Fahad Khalid

Bias correction using Deep learning

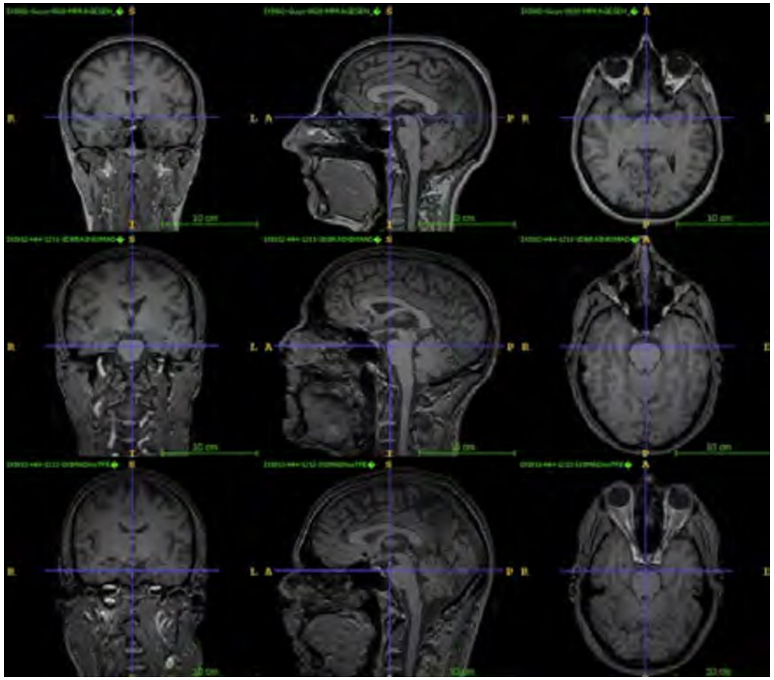
From Maia thesis journal

Outline of the experimentation

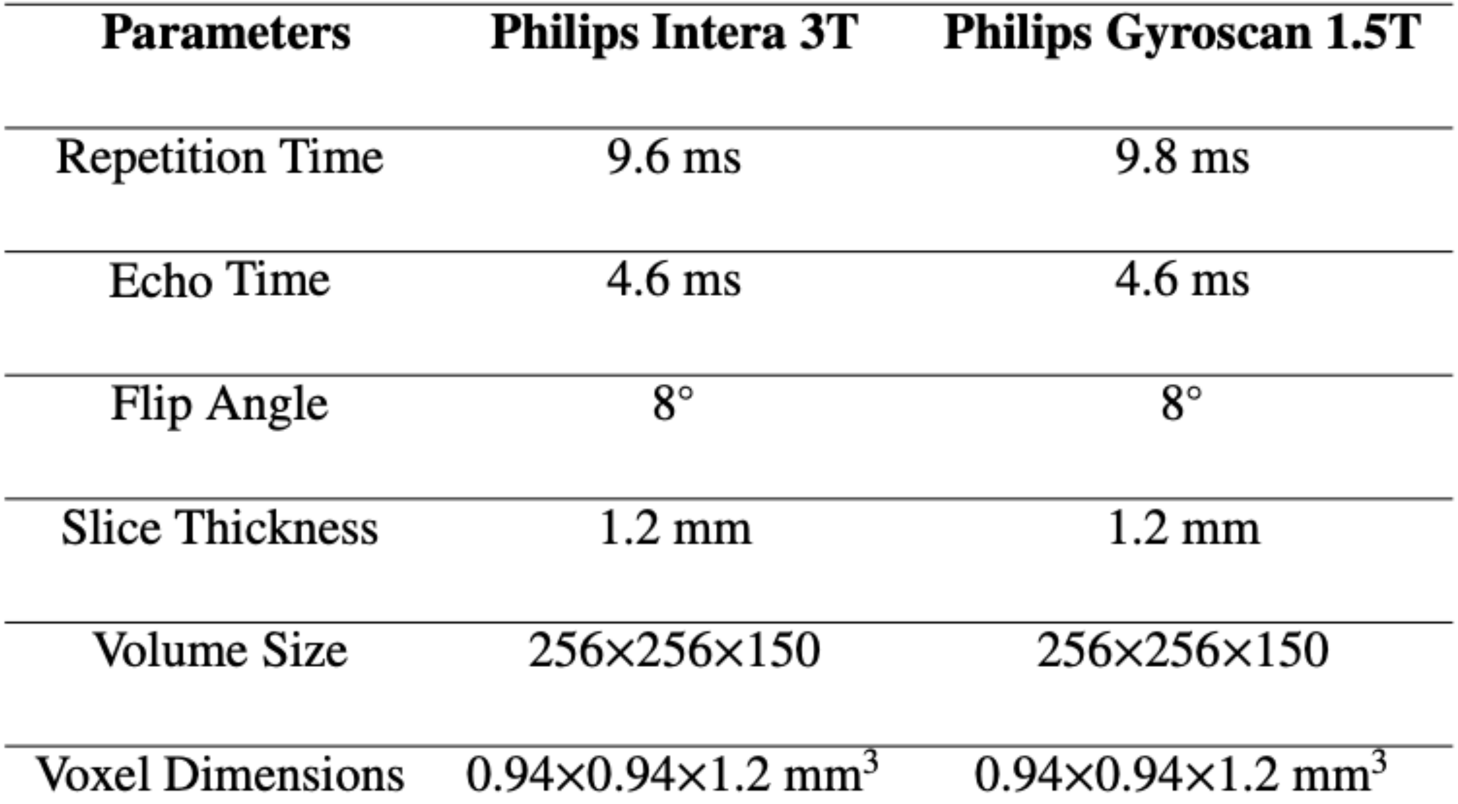
- Inhomogeneity correction.
- Bias signal.
- In this project inhomogeneity correction using deep learning.
- The author compared two different approaches: supervised and unsupervised.
- The goal of this work was to implement a new method to automatically correct the bias field using convolution neural networks (CNN).
- Best results were obtained for the supervised approach.
- Finally, The proposed supervised approach efficiently outperformed related state-of-the-art methods in terms of accuracy, robustness and efficiency.

