

# Brain MRI quality check

Project for CSCE-E2, Fall 2021, Harvard University

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## Abstract

Brain MRI quality checks are a active area of research in the medical imaging community. An MRI can be affected by patient's motion or magnetic artifacts. Research assistants have to spend many hours to visually identify whether an MRI is usable. This project aims to automate that manual labor. A 3D kernel is traversed along the 3D MRI to learn block features. Those features are represented by a continuous distribution named kernel density estimation. The distributions are compared against a pool of known good and bad images using multiple similarity measures. Pearson correlation metric gives the best results for DIAGNOSE CTE data used in this project. An MRI is declared as a good or bad one based on its highest similarity against the particular pool of images. Bootstrapping is used to increase the number of unbalanced samples. Finally, confusion matrix is used to demonstrate results.

```
In [22]: from Python.display import display, Image
```

## Problem

Patients can hardly remain still inside an MRI machine. Their motion affects the quality of an MRI scan. Moreover, magnetic field in the machine can induce artifacts in the MRI. These limitations sometimes make an MRI unusable that must be omitted from population analysis. They are:

- Motion artifact
- Ringing artifact
- Signal drop artifact

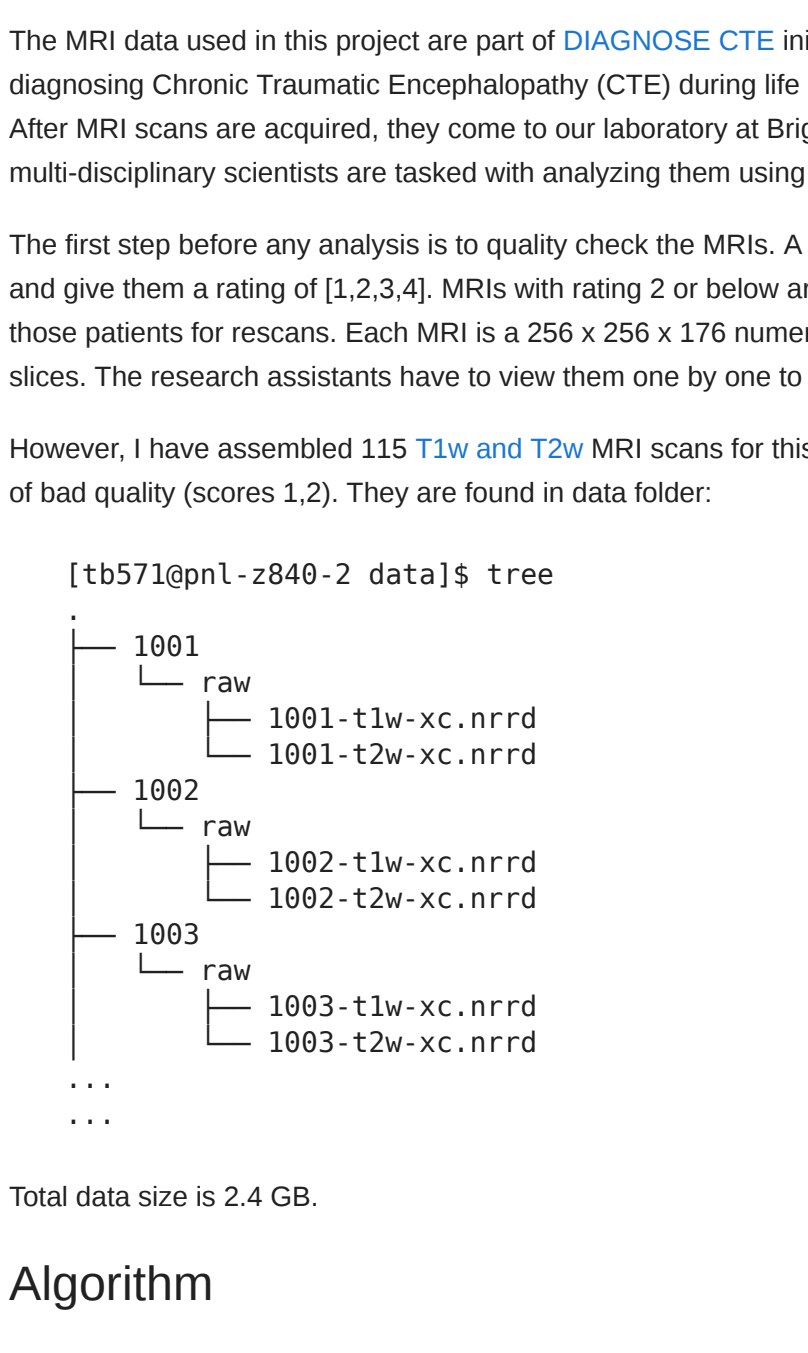
```
In [28]: display(Image(filename="artifacts/motion.png", height=480, width=480))
```



- Motion artifact

Distorted brain

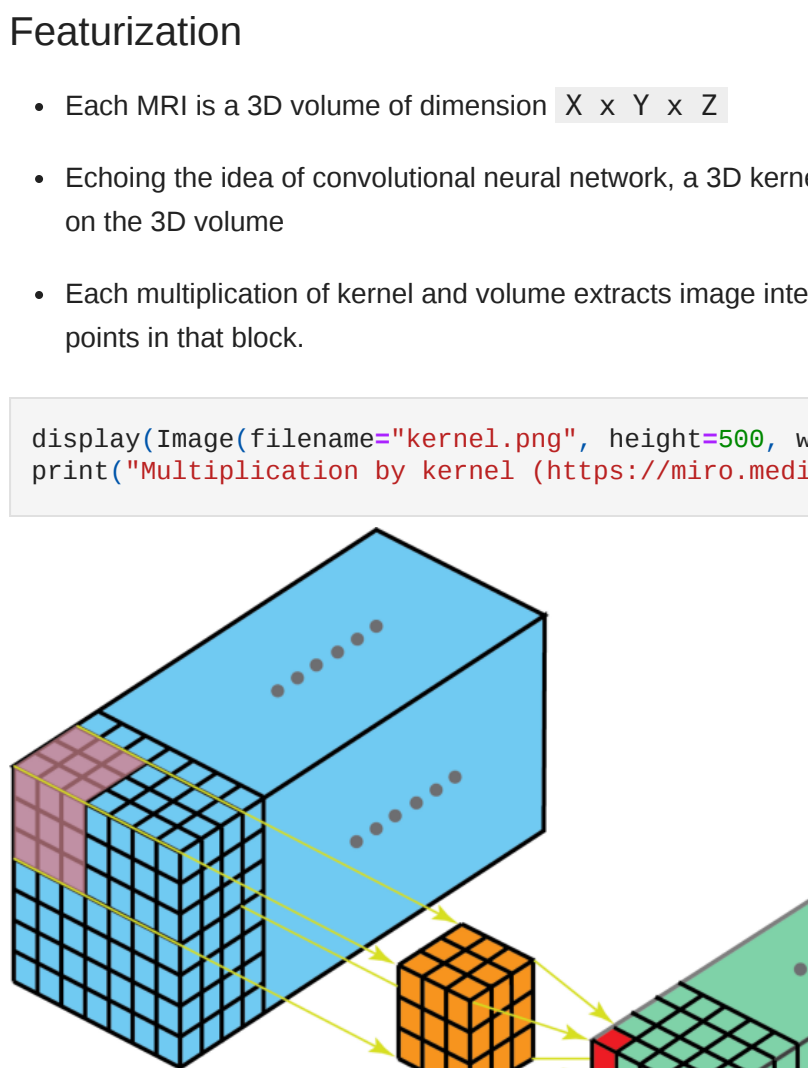
```
In [29]: display(Image(filename="artifacts/ringing.png", height=480, width=480))
```



- Ringing artifact

Circular line over the brain

```
In [30]: display(Image(filename="artifacts/signal_drop.png", height=480, width=480))
```



- Signal drop artifact

Part of back-upper brain is missing

Human has to go through several slices of a 3D MRI scan to determine the existence of artifacts. This project aims to automatically rate an MRI at a scale of 1-4, where 1 is the higher the better quality. I used to use 3-D block features and a histogram matching technique to identify bad scans by comparing them against ground truths.

## Data

The MRI data used in this project are part of **DIAGNOSE CTE** initiative. It is a 7-Year multi-site research project to develop methods of diagnosing Chronic Traumatic Encephalopathy (CTE) during life and to examine potential risk factors for this degenerative brain disease. After MRI scans are acquired, they come to our laboratory at Brigham and Women's Hospital and Harvard Medical School. A group of multi-disciplinary scientists are tasked with analyzing them using various neuroimaging tools.

