MLI-CW-2

February 28, 2019

1 CO416 - Machine Learning for Imaging

1.1 Coursework 2 - Age regression from brain MRI

Predicting age from a brain MRI scan can have diagnostic value for a number of diseases that cause structural changes and damage to the brain. Discrepancy between the predicted, biological age and the real, chronological age of a patient might indicate the presence of disease and abnormal changes to the brain. For this we need an accurate predictor of brain age which may be learned from a set of healthy reference subjects. The objective for the coursework is to implement two different supervised learning approaches for age regression from brain MRI. Data from 600 healthy subjects will be provided. Each approach will require a processing pipeline with different components that you will need to implement using methods that were discussed in the lectures and tutorials. There are dedicated sections in the Jupyter notebook for each approach which contain some detailed instructions, hints and notes.

You may find useful ideas and implementations in the tutorial notebooks. Make sure to add documentation to your code. Markers will find it easier to understand your reasoning when sufficiently detailed comments are provided in your implementations.

Read the descriptions and provided code cells carefully and look out for the cells marked with 'TASK'.

1.1.1 Getting started and familiarise ourselves with the data

The following cells provide some helper functions to load the data, and provide some overview and visualisation of the statistics over the population of 600 subjects. Let's start by loading the meta data, that is the data containing information about the subject IDs, their age, and gender.

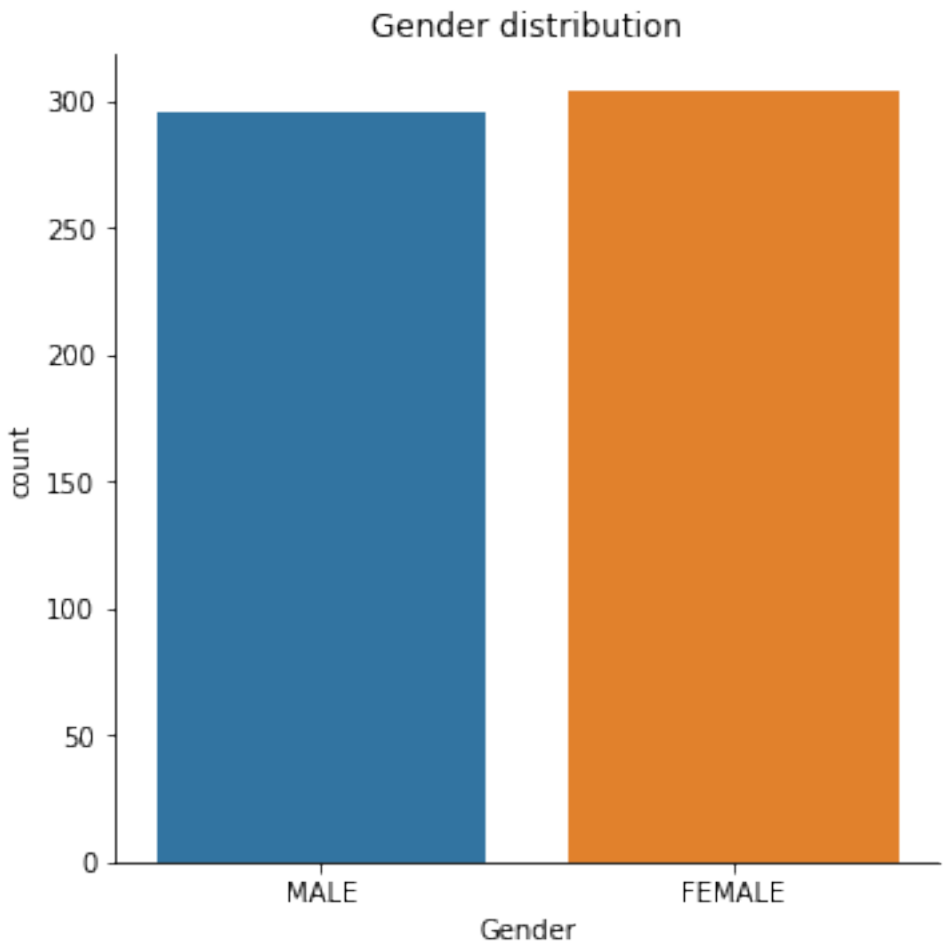
```
In [1]: # Read the meta data using pandas
        import pandas as pd

        data_dir = "./data/brain/"

        meta_data = pd.read_csv(data_dir + 'meta/clean_participant_data.csv')
        meta_data.head() # show the first five data entries
```

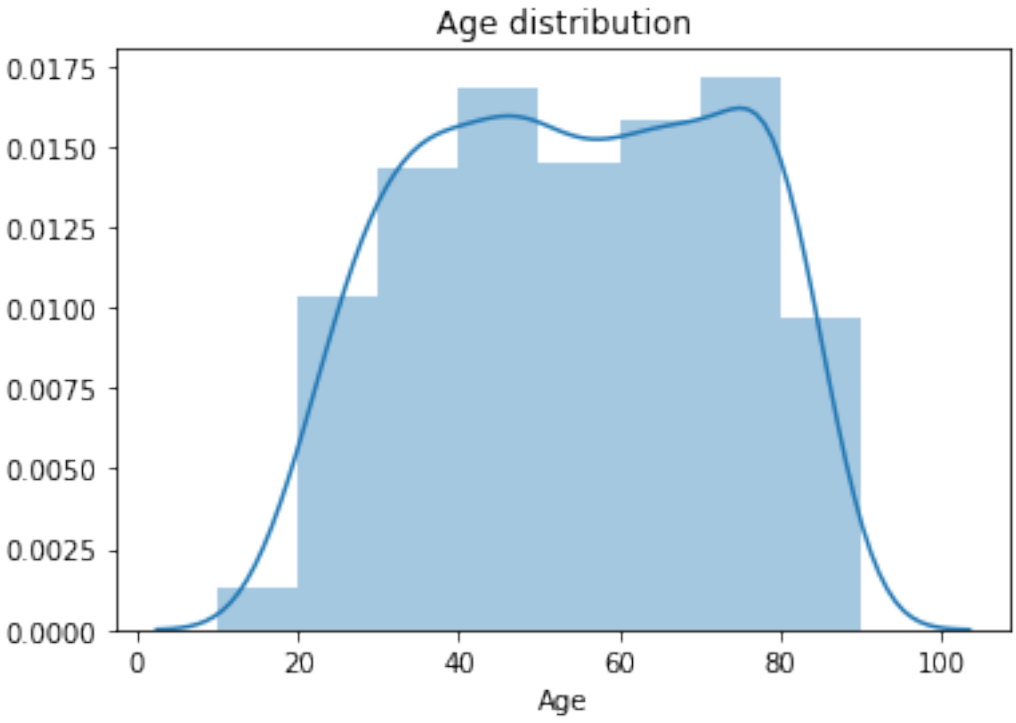
```
Out[1]:          ID  age  gender_code gender_text
        0  CC110033   24            1        MALE
        1  CC110037   18            1        MALE
```

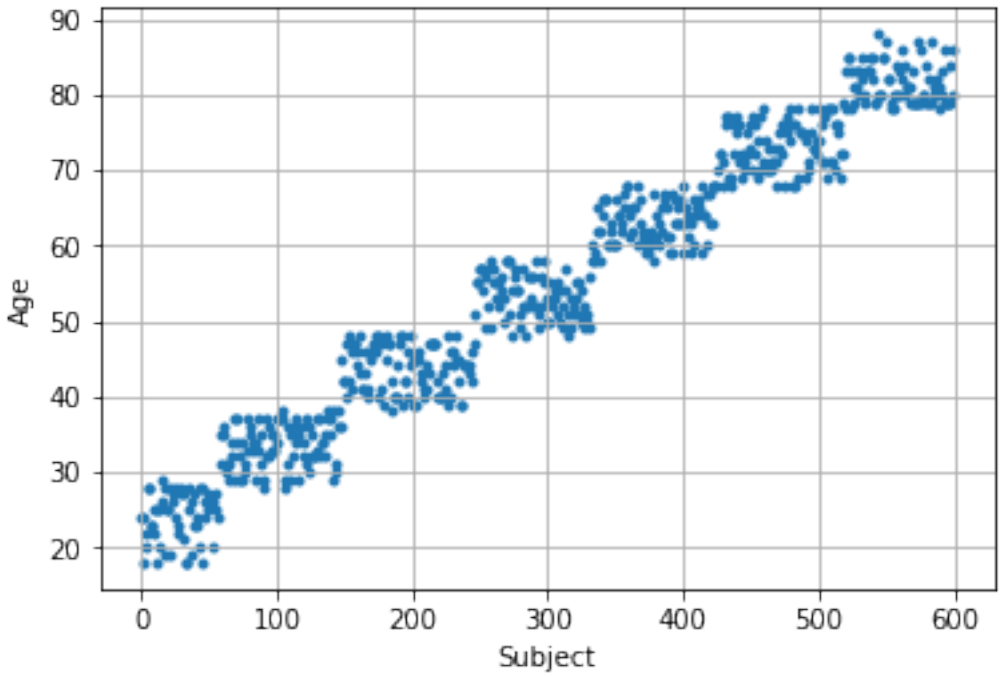
```
2  CC110045   24            2      FEMALE
3  CC110056   22            2      FEMALE
4  CC110062   20            1        MALE
```

Let's have a look at some population statistics.

In [2]:
```
%matplotlib inline

import matplotlib.pyplot as plt
import seaborn as sns

sns.catplot(x="gender_text", data=meta_data, kind="count")
plt.title('Gender distribution')
plt.xlabel('Gender')
plt.show()

sns.distplot(meta_data['age'], bins=[10,20,30,40,50,60,70,80,90])
plt.title('Age distribution')
plt.xlabel('Age')
plt.show()

plt.scatter(range(len(meta_data['age'])),meta_data['age'], marker='.')
plt.grid()
plt.xlabel('Subject')
plt.ylabel('Age')
plt.show()
```


Gender distribution
300
250
200
150
100
50
0
count
MALE
FEMALE
Gender


Age distribution
0.0175
0.0150
0.0125
0.0100
0.0075
0.0050
0.0025
0.0000
0
20
40
60
80
100
Age


90
80
70
60
50
40
30
20
Age
0
100
200
300
400
500
600
Subject

1.1.2 Set up a simple medical image viewer and import SimpleITK

In [4]:
```
import numpy as np
import SimpleITK as sitk
import matplotlib.pyplot as plt

from ipywidgets import interact, fixed
from IPython.display import display

from image_viewer import display_image
```

1.1.3 Imaging data

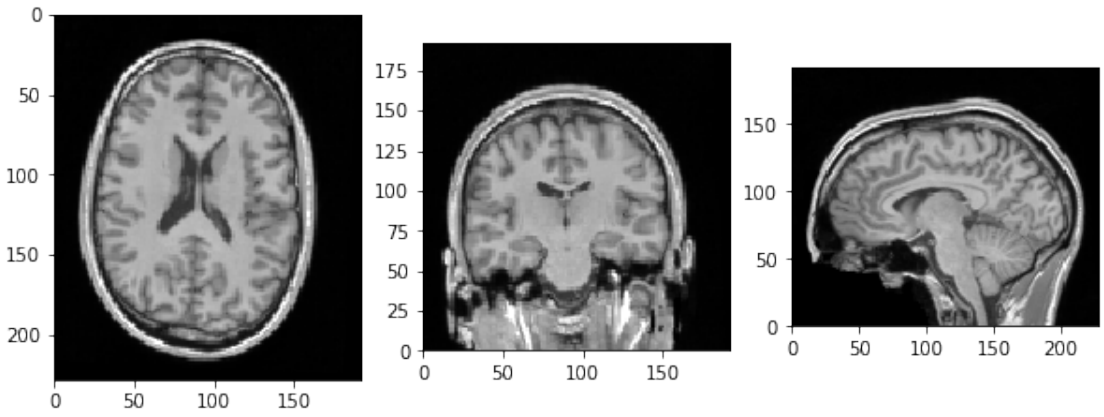
Let's check out the imaging data that is available for each subject. This cell also shows how to retrieve data given a particular subject ID from the meta data.