The Dataset

- The dataset used consists of 580 MRI images from healthy subjects with different sex and ages. Publicly available (IXI dataset).
- The scans were acquired using 2 different scanners; Phillips Intera 3T and Phillips Gyroscan 1.5T. Collected at three different hospitals in the London (UK).



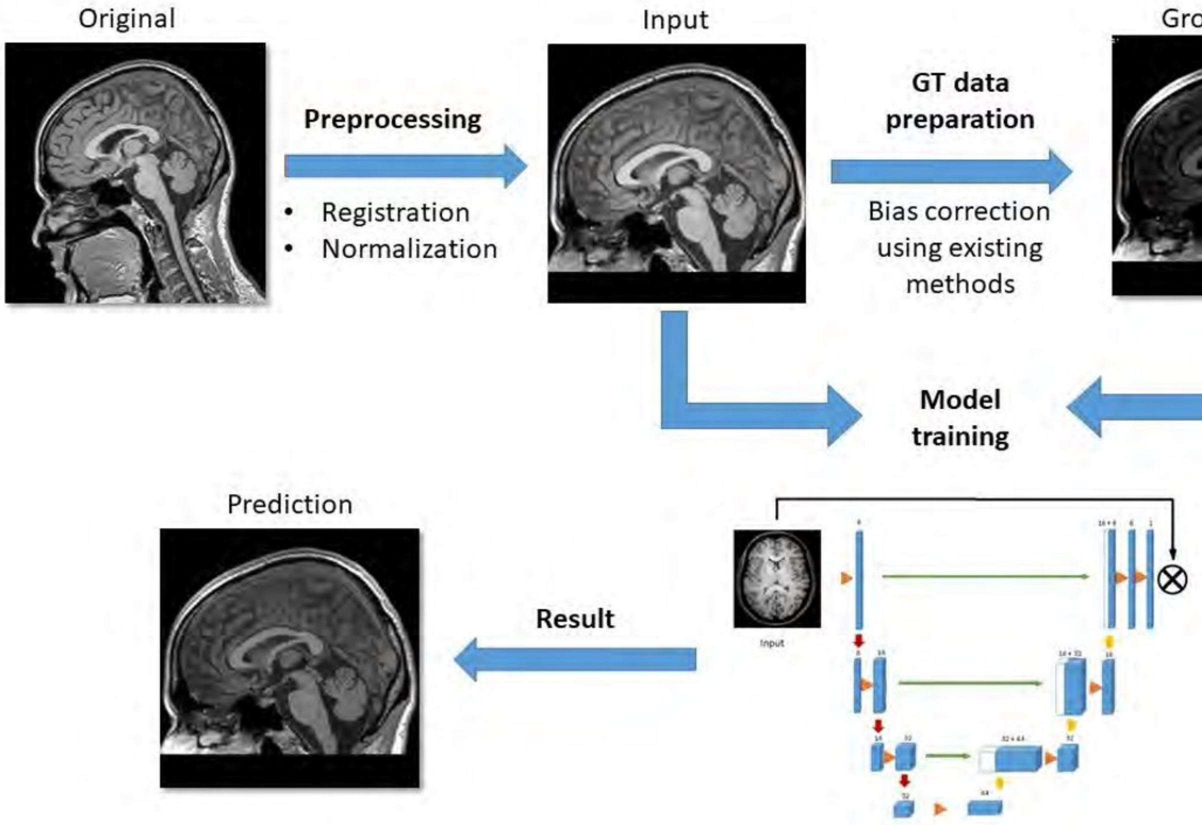
Scanner details



Parameters	Philips Intera 3T	Philips Gyroscan 1.5T
Repetition Time	9.6 ms	9.8 ms
Echo Time	4.6 ms	4.6 ms
Flip Angle	8°	8°
Slice Thickness	1.2 mm	1.2 mm
Volume Size	256×256×150	256×256×150
Voxel Dimensions	$0.94 \times 0.94 \times 1.2$ mm^3	$0.94 \times 0.94 \times 1.2$ mm^3

Preprocessing

- Affine registering the original images to the standard Montreal Neurological Institute (MNI152) space using the ANTS (Avants et al., 2008) software.
- The standard image in the MNI space has a fixed resolution of 1 mm3 and dimensions of 181×217×181 voxels. By fixing the orientation and resolution of the images will require less training data because the issue of dealing with different orientations and resolutions will be removed.
- Normalization using mean normalization and the other approach is the classical Z-scoring.



