



# UNIVERSITY VISVESVARAYA COLLEGE OF ENGINEERING

## DEPARTMENT OF COMPUTER SCIENCE

### Application of Deep Learning in Medical Image Classification and Segmentation

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# Acknowledgements

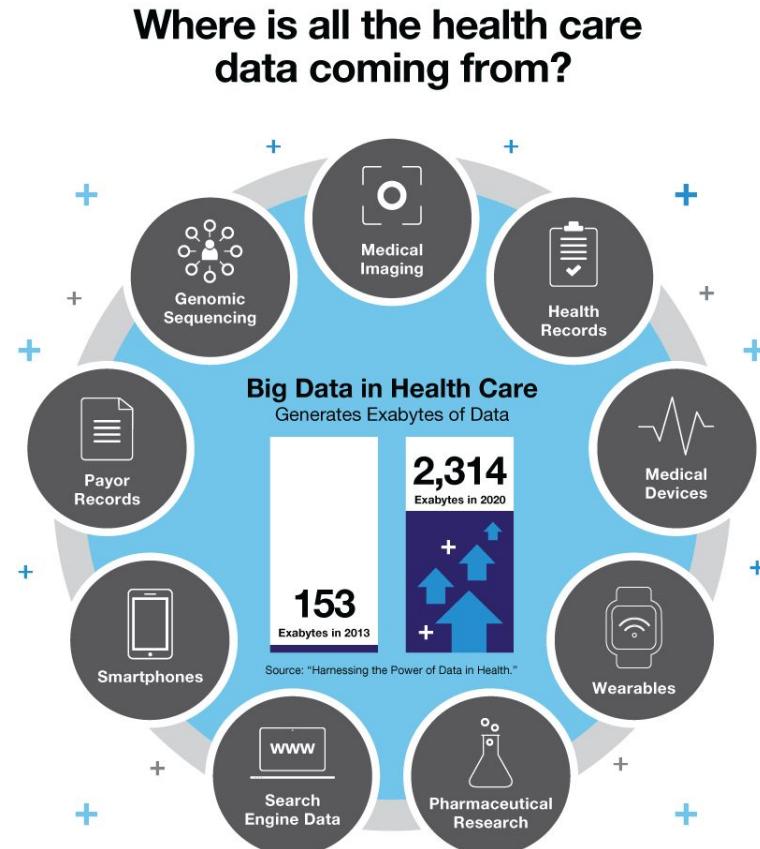
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- Dr Thriveni J, Professor, Department of CSE

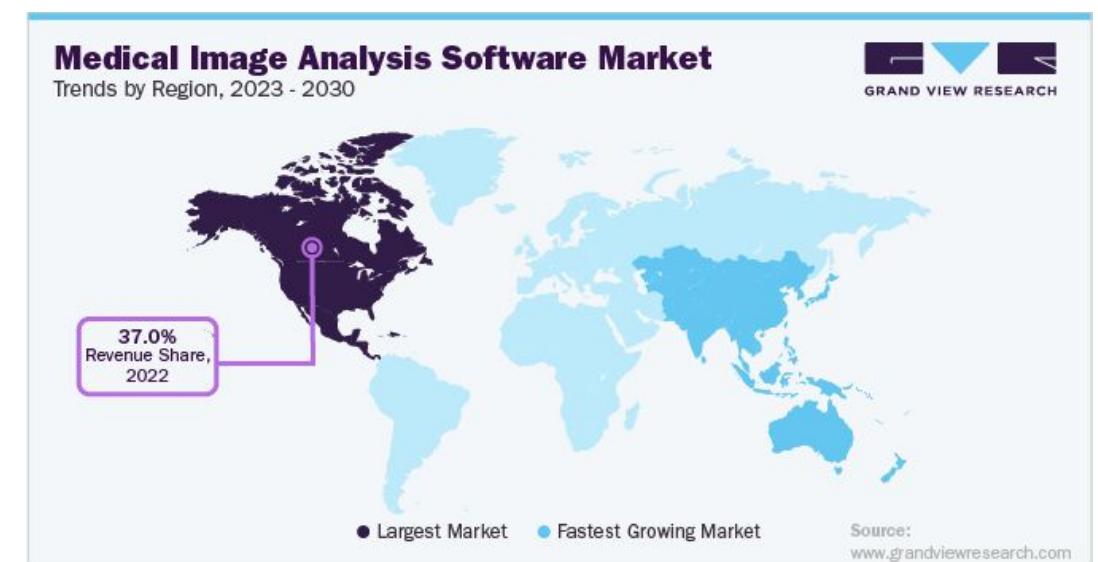
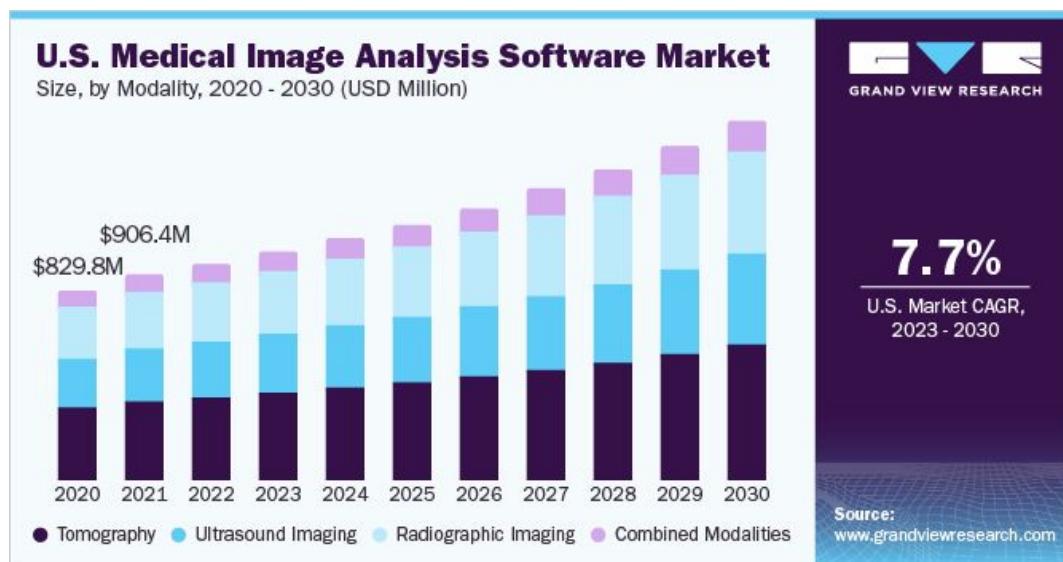
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# Background

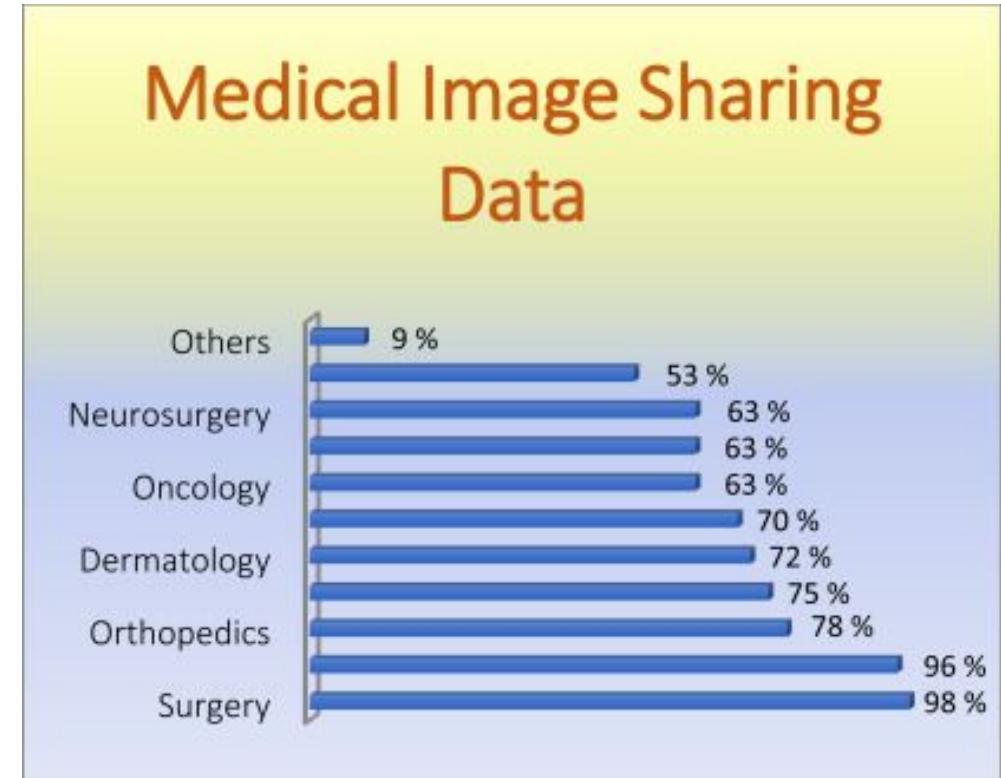
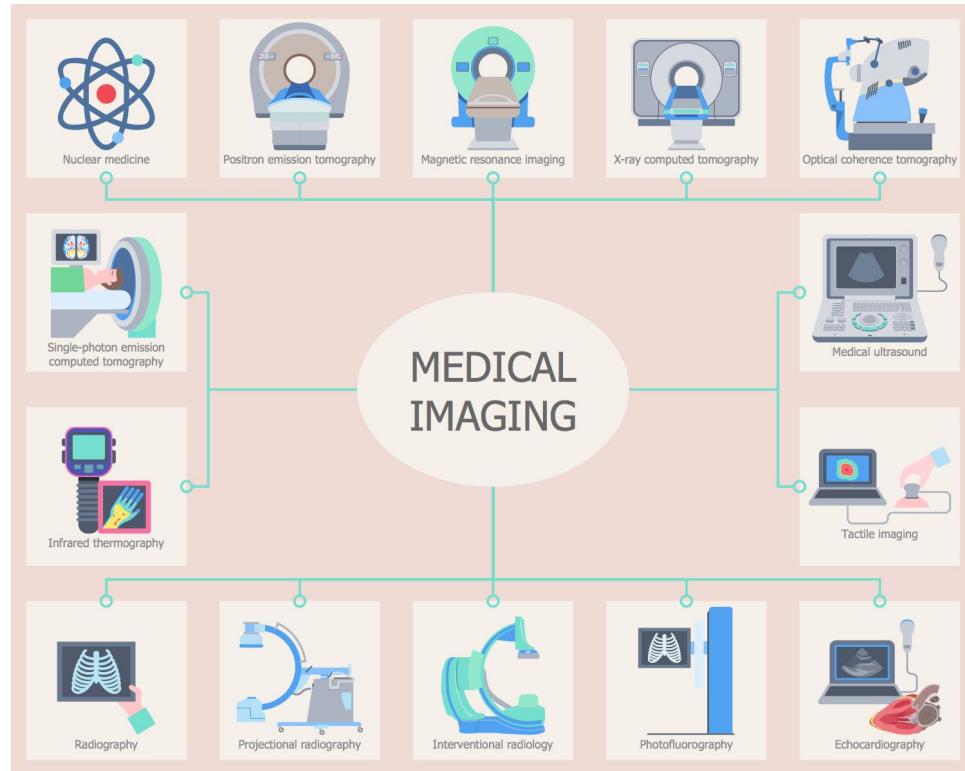


# Background



Source: <https://www.grandviewresearch.com/industry-analysis/medical-image-analysis-software-market>

# Background



# Problem Statement

- **Background:** Medical image data account for the vast majority of medical data.
- **Problem:** How to utilise big medical data for best clinical practices to improve diagnosing techniques?
- **Solution:** Using intelligent imaging and deep learning in the field of big data analysis, combining the latest research progress and the work in the field, especially the classification and segmentation of medical images.
- **Outcome:** Early diagnosis of diseases

# Project Focus

- **Medical Image Segmentation**
  - Brain Tumor Segmentation
- **Medical Image Classification**
  - Acute Lymphoblastic Leukemia
  - Brain Cancer
  - Breast Cancer
  - Cervical Cancer
  - Kidney Cancer
  - Lung Cancer
  - Colon Cancer
  - Lymphoma
  - Oral Cancer

# Methodology

## Transfer learning for Classification Models

- Transfer learning is a machine learning technique where knowledge gained from solving one problem is applied to a different but related problem.
- In transfer learning, a pre-trained model that has been trained on a large dataset and has learned useful patterns and representations is utilized as a starting point for solving a new task.