The first step before any analysis is to quality check the MRIs. A pool of postbacalaureate research assistants observe the MRIs visually and give them a rating of {1,2,3,4}. MRIs with rating 2 or below are discarded from further study. MRI acquisition sites are advised to recall those patients for rescans. Each MRI is a 256 x 256 x 176 numeric array of intensities. Each slice is 256 x 256. Therefore there are 176 slices. These research assistants have to view them one by one to determine usability. This step is burdensome.

However, I have assembled 115 T1w and 12w MRI scans for this project. Most of them are of good quality (scores 3,4). Some of them are of bad quality (scores 1,2). They are found in data folder:

```
[tbs7]epnl-2840-2 data$ tree
├── 1001
│   ├── raw
│   │   ├── 1001-t1w-xc-nrrd
│   │   └── 1001-t2w-xc-nrrd
│   └── hist
│       ├── 1002-t1w-xc-nrrd
│       └── 1002-t2w-xc-nrrd
├── 1002
│   ├── raw
│   │   ├── 1002-t1w-xc-nrrd
│   │   └── 1002-t2w-xc-nrrd
│   └── hist
│       ├── 1003-t1w-xc-nrrd
│       └── 1003-t2w-xc-nrrd
├── ...
└── 1003
    ├── raw
    │   ├── 1003-t1w-xc-nrrd
    │   └── 1003-t2w-xc-nrrd
    └── hist
        ├── 1003-t1w-xc-nrrd
        └── 1003-t2w-xc-nrrd
```

Total data size is 2.4 GB.

## Algorithm

This section is divided into three subsections:

- Preprocessing
- Featurization
- Comparison
- Decision

### Preprocessing

All MRIs are non-linearly registered to a reference MRI. This step omits the effect of size/shape difference among brain scans. It also reduces motion artifact in the brain scans.

### Featurization

- Each MRI is a 3D volume of dimension  $X \times Y \times Z$ .

Echoing the idea of convolutional neural network, a 3D kernel of dimension  $nx \times ny \times nz$  with strides  $sx \times sy \times sz$  is applied on the 3D volume

- Each multiple application of kernel and volume extracts image intensities (features) over the 3D block. There are  $nx \times ny \times nz$  data points in that block.

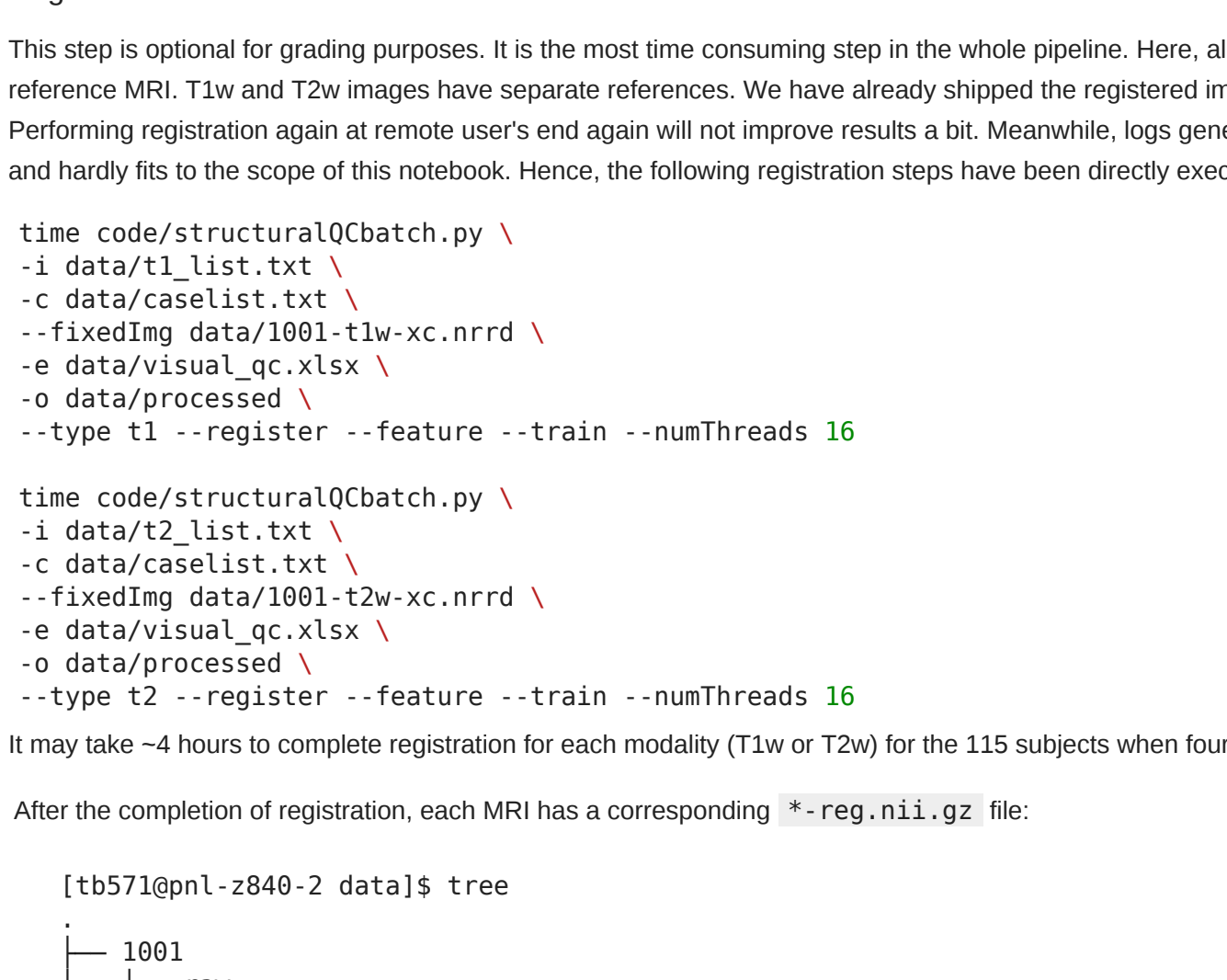
```
In [31]: display(Image(filename="kernel.png", height=580, width=580))
print("Multiplication by kernel (https://medium.com/max/7906/1?wUvVqZn2hwVKqy0TBK_5sq.png)")
```



Multiplication by kernel (https://medium.com/apache-mxnet/3d-3d-convolutions-explained-with-ms-excel-5f88c0f95943)

- A histogram is calculated for each 3D block. To facilitate further calculation, a smoothing technique e.g. kernel density estimation is adopted on the 3D block. Thus, we derive a continuous distribution of features at each 3D block.

```
In [26]: display(Image(filename=" KDE.png", height=480, width=680))
print("Histogram to kernel density (https://en.wikipedia.org/wiki/kernel_density_estimation)")
```



Histogram to kernel density (https://en.wikipedia.org/wiki/kernel\_density\_estimation)

### Comparison

- To decide whether an MRI is good or bad, we compare it against a pool of known good and bad ones. The latter ground truth is developed by human raters. Human raters are trained research assistants who visually observe each MRI and gives it a rating {1,2,3,4} where 1 is the most artifact affected and 4 is the perfect one.

- Image similarity is compared at that 3D block level. The algorithm is equipped to use one of the four techniques for comparing two distributions:
  - Pearson correlation coefficient
  - Bhattacharyya distance
  - Kullback-Leibler divergence
  - Mean squared error

The higher the Pearson correlation coefficient, the more is the similarity. Meanwhile, the lower the other measures, the more is the similarity.

- Each of the techniques yields some number for each comparison. Thereby, we represent each 3D block by a single number. In total, there are  $X \times Y \times Z$  number of features. They are averaged to reduce to one single number for each MRI. Thus, we have a score for each MRI when compared against a ground truth image.

- Since we have four discrete human ratings {1,2,3,4}, we have four pool of ground truth images. An MRI gets a pool of comparison scores for each rating. We average them to get a single score for each rating.

- An input MRI is assigned a rating corresponding to the highest/lowest similarity score. Let's take a look at the following example:

Ground truth rating	Pool of scores	Average score	Final rating
1	[0.2, 0.2, 0.1, 0.3]	0.2	2
2	[0.8, 0.8, 0.9, 0.7]	0.8	
3	[0.1, 0.1, 0.1, 0.1]	0.1	
4	[0.9, 0.1, 0.1, 0.9]	0.5	

The MRI got rating 2 since its average similarity score (Pearson correlation coefficient) is the highest for pool of ground truth images with rating 2.

### Decision

Did the above MRI pass or fail the goodness check algorithm? To answer that question, the user needs to define a 'decisionFactor' in the code/code\_xml.ini file. The decision criterion is:

```
'pass' if similarity_scores > score_range / decisionFactor else 'fail'
```

In the above example, `score_range=4`. If `decisionFactor=2`, then the threshold is `4/2=2`. Since it got a rating of 2, it failed the goodness check algorithm. So either the patient should be called in for a rescans or this image should be omitted from further population analysis.

## Program

In this section, we shall describe how to run this project at a remote user's end. This section is divided into following subsections:

- Dependencies
- Installation
- Execution
  - Registration
  - Training and testing

### Dependencies

The dependencies are noted in `environment.yml` file:

```
name: ANTs-2.3.0
channels:
  - conda-forge
dependencies:
  - ANTs==2.3.0
  - numpy
  - nibabel
  - pandas
  - xarray
  - scipy
  - psutil
  - plumbum
  - ants
  - conda-build
  - sklearn
  - openpyxl
  - pytorch
```

The only outstanding dependency is **ANTs**. It is the state of the art tool for performing registration among neuroimages.

### Installation

Please run the following commands in your terminal:

```
# install Python 3
wget https://raw.githubusercontent.com/miniconda3/miniconda3-latest-linux-x86_64.sh
sh miniconda3-latest-linux-x86_64.sh -b -p miniconda3
source miniconda3/bin/activate

# clone this project
git clone https://github.com/tashrifbillah/csci_e82_project.git
cd csci_e82_project

# build Python environment
conda env create -f environment.yml
conda activate structQC

export ANTS_PATH=$(dirname $(which ANTsApplyTransforms))

Now launch Jupyter notebook from that terminal to run csci_e82_project.ipynb at your end.
```

Finally, you should download the data used in this project as:

```
cd csci_e82_project/
wget https://www.dropbox.com/s/y3mb3l5y17rP49/csci_e82_project_data.tar.gz
tar -xvzf csci_e82_project_data.tar.gz
```

Please make sure the data got extracted to `csci_e82_project/data/`:

- Click here

### Execution

After installation is complete, the `code/config.ini` file needs to be updated with user's paths:

```
train_visual_qc = /home/tbs7/ml_class/csci_e82_project/data/train_visual_qc.xlsx
test_visual_qc = /home/tbs7/ml_class/csci_e82_project/data/test_visual_qc.xlsx
fixedimage1 = /home/tbs7/ml_class/csci_e82_project/data/1001-t1w-xc-nrrd
fixedimage2 = /home/tbs7/ml_class/csci_e82_project/data/1001-t2w-xc-nrrd
fixedmask1 = /home/tbs7/ml_class/csci_e82_project/data/patch_histograms_t1.npy
t2histogram = /home/tbs7/ml_class/csci_e82_project/data/patch_histograms_t2.npy
```

Now you can proceed to executing the codes.

### Registration

This step is optional for grading purposes. It is the most time consuming step in the whole pipeline. Here, all MRIs are registered to a reference MRI. T1w and T2w images have separate references. We have already shipped the registered images with the submission.

Performing registration again at remote user's end again will not improve results a bit. Meanwhile, logs generated from ANTs are pretty big and hardly fits to the scope of this notebook. Hence, the following registration steps have been directly executed in a Linux terminal.

```
time code/structuralQCbatch.py \
-i data/t1_list.txt \
-c data/caselist.txt \
-f fixeding_data/1001-t1w-xc-nrrd \
-e data/train_visual_qc.xlsx \
-o data/processed \
--type t1 --register --feature --train --numThreads 16

time code/structuralQCbatch.py \
-i data/t2_list.txt \
-c data/caselist.txt \
-f fixeding_data/1001-t2w-xc-nrrd \
-e data/test_visual_qc.xlsx \
-o data/processed \
--type t2 --register --feature --train --numThreads 16
```

It may take ~4 hours to complete registration for each modality (T1w or T2w) for the 115 subjects when four threads are used.