Original

Preprocessing

- Registration
- Normalization

Input

GT data preparation

Bias correction using existing methods

Ground truth

Model training

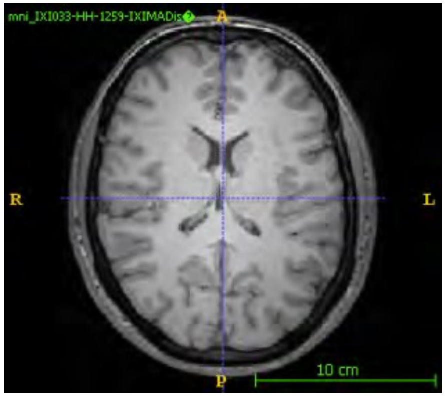
Prediction

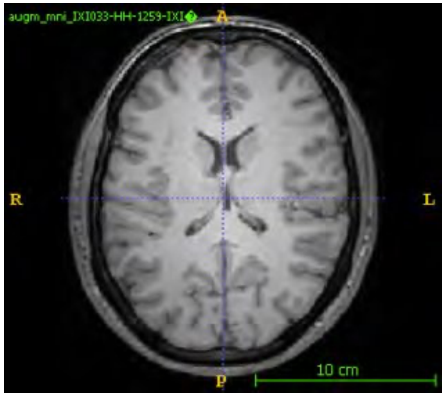
Result

Graphical representation of the general pipeline of the proposed supervised approach for MRI intensity inhomogeneity correction.

Data Augmentation

- Augmentation is done by left-right flipping the input and output images randomly taking benefit from the pseudo-symmetry of the human brain.



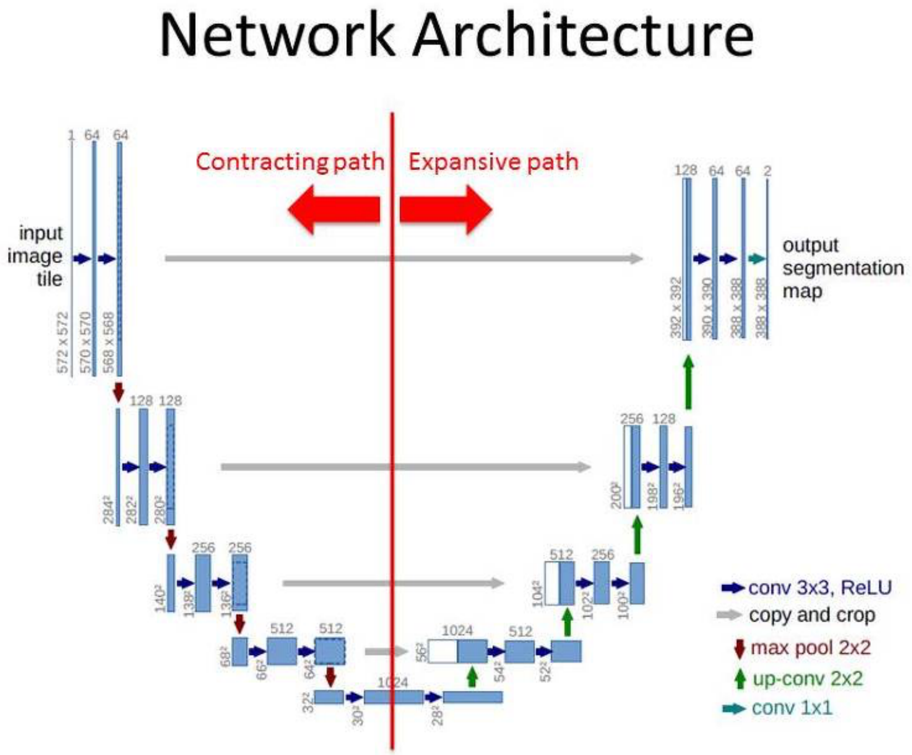


Training

- All the Images were bias corrected using SPM12 tool (Friston et al., 2011).
- The author chose SPM12 method based on the results of the comparison (Figure 4) of three different bias correction methods (SPM12, N4 and CFBC).
- To measure the homogeneity of the different brain tissues, they used the tissue segmentations provided by SPM12 (white matter, gray matter, cerebrospinal fluid).