# Methodology

## Ensembling

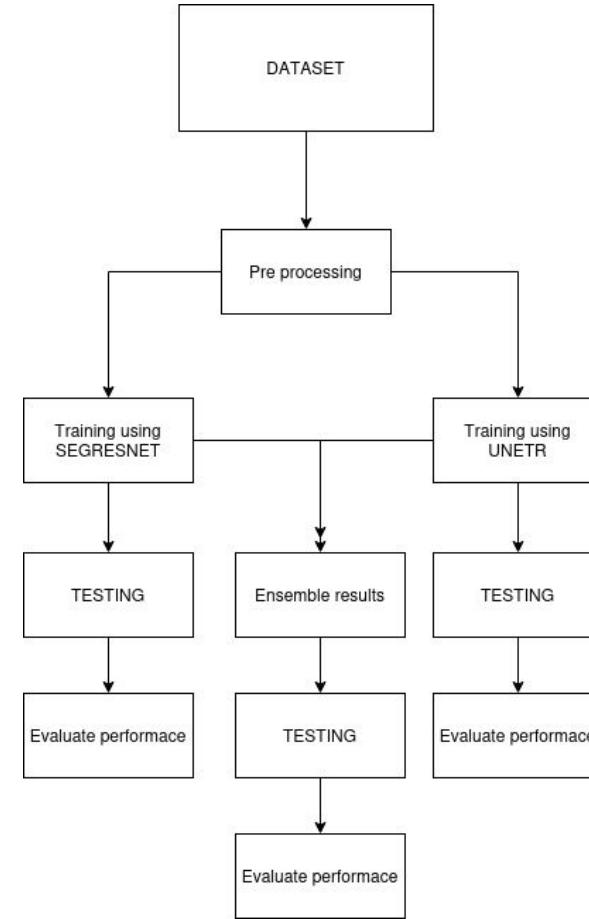
- Machine learning technique where multiple models are combined to make predictions
- Using strengths of different models and reducing individual model errors for improved accuracy
- Reduces the risk of overfitting, enhances stability, and leverages the "wisdom of the crowd" principle

# System Requirements

- **Hardware Requirements**
  - Intel i7 or higher
  - 16 GB RAM or higher
  - 12 GB CPU
- **Software Requirements**
  - Python 3.0 or higher
  - Jupyter
  - VSCode
  - Python Libraries: Pandas, Torchvision, Matplotlib, Numpy, Sklearn, Keras, TensorFlow, PyTorch, Monai

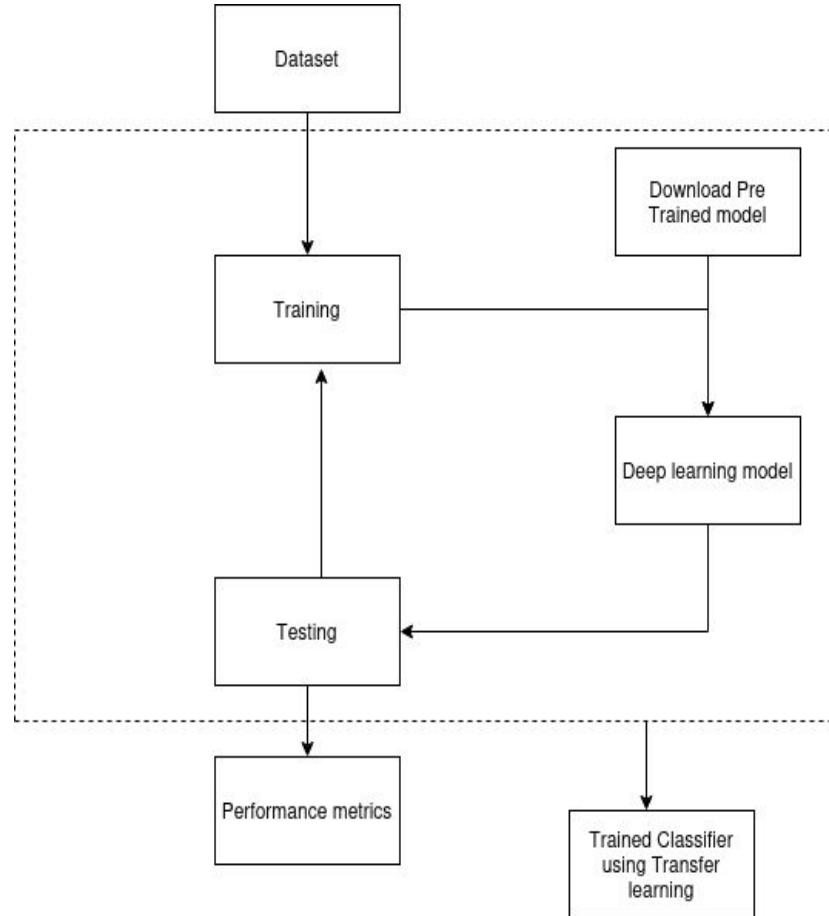
# System Design

## System Design for Brain Tumor Segmentation



# System Design

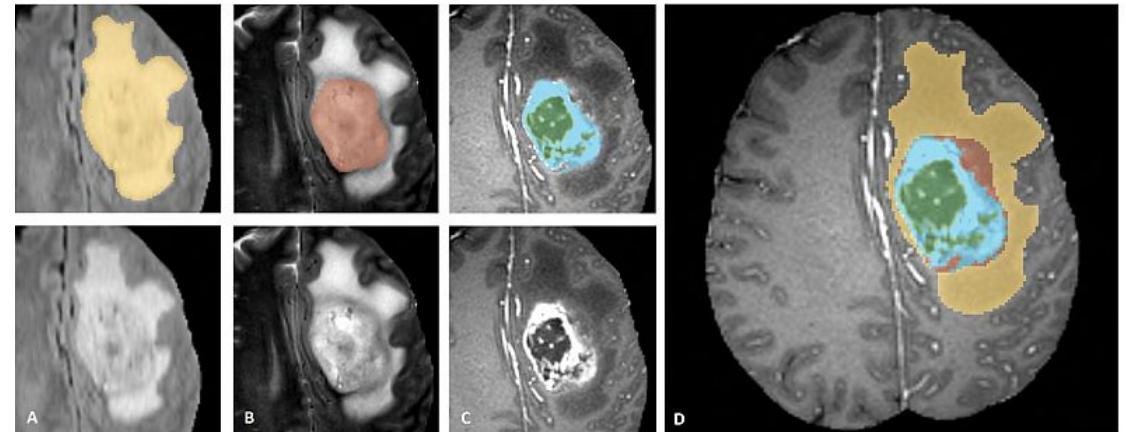
System Design for  
Classification



# System Architecture

## System Architecture for Brain Tumor Segmentation

- Dataset:
  - Size: 750 4D volumes (484 Training + 266 Testing) MRI images
  - Types: FLAIR, T1w, T1gd, T2w
  - Sources: BRATS 2016 and 2017



Glioma Sub-Regions

# System Architecture

## System Architecture for Brain Tumor Segmentation

Each MRI has 3 label images (Ground truth).

The labels are:-

- Label 1 is the peritumoral edema
- Label 2 is the GD-enhancing tumor
- Label 3 is the necrotic and non-enhancing tumor core

These labels are converted to brats classes which are TC (Tumor core), WT (Whole tumor) and ET (Enhancing tumor).

## System Architecture for Brain Tumor Segmentation

Label 2 and label 3 are merged to construct the tumor core.

Label 1, label 2 and label 3 are merged to construct Whole tumor.

Label 2 is enhancing tumors.

Each Image is cropped to a specific dimension.

# System Architecture

## System Architecture for Brain Tumor Segmentation

- Data Augmentation:
  - Transform the data by randomly adjusting the intensity and producing rotations and flips of the MRI image.
  - We apply a random (per channel) intensity shift ( $-0.1..0.1$  of image std) and scale (0.9..1.1) on input image channels. We also apply a random axis mirror flip (for all 3 axes) with a probability 0.5.
- Modeling:
  - 2 architectures: SegResNet and UNETR

## System Architecture for Classification

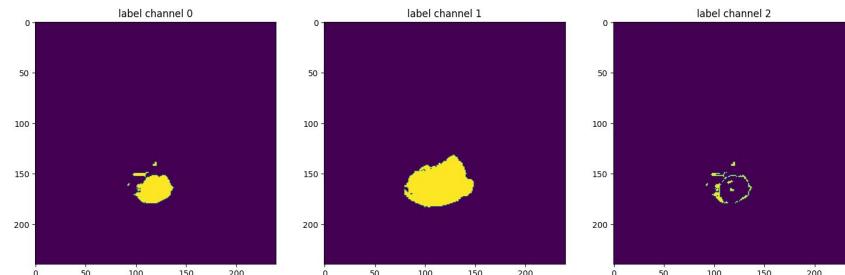
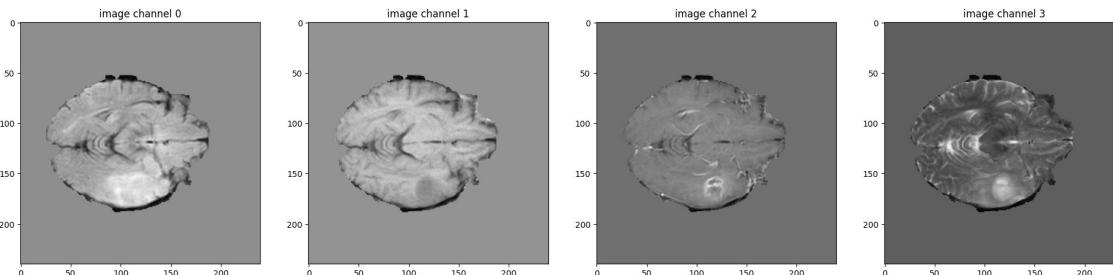
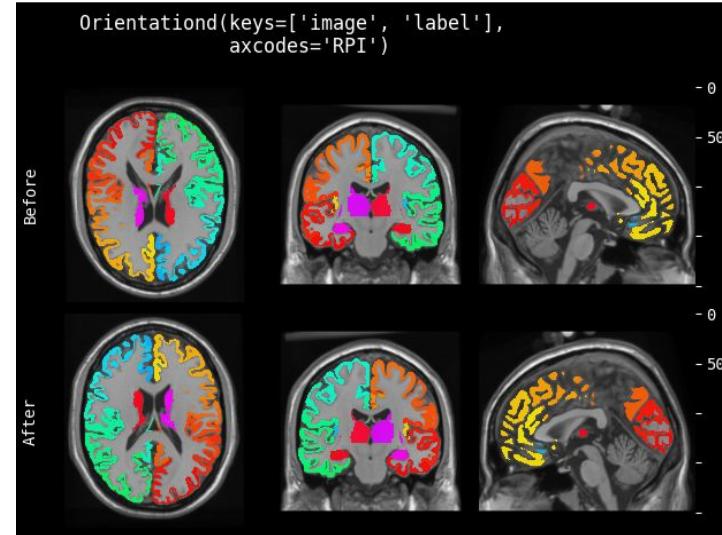
- Dataset:
  - Multi-cancer dataset from Kaggle
  - 5000 images in each sub-class
  - Image size 512x512
- Pre-processing:
  - Data Normalization
  - Image pre-processing
- Modeling:
  - CNN - ResNet, MobileNet, VGGNet, DenseNet

Cancer	Classes	Images
Acute Lymphoblastic Leukemia	4	20000
Brain Cancer	3	15000
Breast Cancer	2	10000
Cervical Cancer	5	25000
Kidney Cancer	2	10000
Lung and Colon Cancer	5	25000
Lymphoma	3	15000
Oral Cancer	2	10000