In [5]:
```
import glob

# Subject with index 0
ID = meta_data['ID'][0]
age = meta_data['age'][0]

# Data folders
image_dir = data_dir + 'images/'
image_filenames = glob.glob(image_dir + '*.nii.gz')

mask_dir = data_dir + 'masks/'
mask_filenames = glob.glob(mask_dir + '*.nii.gz')

greymatter_dir = data_dir + 'greymatter/'
greymatter_filenames = glob.glob(greymatter_dir + '*.nii.gz')


image_filename = [f for f in image_filenames if ID in f][0]
img = sitk.ReadImage(image_filename)

mask_filename = [f for f in mask_filenames if ID in f][0]
msk = sitk.ReadImage(mask_filename)

greymatter_filename = [f for f in greymatter_filenames if ID in f][0]
gm = sitk.ReadImage(greymatter_filename)

print('Imaging data of subject ' + ID + ' with age ' + str(age))

print('\nMR Image (used in part A)')
display_image(img, window=400, level=200)

print('Brain mask (used in part A)')
display_image(msk)
```

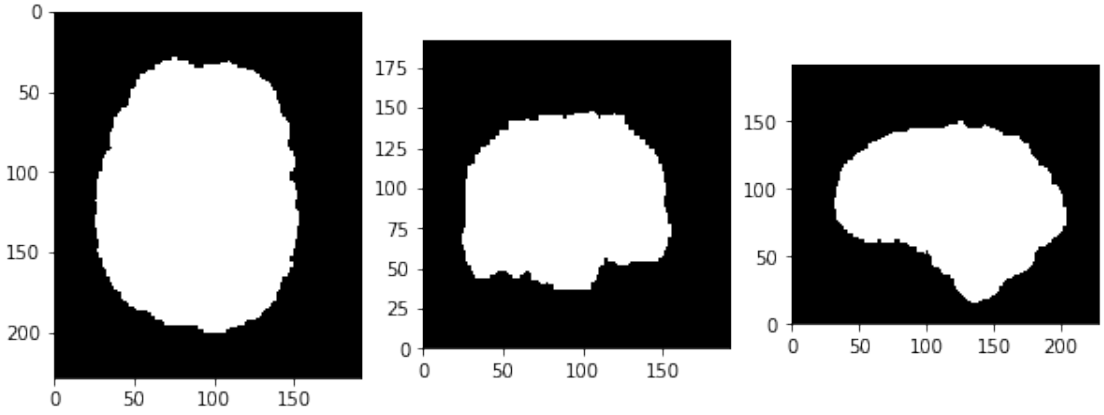
```
print('Spatially normalised grey matter maps (used in part B)')
display_image(gm)
```

```
Imaging data of subject CC110033 with age 24
```

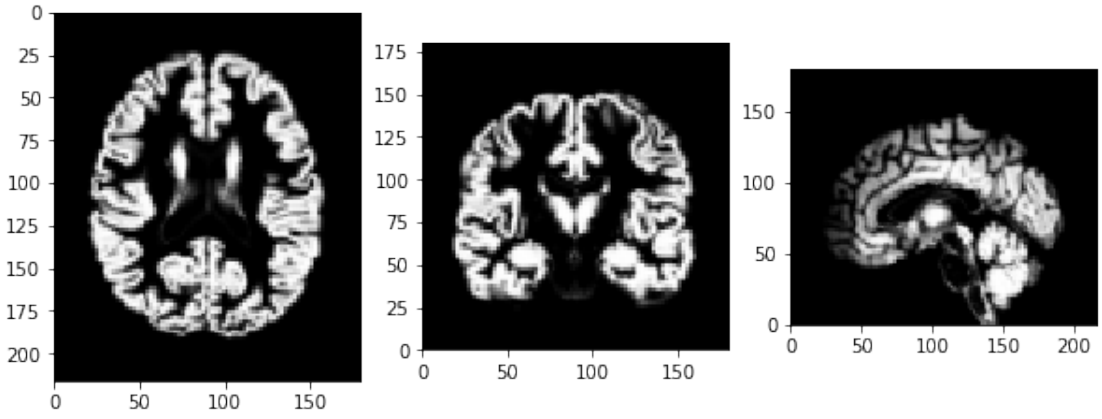
```
MR Image (used in part A)
```




```
Brain mask (used in part A)
```




```
Spatially normalised grey matter maps (used in part B)
```



1.2 Part A: Volume-based regression using brain structure segmentation

The first approach aims to regress the age of a subject using the volumes of brain tissues as features. The structures include grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF). It is known that with increasing age the ventricles enlarge (filled with CSF), while it is assumed that grey and white matter volume may decrease over time. However, as overall brain volume varies across individuals, taking the absolute volumes of tissues might not be predictive. Instead, relative volumes need to be computed as the ratios between each tissue volume and overall brain volume. To this end, a four-class (GM, WM, CSF, and background) brain segmentation needs to be implemented and applied to the 600 brain scans. Brain masks are provided which have been generated with a state-of-the-art neuroimaging brain extraction tool.

Different regression techniques should be explored, and it might be beneficial to investigate what the best set of features is for this task. Are all volume features equally useful, or is it even better to combine some of them and create new features. How does a simple linear regression perform compared to a model with higher order polynomials? Do you need regularisation? How about other regression methods such as regression trees or neural networks? The accuracy of different methods should be evaluated using two-fold cross-validation, and average age prediction accuracy should be compared and reported appropriately.

Note: For part A, only the MR images and the brain masks should be used from the imaging data. The spatially normalised grey matter maps are used in part B only. If you struggle with task A-1, you can continue with A-2 using the provided reference segmentations in subfolder `segs_refs`.

1.2.1 TASK A-1: Brain tissue segmentation

Implement a CNN model for brain tissue segmentation which can provide segmentations of GM, WM, and CSF. For this task (and only for this task), we provide a separate dataset of 52 subjects which are split into 47 images for training and 5 for validation. The template code below has the data handling and main training routines already implemented, so you can focus on implementing a suitable CNN model. A simple model is provided, but this won't perform very well.

Once your model is trained and you are happy with the results on the validation data you should apply it to the 600 test images. We provide reference segmentations in a subfolder

`segs_refs` for all subjects. Calculate Dice similarity coefficients per tissue when comparing your predicted segmentations for the 600 test images to the reference segmentations. Summarise the statistics of the 600 Dice scores for each tissue class in box-and-whisker-plots.

Note: Implementing a full-fledged machine learning pipeline with training and testing procedures in Jupyter notebooks is a bit cumbersome and a pain to debug. Also, running bigger training tasks can be unstable. The code below should work as is on your VM. However, if you want to get a bit more serious about implementing an advanced CNN approach for image segmentation, you may want to move code into separate Python scripts and run them from the terminal.

Imports

```
In [7]: import os
        import torch
        import torch.nn as nn
        import torch.nn.functional as F
        from data_helper import ImageSegmentationDataset
```

Check that the GPU is up and running

```
In [8]: cuda_dev = '0' #GPU device 0 (can be changed if multiple GPUs are available)

        use_cuda = torch.cuda.is_available()
        device = torch.device("cuda:" + cuda_dev if use_cuda else "cpu")

        print('Device: ' + str(device))
        if use_cuda:
            print('GPU: ' + str(torch.cuda.get_device_name(int(cuda_dev))))
```

```
Device: cuda:0
GPU: GeForce GTX 1080
```

Config and hyper-parameters Here we set some default hyper-parameters and a starting configuration for the image resolution and others.

This needs to be revisited to optimise these values. In particular, you may want to run your final model on higher resolution images.

```
In [9]: rnd_seed = 42 #fixed random seed

        #Highest possible definition (original image definition)
        img_size = [128, 152, 128]
        img_spacing = [1.5, 1.5, 1.5]

        num_epochs = 30
        learning_rate = 0.001
        batch_size = 1 #Max batch size in order to fit in memory: Unet is quite large in memor
        val_interval = 10
```

```
num_classes = 4

out_dir = './output'

# Create output directory
if not os.path.exists(out_dir):
    os.makedirs(out_dir)
```

Loading and pre-processing of training and validation data We apply some standard pre-processing on the data such as intensity normalization (zero mean unit variance) and downsampling according to the configuration above.

We provide a 'debug' csv file pointing to just a few images for training. Replace this with the full training dataset when you train your full model.

```
In [10]: # USE THIS FOR TRAINING ON ALL 47 SUBJECTS
         train_data = data_dir + 'train/csv/train.csv'

         # USE THIS FOR DEBUGGING WITH JUST 2 SUBJECTS
         # train_data = data_dir + 'train/csv/train_debug.csv'

         val_data = data_dir + 'train/csv/val.csv'

         print('LOADING TRAINING DATA...')
         dataset_train = ImageSegmentationDataset(train_data, img_spacing, img_size)
         dataloader_train = torch.utils.data.DataLoader(dataset_train, batch_size=batch_size, s

         print('\nLOADING VALIDATION DATA...')
         dataset_val = ImageSegmentationDataset(val_data, img_spacing, img_size)
         dataloader_val = torch.utils.data.DataLoader(dataset_val, batch_size=1, shuffle=False
```

```
LOADING TRAINING DATA...
+ reading image msub-CC110319_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110319.nii.gz
+ reading mask sub-CC110319_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120208_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120208.nii.gz
+ reading mask sub-CC120208_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120462_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120462.nii.gz
+ reading mask sub-CC120462_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC121144_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC121144.nii.gz
+ reading mask sub-CC121144_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC122405_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC122405.nii.gz
+ reading mask sub-CC122405_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC210422_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC210422.nii.gz
```

```
+ reading mask sub-CC210422_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC220203_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC220203.nii.gz
+ reading mask sub-CC220203_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC220518_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC220518.nii.gz
+ reading mask sub-CC220518_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC221220_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC221220.nii.gz
+ reading mask sub-CC221220_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC221595_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC221595.nii.gz
+ reading mask sub-CC221595_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC222120_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC222120.nii.gz
+ reading mask sub-CC222120_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC222956_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC222956.nii.gz
+ reading mask sub-CC222956_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC310203_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC310203.nii.gz
+ reading mask sub-CC310203_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC310407_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC310407.nii.gz
+ reading mask sub-CC310407_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC320089_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC320089.nii.gz
+ reading mask sub-CC320089_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC320336_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC320336.nii.gz
+ reading mask sub-CC320336_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC320574_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC320574.nii.gz
+ reading mask sub-CC320574_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC321069_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC321069.nii.gz
+ reading mask sub-CC321069_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC321428_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC321428.nii.gz
+ reading mask sub-CC321428_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC321899_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC321899.nii.gz
+ reading mask sub-CC321899_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC410113_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC410113.nii.gz
+ reading mask sub-CC410113_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC410243_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC410243.nii.gz
```

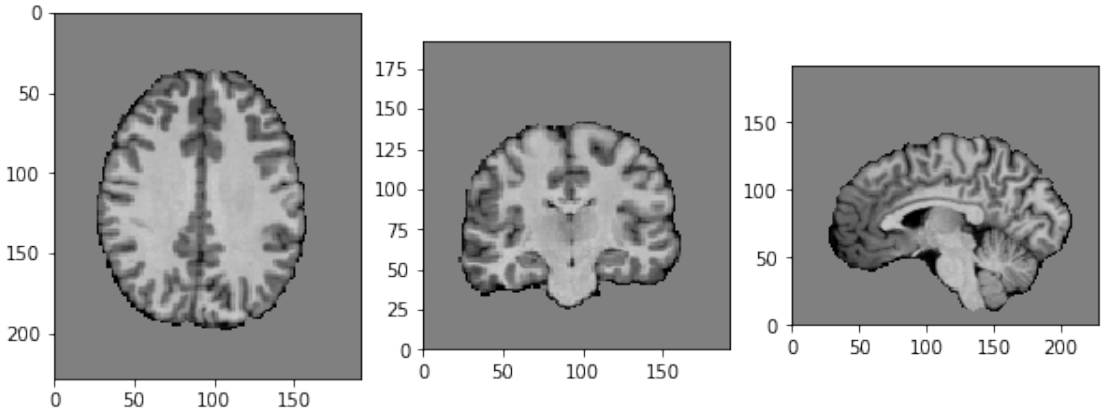
```
+ reading mask sub-CC410243_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC410432_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC410432.nii.gz
+ reading mask sub-CC410432_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC420137_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC420137.nii.gz
+ reading mask sub-CC420137_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC420202_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC420202.nii.gz
+ reading mask sub-CC420202_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC420286_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC420286.nii.gz
+ reading mask sub-CC420286_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC420888_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC420888.nii.gz
+ reading mask sub-CC420888_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC510226_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC510226.nii.gz
+ reading mask sub-CC510226_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC510329_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC510329.nii.gz
+ reading mask sub-CC510329_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC510474_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC510474.nii.gz
+ reading mask sub-CC510474_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC520002_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC520002.nii.gz
+ reading mask sub-CC520002_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC520134_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC520134.nii.gz
+ reading mask sub-CC520134_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC520253_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC520253.nii.gz
+ reading mask sub-CC520253_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC520503_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC520503.nii.gz
+ reading mask sub-CC520503_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC520775_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC520775.nii.gz
+ reading mask sub-CC520775_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC610288_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC610288.nii.gz
+ reading mask sub-CC610288_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC610575_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC610575.nii.gz
+ reading mask sub-CC610575_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC620073_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC620073.nii.gz
```

```
+ reading mask sub-CC620073_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC620262_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC620262.nii.gz
+ reading mask sub-CC620262_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC620444_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC620444.nii.gz
+ reading mask sub-CC620444_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC620557_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC620557.nii.gz
+ reading mask sub-CC620557_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC620821_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC620821.nii.gz
+ reading mask sub-CC620821_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC621642_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC621642.nii.gz
+ reading mask sub-CC621642_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC710416_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC710416.nii.gz
+ reading mask sub-CC710416_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC720103_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC720103.nii.gz
+ reading mask sub-CC720103_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC720511_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC720511.nii.gz
+ reading mask sub-CC720511_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721291_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721291.nii.gz
+ reading mask sub-CC721291_T1w_rigid_to_mni_brain_mask.nii.gz

LOADING VALIDATION DATA...
+ reading image msub-CC220901_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC220901.nii.gz
+ reading mask sub-CC220901_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC320698_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC320698.nii.gz
+ reading mask sub-CC320698_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC420454_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC420454.nii.gz
+ reading mask sub-CC420454_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC610058_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC610058.nii.gz
+ reading mask sub-CC610058_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC710679_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC710679.nii.gz
+ reading mask sub-CC710679_T1w_rigid_to_mni_brain_mask.nii.gz
```

