

## Pre-processing Report

In folder [/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases\\_project/preprocessed\\_CAP\\_final/](/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases_project/preprocessed_CAP_final/) there are three files for each patient:

- **img\_reg\_cropped.nii.gz**: image after resizing to 350 x 350 x 350 pixels, resampling to 0.6 x 0.6 x 0.6 mm, bias corrected, intensity normalized between 0-1, and registered.
- **img\_reg\_cropped\_stripped.nii.gz**: image after resizing to 350 x 350 x 350 pixels, resampling to 0.6 x 0.6 x 0.6 mm, bias corrected, intensity normalized between 0-1, registered and skull stripped.
- **mask\_reg\_cropped.nii.gz**: mask after resizing to 350 x 350 x 350 pixels, resampling to 0.6 x 0.6 x 0.6 mm, and registered.

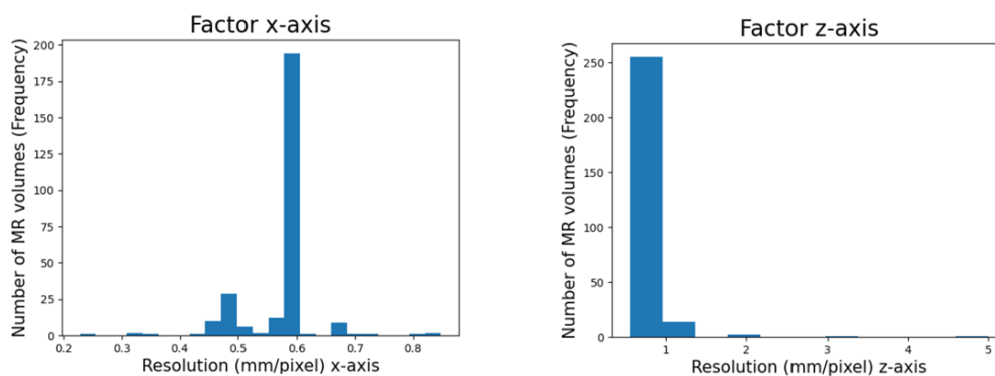
## Pre-processing pipeline

### Step 1. Resampling

The dataset consists of 273 patient volumes with different dimensions and different voxel sizes. The original images are saved in the folder below under the name image.nii.gz (or image.nii):

[/usr/bmicnas01/data-biwi-01/bmicdatasets originals/Originals/USZ/metastases\\_segmentation/Processed/Processed/](/usr/bmicnas01/data-biwi-01/bmicdatasets originals/Originals/USZ/metastases_segmentation/Processed/Processed/)

The distribution of voxel sizes is the following:



Most of the volumes (179 out of the 273) have isotropic voxel resolutions 0.6mm x 0.6mm x 0.6 mm.

Hence, 0.6mm x 0.6mm x 0.6mm was chosen as the reference resolution and all volumes were resampled to this resolution value.

Resampled volumes are saved in the folder below under the name image\_resampled.nii.gz

[/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases\\_project/preprocessed\\_CAP/](/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases_project/preprocessed_CAP/)

### **Step 2. Bias correction**

MR volumes were bias corrected using the N4 algorithm.

Images at this stage are saved in the folder below under the name `image_resampled_bias_corrected1.nii.gz`  
[/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases\\_project/preprocessed\\_CAP/](/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases_project/preprocessed_CAP/)

### **Step 3. Normalization and resizing I**

At this point MR volumes have the same voxel size but not the same image dimensions. 210 volumes (out of 273) have after resampling 400 pixels in the x dimension, 221 (out of 273) have 400 pixels in the y dimension, and 200 (out of 273) have 400 pixels in the z dimension.

Hence, I padded/cropped all volumes so all have 400 x 400 x 400 pixels in the x, y and z dimensions. The value for padding finally chosen was the minimum intensity value of the image.

Finally, images were normalized between 0-1.

Images at this stage are saved in the folder below with the name `img_resampled_bias_corrected1_resized3.nii.gz`  
[/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases\\_project/preprocessed\\_CAP/](/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases_project/preprocessed_CAP/)

Corresponding mask volumes were at this stage resampled and resized and saved in the same folder under the name `mask_resized1.nii.gz`

### **Step 4. Registration**

Images were registered using ANTS software and employing rigid registration. The patient used as reference or fix image was 000001-12 (within `Breast_nii`).

Segmentation masks were registered accordingly.

Images at this stage are saved in the folder below with the name `img_reg.nii.gz`  
[/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases\\_project/preprocessed\\_CAP/](/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases_project/preprocessed_CAP/)

Registration results can be visualized inside the folder [/visualize\\_registration/](/visualize_registration/). Furthermore, are also included in the [/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases\\_project/preprocessed\\_CAP\\_final/](/usr/bmicnas01/data-biwi-01/bmicdatasets/Processed/metastases_project/preprocessed_CAP_final/) folder.

### **Step 5. Skull stripping and resizing II**

Images were skull stripped using the HD-BET algorithm.

At this stage, images have dimensions 400 pixels x 400 pixels x 400 pixels. After skull stripping, we can crop the images so only the brain comprising the brain is included. We find the smallest and largest x, y and z position that include brain in all patients. For completeness values included here:

`x_min: 65, x_max: 327, y_min: 52, y_max: 389, z_min: 65, z_max: 354`

`x_range: 262, y_range: 337, z_range: 289`

Images were finally cropped to isotropic image dimensions: 350 x 350 x 350.

Final results are included in the folder stated in the first paragraph of this document.