# Implementation

## Dataset

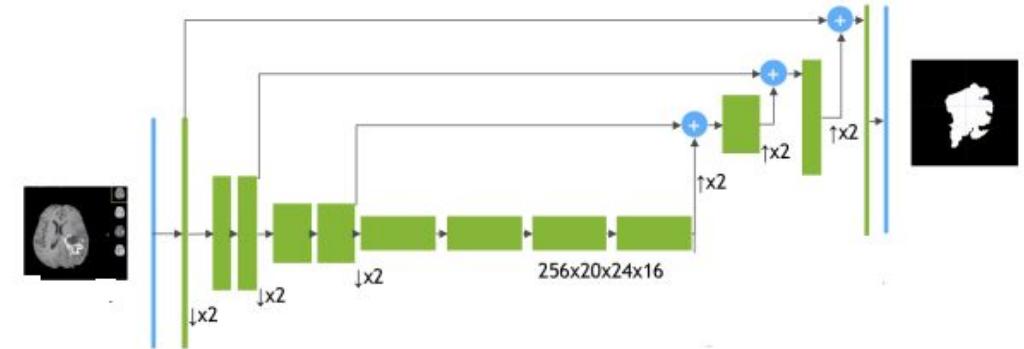
- Source: Medical Segmentation Decathlon (MSD)
- 80% training, 20% validation
- 484 mp-MRI images from patients diagnosed with either glioblastoma or lower-grade glioma



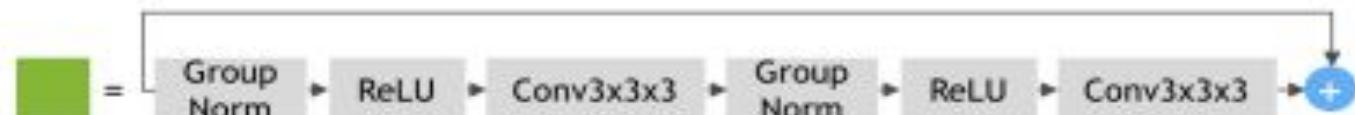
# Implementation

## SEGRESNET Architecture

- Based on ResNet, a CNN model
- SEGRESNET uses skip connections
- ResNet has powerful feature extraction capabilities
- Encoder-decoder based architecture



Schematic visualization of the network architecture



Architecture of each block

$\downarrow \times 2 = \text{conv}3 \times 3 \times 3 \text{ stride } 2$

$\uparrow \times 2 = \text{conv}1 \times 1 \times 1, 3D \text{ bilinear upsizing}$

# Implementation

## Encoder

- The encoder part uses ResNet blocks, where each block consists of two convolutions with normalization and ReLU, followed by additive identity skip connection.
- For normalization, we use Group Normalization (GN), which shows better than BatchNorm performance when batch size is small (batch size of 1 in our case).
- We follow a common CNN approach to progressively downsize image dimensions by 2 and simultaneously increase feature size by 2. For downsizing we use strided convolutions.

# Implementation

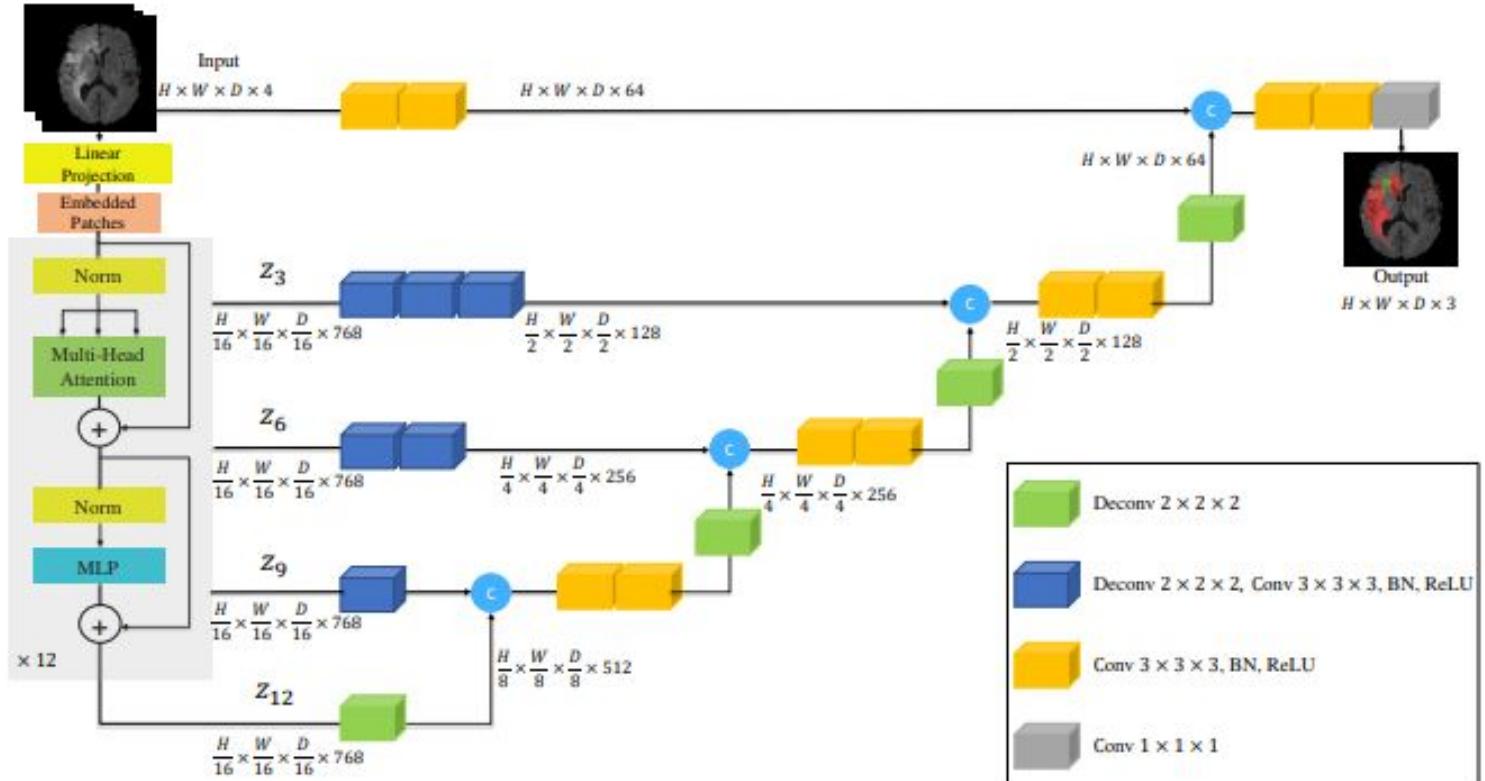
## Decoder

- The decoder structure is similar to the encoder one, but with a single block per each spatial level.
- Each decoder level begins with upsizing: reducing the number of features by a factor of 2 (using  $1 \times 1 \times 1$  convolutions) and doubling the spatial dimension (using 3D bilinear upsampling), followed by an addition of encoder output of the equivalent spatial level.
- The end of the decoder has the same spatial size as the original image, and the number of features equal to the initial input feature size, followed by  $1 \times 1 \times 1$  convolution into 3 channels and a sigmoid function.

# Implementation

## UNETR Architecture

UNETR is a 3D medical image segmentation model that uses a **transformer encoder** and a **CNN-based decoder** to predict the segmentation mask.

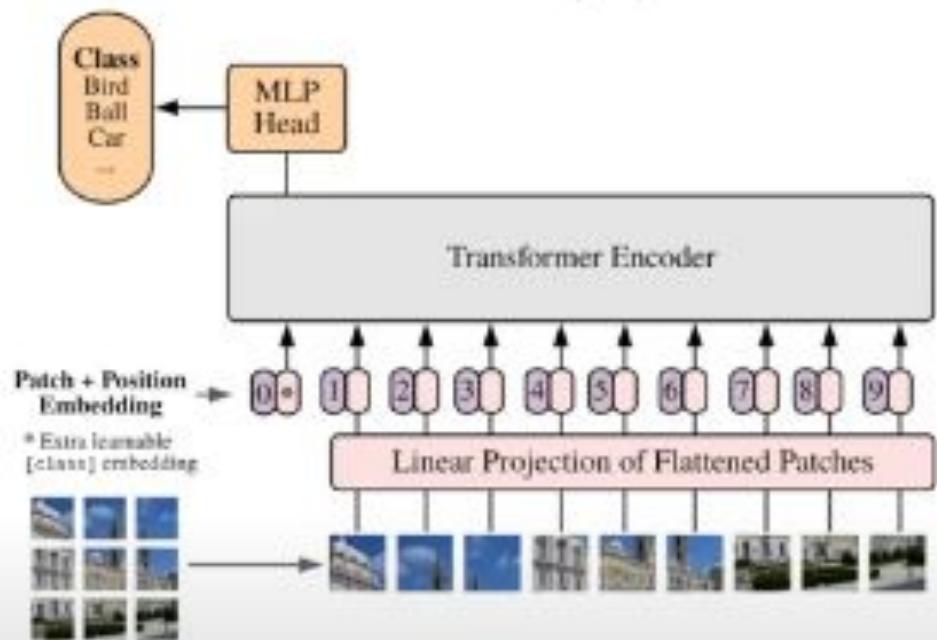


## Key Features of UNETR?

1. It uses **Vision Transformer** as encoder to learn global contextual representations.
2. It uses a **CNN Decoder** to upsample the global representations and generate the final segmentation mask.

## What is Vision Transformer?

Vision Transformer (ViT) is an architecture that is used for image recognition. It is based on the Transformer architecture, which was originally developed for natural language processing. ViTs have been shown to achieve state-of-the-art results on a variety of image recognition tasks, including ImageNet classification.



# Implementation

## Training

$$L_{dice} = \frac{2 * \sum p_{true} * p_{pred}}{\sum p_{true}^2 + \sum p_{pred}^2 + \epsilon}$$

**Loss function**

$$\alpha = \alpha_0 * \left(1 - \frac{e}{N_e}\right)^{0.9}$$

**Optimizer function**

## Ensemble

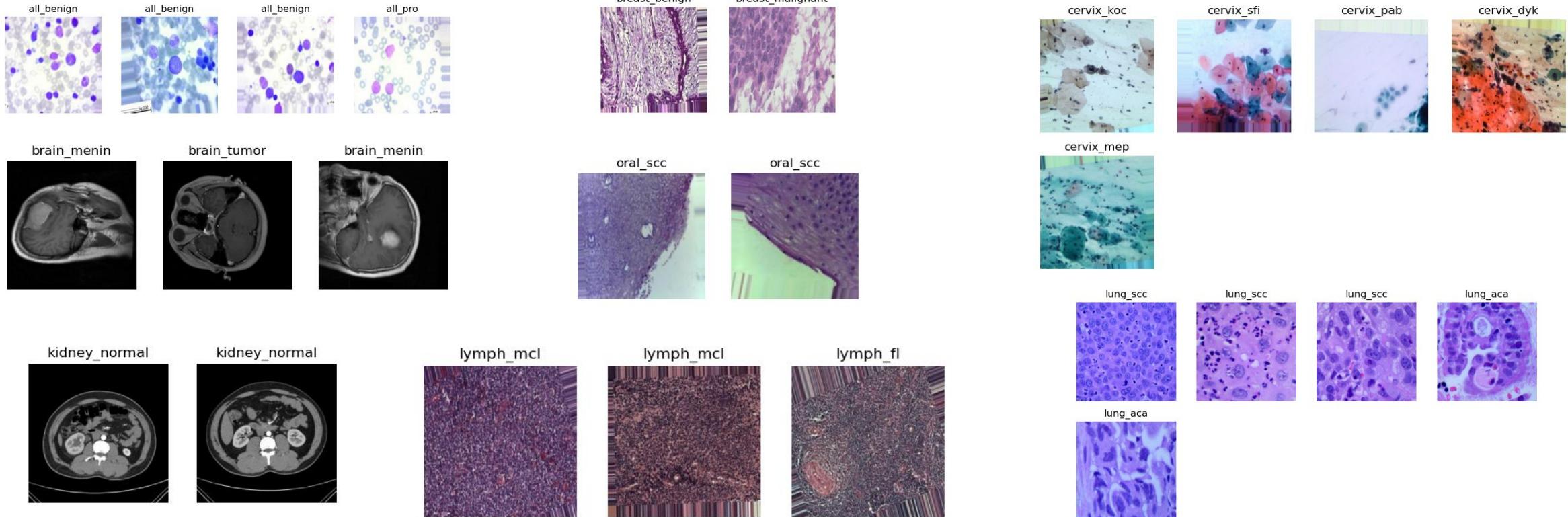
```
def __call__(self, img: Union[Sequence[NdarrayOrTensor], NdarrayOrTensor])
    img_ = self.get_stacked_torch(img)
    if self.weights is not None:
        self.weights = self.weights.to(img_.device)
        shape = tuple(self.weights.shape)
        for _ in range(img_.ndimension() - self.weights.ndimension()):
            shape += (1,)
        weights = self.weights.reshape(*shape)

        img_ = img_ * weights / weights.mean(dim=0, keepdim=True)

    out_pt = torch.mean(img_, dim=0)
    return self.post_convert(out_pt, img)
```