Unet Architecture

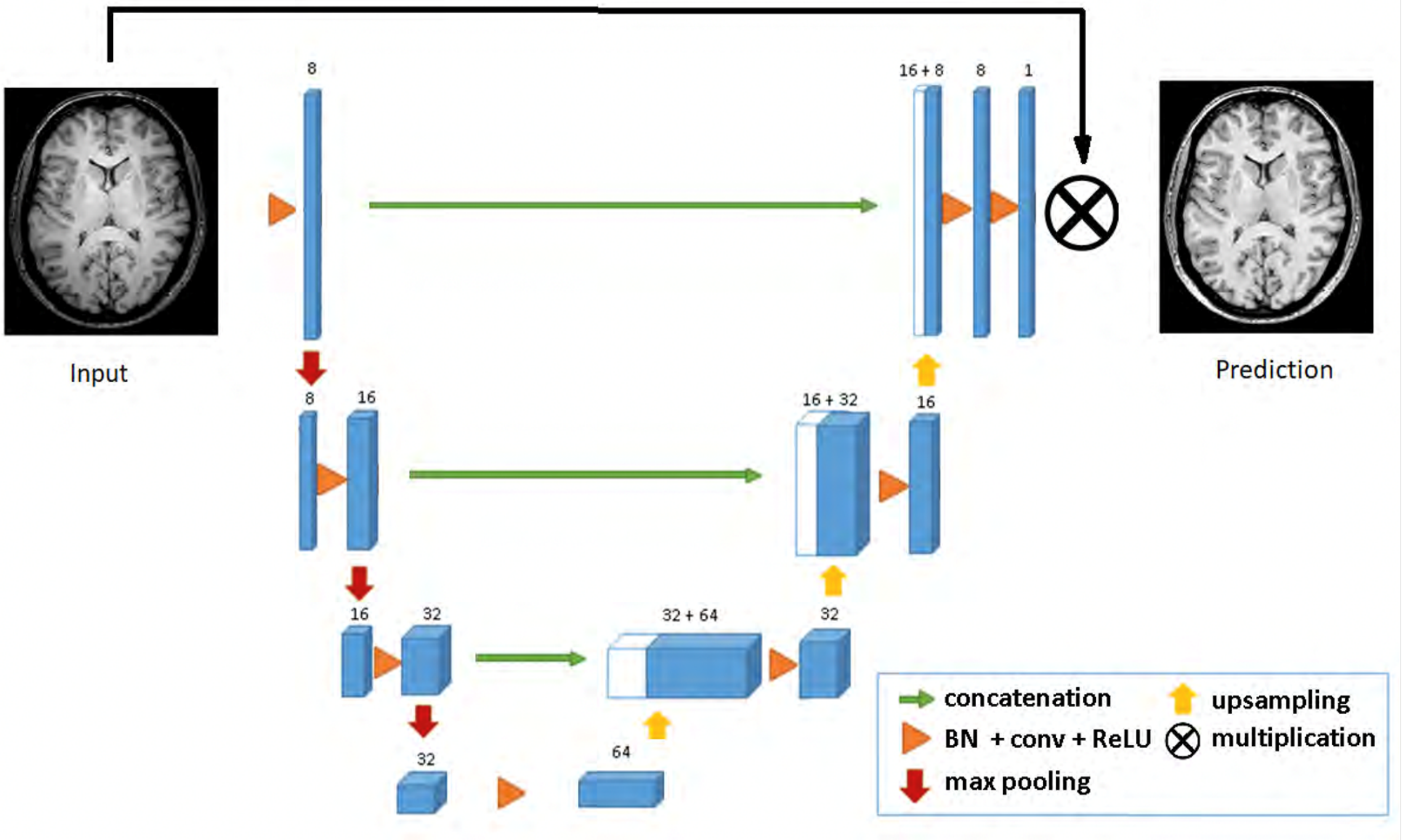
- Convolutional neural network, autoencoder with resolution dependent shortcuts.
- Four main parts; encoder, bottleneck, decoder and shortcuts.



UNET Model 1

- The encoding part of the model is composed of three blocks. Each block is made of a 3D convolution layer (7×7×7) with ReLU activation function.
- The batch normalization followed by the max- pooling layer.
- The number of filters in the first resolution level are 8, 16 and 32 in the following levels.
- The bottleneck is composed of a 3D convolution layer with the ReLU activation, 64 filters and the batch normalization.
- An important thing to highlight in Model 1 is that to generate bias-free volume in the last layer was multiplied by the inverse of the bias field with the original input volume.
- Thus the network predicts the inverse bias field and multiplies it to the input volume to generate the bias free output.

Model 1 illustration



UNET Modification 2

- The only change compared to Model 1 is that its output is modified to have a feature encoding branch that measures feature differences between the predicted image and the target image.
- This is accomplished using a loss function that not only measures the reconstruction error of the predicted image but also its feature error through the use of a multiscale encoder with shared weights. The Model 2 has 33 layers and 2,769,497 trainable parameters.
- Adaptive smoothing layer. Since the proposed network tries to predict a low-frequency bias field, we thought that blurring the input volume will help in the estimation.

Adaptive smoothing layer

- An adaptive smoothing layer is added as the network tries to predict a low-frequency bias field, the authors thought that blurring the input volume will help in the estimation.
- The layer performs gaussian smoothing and is hoped to increase the signal to noise ratio. (Theory of matched filter)
- Maximize the coefficient hence detecting a strong bias signal.

Loss function

- Mean Absolute Error (MAE); The MAE is calculated by taking the average of the absolute difference between the ground truth value and the model prediction. Compared to the Mean Squared Error loss MAE encourages less blurry and higher quality images (Thomas, 2020).
- Custom loss.

Unsupervised Approach

- The model is trained without the ground truth labels.
- The model is forced to learn connections inside the image and make assumptions based on them.

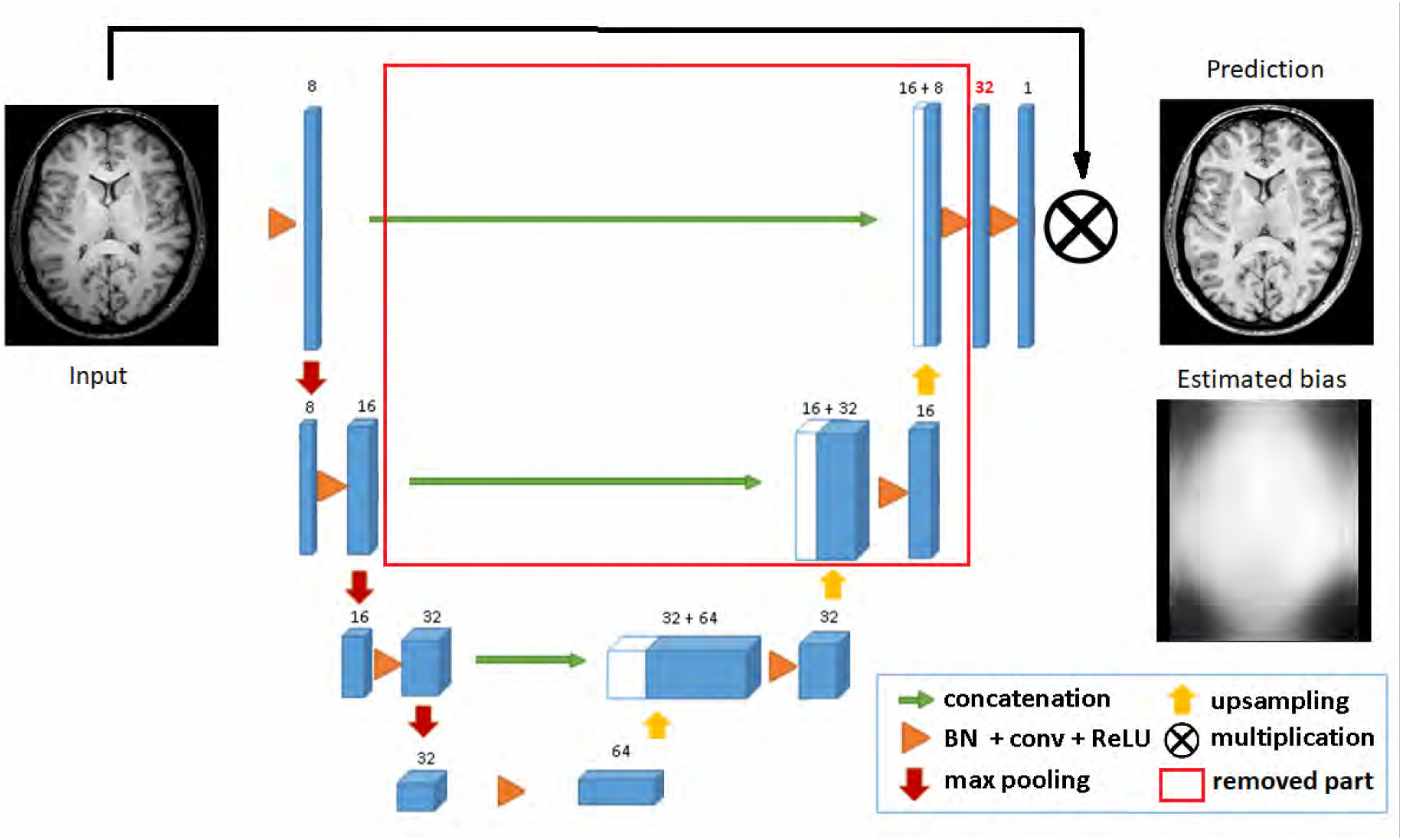
Unsupervised approach (Model 3)

- The architecture used in the unsupervised approach has the same structure as Model 1 but with two outputs instead of one, the inhomogeneity corrected volume and the estimated inverse bias field.
- The input of the model is the original raw volume registered to the MNI space.
- The output of the model is not known in this case. Therefore, we used loss metrics that are related to enforce the image homogeneity.
- The last layer multiplies the estimation of the inverse of the bias field with the input image to generate a bias-corrected volume.
- As a result, we receive the approximation of the bias field and the bias-corrected volume.

Unsupervised approach (R-Model *3)*

- Reduce version of Model-3.
- Two resolution levels were jumped over from the decoder path and directly up sampled the image from the lower resolution to the spatial resolution of the original input image.
- Therefore, the model architecture be- came an asymmetrical encoder-decoder with simplified decoder part.