After the completion of registration, each MRI has a corresponding `*-reg.nii.gz` file:

```
[tbs7]epnl-2840-2 data$ tree
├── 1001
│   ├── raw
│   │   ├── 1001-t1w-xc-nrrd
│   │   ├── 1001-t1w-xc-reg.nii.gz
│   │   ├── 1001-t2w-xc-nrrd
│   │   └── 1001-t2w-xc-reg.nii.gz
│   └── hist
│       ├── 1002-t1w-xc-nrrd
│       └── 1002-t2w-xc-nrrd
├── 1002
│   ├── raw
│   │   ├── 1002-t1w-xc-nrrd
│   │   ├── 1002-t1w-xc-reg.nii.gz
│   │   ├── 1002-t2w-xc-nrrd
│   │   └── 1002-t2w-xc-reg.nii.gz
│   └── hist
│       ├── 1003-t1w-xc-nrrd
│       └── 1003-t2w-xc-nrrd
├── ...
└── 1003
    ├── raw
    │   ├── 1003-t1w-xc-nrrd
    │   ├── 1003-t1w-xc-reg.nii.gz
    │   ├── 1003-t2w-xc-nrrd
    │   └── 1003-t2w-xc-reg.nii.gz
    └── hist
        ├── 1003-t1w-xc-nrrd
        └── 1003-t2w-xc-nrrd
```

Before we begin training and testing, let's take a look at the rating distribution:

```
In [84]: import pandas as pd
from sklearn.model_selection import train_test_split

# load lists
df = pd.read_excel('data/visual_qc.xlsx')

for score in range(1,5):
    print('Score', score)
    train_visual, test_visual, train_cases, test_cases, train_files, test_files = \
        train_test_split(df[df['score']==score], df[df['score']==score].get_group(score).shape[0],
                        df[df['score']==score].get_group(score).shape[8])
    print('t1')
    print('t2')
```

Score 1  
T1w 11  
T2w 4

Score 2  
T1w 9  
T2w 28

Score 3  
T1w 66  
T2w 38

Score 4  
T1w 29  
T2w 61

There is imbalance in rating distribution. The number of scores 1 and 2 (bad images) are quite less than that of 3 and 4 (good images). So we shall apply bootstrapping to increase the bad samples.

```
In [89]: def partition(modality):
    # load lists
    df = pd.read_excel('visual_qc.xlsx')

    with open('caselist.txt') as f:
        cases = f.read().strip().split()

    with open('modality_reg_list.txt') as f:
        files = f.read().strip().split()

    # Bootstrapping begins == #

    # bootstrap 1 and 2 ratings to obtain twice as many as given samples
    df1 = df[df['modality'] == modality]
    df2 = df1.append(df1.sample(frac=1, replace=True))

    df2 = df2[df2['modality'] == modality]
    df2 = df2.append(df2.sample(frac=1, replace=True))

    # update df
    df = df.append(df1)
    df = df.append(df2)

    # update cases
    cases = df['Subject ID'].values

    # update files
    template_files[]
    for new_case in df1['Subject ID'].values:
        files.append(template.replace(str(cases[0]), str(new_case)))

    for new_case in df2['Subject ID'].values:
        files.append(template.replace(str(cases[0]), str(new_case)))

    # Bootstrapping ends == #

    # define train test split
    train_visual, test_visual, train_cases, test_cases, train_files, test_files = \
        train_test_split(df, cases, files, test_size=0.25, stratify=df['modality'] * score))

    # save lists
    train_visual.to_excel('train_visual_qc.xlsx', index=False)
    test_visual.to_excel('test_visual_qc.xlsx', index=False)

    with open('train_reg_list.txt', 'w') as f:
        for i in train_files:
            f.write(f'{i}\n')

    with open('test_reg_list.txt', 'w') as f:
        for i in test_files:
            f.write(f'{i}\n')

    with open('train_cases.txt', 'w') as f:
        for i in train_cases:
            f.write(f'{i}\n')

    with open('test_cases.txt', 'w') as f:
        for i in test_cases:
            f.write(f'{i}\n')
```

### Training and testing

We have already shipped the training features (t1histogram and t2histogram) with this submission. Performing training again will overwrite those features. If you want to use packaged training features, you can skip to the testing step. Otherwise, you can obtain new training features as follows:

```
In [75]: !cd data/
!python code/structuralQCbatch.py \
-i data/train_reg_list.txt \
-c data/test_cases.txt \
-f fixeding_data/1001-t1w-xc-nrrd \
-e data/train_visual_qc.xlsx \
-o data/processed \
--type t1 \
--feature --train \
--numThreads 16
```

antsApplyTransformsByQuick.sh found

Registration found

All executables are found, program will begin now ...

Calculating histogram of 5887-t1w-xc-reg.nii.gz

Calculating histogram of 5894-t1w-xc-reg.nii.gz

Calculating histogram of 5895-t1w-xc-reg.nii.gz

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