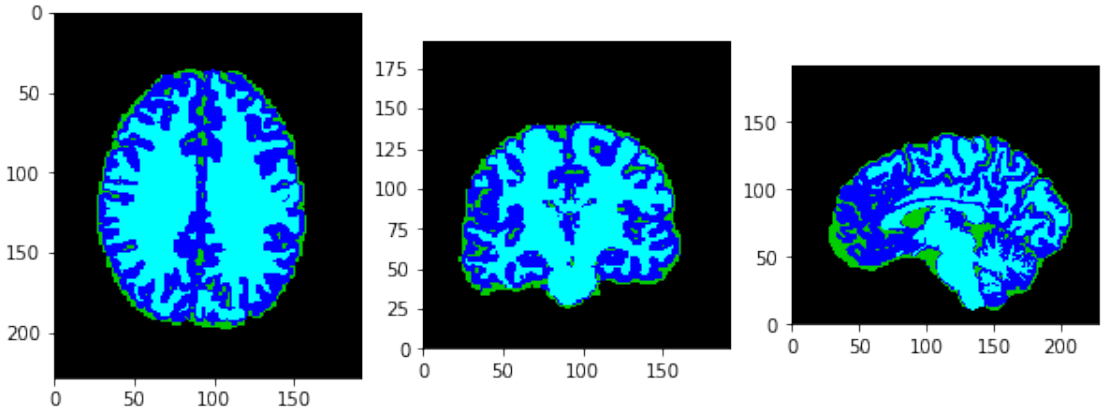
Visualise training example Just to check how a training image looks like after pre-processing.

```
In [11]: sample = dataset_train.get_sample(0)
         img_name = dataset_train.get_img_name(0)
         seg_name = dataset_train.get_seg_name(0)
         print('Image: ' + img_name)
         display_image(sample['img'], window=5, level=0)
         print('Segmentation: ' + seg_name)
         display_image(sitk.LabelToRGB(sample['seg']))
         print('Mask')
         display_image(sample['msk'])
```

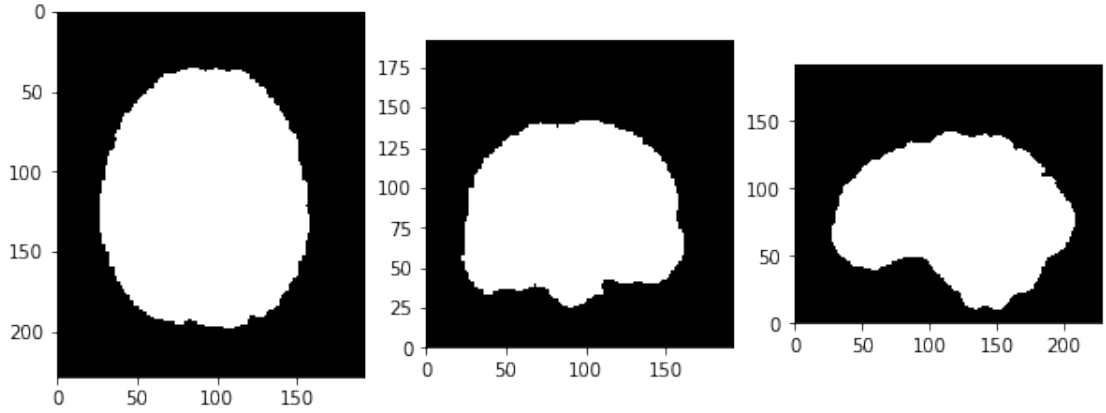
```
Image: msub-CC110319_T1w_rigid_to_mni.nii.gz
```



```
Segmentation: CC110319.nii.gz
```



Mask



The Model This is the **key part of task A-1** where you have to design a suitable CNN model for brain segmentation. The simple model provided below works to some degree (it let's you run through the upcoming cells), but it will not perform very well. Use what you learned in the lectures to come up with a good architecture. Start with a simple, shallow model and only increase complexity (e.g., number of layers) if needed.

```
In [12]: class SimpleNet3D(nn.Module):

             def __init__(self, num_classes):
                 super(SimpleNet3D, self).__init__()
                 self.conv1 = nn.Conv3d(1, 16, kernel_size=3, padding=1)
                 self.conv2 = nn.Conv3d(16, 16, kernel_size=3, padding=1)
                 self.conv3 = nn.Conv3d(16, 32, kernel_size=3, padding=1)
                 self.conv4 = nn.Conv3d(32, num_classes, kernel_size=3, padding=1)

             def forward(self, x):
                 x = F.relu(self.conv1(x))
                 x = F.relu(self.conv2(x))
                 x = F.relu(self.conv3(x))
                 x = self.conv4(x)
                 return F.softmax(x, dim=1)
```

```
In [13]: class LeNet3D(nn.Module):

             def __init__(self, num_classes):
                 super(LeNet3D, self).__init__()
                 self.conv1 = nn.Conv3d(1, 6, kernel_size=3, padding=1)
                 self.conv2 = nn.Conv3d(6, 16, kernel_size=3, padding=1)
                 self.conv3 = nn.Conv3d(16, 120, kernel_size=3, padding=1)
```

```
        self.conv4 = nn.Conv3d(120, 84, kernel_size=1)
        self.conv5 = nn.Conv3d(84, num_classes, kernel_size=1)

    def forward(self, x):
        x = F.relu(self.conv1(x))
        x = F.relu(self.conv2(x))
        x = F.relu(self.conv3(x))
        x = F.relu(self.conv4(x))
        x = self.conv5(x)
        return F.softmax(x, dim=1)
```

In [14]:
```
def make_conv_bn_relu(in_channels, out_channels, kernel_size=3, stride=1, padding=1):
    #Perform a block of the Unet
    return [
        nn.Conv3d(in_channels, out_channels, kernel_size=kernel_size,  stride=stride,
        nn.BatchNorm3d(out_channels),
        nn.ReLU(inplace=True)]

class UNet3D(nn.Module):
    #Unet presented in lecture but smaller
    def __init__(self, num_classes):
        super(UNet3D, self).__init__()
        #Downsampling part
        self.down1 = nn.Sequential(
            *make_conv_bn_relu(1, 32, kernel_size=3, stride=1, padding=1 ),
            *make_conv_bn_relu(32, 32, kernel_size=3, stride=1, padding=1 ))

        self.down2 = nn.Sequential(
            *make_conv_bn_relu(32, 64, kernel_size=3, stride=1, padding=1 ),
            *make_conv_bn_relu(64, 64, kernel_size=3, stride=1, padding=1 ))

        self.bottom = nn.Sequential(
            *make_conv_bn_relu(64, 128, kernel_size=3, stride=1, padding=1 ),
            *make_conv_bn_relu(128, 128, kernel_size=3, stride=1, padding=1 ))

        #Upsampling part
        self.upsample1 = nn.ConvTranspose3d(128, 64, kernel_size=2, stride=2)

        self.up1 = nn.Sequential(
            *make_conv_bn_relu(128, 64, kernel_size=3, stride=1, padding=1 ),
            *make_conv_bn_relu(64, 64, kernel_size=3, stride=1, padding=1 ))

        self.upsample2 = nn.ConvTranspose3d(64, 32, kernel_size=2, stride=2)

        self.up2 = nn.Sequential(
            *make_conv_bn_relu(64, 32, kernel_size=3, stride=1, padding=1 ),
            *make_conv_bn_relu(32, 32, kernel_size=3, stride=1, padding=1 ))
```

```
        self.final_conv = nn.Conv3d(32, num_classes, kernel_size=1)

    def forward(self, x):
        first_down = self.down1(x) #64*64
        first_out = F.max_pool3d(first_down, kernel_size=2, stride=2)

        second_down = self.down2(first_out) #32*32
        second_out = F.max_pool3d(second_down, kernel_size=2, stride=2)

        bottom = self.bottom(second_out) # 16*16

        first_up = self.upsample1(bottom) #32*32
        first_up = torch.cat([second_down, first_up], 1)#skip connections
        first_up = self.up1(first_up)

        second_up = self.upsample2(first_up) #64*64
        second_up = torch.cat([first_down, second_up], 1)#skip connections
        second_up = self.up2(second_up)

        x = self.final_conv(second_up)
        return F.softmax(x, dim=1)
```

My architecture is an U-Net adapted for 32323 images based on the paper https://arxiv.org/abs/1505.04597

TRAINING Below is an implementation of a full training procedure including a loop for intermediate evaluation of the model on the validation data. Feel free to modify this procedure. For example, in addition to the loss you may want to monitor precision, recall and Dice scores (or others).

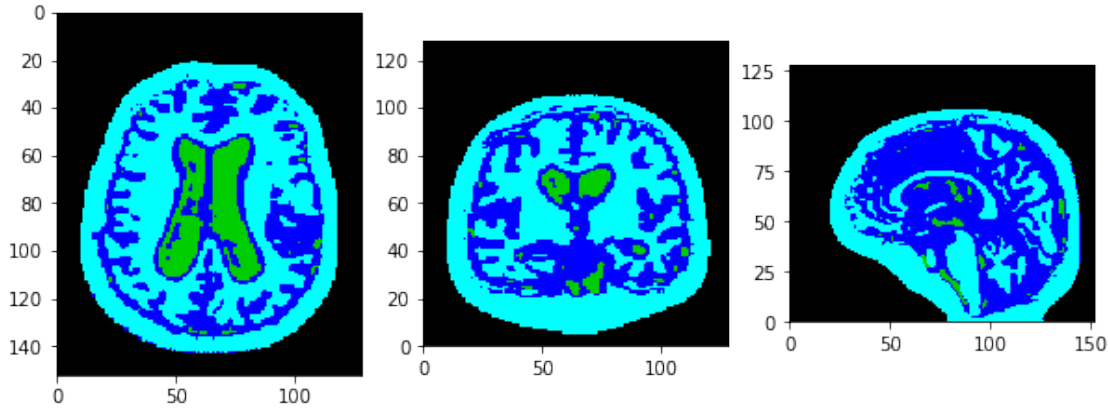
```
In [15]: def evaluate_metrics(prediction, gold_standard):
             """
             Compute and average some metrics for of the 4 segmentations classes
             """
             accuracy = 0
             recall = 0
             dice_score = 0
             prediction = torch.argmax(prediction, dim=1)
             prediction = prediction[0]
             gold_standard = gold_standard[0][0]
             for i in range(4):
                 TP= float((prediction[gold_standard==i] == i).sum())
                 FP = float((prediction[gold_standard!=i] == i).sum())
                 TN = float(len(prediction[gold_standard!=i]) - FP )
                 FN = float(len(prediction[gold_standard==i]) - TP)
                 accuracy += (TP + TN)/(TP + FN + TN + FP)
                 recall += TP / (TP + FN)
```

```
            dice_score += 2*TP / (2*TP+FP+FN)
        return accuracy/4, recall/4, dice_score/4
```

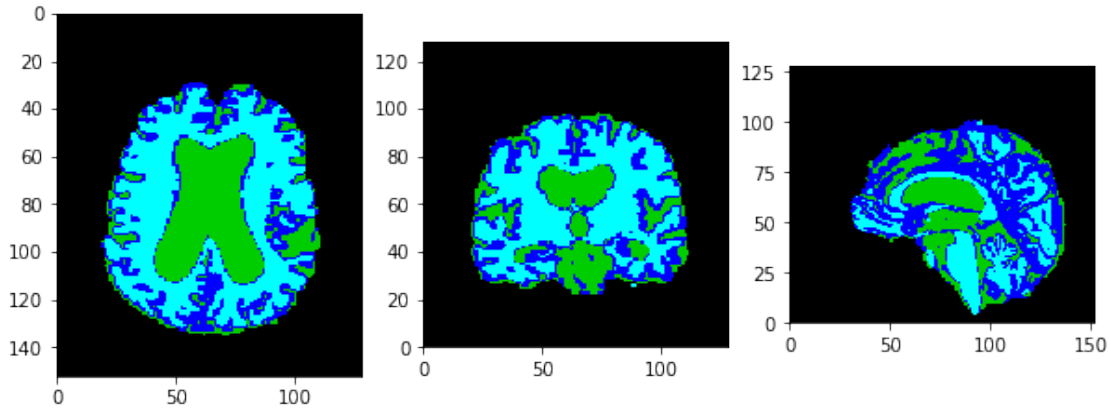
In [16]:
```
model_dir = os.path.join(out_dir, 'model')
if not os.path.exists(model_dir):
    os.makedirs(model_dir)

torch.manual_seed(rnd_seed) #fix random seed

#model = SimpleNet3D(num_classes=num_classes).to(device)
#model = LeNet3D(num_classes=num_classes).to(device)
model = UNet3D(num_classes=num_classes).to(device)
model.train()

optimizer = torch.optim.Adam(model.parameters(), lr=learning_rate)

dsc_train_log = []
accuracy_train_log = []
recall_train_log = []
dsc_val_log = []
accuracy_val_log = []
recall_val_log = []

loss_train_log = []
loss_val_log = []
epoch_val_log = []

print('START TRAINING...')
for epoch in range(1, num_epochs + 1):

    dsc_score = 0
    accuracy = 0
    recall = 0


    # Training
    for batch_idx, batch_samples in enumerate(dataloader_train):
        img, seg = batch_samples['img'].to(device), batch_samples['seg'].to(device)
        optimizer.zero_grad()
        prd = model(img)
        prd_flat = prd.view(prd.size(0), prd.size(1), -1)
        seg_flat = seg.view(seg.size(0), seg.size(1), -1)
        loss = F.cross_entropy(prd_flat, seg_flat.squeeze(1))
        loss.backward()
        optimizer.step()

        #monitor precision, recall and Dice scores
        metrics = evaluate_metrics(prd_flat, seg_flat)
```

```
            dsc_score += metrics[2]
            accuracy += metrics[0]
            recall += metrics[1]

        dsc_train_log.append(dsc_score/len(dataloader_train))
        accuracy_train_log.append(accuracy/len(dataloader_train))
        recall_train_log.append(recall/len(dataloader_train))
        loss_train_log.append(loss.item())

        print('+ TRAINING \tEpoch: {} \tLoss: {:.6f}'.format(epoch, loss.item()))

        # Validation
        if epoch == 1 or epoch % val_interval == 0:
            loss_val = 0
            sum_pts = 0
            with torch.no_grad():
                for data_sample in dataloader_val:
                    img, seg = data_sample['img'].to(device), data_sample['seg'].to(device
                    prd = model(img)
                    prd_flat = prd.view(prd.size(0), prd.size(1), -1)
                    seg_flat = seg.view(seg.size(0), seg.size(1), -1)
                    loss_val += F.cross_entropy(prd_flat, seg_flat.squeeze(1), reduction=
                    sum_pts += seg_flat.size(2)

            prd = torch.argmax(prd, dim=1)
            prediction = sitk.GetImageFromArray(prd.cpu().squeeze().numpy().astype(np.uint


            loss_val /= sum_pts

            loss_val_log.append(loss_val)
            epoch_val_log.append(epoch)

            print('-------------------------------------------------')
            print('+ VALIDATE \tEpoch: {} \tLoss: {:.6f}'.format(epoch, loss_val))
            display_image(sitk.LabelToRGB(prediction))
            print('-------------------------------------------------')

    torch.save(model.state_dict(), os.path.join(model_dir, 'model.pt'))
```

```
START TRAINING...
+ TRAINING         Epoch: 1         Loss: 1.215635
-------------------------------------------------
+ VALIDATE         Epoch: 1         Loss: 1.219756
```