R-Model 3 illustration



Loss function

$$L_{total} = \lambda_1 L_{image} + \lambda_2 L_{bias}$$

- L image is a custom loss function that is applied to the bias corrected image prediction.
- L bias is another custom loss function that measures the properties of the estimated bias field of the image.
- $\lambda 1$ and $\lambda 2$ are corresponding loss weights.
- The function used to measure the homogeneity of the image

$$L_{image} = (1 - NCC) * \mu(G_{image})$$

Loss functions

- Where *NCC* is the Normalized Cross Correlation and μ(*Gimage*) is the mean gradient of the image.
- NCC is commonly used in the evaluation of the similarity between two images.
- *Gradient loss (Gimage and Gbias)*. Homogeneous images show well-ordered intensities and well clustered low gradient values in homogenous regions

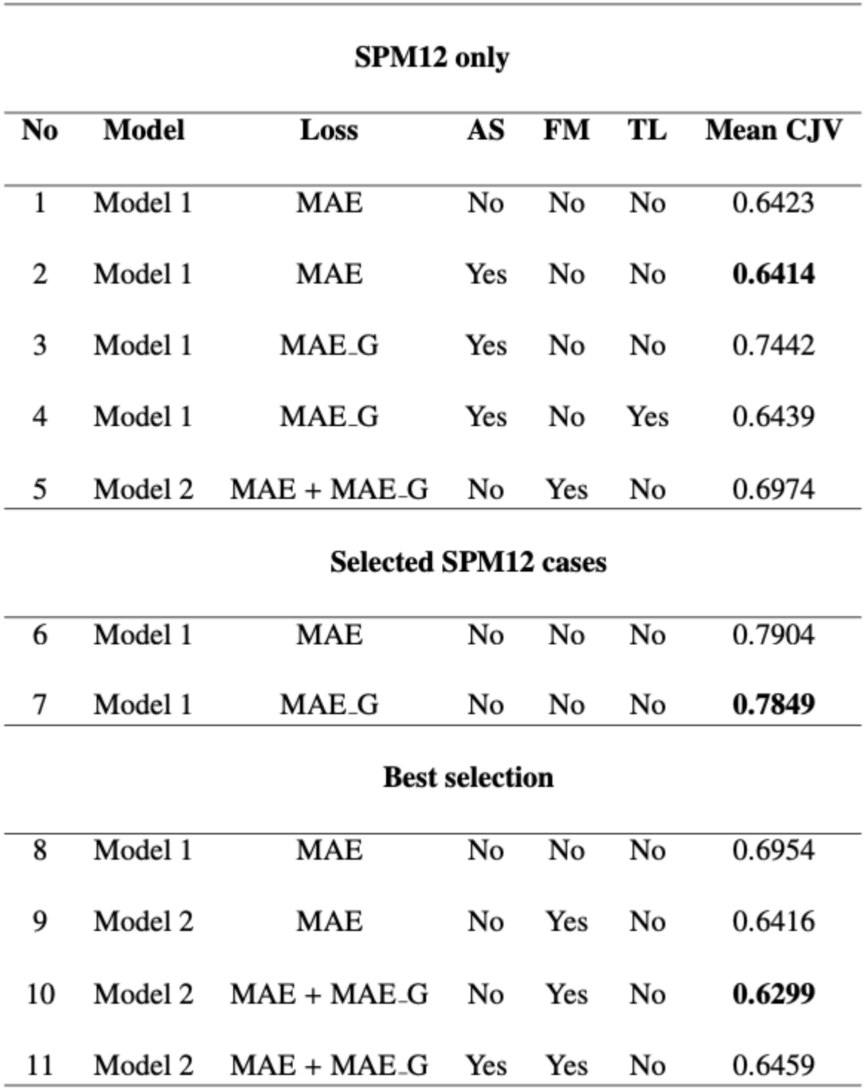
Processor and Environment

- The data processing and all experiments were carried out at IBIME lab at the Polytechnic University of Valencia using a desktop PC with an AMD Ryzen 7 processor with 16 GB RAM running Windows 10. The model was implemented using the Keras 2.3.1 (Chollet, 2015) deep learning library on top of the Tensorflow 1.15 (Abadi et al., 2016) in Python 3.6.

Training Images

- SPM12 only; 550 images were used for training and 10 for validation.
- *Selected SPM12 cases; CJV value was threshold to select only the best corrected. 303 MRI images were chosen. 10 for validation.*
- *Best selection; best bias corrected images were selected from the 3 different correction approaches* (SPM12, ANTS, and CFBC).
  - In this case, 550 images were used for training and 10 for validation.

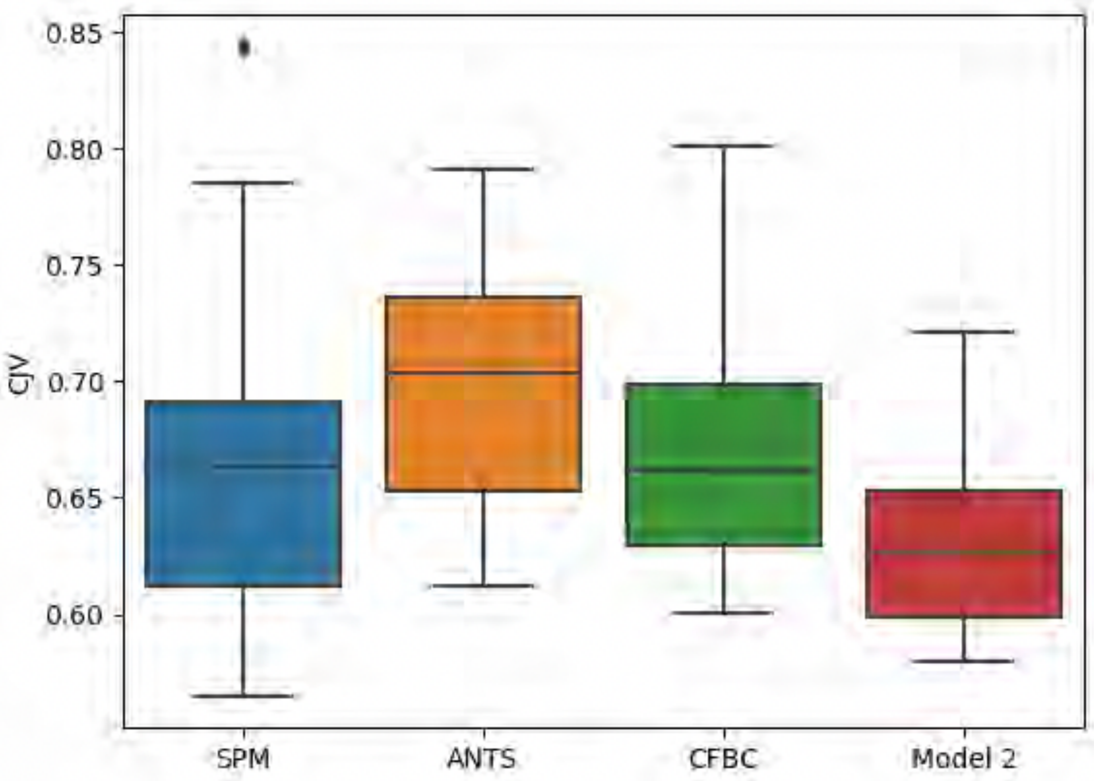
Results



SPM12 only

No	Model	Loss	AS	FM	TL	Mean CJV
1	Model 1	MAE	No	No	No	0.6423
2	Model 1	MAE	Yes	No	No	**0.6414**
3	Model 1	MAE_G	Yes	No	No	0.7442
4	Model 1	MAE_G	Yes	No	Yes	0.6439
5	Model 2	MAE + MAE_G	No	Yes	No	0.6974
Selected SPM12 cases						
6	Model 1	MAE	No	No	No	0.7904
7	Model 1	MAE_G	No	No	No	**0.7849**
Best selection						
8	Model 1	MAE	No	No	No	0.6954
9	Model 2	MAE	No	Yes	No	0.6416
10	Model 2	MAE + MAE_G	No	Yes	No	**0.6299**
11	Model 2	MAE + MAE_G	Yes	Yes	No	0.6459

Comparison of the best obtained result with state-of-the-art



Mean CJV values for the test dataset corrected by three different bias correction methods and by proposed Model 2. The pro- posed network was trained on 580 images (filtered by an ensemble of methods) for 300 epochs.

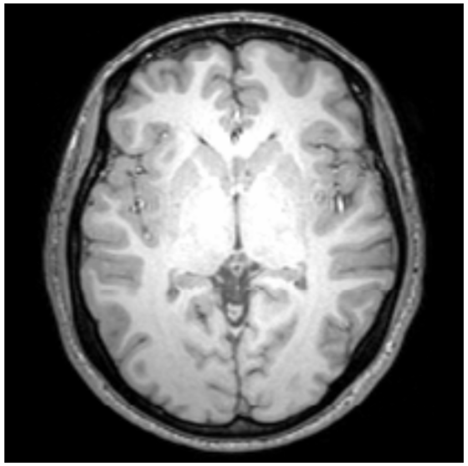
Results

Example of the bias correction.

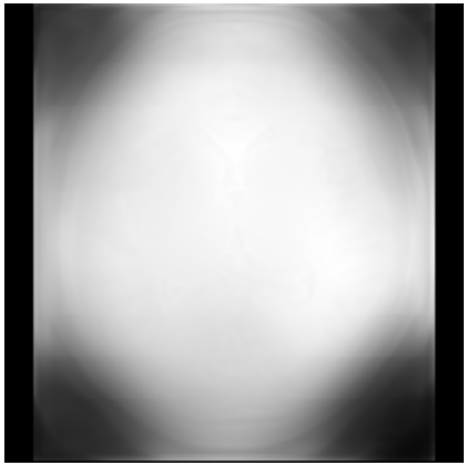
(a) original not corrected data.
(b) estimated bias field.

(c) corrected brain MRI volume.

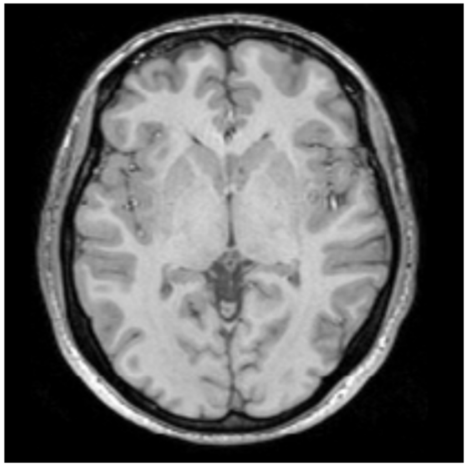
(d) intensity distributions histogram of the original and corrected volume.



