

GENERATIVE ADVERSARIAL NETWORKS IN HEALTHCARE: A CASE STUDY ON MRI IMAGE GENERATION

BEATRIZ CEPA, CLÁUDIA BRITO, ANTÓNIO SOUSA

INESC TEC & UNIVERSITY OF MINHO

MOTIVATION

- Deep Learning (DL) models present a viable option to reduce diagnostic errors. However, the publicly available medical data for model training and research are limited
- GANs have received increased interest and attention for their application in data augmentation because of their ability to synthesize new training samples
- Traditional methods become obsolete when deployed to large-scale medical data environments. The use of distributed techniques and frameworks is an alternative to address this challenge

DATA

- Brain Tumor Segmentation (BraTS) 2020 Dataset
- T2-FLAIR volumes from 15 subjects (subject ID 001 to 015) sliced by the axial plane
- From the 155 slices obtained for each subject, only 48 were selected due to their better representation of the brain and tumor structures,
- Total of 720 images

MODEL DEVELOPED

- Based on the DCGAN architecture

TABLE I
Summary of the Generator architecture*, where T. Conv is Transposed Convolution

Generator	Activation	Output shape
Input noise	—	$128 \times 1 \times 1$
Fully-connected layer	—	16384
Reshape	—	$1024 \times 4 \times 4$
T. Conv 4 × 4	Leaky ReLU	$512 \times 8 \times 8$
T. Conv 4 × 4	Leaky ReLU	$256 \times 16 \times 16$
T. Conv 4 × 4	Leaky ReLU	$128 \times 32 \times 32$
T. Conv 4 × 4	Leaky ReLU	$64 \times 64 \times 64$
T. Conv 4 × 4	Leaky ReLU	$32 \times 128 \times 128$
T. Conv 4 × 4	Leaky ReLU	$3 \times 256 \times 256$
T. Conv 3 × 3	Tanh	$3 \times 256 \times 256$

* The initial seven layers were followed by a batch normalization layer and dropout was applied for every layer

TABLE II
Summary of the Discriminator architecture**

Discriminator	Activation	Output shape
Input	—	$3 \times 256 \times 256$
Conv 4 × 4	ReLU	$32 \times 128 \times 128$
Conv 4 × 4	ReLU	$64 \times 64 \times 64$
Conv 4 × 4	ReLU	$128 \times 32 \times 32$
Conv 4 × 4	ReLU	$156 \times 16 \times 16$
Conv 3 × 3	ReLU	$156 \times 16 \times 16$
Conv 4 × 4	ReLU	$512 \times 8 \times 8$
Conv 3 × 3	ReLU	$512 \times 8 \times 8$
Conv 4 × 4	ReLU	$1024 \times 4 \times 4$
Conv 3 × 3	Sigmoid	$1024 \times 4 \times 4$
Fully-connected layer	—	1

** Each layer was followed by batch normalization (except for the input and fully-connected layers) and noise samples were added as input in every layer

TRAINING PARAMETERS

- Wasserstein loss concept and batch size of 8
- Optimization with Adam ($\alpha=0.0002$, $\beta_1=0.5$ and a Weight Decay rate of 0.001)
- Implementation using ChainerMN