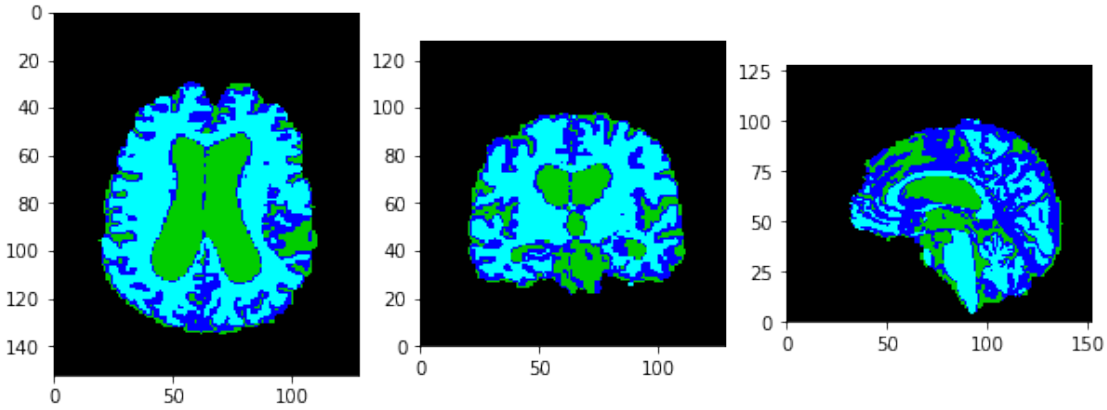


```
------------------------------------------------
+ TRAINING          Epoch: 2          Loss: 1.026881
+ TRAINING          Epoch: 3          Loss: 0.875002
+ TRAINING          Epoch: 4          Loss: 0.805281
+ TRAINING          Epoch: 5          Loss: 0.781606
+ TRAINING          Epoch: 6          Loss: 0.768757
+ TRAINING          Epoch: 7          Loss: 0.766274
+ TRAINING          Epoch: 8          Loss: 0.761625
+ TRAINING          Epoch: 9          Loss: 0.759130
+ TRAINING          Epoch: 10          Loss: 0.758819
------------------------------------------------
+ VALIDATE          Epoch: 10          Loss: 0.759171
```

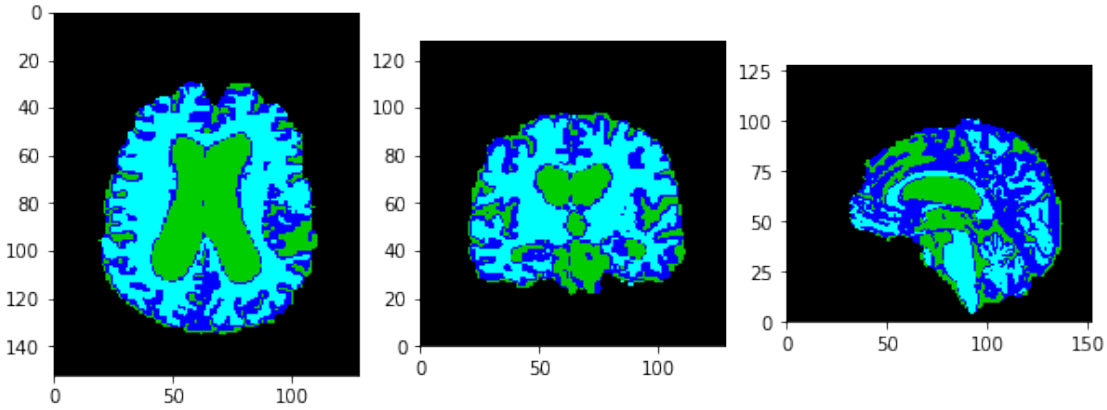


```
------------------------------------------------
+ TRAINING          Epoch: 11          Loss: 0.754410
+ TRAINING          Epoch: 12          Loss: 0.757050
```

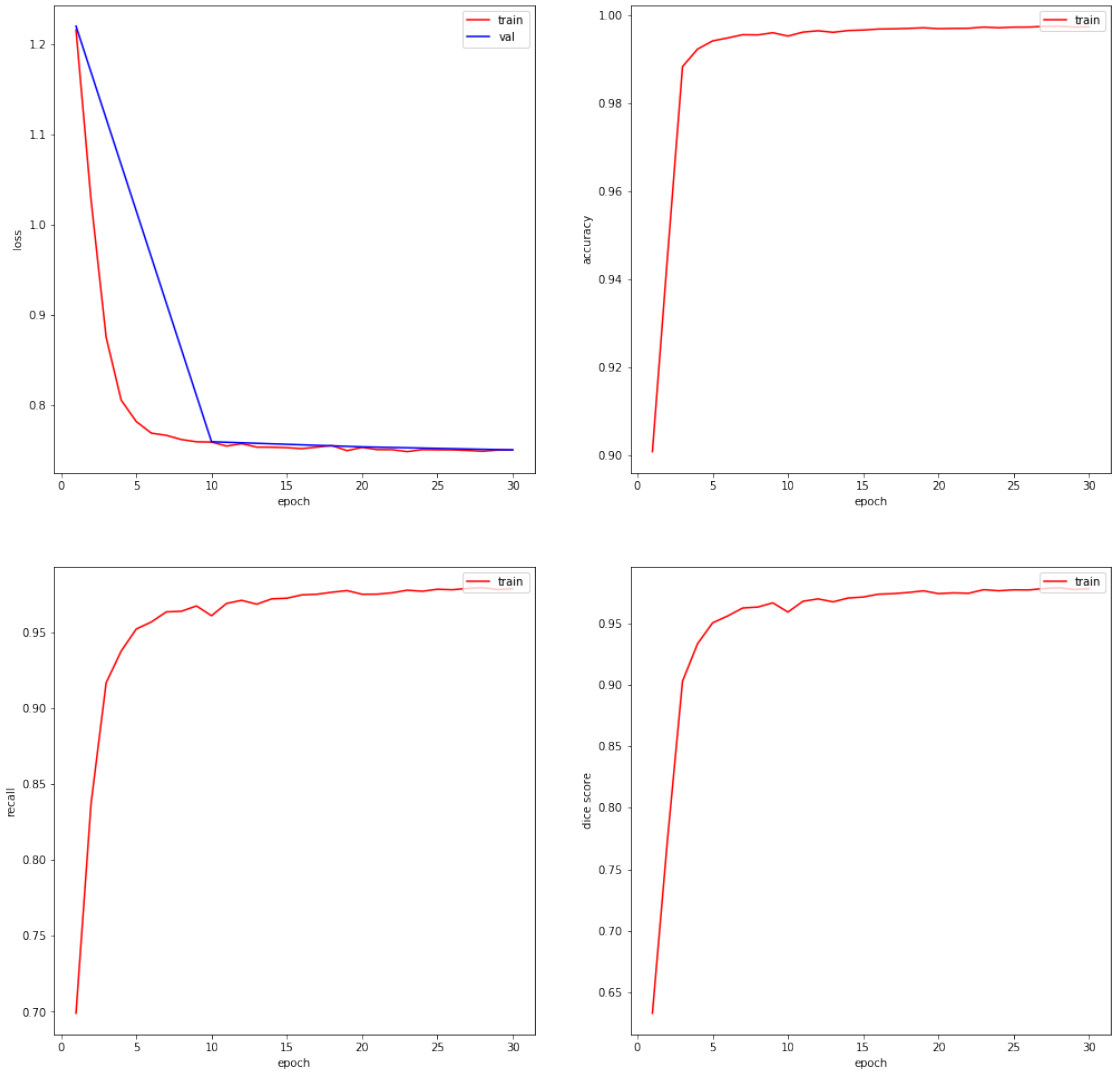
```
+ TRAINING          Epoch: 13          Loss: 0.753254
+ TRAINING          Epoch: 14          Loss: 0.753127
+ TRAINING          Epoch: 15          Loss: 0.752637
+ TRAINING          Epoch: 16          Loss: 0.751523
+ TRAINING          Epoch: 17          Loss: 0.753209
+ TRAINING          Epoch: 18          Loss: 0.754919
+ TRAINING          Epoch: 19          Loss: 0.749320
+ TRAINING          Epoch: 20          Loss: 0.752874
-------------------------------------------------
+ VALIDATE          Epoch: 20          Loss: 0.753533
```




```
-------------------------------------------------
+ TRAINING          Epoch: 21          Loss: 0.750473
+ TRAINING          Epoch: 22          Loss: 0.750360
+ TRAINING          Epoch: 23          Loss: 0.748271
+ TRAINING          Epoch: 24          Loss: 0.750446
+ TRAINING          Epoch: 25          Loss: 0.750219
+ TRAINING          Epoch: 26          Loss: 0.750194
+ TRAINING          Epoch: 27          Loss: 0.749523
+ TRAINING          Epoch: 28          Loss: 0.748635
+ TRAINING          Epoch: 29          Loss: 0.749910
+ TRAINING          Epoch: 30          Loss: 0.750042
-------------------------------------------------
+ VALIDATE          Epoch: 30          Loss: 0.750109
```



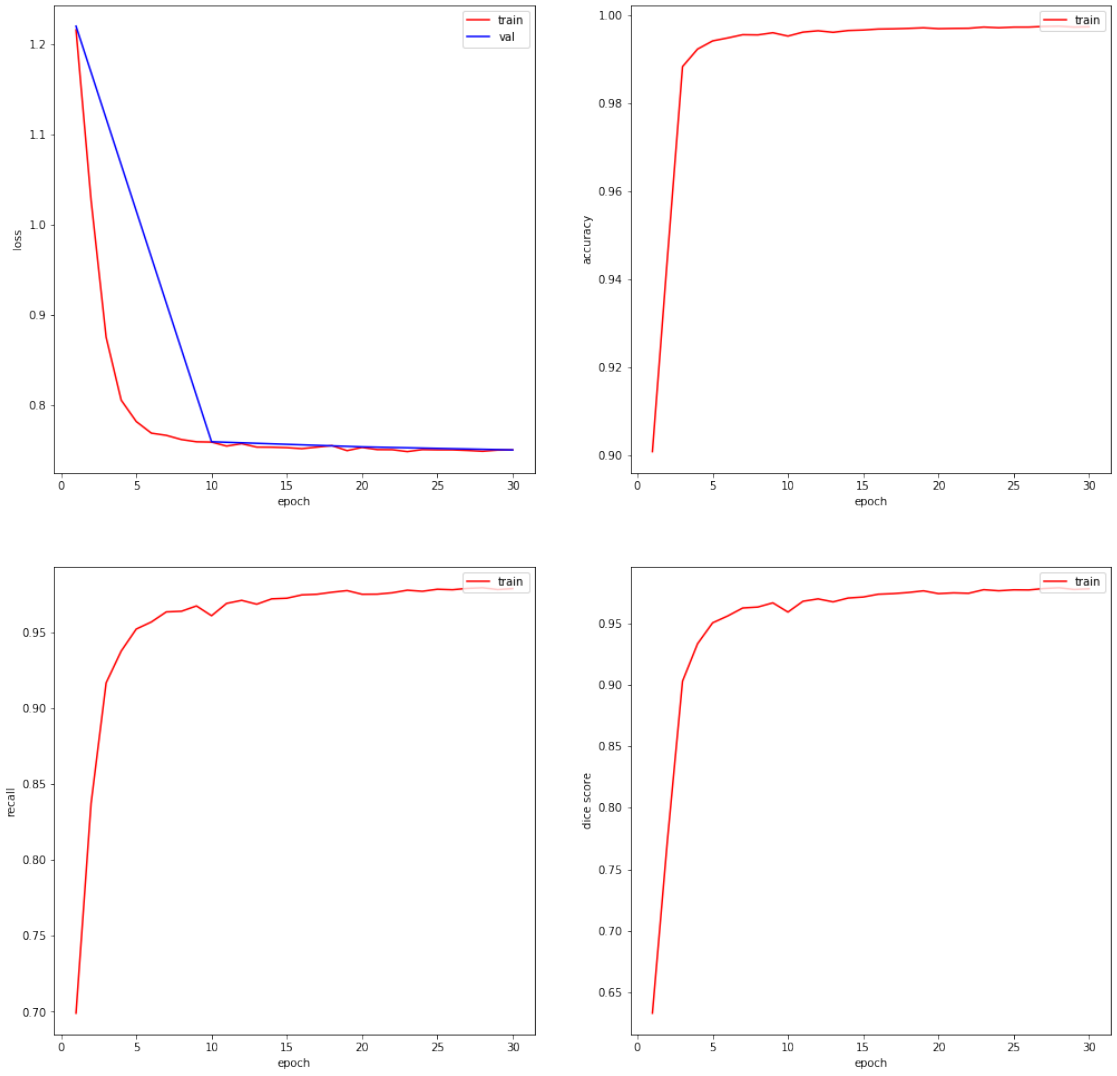
Finished TRAINING.