# Implementation

## Implementation of Classification Models

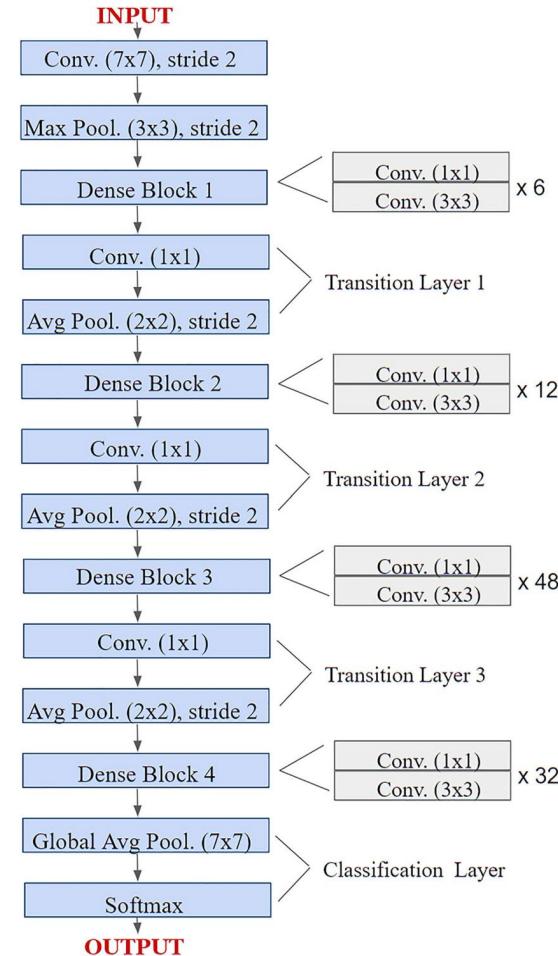


- What is a neuron?
- What is a neural network?
- What is a Convolutional Neural Network?

# Implementation

## DenseNet-201

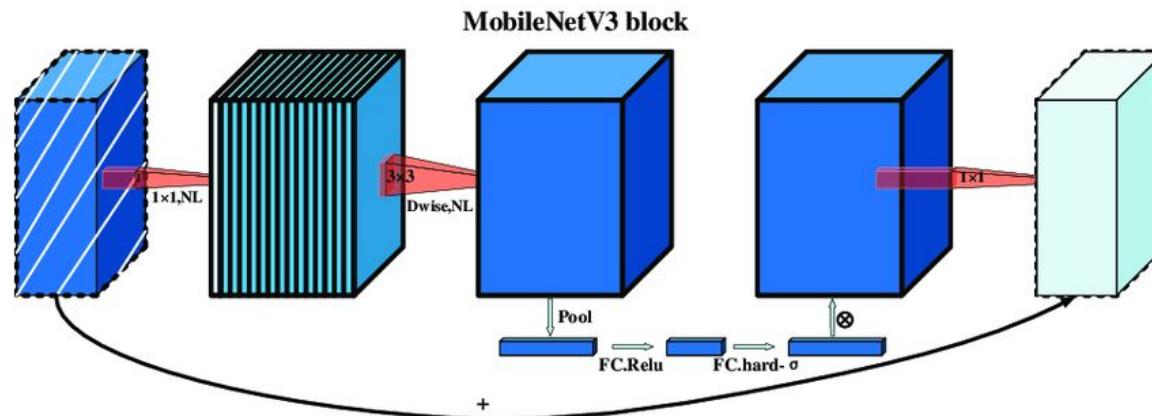
- Dense convolutional network
- Basic building block - dense block
- 201 layers
- Addresses vanishing gradients
- Strengthens feature propagation



# Implementation

## MobileNetv3Small

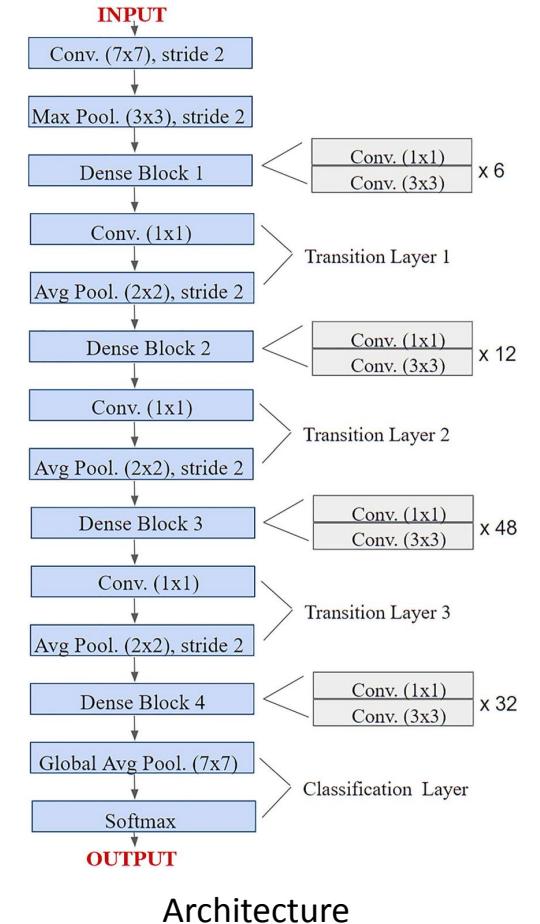
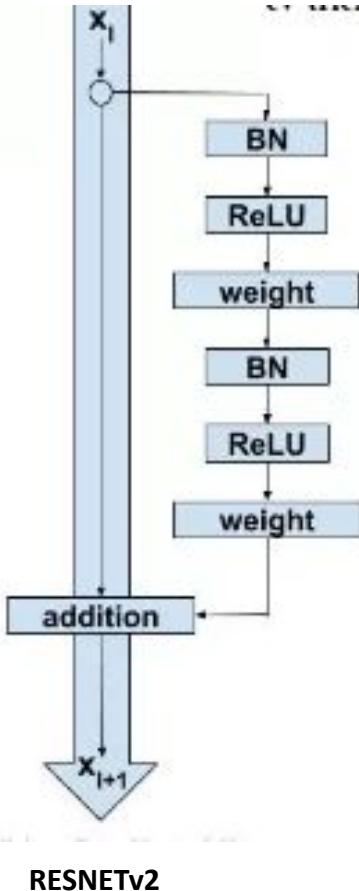
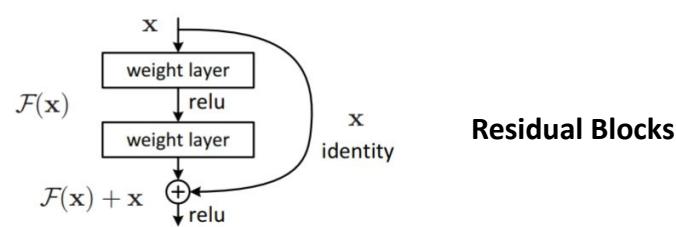
- Lightweight MobileNetv3
- Balance between model size and accuracy
- Depth-wise separable convolutions
- Inverted residuals
- Efficient use of activations



# Implementation

## ResNet50v2

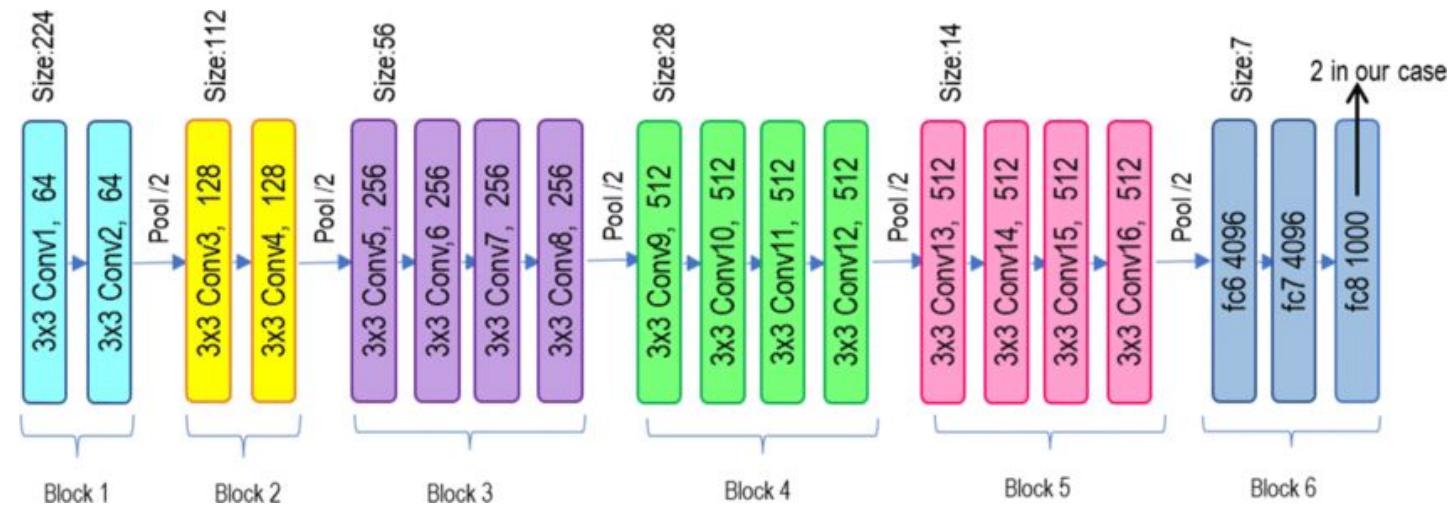
- Residual network architecture
- 50 layers
- Building blocks - residual blocks
- Residual connections
- Identity mapping
- Bottleneck structure
- Pre-activation
- Deeper architecture



# Implementation

## VGG19 Architecture

- Visual Geometry Group, 19 layers
- Convolutional layers, max pooling layers, fully connected layers, increasing depth
- Captures both local and global information from images



# Implementation

## Training

Optimiser - Adam Optimiser

- Adam + RMSprop
- Adaptive Learning Rates
- Momentum Optimization
- Bias Correction
- Weight Decay
- Computational Efficiency

Set learning rate = 0.01

## Annealer - ReduceLROnPlateau

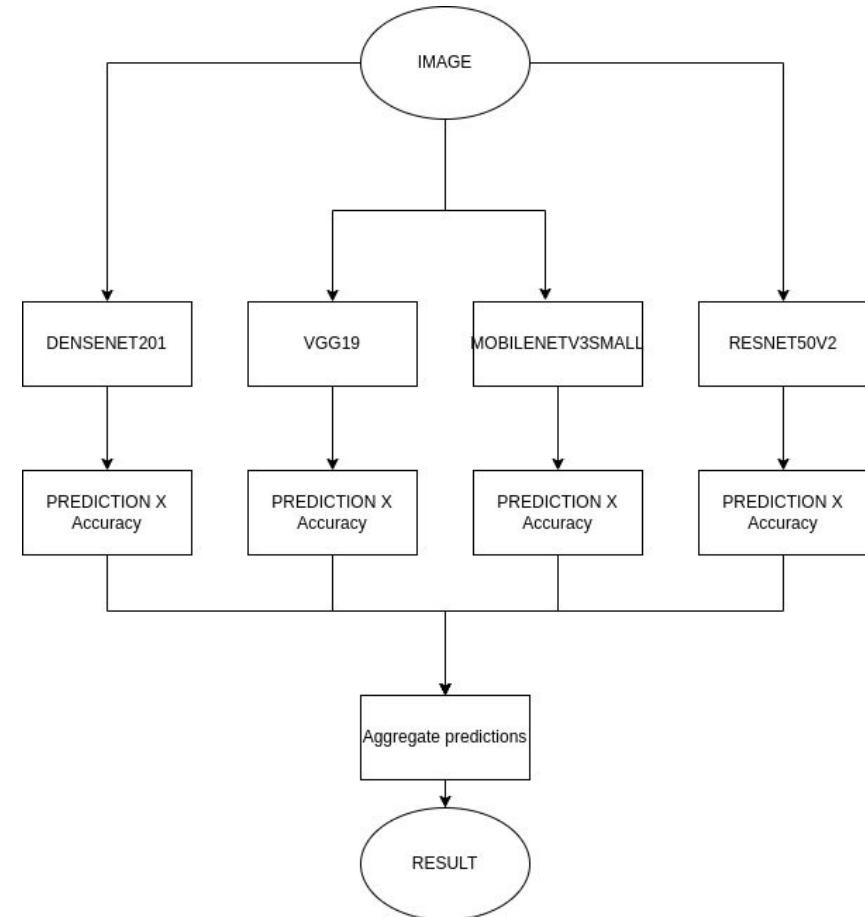
- ReduceLROnPlateau
- Monitor Metric
- Patience
- Factor
- Mode
- Threshold
- Cool-down

```
"ReduceLROnPlateau(monitor='val_accuracy',  
                    factor=0.5, patience=5, verbose=1,  
                    min_lr=1e-3)"
```

# Implementation

## Ensemble

- ML technique that involves combining multiple individual models, called base models or weak learners, to create a more robust and accurate prediction model.
- We have tried to ensemble the predictions of all the models based on the accuracy as a heuristic knowledge to weight the predictions of each model.



