imaging applications.

1. INTRODUCTION

Brain tumors pose a significant threat to human health, and early detection through imaging technologies like Magnetic Resonance Imaging (MRI) plays a vital role in improving treatment outcomes. With the rapid growth of AI in healthcare, deep learning models have shown great promise in automating tumor classification from MRI scans. However, these models require extensive labeled datasets for training, which are scarce in the medical field. Furthermore, conventional models pretrained on generic datasets like ImageNet may not capture the nuanced patterns found in medical images. To address these challenges, our project proposes a self-supervised learning-based solution—SSCLNet—which learns effective image representations from

unlabeled data and enhances performance with limited supervision.

Existing System

The existing systems for brain MRI classification rely heavily on pre-trained convolutional neural networks (CNNs) like ResNet. These models use transfer learning and fine-tuning approaches, where pre-trained weights are adapted to medical imaging tasks. The training process depends on large, labeled datasets such as ImageNet to initialize these models, followed by supervised learning using domain-specific medical datasets.

Proposed System

The proposed system introduces SSCLNet (Self-Supervised Contrastive Loss Network). It learns feature representations directly from unlabeled data using contrastive loss, which enhances the learning process by maximizing the similarity between augmented views of the same data while minimizing the similarity with other data samples. This proposed framework significantly reduces the reliance on labeled data while achieving superior performance on brain MRI classification tasks.

2.LITERATURE SURVEY

G. Velonakis, N. Kelekis, and E. Efstathopoulos (2024) “Evaluating Brain Tumor Detection with Deep Learning CNNs Across Multiple MRI Modalities”, the authors assessed how different CNN models performed on MRI scans taken from various imaging protocols. Their research emphasized that multi-modal MRI data significantly improves tumor classification accuracy. However,

they also noted a major limitation: the requirement of annotated datasets for every modality.

R. Gupta et al. (2023) “*Advanced Deep Learning Applications for Brain Tumor MRI Classification*” comprehensively discussed state-of-the-art models including ResNet, VGG, and DenseNet. They concluded that transfer learning enhances performance but is often insufficient for domain-specific tasks due to the non-medical nature of datasets like ImageNet.

H. A. Moradi et al. (2023) “*Brain Tumor Classification Using Hybrid Architectures and Transfer Learning*”, the authors combined CNNs with Long Short-Term Memory (LSTM) networks to capture spatial and sequential patterns in MRI slices. Though this method improved classification accuracy, the system's complexity and reliance on labeled data remained significant bottlenecks.

M. Badza and M. C. Barjaktarović (2020) “*Classification of Brain Tumors from MRI Images Using a Convolutional Neural Network*” demonstrated successful binary classification (tumor vs. no tumor) using CNNs. While effective, the model lacked fine-grained classification (e.g., glioma vs. meningioma), which limits clinical usability.

Chen et al. (2020) “*A Simple Framework for Contrastive Learning of Visual Representations*”. Their work inspired the use of NT-Xent loss and augmentation strategies used in SSCLNet for learning visual representations without labels.

Azizi et al. (2021) “*Big Self-Supervised Models Advance Medical Image Classification*”, Google Research applied contrastive self-supervised learning to retinal and dermatological images. Their results demonstrated that self-supervised pre-training followed by minimal fine-tuning outperformed fully supervised models, especially when labeled data was limited.

3.METHODOLOGY

The SSCLNet methodology is structured in two phases: **Self-Supervised Pre-training** and **Supervised Fine-tuning**, designed to reduce the need for labeled data and improve accuracy.

3.1 System Architecture

The system follows a layered architecture:

Step 1: Data Collection

- **Unlabeled Data:** 5000+ brain MRI images without any annotations are collected for pre-training using self-supervised learning.
- **Labeled Data:** A small labeled dataset (~500 images) is used for the fine-tuning phase, with four categories: Glioma, Meningioma, Pituitary Tumor, and No Tumor.

Step 2: Data Augmentation

- For each image, two distinct augmented views are generated.
- **Augmentation Techniques Used:**
 - **Rotation:** Randomly rotate by $\pm 15^\circ$.
 - **Flipping:** Horizontal/vertical flip.
 - **Zooming:** Crop and zoom into 80–90% of the image.
 - **Cropping:** Random crop of central or peripheral regions.

This creates "positive pairs" (different views of the same image) and "negative pairs" (views from different images).

Step 3: Feature Extraction using Encoder

- A pre-trained **ResNet-18** model is used as the encoder.
- The final classification layer is removed and replaced with a **projection head** that maps features to a **128-dimensional vector space**.
- This encoder is trained to extract high-level features from each augmented image.

Step 4: Self-Supervised Contrastive Learning

- **Loss Function:** NT-Xent (Normalized Temperature-Scaled Cross Entropy Loss).
- Objective:
 - Minimize distance between **positive pairs**.
 - Maximize distance between **negative pairs**.
- Optimizer: Adam
- Epochs: ~100 (until representation space stabilizes)
This phase helps the model learn visual representations without any labels.

Step 5: Fine-Tuning with Labeled Data

- A **fully connected classifier** is added on top of the encoder.
- Classifier output: **4 units** for the 4 tumor categories.
- The encoder is either:
 - **Frozen** (to retain learned representations), or
 - **Fine-tuned slightly** using backpropagation.
- **Loss Function:** Cross-Entropy Loss
- Training Set: 400 labeled images
- Validation Set: 100 labeled images

Step 6: Inference and Prediction

- New images are passed through the encoder and classifier.
- The model outputs **probabilities for each class**.
- Final prediction is the class with the highest confidence score.

Step 7: Evaluation

- **Metrics Used:**
 - Accuracy
 - Confusion Matrix
 - Precision, Recall, F1-score (optional)
- **Evaluation Dataset:** 100+ labeled test images
- System demonstrates robust generalization even with limited labeled data.

3.2 Workflow

The workflow of the proposed system, SSCLNet, is a structured pipeline that combines self-supervised representation learning with supervised classification. It ensures high performance in

classifying brain MRI images while minimizing dependence on labeled data.

1. Image Input and Upload

- The user accesses a web interface built using Flask.
- An MRI scan image is uploaded via the browser UI.
- The system supports common formats like JPG, PNG.

2. Preprocessing

- The uploaded image is resized to a standard dimension (224x224).
- Converted to RGB if originally grayscale.
- Normalized pixel values to improve training consistency.

3. Data Augmentation

- Two augmented views are created per image using:
 - Random rotation (± 15 degrees)
 - Random cropping (80-90%)
 - Horizontal/vertical flipping
 - Random zooming
- These two views form a positive pair for contrastive learning.

4. Feature Encoding

- Both augmented images are passed through a shared encoder (ResNet-18).
- The encoder maps each image to a 128-dimensional feature vector.
- This representation captures high-level features (edges, texture, tumor patterns, etc.).

5. Contrastive Learning Phase (Self-Supervised Training)

- The NT-Xent loss function is applied:
 - Pulls positive pairs (views of same image) closer in vector space.
 - Pushes negative pairs (views from different images) apart.
- Trains only on unlabeled data, allowing the model to learn robust visual representations without requiring tumor labels.

6. Fine-Tuning Phase (Supervised Training)

- The learned encoder is connected to a fully connected classifier head.
- The classifier is trained on a small labeled dataset (e.g., 500 images).
- Loss Function: Cross-entropy loss.
- The output layer classifies images into 4 categories:
 - Glioma
 - Meningioma
 - Pituitary Tumor
 - No Tumor

7. Inference and Prediction

- For a newly uploaded MRI:
 - It is passed through the trained encoder and classifier.
 - The system outputs class probabilities, e.g.:
 - Glioma : 0.93
 - Meningioma : 0.03
 - Pituitary : 0.02

- No Tumor : 0.00
- The final predicted tumor type is displayed to the user.