In [37]: *### Display training logs such as loss, accuracy, dice score, recall*

```
print('\nFinished TRAINING.')
fig = plt.figure(figsize=(17,17))

plt.subplot(2, 2, 1)
plt.plot(range(1, num_epochs + 1), loss_train_log, c='r', label='train')
plt.plot(epoch_val_log, loss_val_log, c='b', label='val')
plt.legend(loc='upper right')
plt.xlabel('epoch')
plt.ylabel('loss')

plt.subplot(2, 2, 2)
plt.plot(range(1, num_epochs + 1), accuracy_train_log, c='r', label='train')
```

```
        plt.legend(loc='upper right')
        plt.xlabel('epoch')
        plt.ylabel('accuracy')

        plt.subplot(2, 2, 3)
        plt.plot(range(1, num_epochs + 1), recall_train_log, c='r', label='train')
        plt.legend(loc='upper right')
        plt.xlabel('epoch')
        plt.ylabel('recall')

        plt.subplot(2, 2, 4)
        plt.plot(range(1, num_epochs + 1), dsc_train_log, c='r', label='train')
        plt.legend(loc='upper right')
        plt.xlabel('epoch')
        plt.ylabel('dice score')
        plt.show()


Finished TRAINING.
```



The above plots are metrics over the epochs averaged between the 4 segmentation classes.

We can see that the model is still improving at between the 25th and 30th epoch. It could be worth to do more epochs but since it is very computationally expensive we decided to stop at 30.

We don't observe any overfitting since the validation loss is also decreasing in the last epoch. Thus regularization does not seem to be needed here.

Loading and pre-processing of testing data Now that we have trained a model, the next cells are about applying that model to our test dataset. Before testing on the full 600 subjects, you may want to initially just test on the 5 validation subjects.

```
In [17]: # USE THIS FOR TESTING ON THE 600 SUBJECTS
         test_data = data_dir + 'csv/test.csv'

         # USE THIS FOR TESTING ON THE 5 VALIDATION SUBJECTS
         #test_data = data_dir + 'train/csv/val.csv'
```

```
        print('LOADING TESTING DATA...')
        dataset_test = ImageSegmentationDataset(test_data, img_spacing, img_size)
        dataloader_test = torch.utils.data.DataLoader(dataset_test, batch_size=1, shuffle=Fals
```

```
LOADING TESTING DATA...
+ reading image msub-CC110033_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110033.nii.gz
+ reading mask sub-CC110033_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110037_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110037.nii.gz
+ reading mask sub-CC110037_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110045_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110045.nii.gz
+ reading mask sub-CC110045_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110056_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110056.nii.gz
+ reading mask sub-CC110056_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110062_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110062.nii.gz
+ reading mask sub-CC110062_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110069_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110069.nii.gz
+ reading mask sub-CC110069_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110087_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110087.nii.gz
+ reading mask sub-CC110087_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110098_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110098.nii.gz
+ reading mask sub-CC110098_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110101_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110101.nii.gz
+ reading mask sub-CC110101_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110126_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110126.nii.gz
+ reading mask sub-CC110126_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110174_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110174.nii.gz
+ reading mask sub-CC110174_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110182_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110182.nii.gz
+ reading mask sub-CC110182_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110187_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110187.nii.gz
+ reading mask sub-CC110187_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC110411_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110411.nii.gz
+ reading mask sub-CC110411_T1w_rigid_to_mni_brain_mask.nii.gz
```

```
+ reading image msub-CC110606_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC110606.nii.gz
+ reading mask sub-CC110606_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC112141_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC112141.nii.gz
+ reading mask sub-CC112141_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120008_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120008.nii.gz
+ reading mask sub-CC120008_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120049_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120049.nii.gz
+ reading mask sub-CC120049_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120061_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120061.nii.gz
+ reading mask sub-CC120061_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120065_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120065.nii.gz
+ reading mask sub-CC120065_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120120_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120120.nii.gz
+ reading mask sub-CC120120_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120123_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120123.nii.gz
+ reading mask sub-CC120123_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120166_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120166.nii.gz
+ reading mask sub-CC120166_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120182_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120182.nii.gz
+ reading mask sub-CC120182_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120218_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120218.nii.gz
+ reading mask sub-CC120218_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120234_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120234.nii.gz
+ reading mask sub-CC120234_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120264_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120264.nii.gz
+ reading mask sub-CC120264_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120276_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120276.nii.gz
+ reading mask sub-CC120276_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120286_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120286.nii.gz
+ reading mask sub-CC120286_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120309_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120309.nii.gz
+ reading mask sub-CC120309_T1w_rigid_to_mni_brain_mask.nii.gz
```

```
+ reading image msub-CC120313_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120313.nii.gz
+ reading mask sub-CC120313_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120319_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120319.nii.gz
+ reading mask sub-CC120319_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120347_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120347.nii.gz
+ reading mask sub-CC120347_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120376_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120376.nii.gz
+ reading mask sub-CC120376_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120409_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120409.nii.gz
+ reading mask sub-CC120409_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC120469_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC120469.nii.gz
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+ reading mask sub-CC721532_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721585_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721585.nii.gz
+ reading mask sub-CC721585_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721618_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721618.nii.gz
+ reading mask sub-CC721618_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721648_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721648.nii.gz
+ reading mask sub-CC721648_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721704_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721704.nii.gz
+ reading mask sub-CC721704_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721707_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721707.nii.gz
+ reading mask sub-CC721707_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721729_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721729.nii.gz
+ reading mask sub-CC721729_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721888_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721888.nii.gz
+ reading mask sub-CC721888_T1w_rigid_to_mni_brain_mask.nii.gz
```
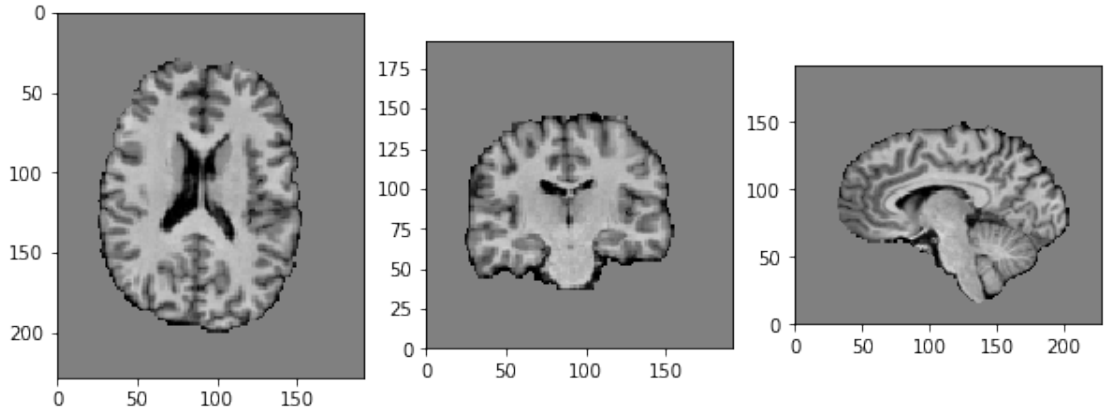

```
+ reading image msub-CC721891_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721891.nii.gz
+ reading mask sub-CC721891_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC721894_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC721894.nii.gz
+ reading mask sub-CC721894_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC722216_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC722216.nii.gz
+ reading mask sub-CC722216_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC722421_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC722421.nii.gz
+ reading mask sub-CC722421_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC722536_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC722536.nii.gz
+ reading mask sub-CC722536_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC722542_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC722542.nii.gz
+ reading mask sub-CC722542_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC722651_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC722651.nii.gz
+ reading mask sub-CC722651_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC722891_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC722891.nii.gz
+ reading mask sub-CC722891_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC723197_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC723197.nii.gz
+ reading mask sub-CC723197_T1w_rigid_to_mni_brain_mask.nii.gz
+ reading image msub-CC723395_T1w_rigid_to_mni.nii.gz
+ reading segmentation CC723395.nii.gz
+ reading mask sub-CC723395_T1w_rigid_to_mni_brain_mask.nii.gz
```

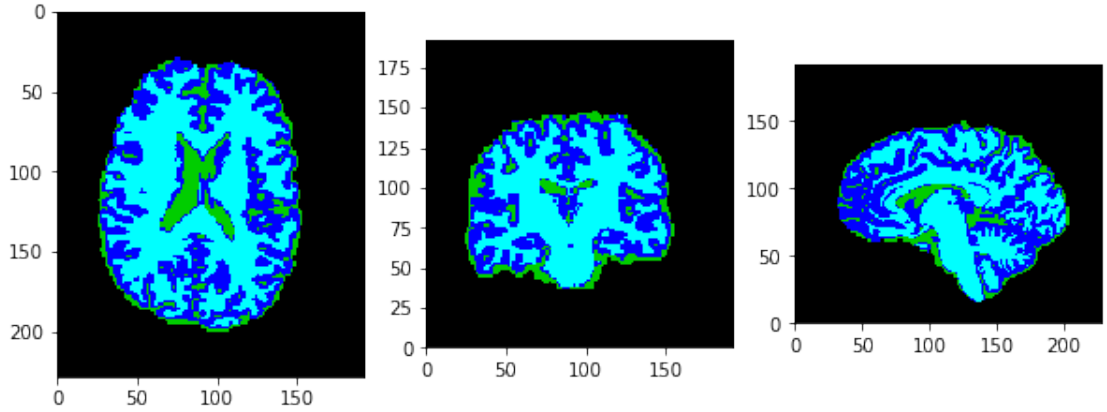
Visualise testing example Just to check how a testing image looks like after pre-processing.

```
In [18]: sample = dataset_test.get_sample(0)
         img_name = dataset_test.get_img_name(0)
         seg_name = dataset_test.get_seg_name(0)
         print('Image: ' + img_name)
         display_image(sample['img'], window=5, level=0)
         print('Segmentation: ' + seg_name)
         display_image(sitk.LabelToRGB(sample['seg']))
         print('Mask')
         display_image(sample['msk'])
```

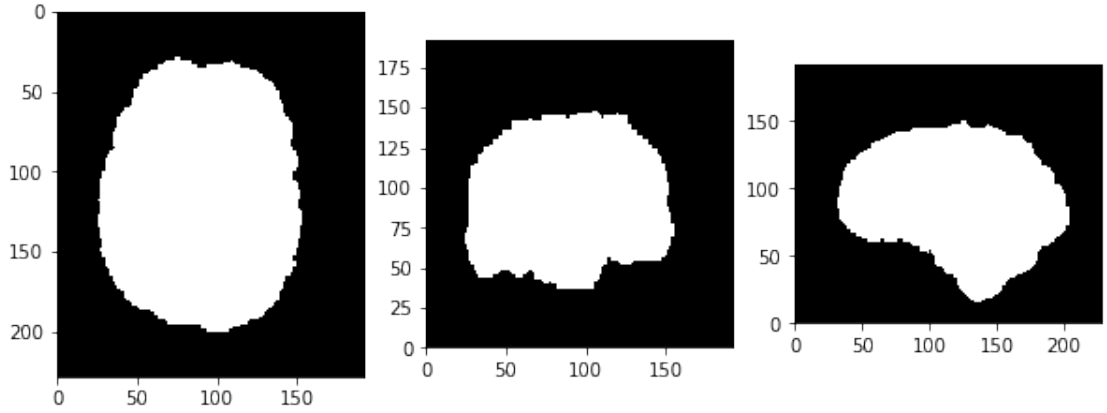
```
Image: msub-CC110033_T1w_rigid_to_mni.nii.gz
```



Segmentation: CC110033.nii.gz



Mask



TESTING Below is an implementation of a full testing procedure that saves the segmentations in an output folder. Feel free to modify this procedure.