RESULTS

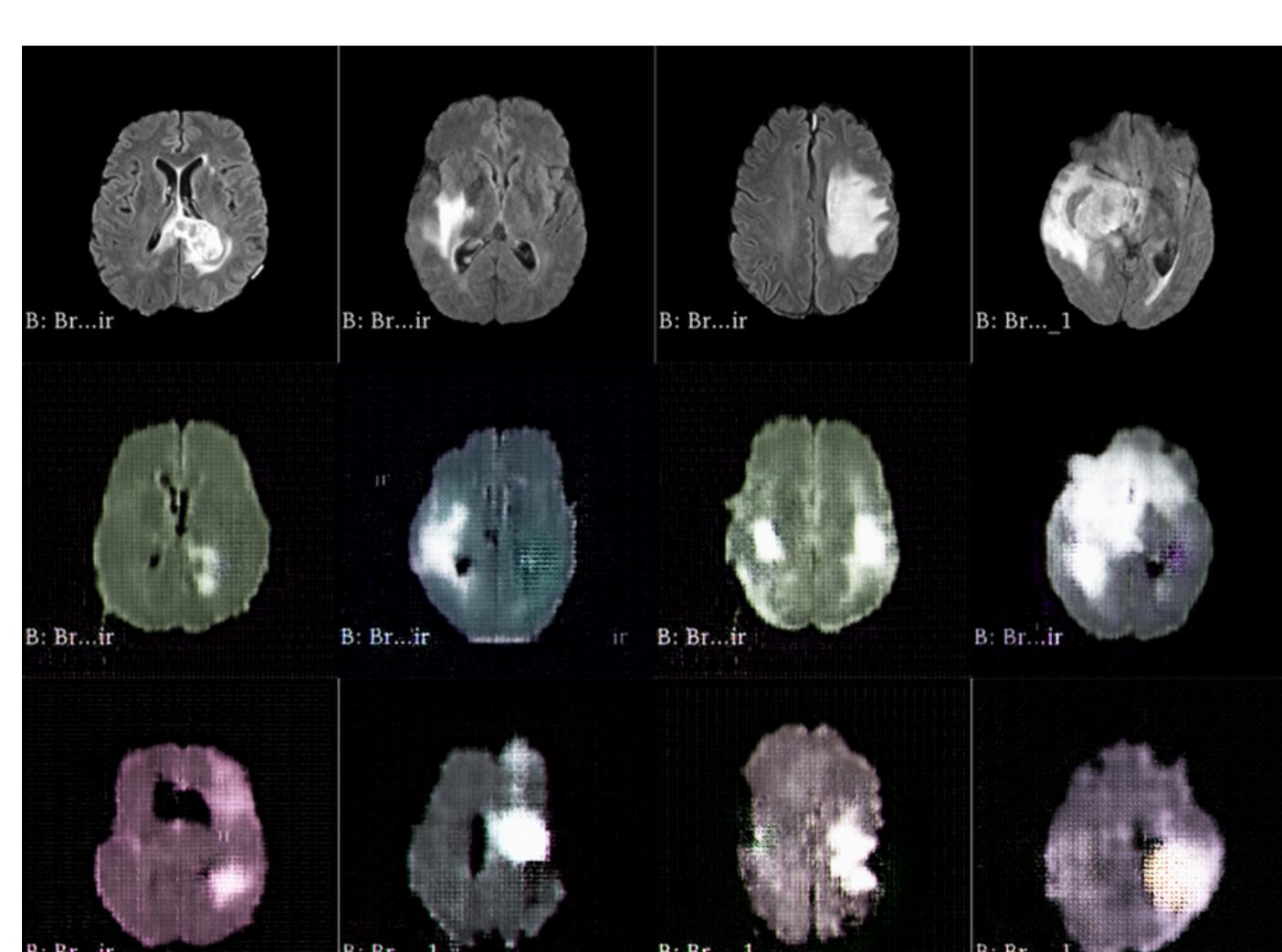


Fig. 1. Comparison between real MRI images (upper row), success cases (middle row), and failure cases (lower row)