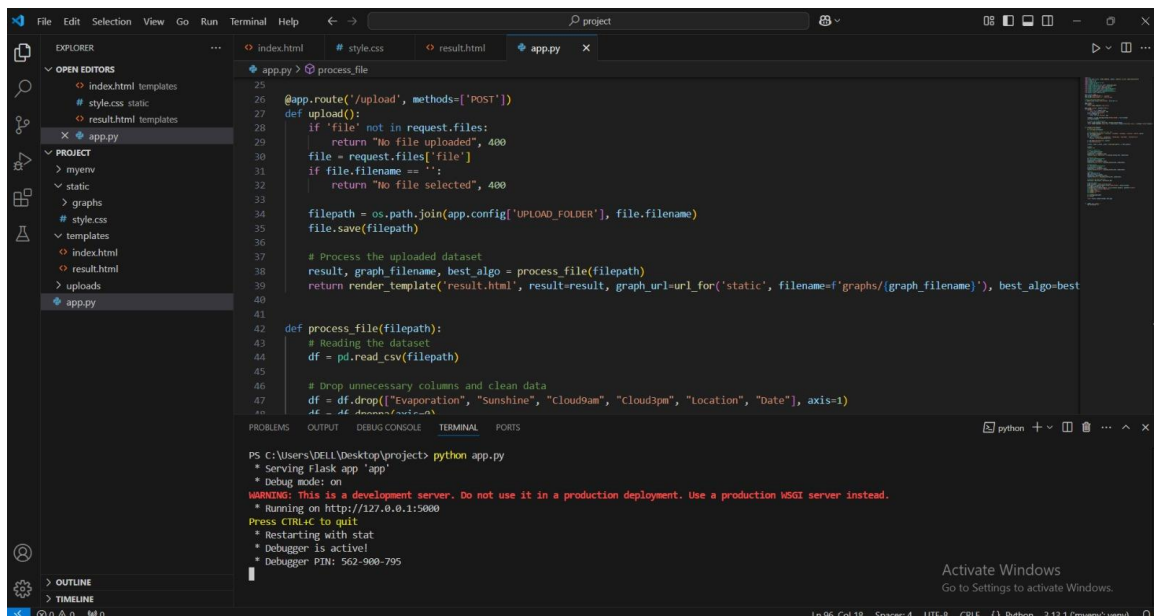
8. Output Display and User Interaction

- The predicted tumor type is shown on the UI.
- Users can:
 - Upload another image.
 - View classification history.
 - Save or export prediction results.

9. Evaluation and Testing (Offline)

- During development, model performance is evaluated on a test set.
- Metrics used:
 - Accuracy
 - Confusion Matrix
 - Precision and Recall (optional)
- Confirms the model's ability to generalize to unseen images.

4. RESULTS



```

25
26 @app.route('/upload', methods=['POST'])
27 def upload():
28     if 'file' not in request.files:
29         return "No file uploaded", 400
30     file = request.files['file']
31     if file.filename == '':
32         return "No file selected", 400
33
34     filepath = os.path.join(app.config['UPLOAD_FOLDER'], file.filename)
35     file.save(filepath)
36
37     # Process the uploaded dataset
38     result, graph_filename, best_algo = process_file(filepath)
39     return render_template('result.html', result=result, graph_url=url_for('static', filename=f'graphs/{graph_filename}'), best_algo=best_algo)
40
41
42 def process_file(filepath):
43     # Reading the dataset
44     df = pd.read_csv(filepath)
45
46     # Drop unnecessary columns and clean data
47     df = df.drop(['Evaporation', 'Sunshine', 'Cloud9am', 'Cloud3pm', 'Location', 'Date'], axis=1)
48     df = df.dropna()
49
50     # Feature Engineering
51     # ... (code for feature engineering) ...
52
53     # Model Training and Prediction
54     # ... (code for model training and prediction) ...
55
56     # Return results
57     return result, graph_filename, best_algo
58
59
60 if __name__ == '__main__':
61     app.run(debug=True)
62

```

Figure 4.1: Home Page of the Brain MRI Classification System

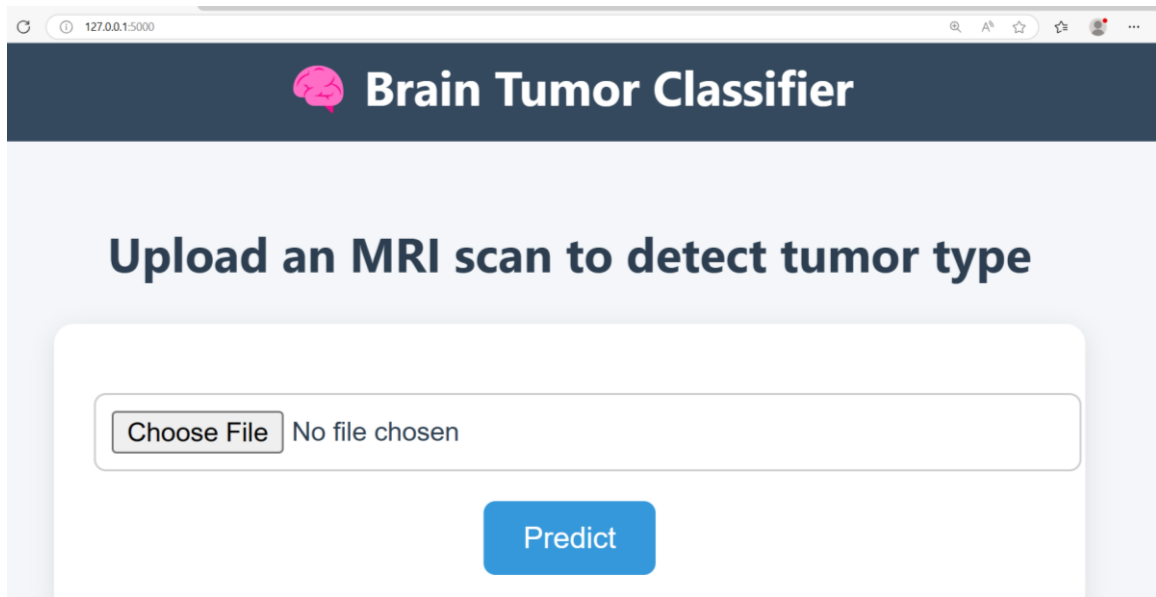


Figure 4.2: Image Upload Interface

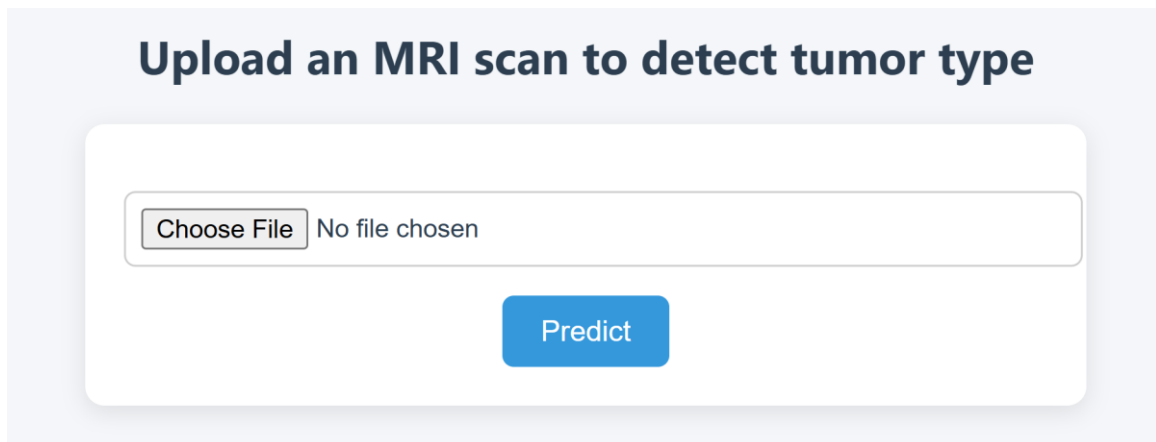


Figure 4.3: Prediction Result Display

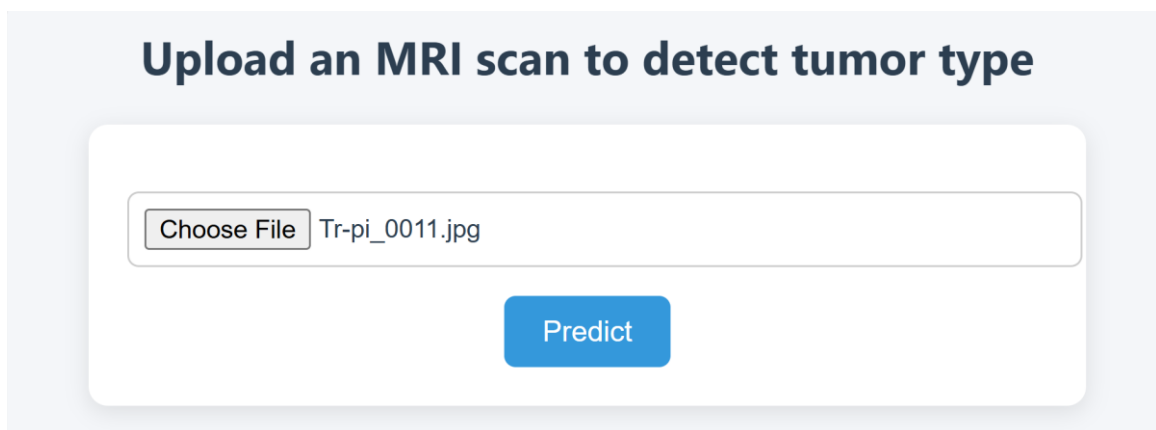


Figure 4.4: Click on predict after uploading the image.



Brain Tumor Classifier

Prediction Result

Tumor Type Detected: **pituitary**

Uploaded MRI Image:

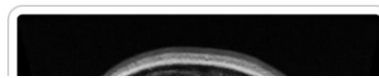
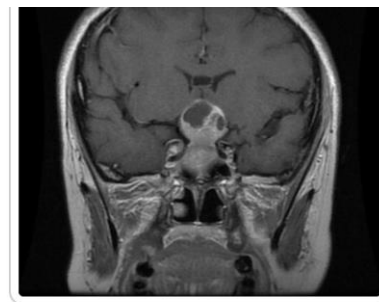


Figure 4.5: Prediction result is given indicating whether tumor is present or not along with type of tumor if present.



← [Classify Another Image](#)

Figure 4.6: Classify Another Image Option

5. CONCLUSION

In conclusion, SSCLNet presents a powerful and practical approach to brain MRI classification using self-supervised contrastive learning. By significantly reducing the dependence on labeled medical data, SSCLNet makes AI-assisted diagnosis more scalable, accessible, and efficient. Our model achieves classification performance comparable to fully supervised methods, while offering advantages in data efficiency and domain adaptability. The results validate the potential of self-supervised learning in the medical imaging

domain and set the foundation for future enhancements in automated diagnostic systems.

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