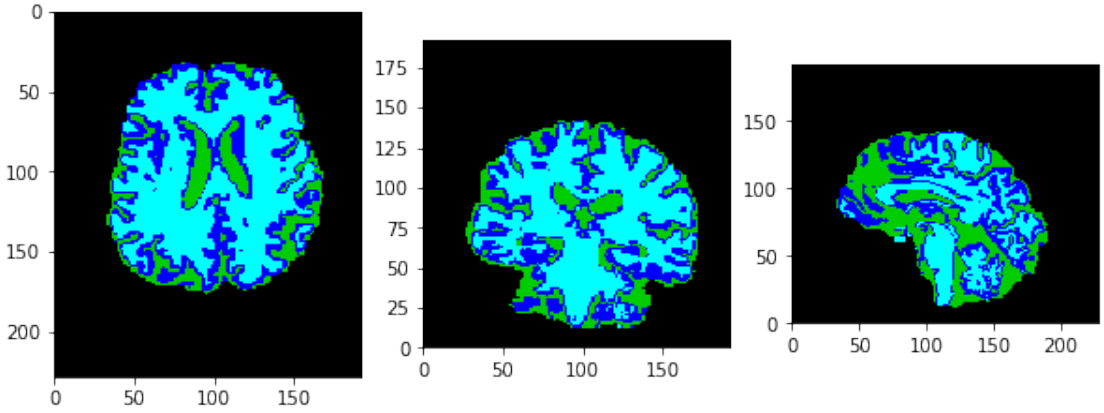
You will need to add the calculations of Dice scores (and possibly others) to evaluate the segmentation performance.

```
In [19]: def evaluate(prediction, gold_standard):
             """
             Compute and average some metrics for of the 4 segmentations classes
             """
             accuracy = torch.zeros(4)
             recall = torch.zeros(4)
             dice_score = torch.zeros(4)
             prediction = torch.argmax(prediction, dim=1)
             prediction = prediction[0]
             gold_standard = gold_standard[0][0]
             for i in range(4):
                 TP= float((prediction[gold_standard==i] == i).sum())
                 FP = float((prediction[gold_standard!=i] == i).sum())
                 TN = float(len(prediction[gold_standard!=i]) - FP )
                 FN = float(len(prediction[gold_standard==i]) - TP)
                 accuracy[i] = (TP + TN)/(TP + FN + TN + FP)
                 recall[i] = TP / (TP + FN)
                 dice_score[i] = 2*TP / (2*TP+FP+FN)
             return accuracy, recall, dice_score

In [20]: pred_dir = os.path.join(out_dir, 'pred')
         if not os.path.exists(pred_dir):
             os.makedirs(pred_dir)

         #model = SimpleNet3D(num_classes=num_classes)
         model = UNet3D(num_classes=num_classes)
         model.load_state_dict(torch.load(os.path.join(model_dir, 'model.pt')))
         model.to(device)
         model.eval()

         global_acc = torch.zeros(4)
         global_recall = torch.zeros(4)
         global_dice = torch.zeros(4)
         all_dice = []
         print('START TESTING...')

         loss_test = 0
         sum_pts = 0
         idx_test = 0
         with torch.no_grad():
```

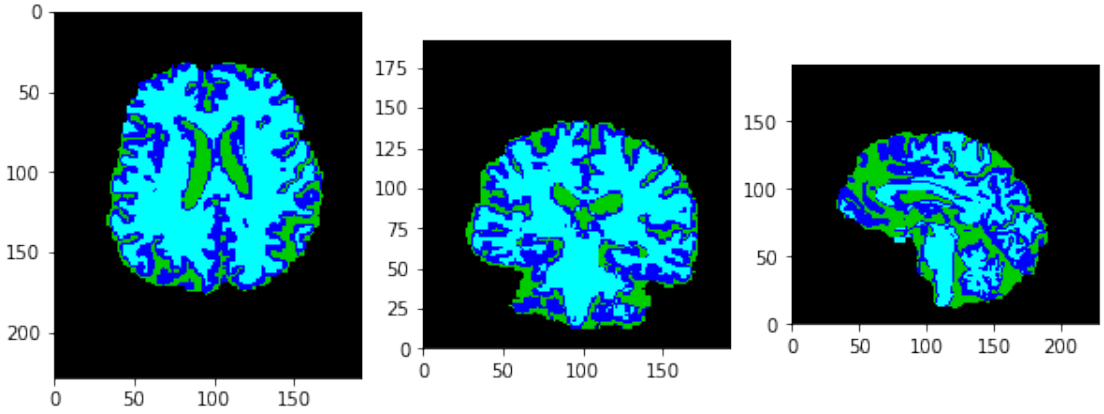
```
            for data_sample in dataloader_test:
                img, seg = data_sample['img'].to(device), data_sample['seg'].to(device)
                prd = model(img)
                prd_flat = prd.view(prd.size(0), prd.size(1), -1)
                seg_flat = seg.view(seg.size(0), seg.size(1), -1)
                loss_test += F.cross_entropy(prd_flat, seg_flat.squeeze(1), reduction='sum').i
                sum_pts += seg_flat.size(2)

                metrics = evaluate(prd_flat, seg_flat)
                global_acc = torch.add(metrics[0], global_acc)
                global_recall = torch.add(metrics[1], global_recall)
                global_dice = torch.add(metrics[2], global_dice)
                all_dice.append(metrics[2])

                prd = torch.argmax(prd, dim=1)

                sample = dataset_test.get_sample(idx_test)
                name = dataset_test.get_seg_name(idx_test)
                prediction = sitk.GetImageFromArray(prd.cpu().squeeze().numpy().astype(np.uint
                prediction.CopyInformation(sample['seg'])
                sitk.WriteImage(prediction, os.path.join(pred_dir, name))

                idx_test += 1

        loss_test /= sum_pts
        global_acc/= len(dataloader_test)
        global_recall /= len(dataloader_test)
        global_dice /= len(dataloader_test)

        print('+ TESTING \tLoss: {:.6f}'.format(loss_test))

        # Show last testing sample as an example
        print('\n\nReference segmentation')
        display_image(sitk.LabelToRGB(sample['seg']))
        print('Predicted segmentation')
        display_image(sitk.LabelToRGB(prediction))

        print("PER TISSU METRICS:")
        print("Overall per tissu Dice score:", global_dice)
        print("Overall per tissu Accuracy:", global_acc)
        print("Overall per tissu Recall", global_recall)

        print('\nFinished TESTING.')
```

```
START TESTING...
+ TESTING         Loss: 0.750655
```

Reference segmentation



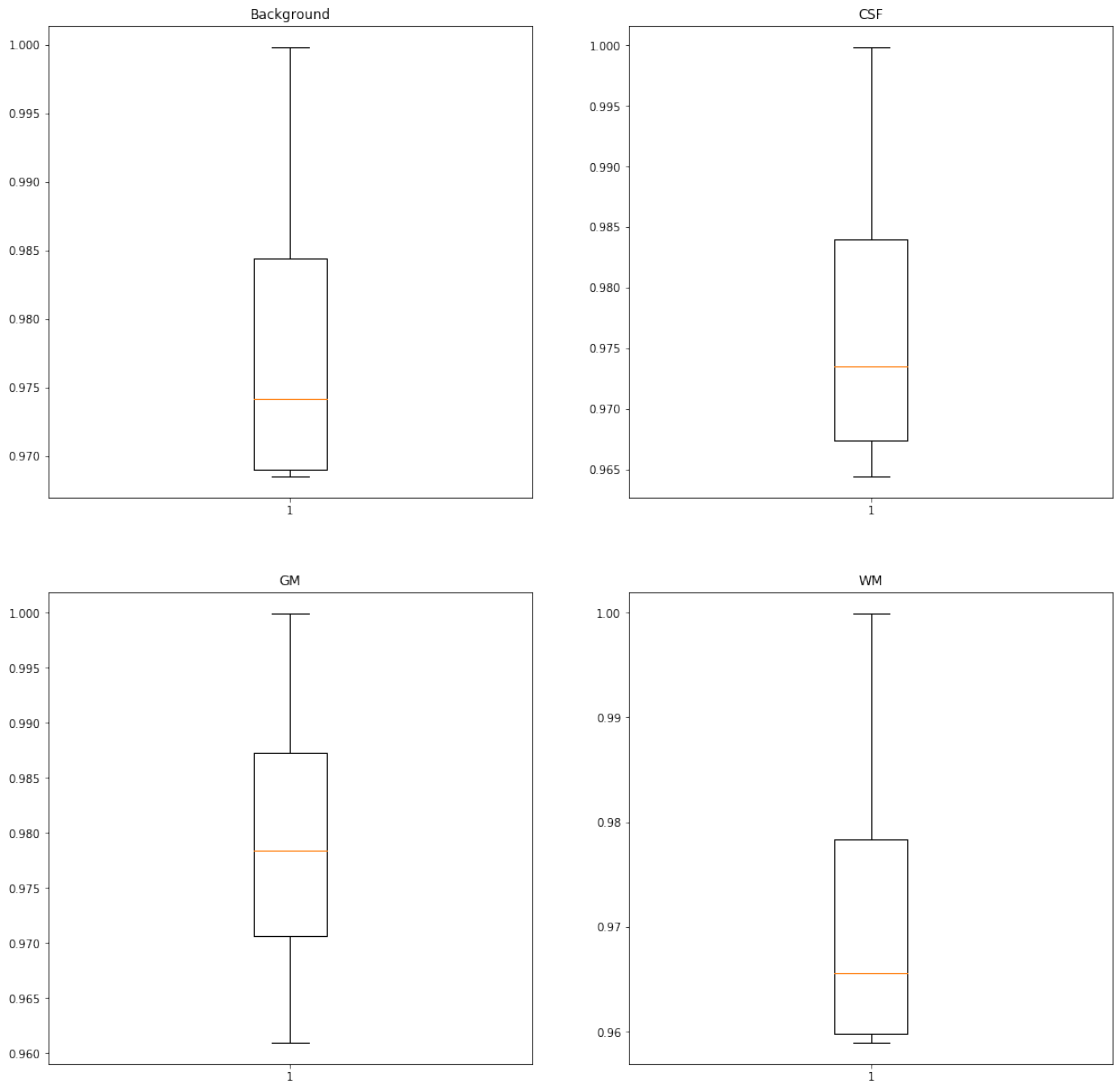
Predicted segmentation



```
PER TISSU METRICS:
Overall Dice score: tensor([0.9998, 0.9552, 0.9539, 0.9779])
Overall Accuracy: tensor([0.9996, 0.9973, 0.9938, 0.9968])
Overall Recall tensor([0.9998, 0.9372, 0.9802, 0.9645])

Finished TESTING.
```

```
In [21]: # Summarize the 600 dice score per tissue in box-and-whisker-plots
         fig = plt.figure(figsize=(17,17))
         plt.subplot(2, 2, 1)
```

```
plt.title("Background")
plt.boxplot(all_dice[:][0])
plt.subplot(2, 2, 2)
plt.title("CSF")
plt.boxplot(all_dice[:][1])
plt.subplot(2, 2, 3)
plt.title("GM")
plt.boxplot(all_dice[:][2])
plt.subplot(2, 2, 4)
plt.title("WM")
plt.boxplot(all_dice[:][3])
plt.show()
```



We observe really good dice score in this box and whisker plot for every segmentation class.

1.2.2 TASK A-2: Feature calculation

Start by calculating the three absolute tissue volumes for each subject. Plot the volumes against the subjects' ages. Taking the absolute volumes of tissues as features, however, might not be predictive. Instead, relative volumes need to be computed as the ratios between each tissue volume and overall brain volume. But you might also want to explore using different combinations or even polynomial features.

Implement a function that constructs a big matrix X with a row for each subject and features across the columns. Start with just calculating three simple features of relative tissue volumes for GM, WM and CSF, and compare these to the absolute volumes plotted above.

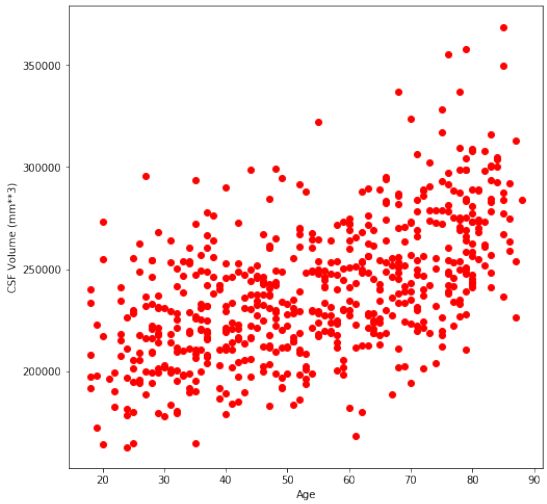
Note: If you are struggling with the previous task on image segmentation, or if you prefer to work on this and the following tasks first, you can continue here using the provided reference segmentations which can be found in a subfolder `segs_refs`.

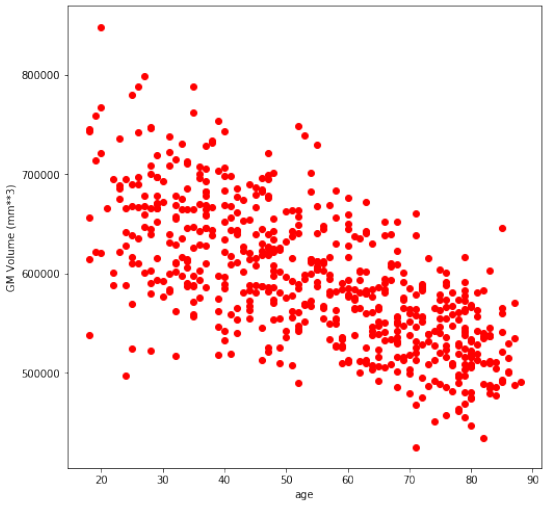
In [22]:
```
## CALCULATE ABSOLUTE TISSUE VOLUMES

import os

# USE THIS TO RUN THE CALCULATIONS ON YOUR SEGMENTATONS
seg_dir = './output/pred/'

# USE THIS TO RUN THE CALCULATIONS ON OUR REFERENCE SEGMENTATIONS
#seg_dir = data_dir + './segs_refs/'

vols = np.zeros((3,meta_data['ID'].count()))
voxel_volume = img_spacing[0]*img_spacing[1]*img_spacing[2]
#seg_filenames = glob.glob(seg_dir + '*.nii.gz')
#seg_filenames = [f for f in seg_filenames if ID in f]

for i in range(meta_data['ID'].count()):
    img = sitk.ReadImage(seg_dir + meta_data['ID'][i]+'.nii.gz')
    img_array = sitk.GetArrayFromImage(img)
    CSF = np.count_nonzero(img_array == 1)
    GM = np.count_nonzero(img_array == 2)
    WM = np.count_nonzero(img_array == 3)
    vols[0][i] = CSF * voxel_volume
    vols[1][i] = GM * voxel_volume
    vols[2][i] = WM * voxel_volume
```

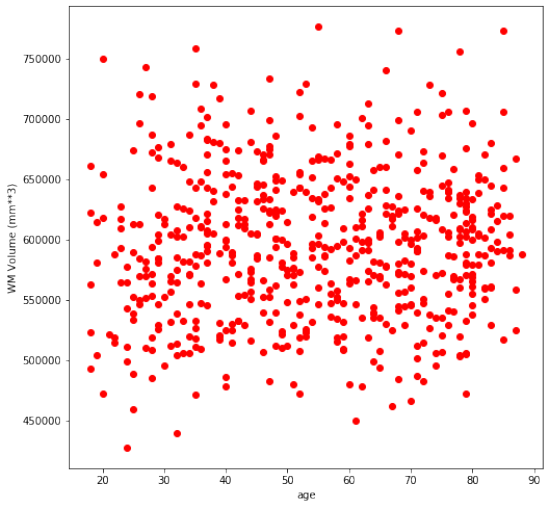
Plot features versus age.

