	Brain MRI goodness check Project for CSCI E-82, Fall 2021, Harvard University By Tashrif Billah Abstract Brain MRI quality check is an 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 usuable. 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
In [22]:	continuous distribution named kernel density estimation. The distributions are compared against a pool of known good and bad images using multiple similarity metrices. 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. from IPython.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
In [28]:	 analysis. They are: Motion artifact Ringing artifact Signal drop artifact display(Image(filename="artifacts/motion.png", height=400, width=400))
	B: 3002-t1w-xc
In [29]:	• Motion artifact Distorted brain display(Image(filename="artifacts/ringing.png", height=400, width=400))
	B _x 1028-t1w-xe • Ringing aritifact
In [30]:	Circular line over the brain display(Image(filename="artifacts/signal_drop.png", height=400, width=400))
	B: 7008-t2w-xc • Signal drop artifact
	Part of back-upper brain is missing A 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 on a scale of 1-4, the higher the better quality. I intend 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 postbaccalaureate 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. The research assistants have to view them one by one to determine usability. This step is burdensome. However, I have assembled 115 TIw and T2w 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: [tb571@pn1-z840-2 data] \$ tree 1001
	Total data size is 2.4 GB. Algorithm This section is divided into three subsections: Preprocessing Featurization Comparision
	 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 x Y x Z Echoing the idea of convolutional neural network, a 3D kernel of dimension nx x ny x nz with strides sx x sy x sz is applied
In [31]:	on the 3D volume • Each multiplication of kernel and volume extracts image intensities (features) over the 3D block. There are nx x ny x nz data points in that block. display(Image(filename="kernel.png", height=500, width=500)) print("Multiplication by kernel (https://miro.medium.com/max/700/1*wUVVgZnzBwYKgQyTBK_5sg.png)")
In [26]:	Multiplication by kernel (https://medium.com/apache-mxnet/1d-3d-convolutions-explained-with-ms-excel-5f88c0f35941) • A histogram is calculated for each 3D block. To facilitate further calculation, a smoothing technique e.g. kernel density estimation is applied on the 3D block. Thus, we derive a continuous distribution of features at each 3D block. display(Image(filename="KDE.png", height=400, width=600)) 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 one number for each comparison. Thereby, we represent each 3D block by a single number. In total,
	there are X x Y x Z such numbers. 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
	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/config.ini file. The decision criterion is:
	'pass' if similarity_score > 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 rescan 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
	 Installation Execution Registration Training and Testing Dependencies The dependencies are noted in environment.yml file: ANTs==2.3.0 numpy nihabel
	 nibabel pandas xlrd scipy psutil plumbum ants conda-build sklearn openpyxl pynrrd
	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://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh sh Miniconda3-latest-Linux-x86_64.sh -b -p mininconda3 source miniconda3/bin/activate
	<pre># 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 # set up bash environment export ANTSPATH=\$(dirname `which antsApplyTransforms`) Now launch jupyter-notebook from that terminal to run csci_e82_project.ipynb at your end.</pre>
	Finally, you should download the data used in this project as: cd csci_e82_project/ wget https://www.dropbox.com/s/yim3blsy17krp49/csci_e82_project_data.tar.gz tar -xzvf 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/tb571/ml_class/csci_e82_project/data/train_visual_qc.xlsx test_visual_qc = /home/tb571/ml_class/csci_e82_project/data/test_visual_qc.xlsx fixedimaget1 = /home/tb571/ml_class/csci_e82_project/data/1001-tlw-xc.nrd fixedimaget2 = /home/tb571/ml_class/csci_e82_project/data/1001-t2w-xc.nrd fixedmaskt1 = fixedmaskt2 = tlhistogram = /home/tb571/ml_class/csci_e82_project/data/patch_histograms_t1.npy t2histogram = /home/tb571/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 \ -fixedImg data/1001-t1w-xc.nrrd \ -e data/visual_qc.xlsx \ -o data/processed \type t1registerfeaturetrainnumThreads 16
	time code/structuralQCbatch.py \ -i data/t2_list.txt \ -c data/caselist.txt \ -fixedImg data/1001-t2w-xc.nrrd \ -e data/visual_qc.xlsx \ -o data/processed \type t2registerfeaturetrainnumThreads 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:
	[tb571@pnl-z840-2 data]\$ tree .
	- 1002-t2w-xc-reg.nii.gz - 1003 - raw - 1003-t1w-xc.nrrd - 1003-t1w-xc-reg.nii.gz - 1003-t2w-xc.nrrd - 1003-t2w-xc.nrrd - 1003-t2w-xc.nrrd - 1003-t2w-xc-reg.nii.gz - 1003-t2w-xc-reg.nii.gz - 1003-t2w-xc-reg.nii.gz
In [84]:	<pre>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) print('T1w', df.groupby('t1 score').get_group(score).shape[0]) print('T2w', df.groupby('t2 score').get_group(score).shape[0]) print('')</pre>
	Score 1 T1W 11 T2W 4 Score 2 T1W 9 T2W 20 Score 3 T1W 66 T2W 30 Score 4 T1W 29 T2W 61
In [89]:	 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. def partition(modality): # load lists df= pd.read_excel('visual_qc.xlsx') with open('caselist.txt') as f: cases= f.read().strip().split()
	<pre>with open(f'{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[f'{modality} score']==1] df1=df1.append(df1.sample(frac=1, replace=True)) df2= df[df[f'{modality} score']==2] df2=df2.append(df1.sample(frac=1, replace=True)) # update df df=df.append(df1)</pre>
	<pre>df=df.append(df2) # update cases cases= df['Subject ID'].values # update files template= files[0] 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 === #</pre>
	<pre># 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[f'{modality} score']) # save lists train_visual.to_excel(f'train_visual_qc.xlsx', index=False) test_visual.to_excel(f'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')</pre>
	<pre>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')</pre> Training and testing
	We have already shipped the training features tlhistogram 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: Tlw MRI **Cd data/partition('t1') **Cd /home/tb571/ml_class/csci_e82_project/data /home/tb571/ml_class/csci_e82_project
[n [77]:	, ,
	antsRegistrationSyNQuick.sh found antsRegistration found All executables are found, program will begin now Calculating histogram of 5007-t1w-xc-reg.nii.gz Calculating histogram of 3024-t1w-xc-reg.nii.gz Calculating histogram of 1035-t1w-xc-reg.nii.gz Calculating histogram of 5030-t1w-xc-reg.nii.gz Calculating histogram of 5016-t1w-xc-reg.nii.gz Calculating histogram of 5015-t1w-xc-reg.nii.gz Calculating histogram of 5003-t1w-xc-reg.nii.gz Calculating histogram of 5003-t1w-xc-reg.nii.gz Calculating histogram of 7028-t1w-xc-reg.nii.gz Calculating histogram of 5025-t1w-xc-reg.nii.gz Calculating histogram of 1030-t1w-xc-reg.nii.gz Calculating histogram of 1030-t1w-xc-reg.nii.gz Calculating histogram of 1018-t1w-xc-reg.nii.gz
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Checking quality ... 2 fail /home/tb571/ml_class/csci_e82_project/data/3023/raw/3023-t1w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/3009/raw/3009-t1w-xc-reg.nii.gz Registered image found ... 1 fail /home/tb571/ml_class/csci_e82_project/data/1010/raw/1010-t1w-xc-reg.nii.gz Registered image found ... Checking quality ... Checking quality ... Checking quality ... 3 pass 4 pass 3 pass 1 fail 4 pass 3 pass Checking quality ... Checking quality ... Checking quality ... 4 pass 3 pass 1 fail 1 fail 4 pass 3 pass 4 pass 3 pass 1 fail 1 fail Time taken in quality checking 486.03051495552063 seconds In [79]: %cat data/processed/confusion_matrix.txt Confusion matrix (columns are true labels, rows are predicted labels): Visual discrete scores are: [1, 2, 3, 4] [[14 0 0 0] [0 3 2 0] [0 0 8 8] $[0 \ 0 \ 0 \ 7]]$ Observation Presence of some off-diagonal elements in the confusion matrix tells us that not all human ratings have been accurately recovered. But we care more about the pass/fail decision where decision threshold of 2 comes into play. This threshold allows us to consolidate each quadrant of the above matrix as: [[17 2] [0 23]] From the consolidated confusion matrix, we conclude that the algorithm has mostly been able to decide which MRIs are good and which are bad ones. The number of misclassification is only 2. Moreover, a -t*w-xc-reg-quality.txt file corresponding to each MRI has been created with the decision to accept/reject: Predicted score: 3 (1 being worst, 4 being best) Decision: pass Furthermore, a combined scores files has been created: [tb571@pnl-z840-2 data]\$ cat processed/t1 QC scores.csv Case #, "Predicted score (1 being worst, 4 being best)", Quality 7024,4,pass 7027,1,fail 3021,1,fail 3005,4,pass . . . Any of the above can be considered to realize algorithm performance. T2w MRI In [93]: %cd data/ partition('t2') %cd .. /home/tb571/ml_class/csci_e82_project/data /home/tb571/ml_class/csci_e82_project In [97]: # Train (calculate histogram) !python code/structuralQCbatch.py \ -i data/train_reg_list.txt \ -c data/train_cases.txt \ --fixedImg data/1001-t2w-xc.nrrd \ -e data/train_visual_qc.xlsx \ -o data/processed \ --type t2 \ --feature --train \ --numThreads 16 antsApplyTransforms found antsRegistrationSyNQuick.sh found antsRegistration found All executables are found, program will begin now ... 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7028-t2w-xc-reg.nii.gz Histogram calculation successful of 7008-t2w-xc-reg.nii.gz Histogram calculation successful of 1027-t2w-xc-reg.nii.gz Completed histogram calculation of all the subjects. Time taken in histogram calculation 96.53516745567322 seconds Time taken in feature extraction for training 96.73375797271729 seconds In [95]: # Test (predict goodness) !python code/structuralQCbatch.py \ -i data/test_reg_list.txt \ -c data/test_cases.txt \ --fixedImg data/1001-t2w-xc.nrrd \ -e data/test_visual_qc.xlsx \ -o data/processed \ --type t2 \ --numThreads 16 antsApplyTransforms found antsRegistrationSyNQuick.sh found antsRegistration found All executables are found, program will begin now ... /home/tb571/ml_class/csci_e82_project/data/5010/raw/5010-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/1028/raw/1028-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/3024/raw/3024-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/5016/raw/5016-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/5015/raw/5015-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/7027/raw/7027-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/1017/raw/1017-t2w-xc-reg.nii.gz /home/tb571/ml_class/csci_e82_project/data/5016/raw/5016-t2w-xc-reg.nii.gz Registered image found ... Registered image found ... /home/tb571/ml_class/csci_e82_project/data/3025/raw/3025-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/3006/raw/3006-t2w-xc-reg.nii.gz /home/tb571/ml_class/csci_e82_project/data/5012/raw/5012-t2w-xc-reg.nii.gz Registered image found ... Registered image found ... /home/tb571/ml_class/csci_e82_project/data/3026/raw/3026-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/7018/raw/7018-t2w-xc-req.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/1005/raw/1005-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/5003/raw/5003-t2w-xc-reg.nii.gz /home/tb571/ml_class/csci_e82_project/data/3023/raw/3023-t2w-xc-reg.nii.gz Registered image found ... Registered image found ... Checking quality ... 1 fail /home/tb571/ml_class/csci_e82_project/data/3003/raw/3003-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/7026/raw/7026-t2w-xc-reg.nii.gz Registered image found ... 2 fail /home/tb571/ml_class/csci_e82_project/data/1031/raw/1031-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/7023/raw/7023-t2w-xc-reg.nii.gz Registered image found ... 2 fail /home/tb571/ml_class/csci_e82_project/data/3017/raw/3017-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/5024/raw/5024-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/7020/raw/7020-t2w-xc-reg.nii.gz Registered image found ... 4 pass /home/tb571/ml_class/csci_e82_project/data/1006/raw/1006-t2w-xc-reg.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/3019/raw/3019-t2w-xc-reg.nii.gz Registered image found ... 4 pass /home/tb571/ml_class/csci_e82_project/data/7023/raw/7023-t2w-xc-reg.nii.gz Registered image found ... 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Checking quality ... /home/tb571/ml_class/csci_e82_project/data/5025/raw/5025-t2w-xc-reg.nii.gz Registered image found ... 4 pass /home/tb571/ml_class/csci_e82_project/data/3012/raw/3012-t2w-xc-reg.nii.gz Registered image found ... 4 pass 4 pass /home/tb571/ml_class/csci_e82_project/data/7007/raw/7007-t2w-xc-req.nii.gz Registered image found ... /home/tb571/ml_class/csci_e82_project/data/7028/raw/7028-t2w-xc-reg.nii.gz Registered image found ... 4 pass /home/tb571/ml_class/csci_e82_project/data/5013/raw/5013-t2w-xc-req.nii.gz Registered image found ... 2 fail /home/tb571/ml_class/csci_e82_project/data/5027/raw/5027-t2w-xc-req.nii.gz Registered image found ... Checking quality ... 1 fail 4 pass Checking quality ... Checking quality ... 4 pass Checking quality ... Checking quality ... 4 pass Checking quality ... 2 fail 4 pass 4 pass 4 pass 4 pass 2 fail 2 fail 4 pass 4 pass 2 fail 4 pass 4 pass Time taken in quality checking 460.45311093330383 seconds In [96]: %cat data/processed/confusion_matrix.txt Confusion matrix (columns are true labels, rows are predicted labels): Visual discrete scores are: [1, 2, 3, 4] [[5 0 0 0][1 7 0 2] [0 0 0 8] [0 0 0 15]] Observation T2w image goodness check yielded as good as T1w image as characterized by the presence of less number of off-diagonal elements in the confusion matrix. Again, we can consolidate each quadrant of it as: [[13 2] [0 23]] From the bottom-corner entry, we conclude that we have been able to correctly predict the score of good images. On the other hand, 2 bad images has been misclassified as good ones. Discussion Similarity metric A remote user can try my algorithm by varying the similarity metric. The metric = PEARSON parameter in code/config.ini file has to be modified with one of { 'PEARSON', 'BC', 'KL', 'MSE'}. I have tried all of them and submitted my best similarity metric for grading. Cross Validation The only cross validation I tried in this project is to find a proper kernel dimension $|nx| \times |ny| \times |nz|$. Although my algorithm allows varying numbers for nx x ny x nz, I have tried equal numbers i.e. cube. I have varied the cube dimension as [3,5,8,10,20] and decided on 8 from the following curve: In [27]: display(Image(filename="cv.png", height=400, width=600)) cross validation mean squared error of (actual-predicted) scores 1.6 1.4 1.2 1.0 0.8 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 kernel dimension Majority voting Since I have coded four similarity metrices: * Pearson correlation coefficient * Bhattacharyya distance * Kullback-Leibler divergence * Mean squared error One would naturally think why I did not use a bagging/majority voting approach to decide a rating for the MRI. I tried that as well. However, bagging does not yield any better accuracy than a single similarity metric. It only complicates the code and probably confuses the algorithm. So I have omitted that untidy code from this submission. Future work Furnish bootstrapping Currently, bootstrapping has been applied at the whole data level. Bootstrapping is synonymous to data duplication. So, there may be some samples that exist in both training and testing sets. Algorithmically, existence of a few train samples in the test set does not affect the outcome at all. But in future, we plan to write complex code that will apply bootstrapping to the train set only. Use ROC AUC In the above, we care more about pass/fail decision than the actual rating of the MRI (1,2 are fail while 3,4 are pass). Thus we have some buffer in evaluating performance of the algorithm. In such case, we can calculate probability of an MRI being a rating. Instead of hard assignment of a rating [1,2,3,4], we can calculate probability as a four element array e.g. [0.1,0.2,0.5,0.2]. Such probabilities would allow AUC calculation from an ROC curve. We intend to use this metric in future. Mask MRIs A significant portion of the MRI is background i.e. black region around the brain. When comparing similarity between two MRIs, we should not need to consider that background. If we could extract the brain from an MRI, then the background would reduce to zero. The zero features should increase efficiency of calculation. In future, we shall look for a good brain extraction tool intrisically in Python that could be used conveniently in the above terminal. Conclusion Despite a few misclassifications, we have mostly been able to decide which MRI passes goodness check. Hence, this project has been a successful one. Upon completion of the future work, I plan to publish this at a machine learning conference. **Appendix** Advanced options There are some other parameters in code/config.ini as follows: [DEFAULT] points = 20nx = 8ny = 8nz = 8eta = 0.9sx = 2sy = 2sz = 2metric = PEARSON decisionfactor = 2points are the number of bins for histogram in each cell of the small cube n* are the dimensions of the small cube that we slide along the 3D image volume eta is the degree of overlap required for comparing each patch to the library images s* is the stride taken to get the next small cube. If you set s* to greater than 1 (usually 2 or 3), the prediction will be faster metric currently supports BC, MSE, KL respectively for Bhattacharya distance, mean squared error, and KL divergence decisionfactor is the factor that determines threshold for predicting an image as pass. For example, if 1 is the worst and 4 is the best, then a decisionfactor of 2 will set halfway (2) as the threshold: score range= np.ptp(discreteScores)+1 if min(discreteScores)>0 else np.ptp(discreteScores) quality= 'pass' if predicted_score>score_range/decisionFactor else 'fail' Visual QC In training mode, visual quality scores are required to train the algorithm. As occurs for most training, someone has to visually look at a batch of data and give it discreteScores. In our training, we have used [1,2,3,4] as the discrete scores while 1 is for worst i.e. an MRI affected by severe ringing, ghosting, motion, and signal drop. On the other hand, 4 is for a good quality MRI free from noticeable artifacts. The scores should be in an excel file as follows: Subject ID t1 score t2 score 1001 1 1002 Make sure to properly write the header: | Subject ID | t1 score | t2 score | The caseids in the caselist should be same as the ones used under Subject ID column in the excel file.

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