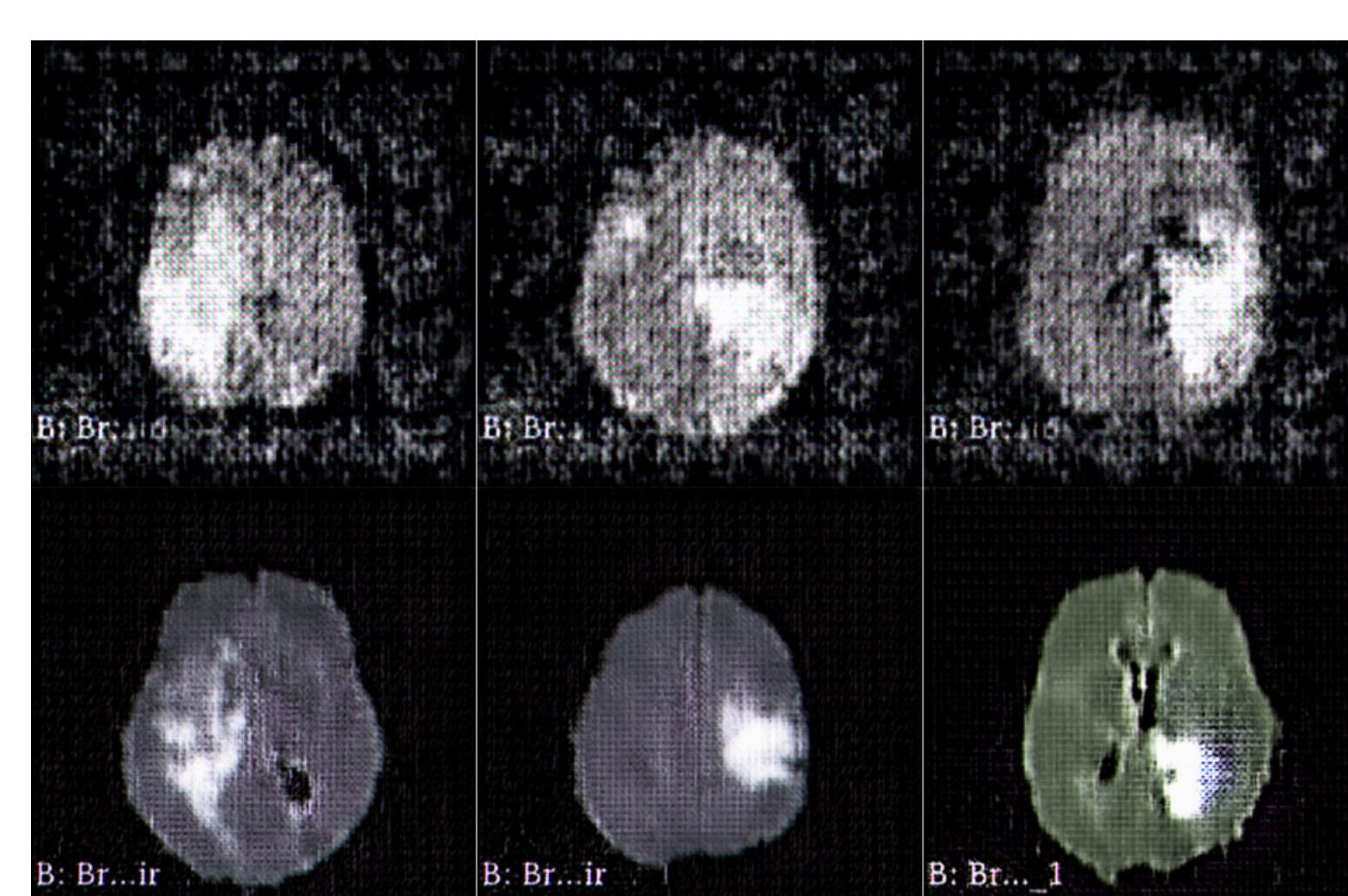


Fig. 2. Images generated in the initial (upper row) and final (lower row) experiments

- The model generates several stacks of 100 3-channel 2D images of size 256×256 pixels
- Each image provides an overall representation of the brain structure and tumoral area
- The images show considerable brain-tumor separation
- Results allow clear recognition of the represented structures and include images representing different axial views of the brain and tumors located in various areas

FUTURE WORK

- The grid effect on the images should be minimized. This can be achieved by changing the transposed convolutions so the kernel size is divisible by the stride or by using a different upsampling strategy
- It is important to obtain high-definition images with more visible details and clearer borders between the brain and the tumoral tissue
- This work should accompany clinical validation of the results and experimental validation in fully-distributed environments and with real-world scenarios

GENERATIVE ADVERSARIAL NETWORKS IN HEALTHCARE: A CASE STUDY ON MRI IMAGE GENERATION

BEATRIZ CEPA, CLÁUDIA BRITO, ANTÓNIO SOUSA

INESC TEC & UNIVERSITY OF MINHO

MOTIVATION

- Deep Learning (DL) models present a viable option to reduce diagnostic errors. However, the publicly available medical data for model training and research are limited.
- GANs have received increased interest and attention for their application in data augmentation because of their ability to synthesize new training samples.
- Traditional methods become obsolete when deployed to large-scale medical data environments. The use of distributed techniques and frameworks is an alternative to address this challenge.

DATA

- Brain Tumor Segmentation (BraTS) 2020 Dataset [1 - 3].
- T2-FLAIR volumes from 15 subjects (subject ID 001 to 015) sliced by the axial plane.
- From the 155 slices obtained for each subject, only 48 were selected due to their better representation of the brain and tumor structures.
- Total of 720 images.

PARAMETERS

- Wasserstein loss [4] concept and batch size of 8.
- Optimization with Adam [5] ($\alpha=0.0002$, $\beta_1=0.5$ and a Weight Decay rate of 0.001).
- Implementation using ChainerMN [6].

RESULTS

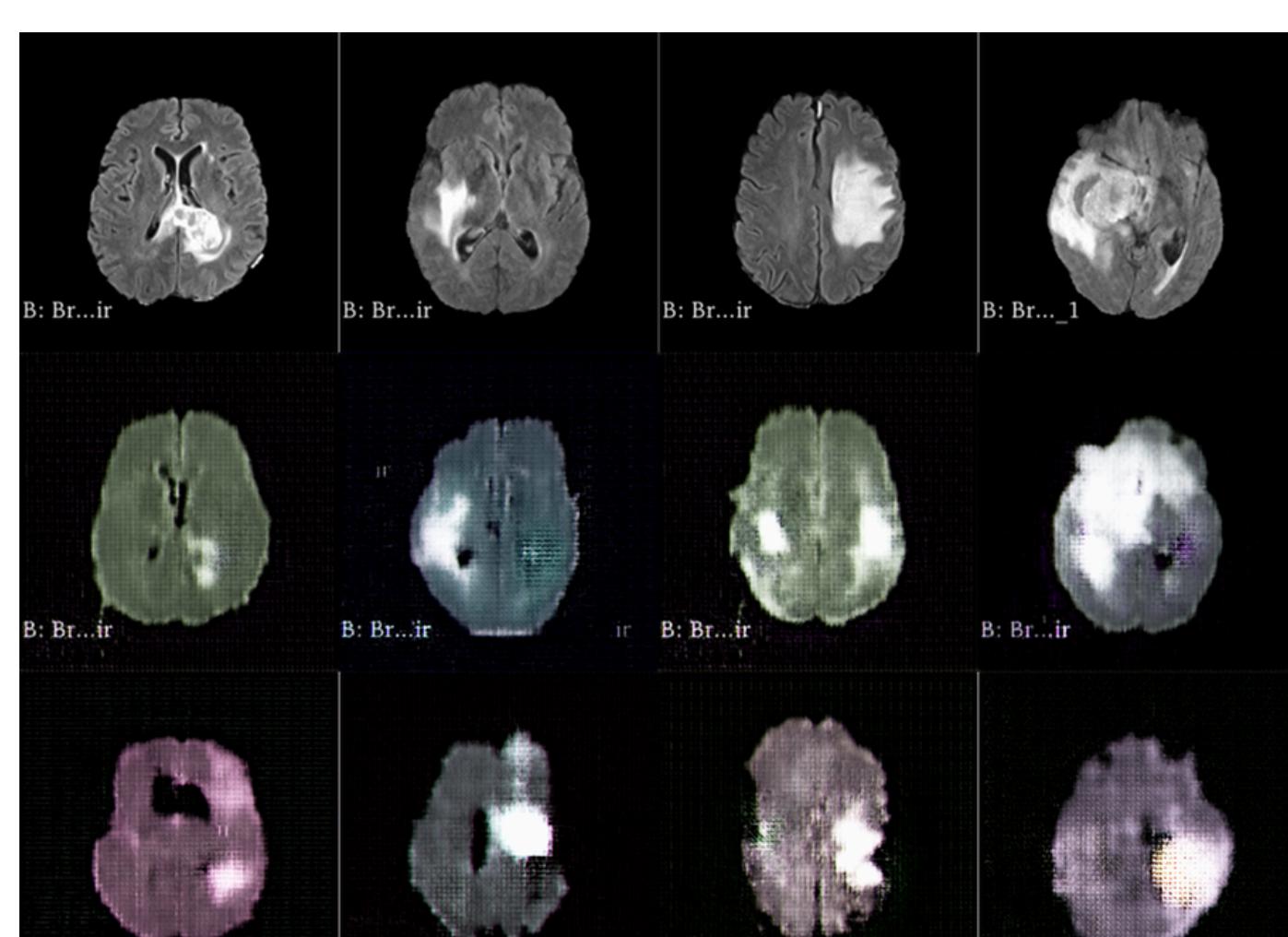


Fig. 1. Comparison between real MRI images (upper row), success cases (middle row), and failure cases (lower row)

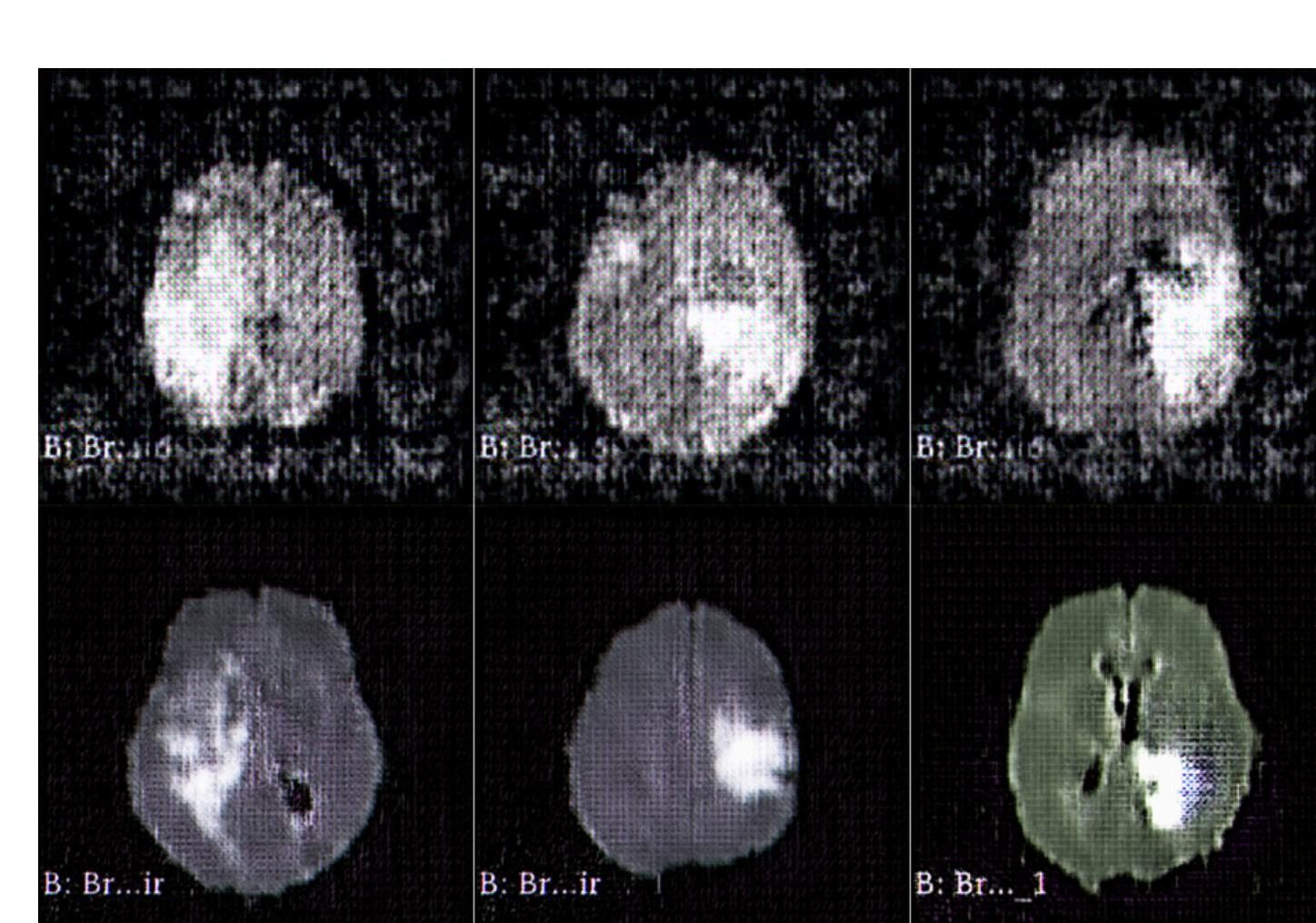


Fig. 2. Images generated in the initial (upper row) and final (lower row) experiments

- The model generates several stacks of 100 3-channel 2D images of size 256×256 pixels.
- Each image provides an overall representation of the brain structure and tumoral area.
- The images show considerable brain-tumor separation.
- Results allow clear recognition of the represented structures and include images representing different axial views of the brain and tumors located in various areas.

MODEL ARCHITECTURE

- Based on the DCGAN architecture [7].

TABLE I
Summary of the Generator architecture*, where T. Conv is Transposed Convolution

Generator	Activation	Output shape
Input noise	—	$128 \times 1 \times 1$
Fully-connected layer	—	16384
Reshape	—	$1024 \times 4 \times 4$
T. Conv 4×4	Leaky ReLU	$512 \times 8 \times 8$
T. Conv 4×4	Leaky ReLU	$256 \times 16 \times 16$
T. Conv 4×4	Leaky ReLU	$128 \times 32 \times 32$
T. Conv 4×4	Leaky ReLU	$64 \times 64 \times 64$
T. Conv 4×4	Leaky ReLU	$32 \times 128 \times 128$
T. Conv 4×4	Leaky ReLU	$3 \times 256 \times 256$
T. Conv 3×3	Tanh	$3 \times 256 \times 256$

* The initial seven layers were followed by a batch normalization layer and dropout was applied for every layer

TABLE II
Summary of the Discriminator architecture**

Discriminator	Activation	Output shape
Input	—	$3 \times 256 \times 256$
Conv 4×4	ReLU	$32 \times 128 \times 128$
Conv 4×4	ReLU	$64 \times 64 \times 64$
Conv 4×4	ReLU	$128 \times 32 \times 32$
Conv 4×4	ReLU	$156 \times 16 \times 16$
Conv 3×3	ReLU	$156 \times 16 \times 16$
Conv 4×4	ReLU	$512 \times 8 \times 8$
Conv 3×3	ReLU	$512 \times 8 \times 8$
Conv 4×4	ReLU	$1024 \times 4 \times 4$
Conv 3×3	Sigmoid	$1024 \times 4 \times 4$
Fully-connected layer	—	1

** Each layer was followed by batch normalization (except for the input and fully-connected layers) and noise samples were added as input in every layer

FUTURE WORK

- The grid effect on the images should be minimized. This can be achieved by changing the transposed convolutions so the kernel size is divisible by the stride or by using a different upsampling strategy.
- It is important to obtain high-definition images with more visible details and clearer borders between the brain and the tumoral tissue.
- This work should accompany clinical validation of the results and experimental validation in fully-distributed environments and with real-world scenarios.

REFERENCES

- [1] B. H. Menze et al., "The multimodal brain tumor image segmentation benchmark (BRATS)", *IEEE Trans. Med. Imaging*, vol. 34, no. 10, pp.1993–2024, Oct. 2015.
- [2] S. Bakas et al., "Advancing the Cancer Genome Atlas glioma MRI collections with expert segmentation labels and radiomic features", *Sci. Data*, vol. 4, Sep. 2017.
- [3] S. Bakas et al., "Identifying the best machine learning algorithms for brain tumor segmentation, progression assessment, and overall survival prediction in the BRATS challenge", Nov. 2018.
- [4] M. Arjovsky, S. Chintala, and L. Bottou, "Wasserstein generative adversarial networks", in *Proceedings of the 34th International Conference on Machine Learning*, Aug. 2017, pp. 214–223.
- [5] D. P. Kingma and J. Ba, "Adam: a method for stochastic optimization", Dec. 2014.
- [6] Preferred Networks, "Distributed Deep Learning with ChainerMN", 2015, [Online]. Available: <https://docs.chainer.org/en/stable/chainermn/index.html>.
- [7] A. Radford, L. Metz, and S. Chintala, "Unsupervised representation learning with deep convolutional generative adversarial networks", Jan. 2016.