In [23]:
```
fig = plt.figure(figsize=(18,18))
plt.subplot(2, 2, 1)

plt.scatter(meta_data['age'], vols[0][:], c='r')
plt.xlabel('Age')
plt.ylabel('CSF Volume (mm**3)')

plt.subplot(2, 2, 2)
```

```
plt.scatter(meta_data['age'], vols[1][:], c='r')
plt.xlabel('age')
plt.ylabel('GM Volume (mm**3)')

plt.subplot(2, 2, 3)
plt.scatter(meta_data['age'], vols[2][:], c='r')
plt.xlabel('age')
plt.ylabel('WM Volume (mm**3)')

plt.show()
```







In [24]:
```
## CALCULATE RELATIVE TISSUE VOLUMES

vols_normalised = np.zeros((3,meta_data['ID'].count()))
```

```
for i in range(len(vols[0])):
    CSF = vols[0][i]
    GM = vols[1][i]
    WM = vols[2][i]
    total = GM + WM + CSF
    vols_normalised[0][i] = CSF / total
    vols_normalised[1][i] = GM / total
    vols_normalised[2][i] = WM / total
```

1.2.3 TASK A-3: Age regression and cross-validation

Experiment with different regression methods from the scikit-learn toolkit. Remember to construct the output vectur y containing the age for each of the subjects.

Evaluate the methods using two-fold cross-validation where the dataset of 600 subjects is split into two equally sized sets (X_1, y_1) and (X_2, y_2) which are used for training and testing in an alternating way (so each set is used as $(X_{\text{train}}, y_{\text{train}})$ and $(X_{\text{test}}, y_{\text{test}})$ exactly once).

Try using at least three different regression methods, and generate a plot allows easy comparison of the performance of the three methods. Useful error metrics to report include mean absolute error and r2 score. You might also want to plot the real vs predicted ages.

Note: These scikit-learn examples might serve as an inspiration.

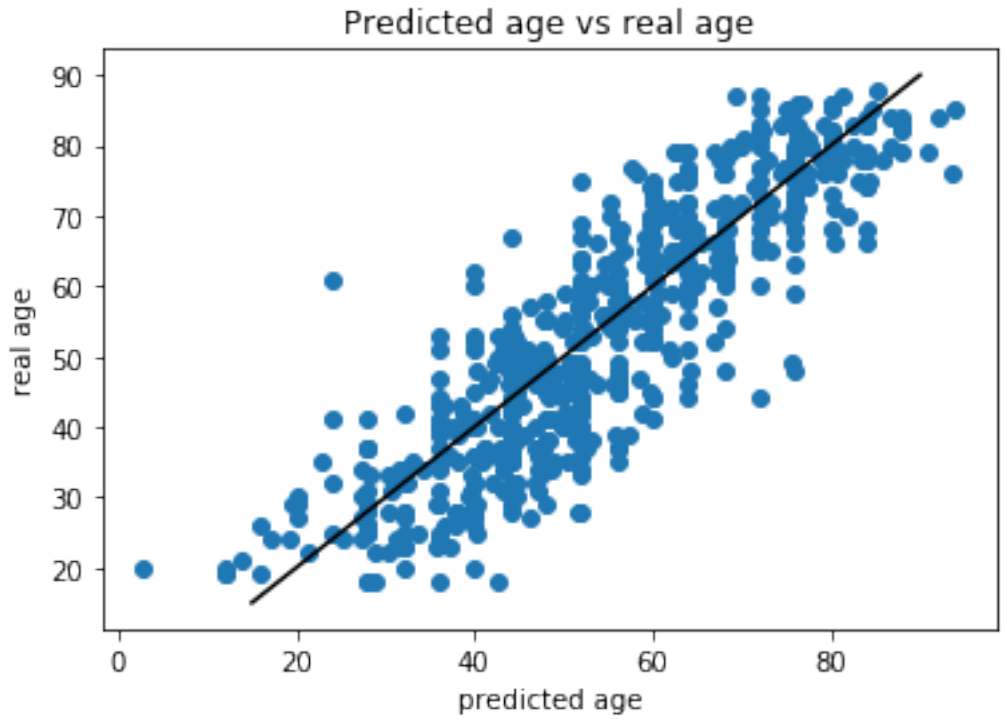
Hint: Be careful how you split the dataset into two folds. Take into account the data characteristics shown at the top of the notebook.

In [25]:
```
from sklearn.preprocessing import PolynomialFeatures
from sklearn.ensemble import RandomForestRegressor, GradientBoostingRegressor
from sklearn.svm import SVR
from sklearn import linear_model
from sklearn.utils import shuffle

# Data preprocessing
np.random.seed(0)
X = vols_normalised.T
y = meta_data['age'].values
X, y = shuffle(X, y)
poly = PolynomialFeatures(degree=2)
X = poly.fit_transform(X)
X_fold1 = X[:300]
X_fold2 = X[300:]
y_fold1 = y[:300]
y_fold2 = y[300:]



#regr = RandomForestRegressor(max_depth=3, random_state=0, n_estimators=1000, n_jobs=
#regr = GradientBoostingRegressor(max_depth=5, learning_rate=0.01, n_estimators=1000)

#fold1
regr1 = linear_model.LinearRegression()
```

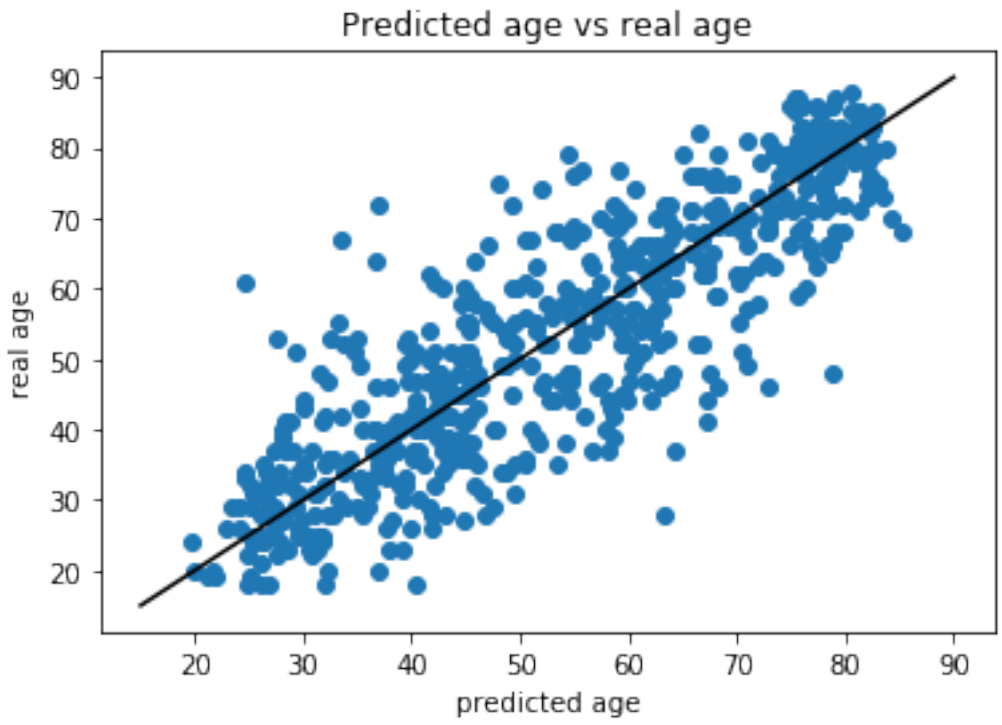
```
regr1.fit(X_fold1, y_fold1)
#fold2
regr2 = linear_model.LinearRegression()
regr2.fit(X_fold2, y_fold2)
#metrics
R2 = (regr1.score(X_fold2, y_fold2) + regr2.score(X_fold1, y_fold1))/2
predictions = np.concatenate((regr2.predict(X_fold1), regr1.predict(X_fold2)), axis=0)
MAE = sum(abs(predictions-y))/len(predictions)
#prints
print("Linear Regression")
print("R2 coefficient:", R2)
print("Mean Absolute Error:", MAE)
plt.scatter(predictions, y)
plt.plot([15,90], [15,90], c='black')
plt.title("Predicted age vs real age")
plt.xlabel('predicted age')
plt.ylabel('real age')
plt.show()

#fold1
regr1 = GradientBoostingRegressor(max_depth=5, learning_rate=0.01, n_estimators=1000)
regr1.fit(X_fold1, y_fold1)
#fold2
regr2 = GradientBoostingRegressor(max_depth=5, learning_rate=0.01, n_estimators=1000)
regr2.fit(X_fold2, y_fold2)
#metrics
R2 = (regr1.score(X_fold2, y_fold2) + regr2.score(X_fold1, y_fold1))/2
predictions = np.concatenate((regr2.predict(X_fold1), regr1.predict(X_fold2)), axis=0)
MAE = sum(abs(predictions-y))/len(predictions)
#prints
print("GradientBoosting Regression")
print("R2 coefficient:", R2)
print("Mean Absolute Error:", MAE)
plt.scatter(predictions, y)
plt.plot([15,90], [15,90], c='black')
plt.title("Predicted age vs real age")
plt.xlabel('predicted age')
plt.ylabel('real age')
plt.show()

#fold1
regr1 = RandomForestRegressor(max_depth=3, random_state=0, n_estimators=1000, n_jobs=
regr1.fit(X_fold1, y_fold1)
#fold2
regr2 = RandomForestRegressor(max_depth=3, random_state=0, n_estimators=1000, n_jobs=
regr2.fit(X_fold2, y_fold2)
#metrics
R2 = (regr1.score(X_fold2, y_fold2) + regr2.score(X_fold1, y_fold1))/2
```

```
        predictions = np.concatenate((regr2.predict(X_fold1), regr1.predict(X_fold2)), axis=0)
        MAE = sum(abs(predictions-y))/len(predictions)
        #prints
        print("RandomForest Regression")
        print("R2 coefficient:", R2)
        print("Mean Absolute Error:", MAE)
        plt.scatter(predictions, y)
        plt.plot([15,90], [15,90], c='black')
        plt.title("Predicted age vs real age")
        plt.xlabel('predicted age')
        plt.ylabel('real age')
        plt.show()
```

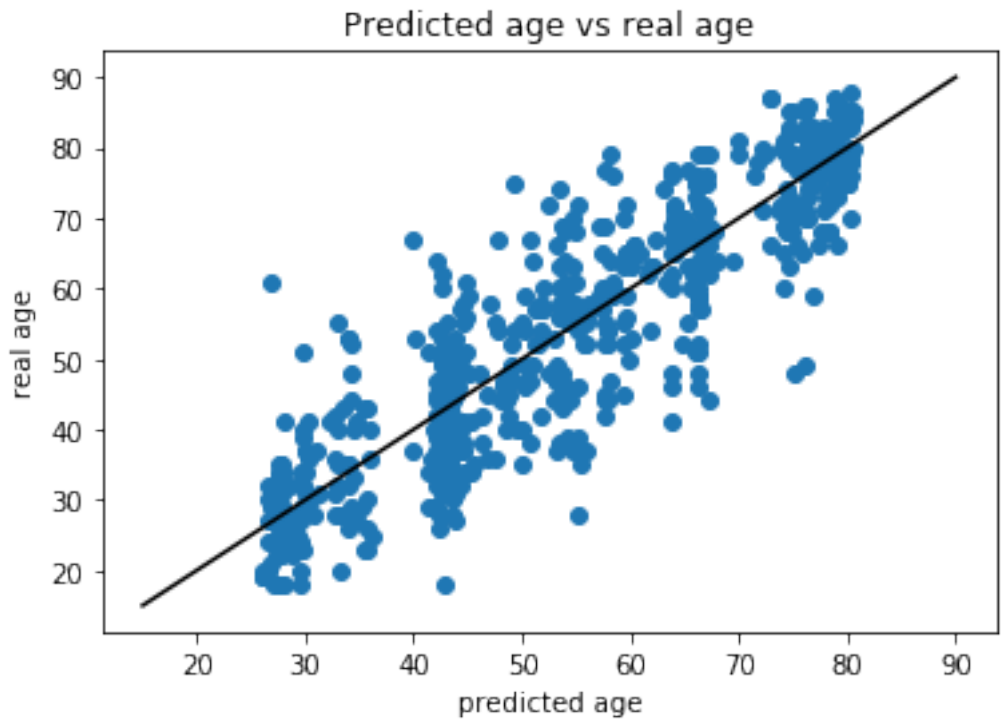
```
Linear Regression
R2 coefficient: 0.7673892837934357
Mean Absolute Error: 7.1258333333333335
```




```
GradientBoosting Regression
R2 coefficient: 0.7417827692724595
Mean Absolute Error: 7.1366001059913335
```




```
RandomForest Regression
R2 coefficient: 0.7970018489698203
Mean Absolute Error: 6.532917525305609
```



1.2.4 MAE of 6.5 with our predicted segmentation

By comparing a LinearRegressor and a fine-tuned RandomForest and GradientBoosting Regressor we are able to get a MAE of 6.5 with our predicted segmentation. The plot represent the predicted age vs the real age for each regessor. We can see how RandomForestRegressor is trying to group the prediction, while the LinearRegressor created a smoother regression.