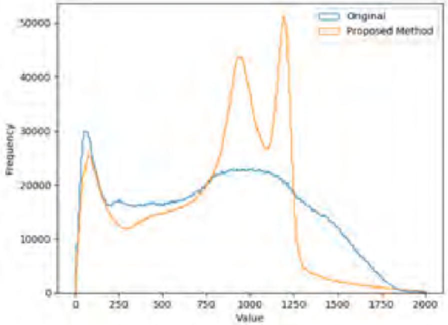
(a) Original brain MRI



(b) Bias field

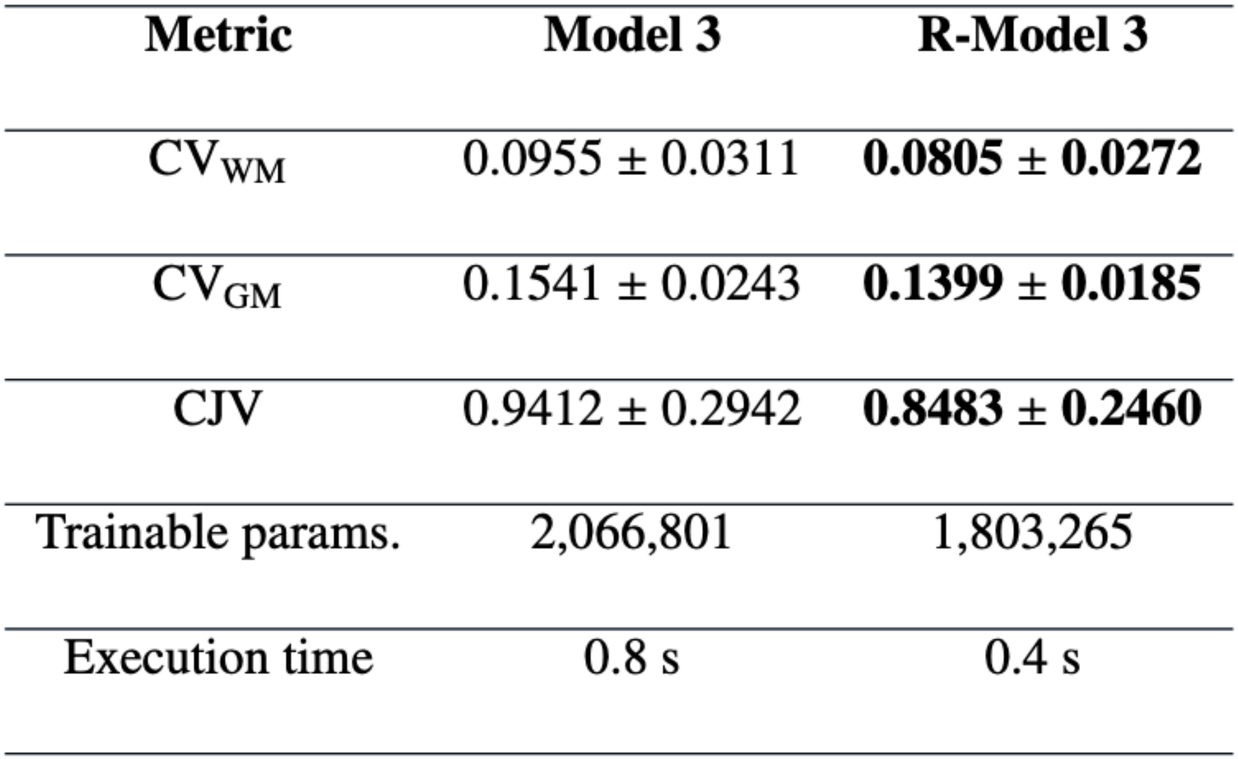


(c) Corrected brain MRI



(d) Intensity distributions

Unsupervised results



Metric	**Model 3**	**R-Model 3**
CV_{WM}	0.0955 ± 0.0311	**0.0805 ± 0.0272**
CV_{GM}	0.1541 ± 0.0243	**0.1399 ± 0.0185**
CJV	0.9412 ± 0.2942	**0.8483 ± 0.2460**
Trainable params.	2,066,801	1,803,265
Execution time	0.8 s	0.4 s

Test results from proposed models. Lower coefficients indicate better correction.

Merci

Supplimentary

Coefficient of joint variation (cjv)

- It is generally accepted that the spatial intensity distribution in the MRI volume is piece-wise constant and that each tissue type is represented by similar intensities corresponding to a unique grayscale level.

- A valid intensity inhomogeneity correction method should decrease the standard deviation in intensity for each tissue (Belaroussi et al., 2006)
- Coefficient of variation is the ratio of std to the mean.
- It is used for measuring the homogeneity of the WM and GM of the brain.
- A modification of the CV value is the Coefficient of Joint Variation (CJV), which also measures the overlap between tissue distributions.

Why SPM12 (Friston et al, 2011)

- We chose SPM12 method based on the results of the comparison (Figure 4) of three different bias correction methods (SPM12, N4 and CFBC).
- Comparison of three existing bias-correction methods on the basis of the mean coefficient of joint variation (CJV) value computed for the IXI dataset. The smaller box the less dispersed the CJV values.
- To measure the homogeneity of the different brain tissues, we used the tissue segmentations provided by SPM12 (white matter, gray matter, cerebrospinal fluid).