# Performance Metrics

## Metrics Used for Segmentation

- Dice score

## Metrics Used for Classification

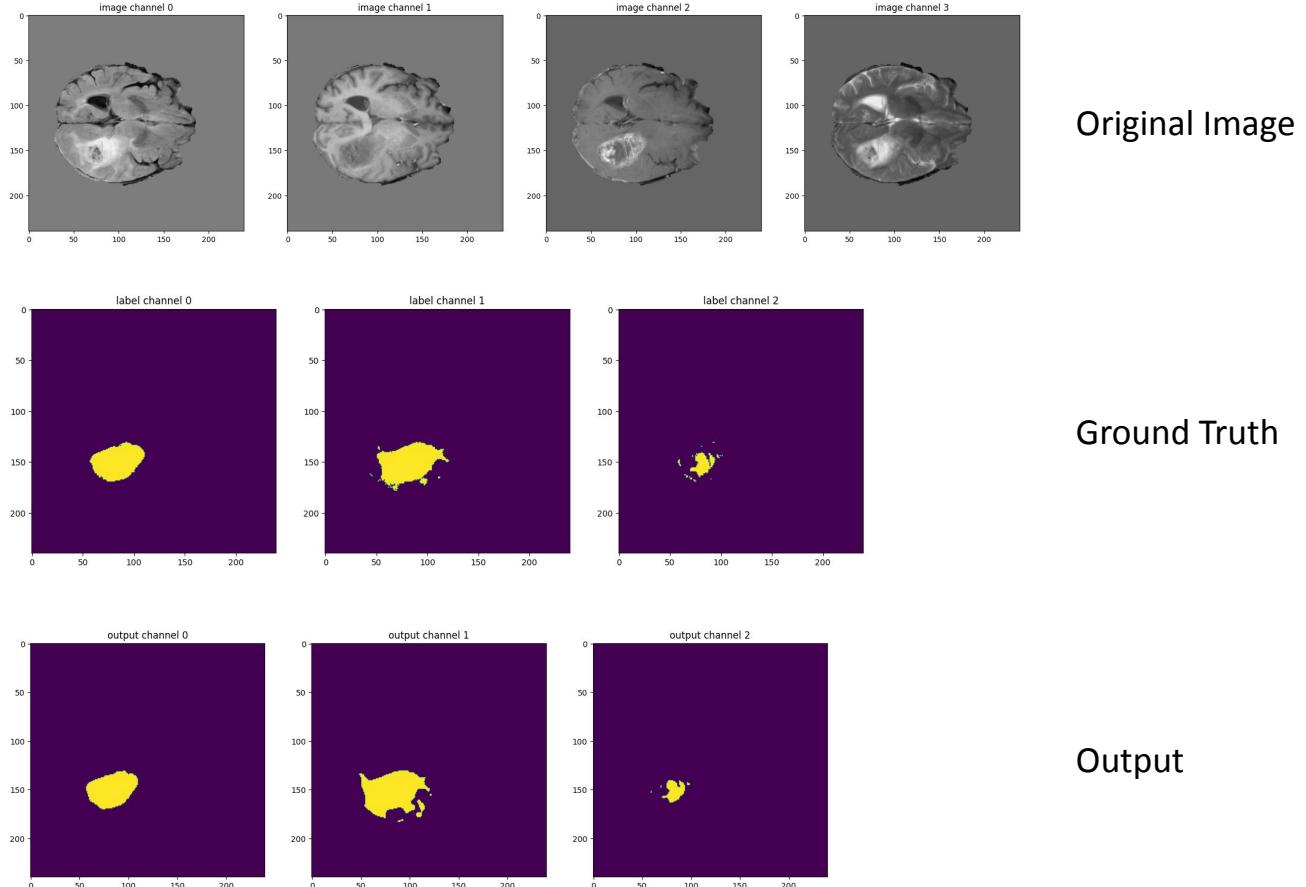
- Performance metrics
- Confusion matrix
- Accuracy
- Precision
- Recall or sensitivity
- F1 score

# Performance Analysis

## Result for Brain Tumor Segmentation - SEGRESNET

Dice Scores:

- Metric on original image spacing:  
0.7625482082366943
- Metric for tumor Core: 0.8078
- Metric for Whole tumor: 0.9002
- Metric enhancing tumor: 0.5796
- Results achieved at 63 epochs

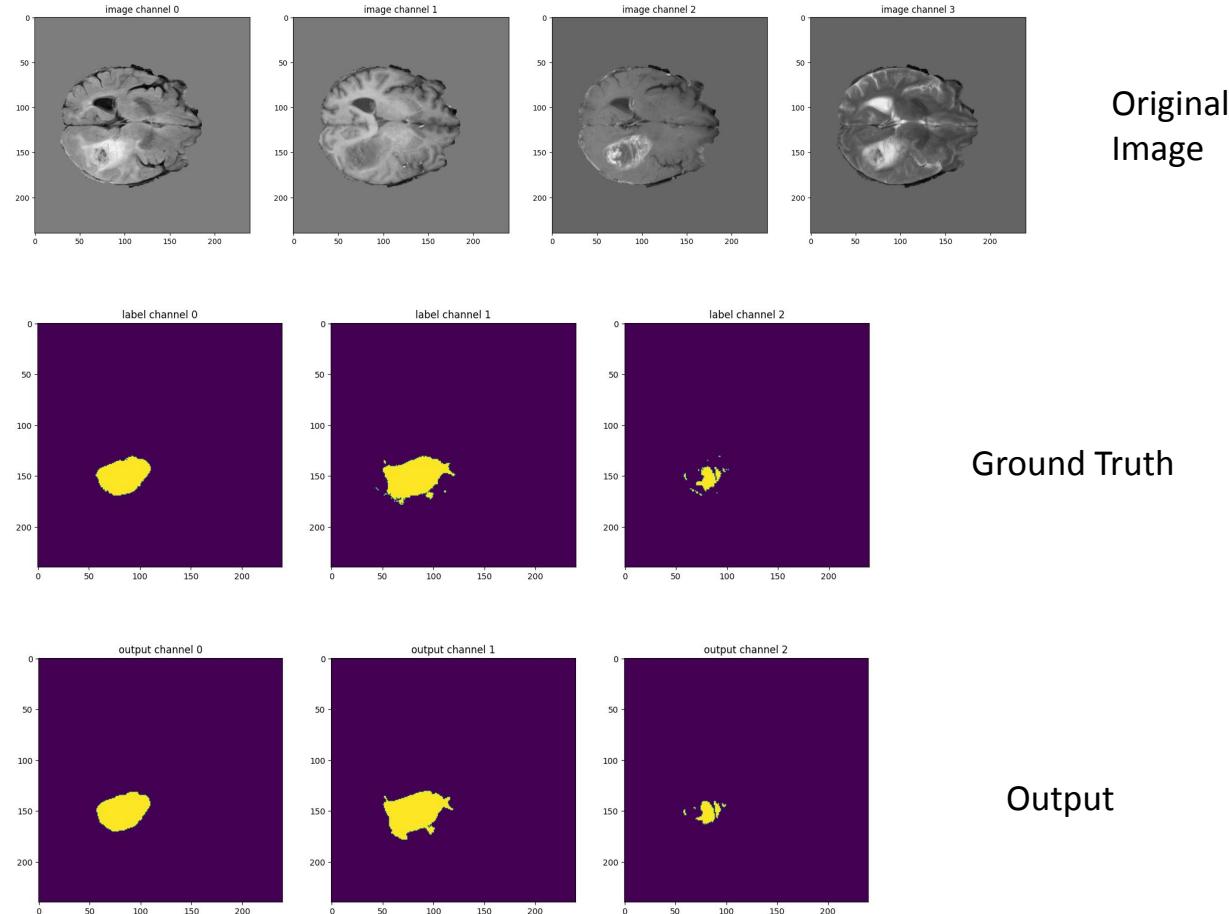


# Performance Analysis

## Brain Tumor Segmentation - UNETR

Dice Scores:

- Metric on original image spacing:  
 $0.737675666809082$
- Metric tumor Core: 0.7786
- Metric Whole tumor: 0.8912
- Metric Enhancing tumor: 0.5432
- Results achieved at 47 epochs

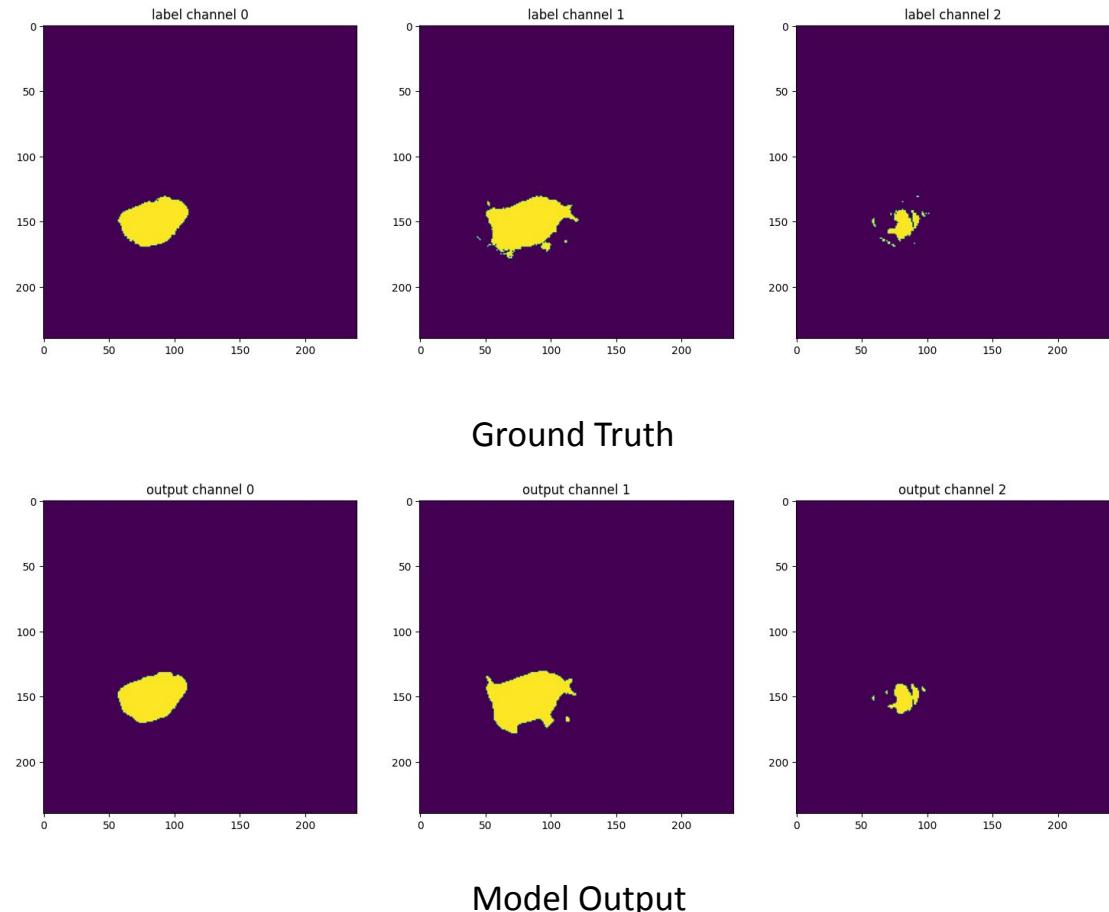


# Performance Analysis

## Brain Tumor Segmentation - Mean Ensemble

### Dice Scores:

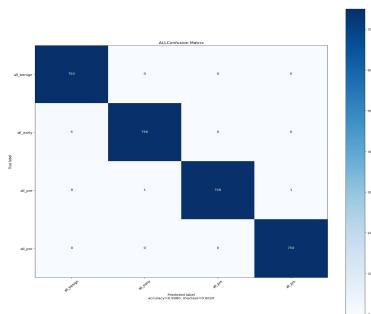
- Metric on original image spacing: **0.7645719647407532**
- Metric Tumor Core: **0.8091**
- Metric Whole tumor: **0.9032**
- Metric enhancing tumor: **0.5814**



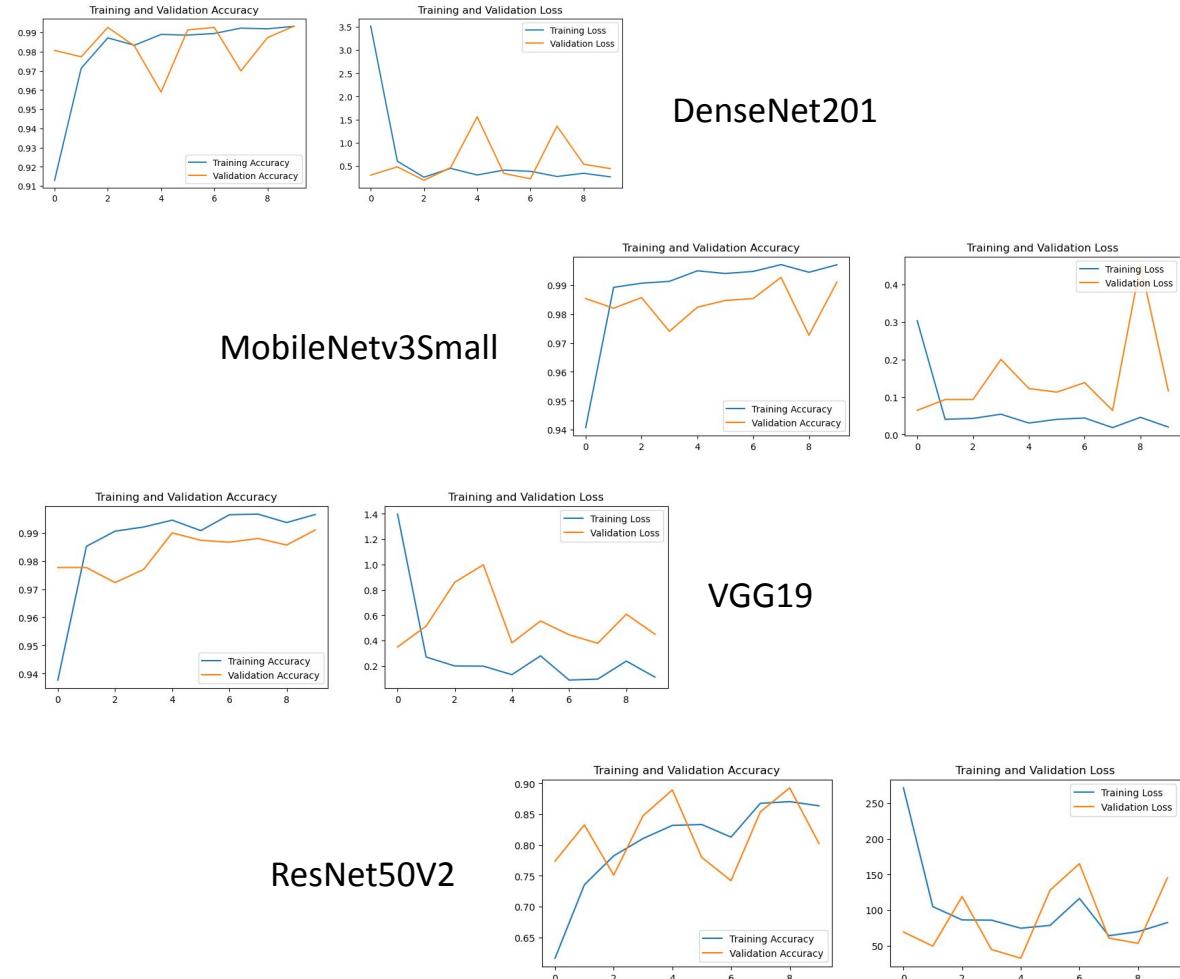
# Performance Analysis

## Acute Lymphoblastic Leukemia

Models	Recall	Precision	F1Score
DenseNet201	0.9903333333333333	0.9904421811723344	0.9903241375685572
MobileNetV3 Small	0.9916666666666667	0.991678857124651	0.9916619096443816
VGG19	0.9913333333333333	0.9913810676610213	0.99133643551295
ResNet50V2	0.7963333333333333	0.8631494378615919	0.7981504464349779
Ensemble	0.998	0.998006178550939	0.9979997690422237



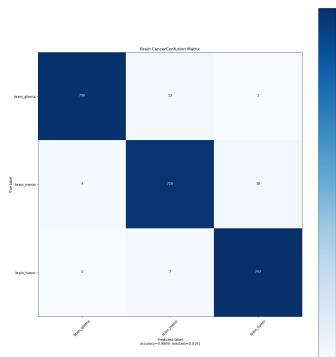
Ensemble



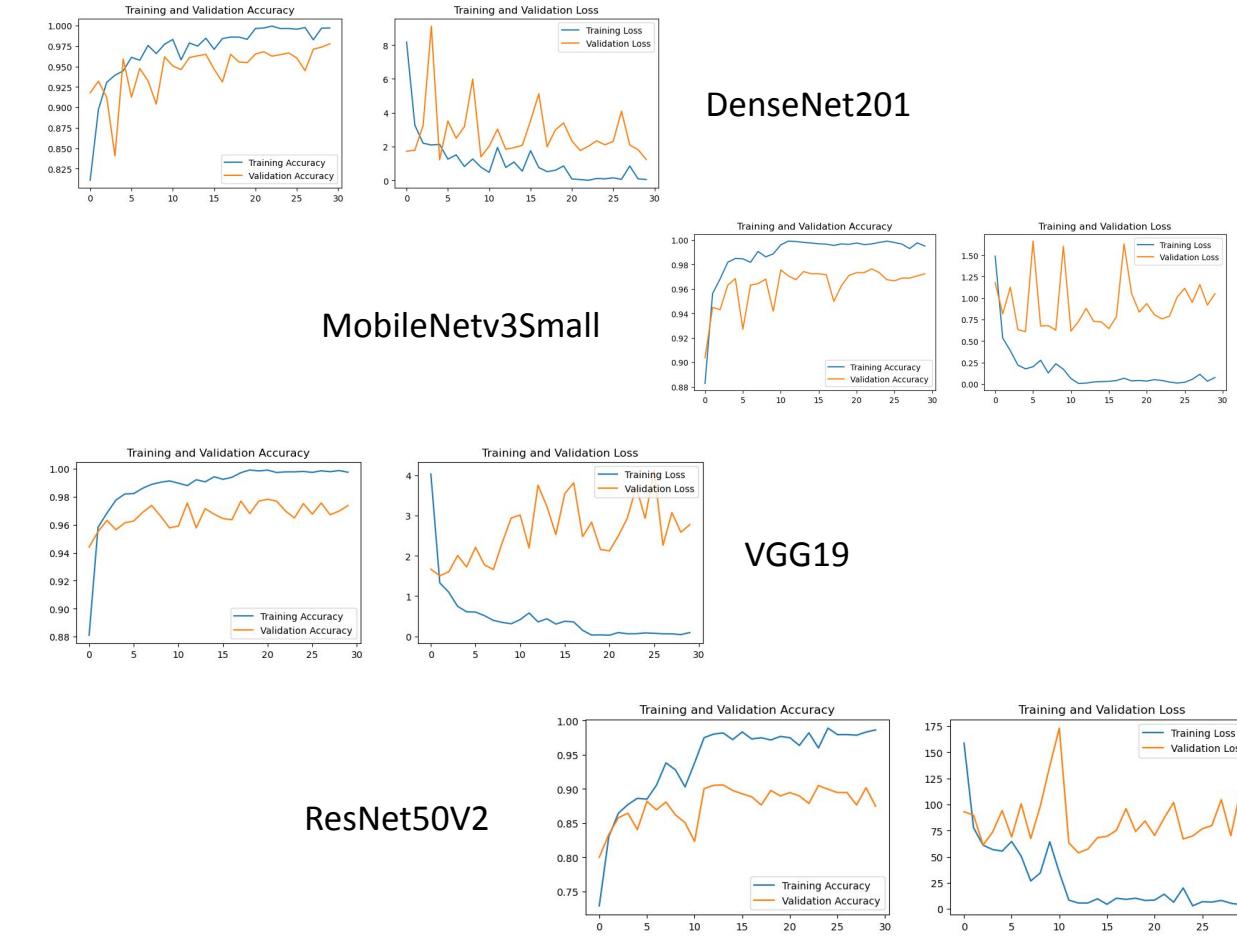
# Performance Analysis

## Brain Cancer

Models	Accuracy	Recall	Precision	F1Score
DenseNet201	0.95955555555556	0.959555555556	0.959682605299268	0.9595922637062334
MobileNetV3Small	0.9697777777777777	0.9697777777777777	0.9699118252039262	0.9697824194666587
VGG19	0.9684444444444444	0.9684444444444444	0.9688725780364567	0.9683784986919409
ResNet50V2	0.8742222222222222	0.8742222222222222	0.8893087706148176	0.8757004946044663
Ensemble	0.9808888888888889	0.9808888888888889	0.980974081159352	0.9808954375713036



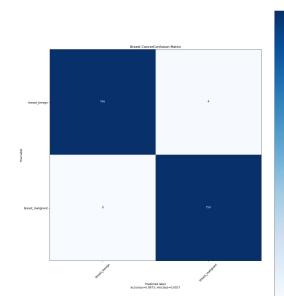
Ensemble



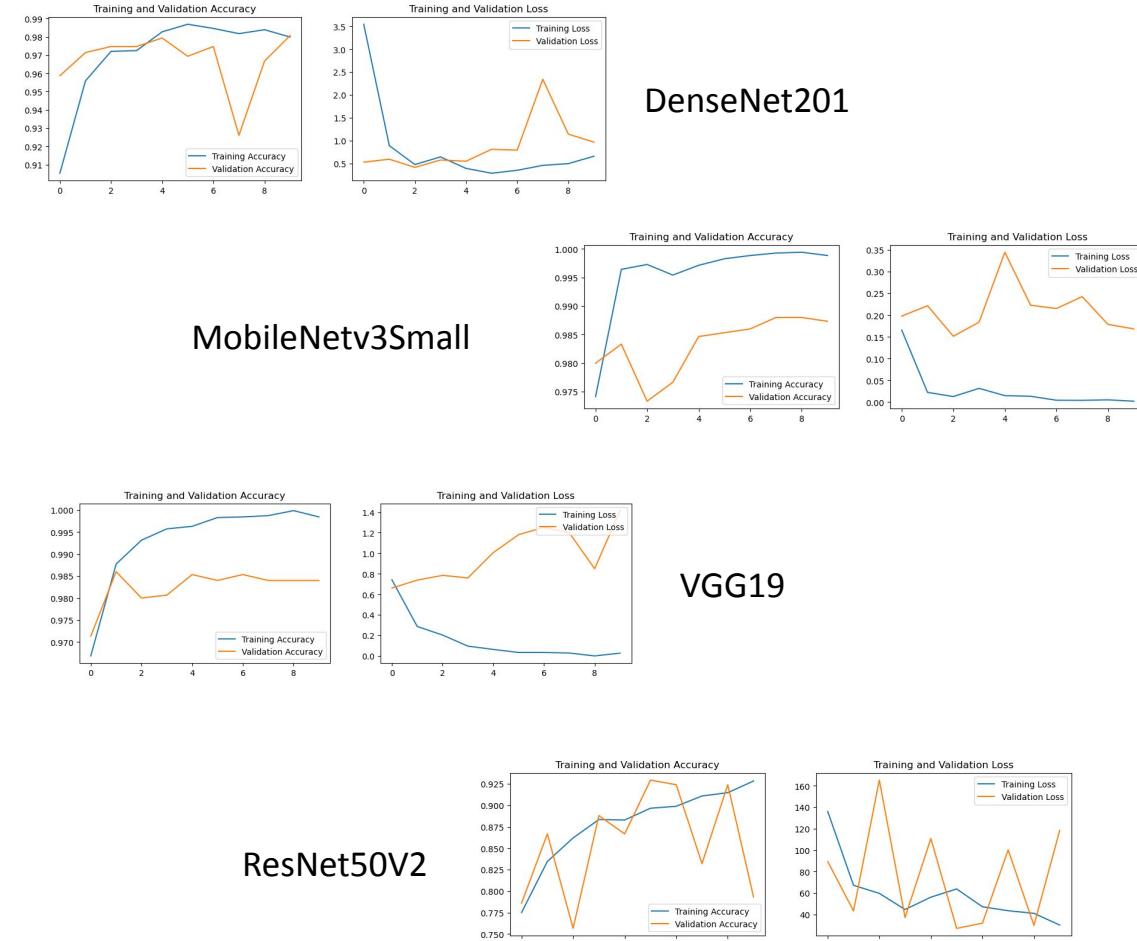
# Performance Analysis

## Breast Cancer

Models	Accuracy	Recall	Precision	F1Score
DenseNet201	0.98	0.98	0.9806699470 907005	0.9799930286 819941
MobileNetV3Small	0.9926666666 666667	0.9926666666 666667	0.9926675425 200756	0.9926666634 07406
VGG19	0.9913333333 333333	0.9913333333 333333	0.9914040955 230887	0.9913330213 22101
ResNet50V2	0.7926666666 666666	0.7926666666 666666	0.8479715662 049592	0.7840876534 70172
Ensemble	0.9973333333 333333	0.9973333333 333333	0.9973474801 061007	0.9973333143 702354



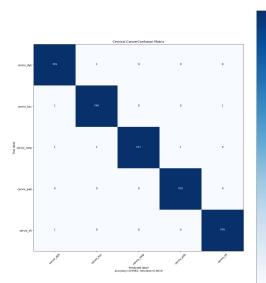
Ensemble



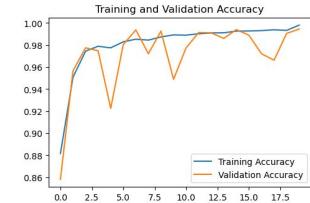
# Performance Analysis

## Cervical Cancer

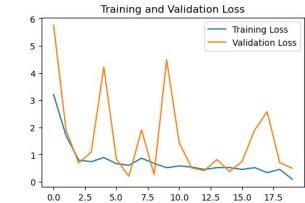
Models	Accuracy	Recall	Precision	F1Score
DenseNet201	0.9944	0.9944	0.99446302996 9946	0.99440384072 41459
MobileNetV3Small	0.98266666666 66667	0.98266666666 66667	0.98293799487 01118	0.98262953557 47524
VGG19	0.98906666666 66666	0.98906666666 66666	0.98916943644 07169	0.98907777524 61215
ResNet50V2	0.8512	0.8512	0.88191196514 5657	0.84764221667 9388
Ensemble	0.99813333333 33333	0.99813333333 33333	0.99813581607 50206	0.99813333072 40217



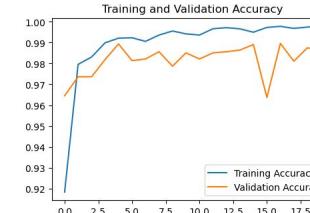
Ensemble



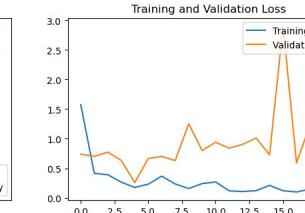
MobileNetv3Small



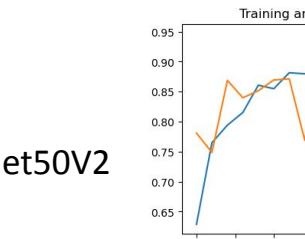
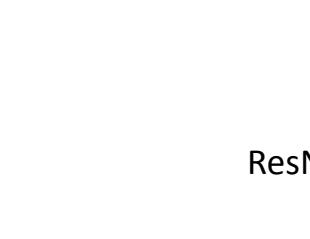
DenseNet201



VGG19



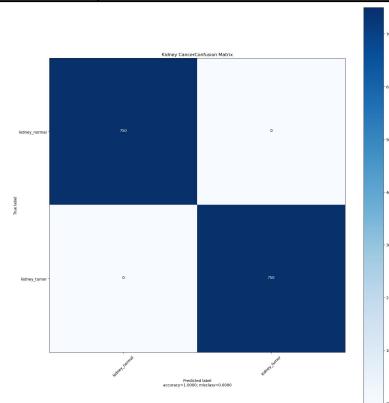
ResNet50V2



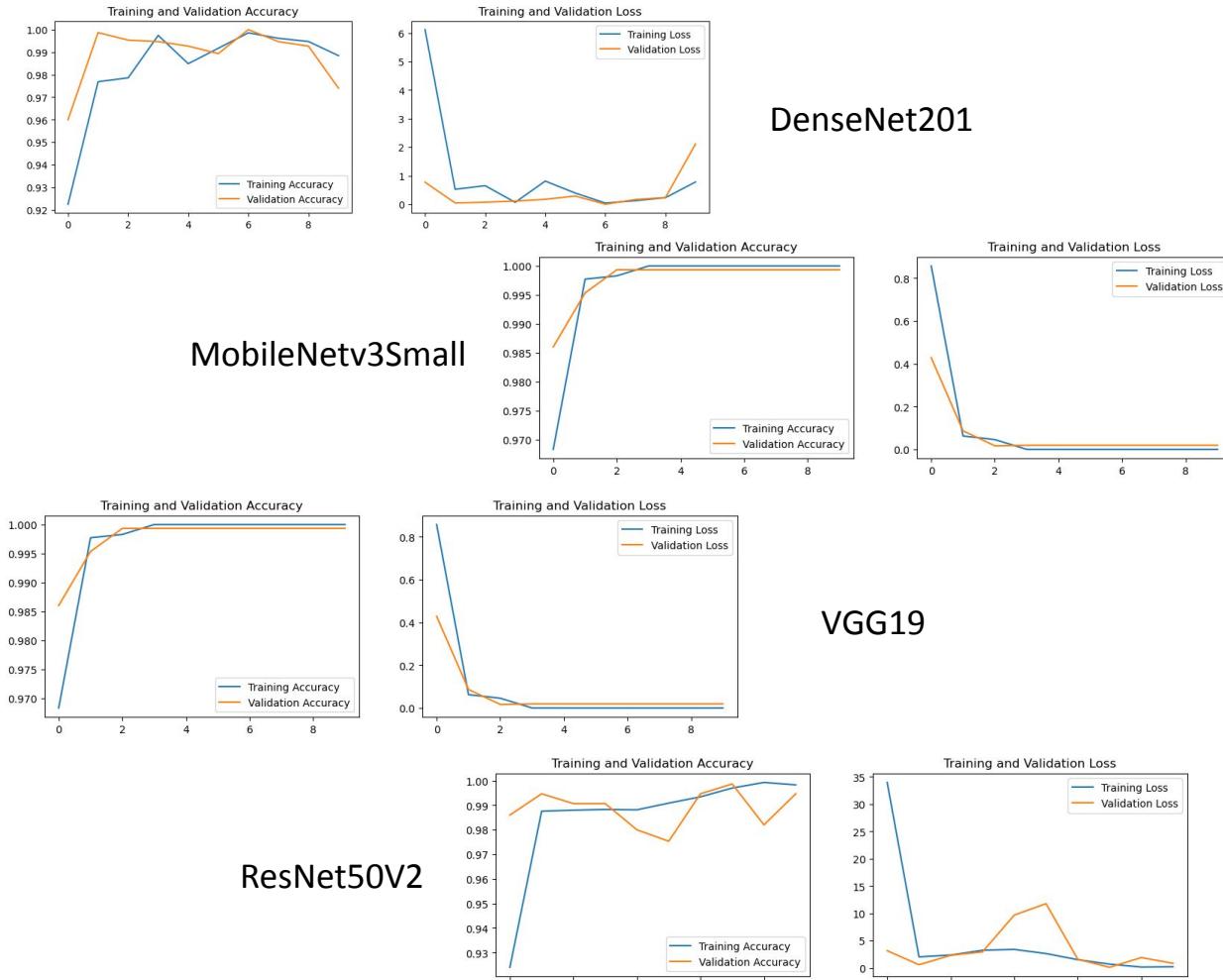
# Performance Analysis

## Kidney Cancer

Models	Recall	Precision	F1Score
DenseNet201	0.9426666666666667	0.997179125528914	0.9691569568197395
MobileNetV3Small	1.0	1.0	1.0
VGG19	1.0	1.0	1.0
ResNet50V2	0.9933333333333333	1.0	0.9966555183946488
Ensemble	1.0	1.0	1.0



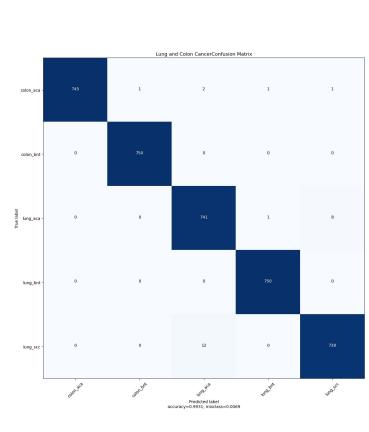
Ensemble



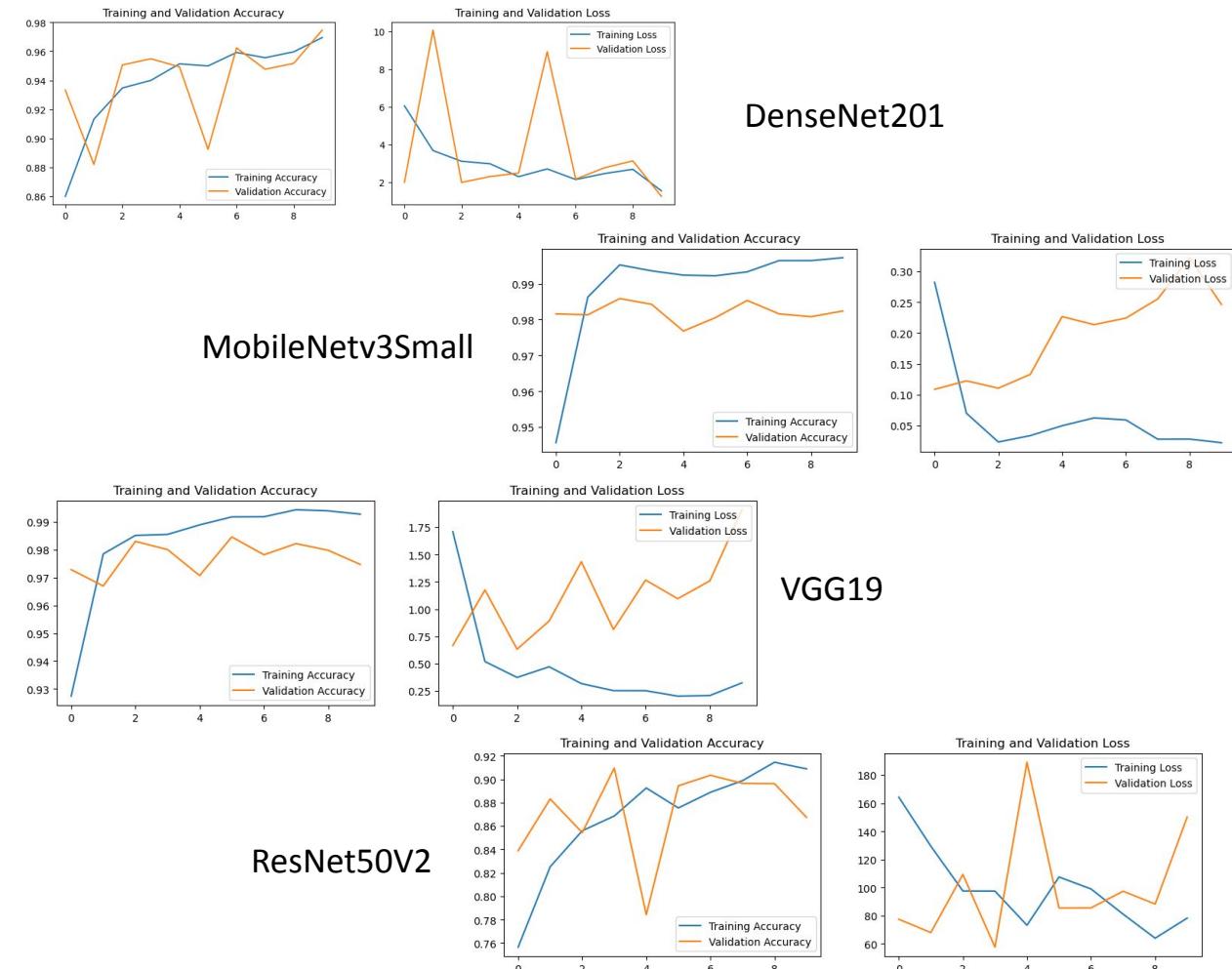
# Performance Analysis

## Lung and Colon Cancer

Models	Recall	Precision	F1Score
DenseNet201	0.9728	0.9729875598804594	0.972848129781705
MobileNetV3Small	0.9864	0.9864941910877201	0.9864197297322221
VGG19	0.9733333333333334	0.974243236543145	0.9732906860342894
ResNet50V2	0.868	0.8908159830262765	0.8611486751050
Ensemble	0.9930666666666667	0.9930835256960889	0.9930694579629511



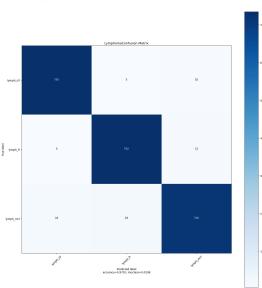
Ensemble



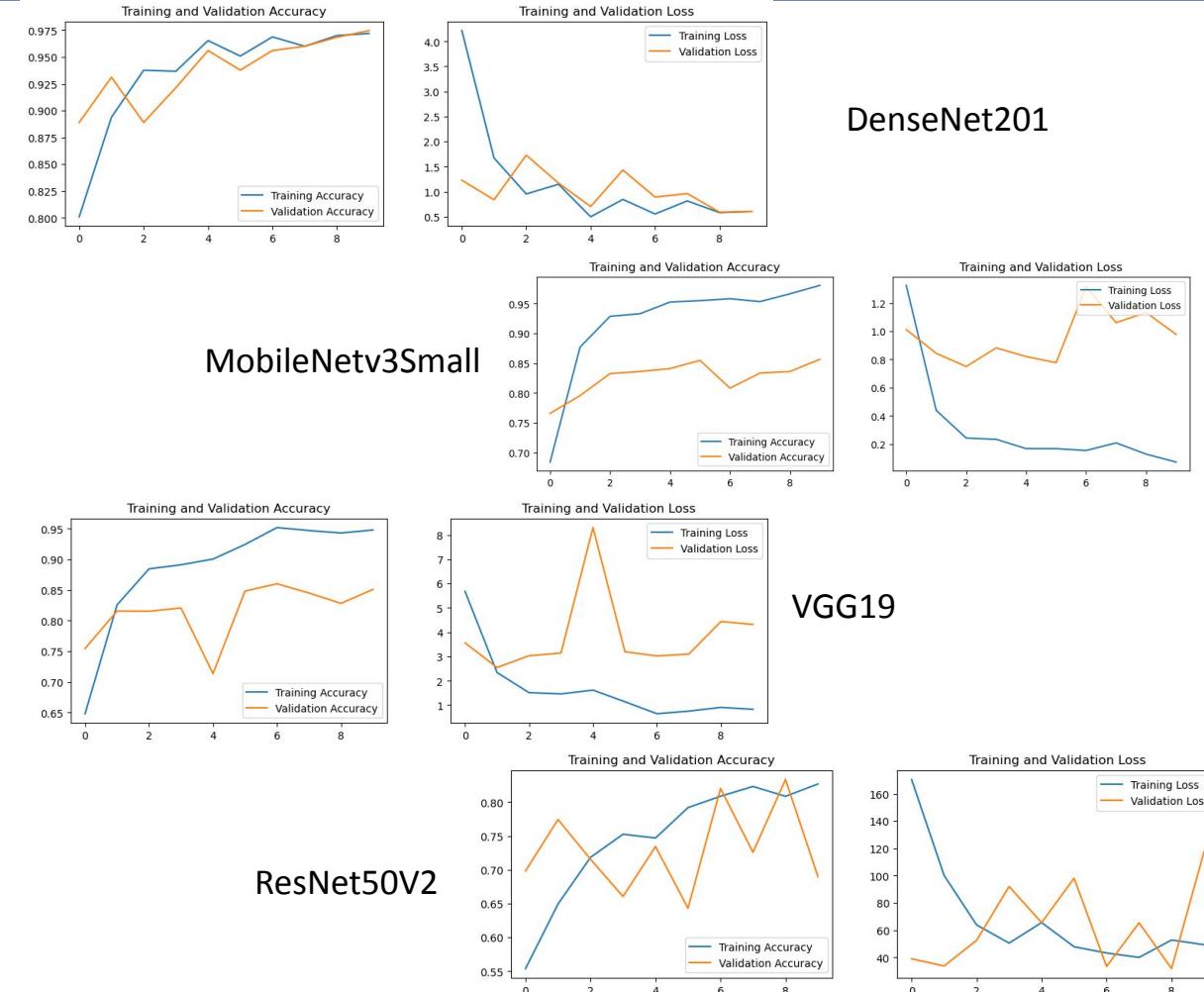
# Performance Analysis

## Lymphoma

Models	Accuracy	Recall	Precision	<u>F1Score</u>
DenseNet201	0.9688888888888889	0.9688888888888889	0.9689020280935331	0.9688874465479973
MobileNetV3Small	0.8613333333333333	0.8613333333333333	0.863749712001629	0.8618748161763887
VGG19	0.8417777777777777	0.8417777777777777	0.8426514454459834	0.8415871408756553
ResNet50V2	0.6862222222222222	0.6862222222222222	0.778109181931267	0.6394392144701045
Ensemble	0.9702222222222222	0.9702222222222222	0.9702118355619148	0.9701907890979771



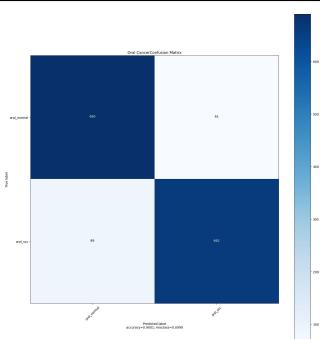
Ensemble



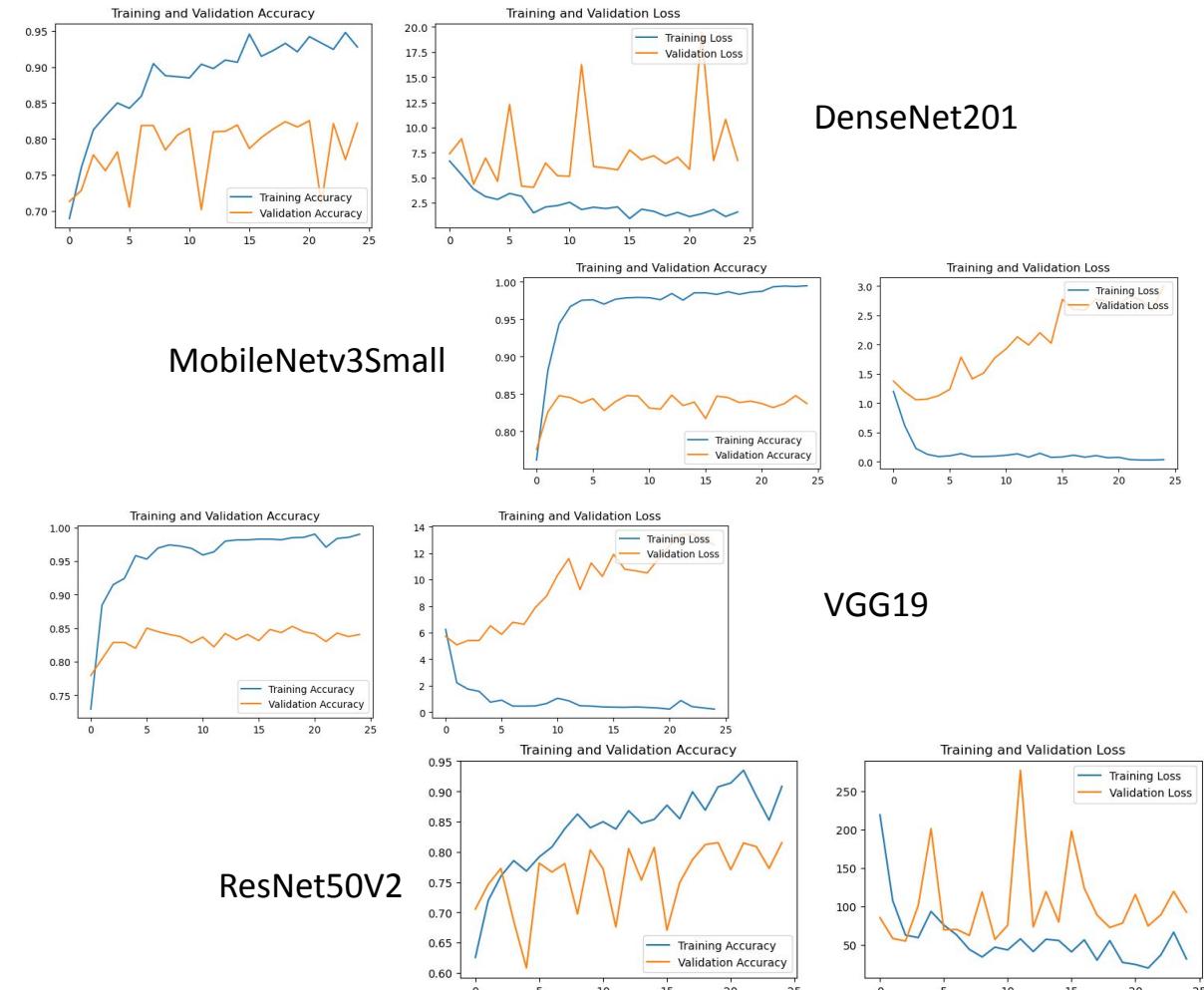
# Performance Analysis

## Oral Cancer

Models	Recall	Precision	F1Score
DenseNet201	0.8362183754993342	0.8406859442513094	0.835679673824873
MobileNetV3Small	0.8495339547270306	0.8495364337044347	0.8495336879432624
VGG19	0.8302263648468708	0.8302269503546099	0.8302262895927
ResNet50V2	0.8055925432756325	0.8071807301923951	0.8053409365280007
Ensemble	0.9001331557922769	0.9006901425205559	0.9000984382898342



Ensemble



# Conclusion and Future Work

- Managed to build 2 models and tried to ensemble it to segment brain tumors and achieved desirable results
- Ensemble-based approaches offer significant advantages in medical image classification and segmentation. They enhance the performance, robustness, and generalization capabilities of the system, enabling more accurate diagnoses and treatment decisions. Leveraging the power of ensembles can lead to improved healthcare outcomes and contribute to advancements in medical imaging technology.
- Conclusion: The detection of cancer using machine learning techniques offers several advantages that can significantly impact healthcare and improve patient outcomes. Traditional cancer diagnosis often requires extensive manual analysis and interpretation of medical images and biopsy samples, which can be time-consuming. Machine learning algorithms can automate and expedite the diagnostic process, analyzing images and data in a fraction of the time, thereby reducing waiting times for patients and enabling faster treatment initiation.

# Conclusion and Future Work

- Scope for improvement:
  - Bigger dataset
  - Cross-validation ensemble
  - Swin-UNETR Architecture
  - Better validation data sourced through key radiologists
- Future Work:
  - More and potentially better models
  - Creating bigger ensemble

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# THANK YOU