1.3 Part B: Image-based regression using grey matter maps

The second approach will make use of grey matter maps that have been already extracted from the MRI scans and aligned to a common reference space to obtain spatially normalised maps. For this, we have used an advanced, state-of-the-art neuroimaging toolkit, called SPM12. The reference space corresponds to the commonly used MNI atlas as seen in the lecture on image segmentation.

Because these grey matter maps are spatially normalised (ie., registered), voxel locations across images from different subjects roughly correspond to the same anatomical locations. This means that each voxel location in the grey matter maps can be treated as an individual feature. Because those maps are quite large at their full resolution there would be a very large number of features to deal with (more than 850,000). A dimensionality reduction using PCA may need to be performed before training a suitable regressor on the low-dimensional feature representation obtained with PCA. It might also be beneficial to apply some pre-processing (downsampling, smoothing, etc.) before running PCA, which should be explored. The implemented pipeline should be evaluated using two-fold cross-validation using the same data splits as in part A, so the two different approaches can be directly compared in terms average age prediction accuracy.

Note: For part B, only the spatially normalised grey matter maps should be used.

1.3.1 TASK B-1: Pre-processing

Before running PCA to reduce the dimensionality of the feature space for grey matter maps, it might be beneficial to run some pre-processing on the maps. In voxel-based analysis where each voxel location is a feature, it is common to apply some smoothing beforehand. This is to reduce noise and to compensate for errors of the spatial normalisation that had been applied to the maps.

Because the maps are quite large, it might also be worthwile to explore whether downsampling could be performed even before PCA. This would further reduce the dimensionality, and might be even needed in the case where PCA on the orignial resolution runs into memory issues. You may want to consider other ways of pre-processing and you can find insipiration in the notebook on medical image computing `MLI-MIC-Summary.ipynb`.

Implement a function that performs suitable pre-processing on each grey matter map.

Hint: You may want to save the pre-processed maps using `sitk.WriteImage` to avoid recomputation each time you run the notebook.

```
In [26]: ID = meta_data['ID']

In [27]: list_filename = []
         for i in range(len(greymatter_filenames)):
             list_filename.append([f for f in greymatter_filenames if ID[i] in f][0])

In [28]: def resample(img, new_size=None, new_spacing=None):
             old_size = img.GetSize()
             old_spacing = img.GetSpacing()

             if new_size is None and new_spacing is None:
                 return img

             if new_size is None:
                 # Compute new image dimensions based on the desired rescaling of the voxel sp
                 new_size = [int(np.ceil(old_size[d] * old_spacing[d] / new_spacing[d])) for d

             if new_spacing is None:
                 # Compute new voxel spacing based on the desired rescaling of the image dimen
                 new_spacing = [old_spacing[d] * old_size[d] / new_size[d] for d in range(3)]

             # Smooth the input image with anisotropic Gaussian filter
             img_smoothed = img
             for d in range(3):
                 # Note how the blurring strength can be different in each direction,
                 # if the scaling factors are different.
                 factor = new_spacing[d] / old_spacing[d]
                 sigma = 0.2 * factor
                 img_smoothed = sitk.RecursiveGaussian(img_smoothed, sigma=sigma, direction=d)

             # Finally, apply the resampling operation
             img_resampled = sitk.ResampleImageFilter().Execute(
                 img_smoothed,        # Input image
                 new_size,            # Output image dimensions
```

```
                sitk.Transform(),     # Coordinate transformation. sitk.Transform() is a dummy
                                      # as we want the brain to be in exactly the same place.
                                      # for example, this can be a linear or nonlinear transfo
                sitk.sitkLinear,      # Interpolation method (cf. also sitk.sitkNearestNeighbo
                img.GetOrigin(),      # Output image origin (same)
                new_spacing,          # Output voxel spacing
                img.GetDirection(),   # Output image orientation (same)
                0,                    # Fill value for points outside the input domain
                img.GetPixelID())     # Voxel data type (same)

            return img_resampled
```

```
In [29]: filename_length = len(list_filename)
         img_data = []
         for i in range(filename_length):
             current_img = sitk.ReadImage(list_filename[i])
             img_diffusion = sitk.GradientAnisotropicDiffusion(current_img)
             #resampling does not offers better performance
             #img_resampled = resample(img_diffusion, new_spacing=[2.5,2.5,2.5])
             img_array = sitk.GetArrayFromImage(img_diffusion)
             img_array = img_array.reshape(-1)
             img_data.append(img_array)

         ########################################
```

```
In [30]: img_data = np.array(img_data)
```

```
In [31]: X = img_data #PRE-PROCESSED IMAGE DATA
         y = meta_data['age'].values.reshape(-1,1)

         print(X.shape)
         print(y.shape)
```

```
(600, 874800)
(600, 1)
```

1.3.2 TASK B-2: Dimensionality reduction

Implement dimensionality reduction for grey matter maps using scitkit-learn's PCA. PCA has an option to set the percentage of variance to be preserved (by setting the parameter `n_components` to a value between 0 and 1). The number of principal modes, that is the new dimensionality of the data, is then automatically determined. Try initially to preserve 95% of the variance (`n_components=0.95`).

Note: When dimensionality reduction is used as pre-processing step for supervised learning, as in this case, it is important that PCA is fitted to the training data only, but then applied to both the training and testing data. So make sure your implementation consists of two separate steps, 1) fitting the PCA model to X_{train} (using the `fit` function), and 2) applying dimensionality reduction to X_{train} and X_{test} using the `transform` function.

1.3.3 TASK B-3: Age regression and cross-validation

Experiment with different regression methods from the scikit-learn toolkit. Evaluate the methods using two-fold cross-validation in the same way as for your approach in Part A so results can be directly compared. Generate the similar plots.

Try using at least three different regression methods.

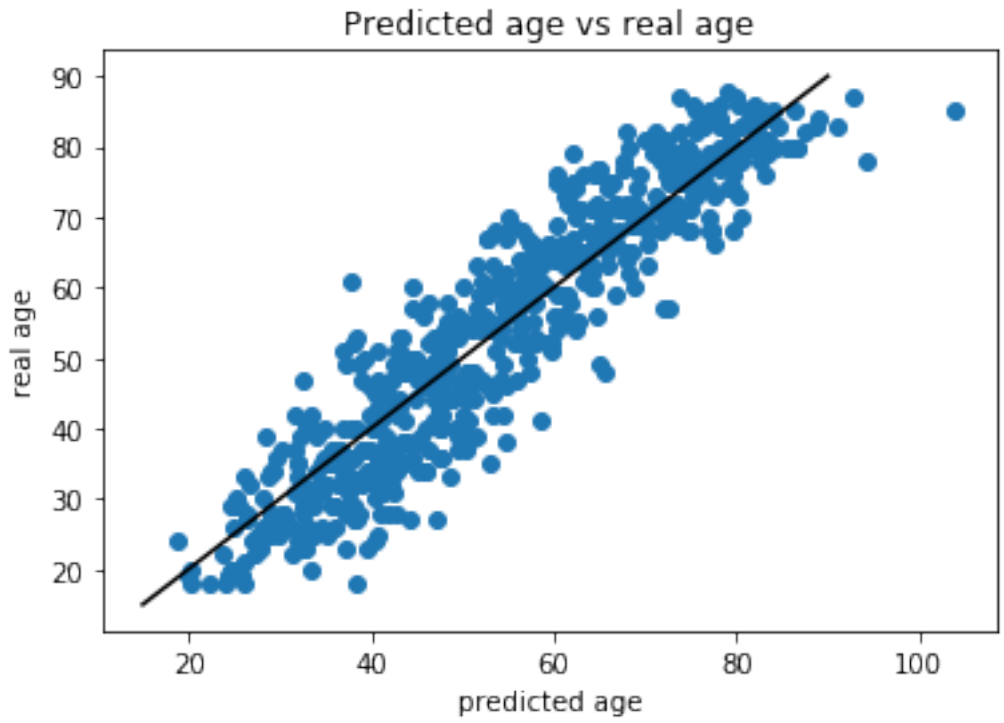
Hint: Remember, when you use cross-validation where you swap training and testing sets in each fold, you need to fit PCA to the training set of each fold.

```
In [32]: idx = np.random.permutation(len(X))
         X,y = X[idx], y[idx]

         X_fold1 = X[:300]
         X_fold2 = X[300:]
         y_fold1 = y[:300]
         y_fold2 = y[300:]
```

```
In [33]: from sklearn.preprocessing import PolynomialFeatures
         from sklearn.ensemble import RandomForestRegressor, GradientBoostingRegressor
         from sklearn.svm import SVR
         from sklearn import linear_model
         from sklearn.decomposition import PCA

         age_prediction = []

         pca1 = PCA(n_components=0.95)
         pca1.fit(X_fold2)

         pca2 = PCA(n_components=0.95)
         pca2.fit(X_fold1)

         X_fold1_pca1 = pca1.transform(X_fold1)
         X_fold2_pca1 = pca1.transform(X_fold2)


         regr1 = linear_model.LinearRegression()
         regr1.fit(X_fold2_pca1, y_fold2)
         pred1 = regr1.predict(X_fold1_pca1)

         X_fold1_pca2 = pca2.transform(X_fold1)
         X_fold2_pca2 = pca2.transform(X_fold2)

         regr2 = linear_model.LinearRegression()
         regr2.fit(X_fold1_pca2, y_fold1)
         pred2 = regr2.predict(X_fold2_pca2)

         predictions = np.concatenate((pred1, pred2), axis=0)
         MAE = sum(abs(predictions-y))/len(predictions)
         #prints
```

```
        print("Linear Regression")
        print("Mean Absolute Error:", MAE)
        plt.scatter(predictions, y)
        plt.plot([15,90], [15,90], c='black')
        plt.title("Predicted age vs real age")
        plt.xlabel('predicted age')
        plt.ylabel('real age')
        plt.show()
```

```
Linear Regression
Mean Absolute Error: [5.61117082]
```

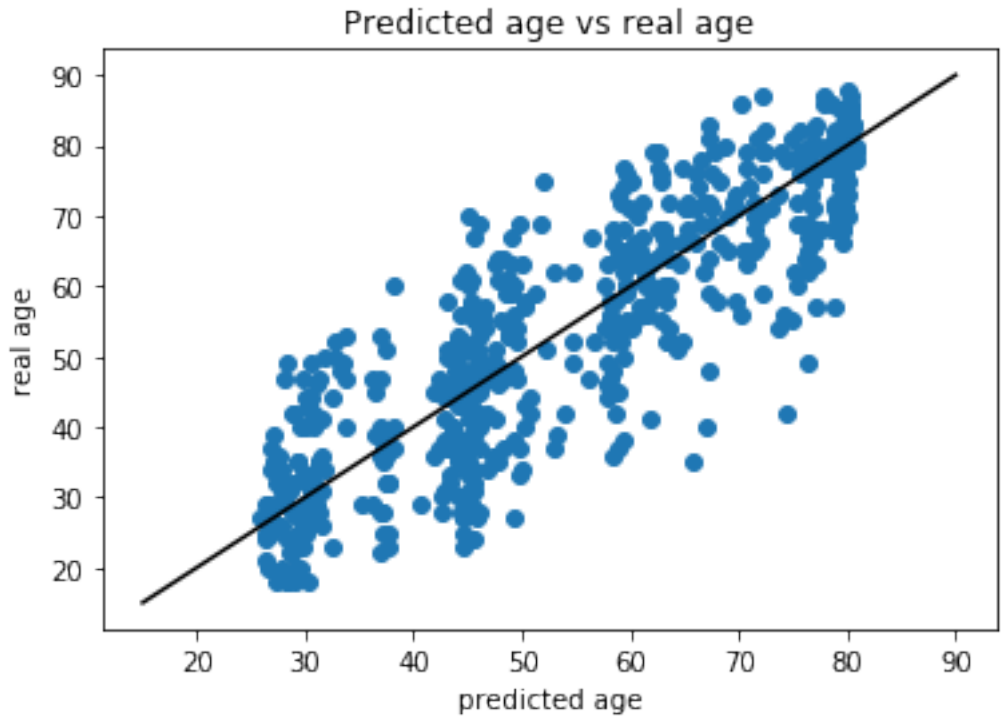



```
In [36]: #fold1
        regr1 = RandomForestRegressor(max_depth=None, n_estimators=200, n_jobs=-1)
        regr1.fit(X_fold2_pca1, y_fold2)
        pred1 = regr1.predict(X_fold1_pca1)

        #fold2
        regr2 = RandomForestRegressor(max_depth=None, n_estimators=200, n_jobs=-1)
        regr2.fit(X_fold1_pca2, y_fold1)
        pred2 = regr2.predict(X_fold2_pca2)

        predictions = np.concatenate((pred1, pred2), axis=0)
```

```
        MAE = np.sum(abs(predictions-y.reshape(600,)))/len(predictions)
        #prints
        print("Random Forest")
        print("Mean Absolute Error:", MAE)
        plt.scatter(predictions, y)
        plt.plot([15,90], [15,90], c='black')
        plt.title("Predicted age vs real age")
        plt.xlabel('predicted age')
        plt.ylabel('real age')
        plt.show()
```

```
c:\users\theoc\appdata\local\programs\python\python36\lib\site-packages\ipykernel_launcher.py:3
  This is separate from the ipykernel package so we can avoid doing imports until
c:\users\theoc\appdata\local\programs\python\python36\lib\site-packages\ipykernel_launcher.py:8
```

```
Random Forest
Mean Absolute Error: 7.258100000000001
```



In [ ]: