

## Quantifying Triple-XAI Disagreement and Attribution Reliability across Grad-CAM, SHAP and LIME for a Hybrid CNN–Transformer Brain Tumor Classifier

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## ABSTRACT

Deep-learning models are accurate to a degree that leaves little scope for improvement; brain tumor classification models from MRI are hard to deploy to practice, typically barely worth the decisions that they make. If there is a justification provided, this is generally produced by only one of the pothooking explanation techniques and refers to an overall explanation of the reasoning of the model. This paper proceeds on the basis of that assumption. We use a patient-disjoint protocol and leakage-safe manner to train a Hybrid CNN–Transformer classifier on the Mendeley dataset of four-level brain tumor MRIs; we then use Grad-CAM, SHAP and LIME to visualize and quantify the explanations, and their agreement to the predictions, as well as the trustworthiness of the three explanations. The classifier achieves a 99.88% accuracy (SD 0.37%, 4-fold patient-disjoint cross validated mean 98.85% (95% CI 98.26–99.44%)) and a 99.88% macro F1-score on a held-out client never seen during training. To eliminate the contribution from ResNet50 (which has the same training opportunity), the same ablating procedure is repeated on the same set of images when the two models disagree in their contribution. The ablating is repeated alone on the same set of images where the two models disagree with each other, and the hybrid is correct on 21 images, wrong on none, for which the McNemar p-value is  $9.54 \times 10^{-7}$ . In the process of explanation analysis, the main

findings of the paper are produced. There is only a 50% to 33% intersection between any two of the three attribution methods with Dice-DW coefficient ranging between 0.3299 and 0.4383. They are generally within a range of each other (0.7008, 0.6922, 0.6750) and both are significantly higher than a random attribution simulation (0.0240), that is, each method gathers the evidence that is relevant to the class, but that is not enough to definitively outperform the other. When the three measurements are combined together in the same proportions to the degrees of the measured reliability, they yield a combined map of fidelity 0.6895, which is just below, instead of above, the items that individually had the highest level of fidelity. We openly report this negative finding because we believe that reliability-weighted fusion can be viewed as a way to reconcile different explanations in addition to being a means of maximising fidelity.

**Keywords:** *Machine Learning; brain tumor classification, magnetic resonance imaging, explainable artificial intelligence, Grad-CAM, SHAP, LIME, attribution reliability, vision transformer*

## 1. Introduction

Manual interpretation is also time consuming and can have significant inter-observer variability, with the diagnosis of brain tumors being at the core of this: measurements of the same tumour by three different radiologists varied significantly, both in clinic and in research [1, 2]. Automated classification has therefore been continuously interested and the reported accuracy rate is in the mid-high nineties now with the use of deep convolutional networks [3, 4]. A high accuracy level has not resulted in clinical uptake. A diagnosis alone that doesn't explain the causes of it cannot be confirmed by the clinician who has to apply it, nor be verified when it is not working. Post-hoc, explainable AI is the answer and there are three dominant techniques to learn: Gradient-based and class-discriminative Grad-CAM [5, 6]; cooperative game theory-based SHAP [7]; and local interpretable surrogate modelling-based LIME [8].

There is set afterward of this plurality a difficulty. Each of the three are based on distinct mathematical principles, and have not been thoroughly examined to determine whether they coincide in the same model predicting the same event [9-13]. One given map, one told (and told as the only one true) to a clinician. Adding to the challenges of the CO's, creating an attribution tells only that a method makes an output, and does not tell that the highlighted region is, indeed, what caused the prediction [14-18].

$$s(t) = (x * w)(t) = \sum_{a=-\infty}^{\infty} x(a)w(t - a) \quad \text{Eq (1)}$$

W stands for the kernel filter, x stands for the input signal, t stands for time and s is the output signal. The convolution process with two-dimensional input data is described by Equation (2).

$$S(i, j) = (I * K)(i, j) = \sum_m a \sum_n I(i, j) * K(i - m, j - n) \quad \text{Eq (2)}$$

The variables iii and jjj are the spatial position in the output matrix following the convolution operation. In this process, the center of the filter is matched with the corresponding image area, so as to achieve the best feature extraction effect. Moreover, the proposed framework uses the cross-entropy loss as the optimization objective, which is shown in Equation (3).

$$S(i, j) = (I * K)(i, j) = \sum_m a \sum_n I(i + m, j + n) * K(m, n) \quad \text{Eq (3)}$$

In this paper, four contributions are made. The first one is the hybrid CNN–Transformer

(CNN-TR) classifier designed for classification of magnetic resonance imaging (MRI) scans of brain tumours in 4 classes, which is then rigorously evaluated using a strictly patient-disjoint protocol for training and testing, to prevent overfitting due to memorisation rather than generalisation. Secondly, we compare the contribution of the transformer with another convolutional network with the same good training to determine if it is statistically significant [19-23]. Third, we quantify how much disagreement there is between Grad-CAM, SHAP, and LIME using five complementary directions. Fourth, warm target deletion is performed and fidelity and stability of each method is compared with that of random-attribution control, and the best among these individual methods' reliability is compared with the reliability of reliability-weighted fusion of all three methods [24-29].

## 2. Related Work

This automated brain tumor analysis has gone through four deliberations. This automated brain tumor analysis has progressed in four families of methods. In the early work the parameters are hand-tuned and the classical image-processing operations are directly applied to the images – without any training data – such as the thresholding, the region growing or the morphological operators – with the success of these degrading when the appearance of the lesions is deviating from the assumption made in the image-processing operator [30-33]. For a second family, classical segmentation was combined with machine learning, deriving classical statistical and textural features (e.g. grey level co-occurrence matrices and local binary patterns) to be used as input features to a number of classifiers including support vector and random forest [34-38]. More focused performances, choice of descriptions by designers.

ReLU

$$f(x) = \begin{cases} 0, & x < 0 \\ x, & x \geq 0 \end{cases}, f'(x) = \begin{cases} 0, & x < 0 \\ 1, & x \geq 0 \end{cases} \quad \text{Eq (4)}$$

Sigmoid

$$f(x) = \frac{1}{1+e^{-x}}, f'(x) = f(x)(1 - f(x)) \quad \text{Eq (5)}$$

Tanh:

$$\tanh(x) = \frac{e^x - e^{-x}}{e^x + e^{-x}}, f'(x) = 1 - f(x)^2 \quad \text{Eq (6)}$$

Clipped ReLU:

$$f(x) = \begin{cases} 0, & x < 0 \\ x, & 0 \leq x < \text{ceiling} \\ \text{ceiling}, & x \geq \text{ceiling} \end{cases} \quad \text{Eq (7)}$$

Leaky ReLU:

$$f(x) = \begin{cases} 0, & x < 0 \\ \text{scale} * x, & x \geq 0 \end{cases} \quad \text{Eq (8)}$$

The third family got rid of all hand engineering. The hierarchical properties were well captured directly by convolutional networks and transfer learning from scale pretraining of natural images was the common strategy with medical data scarcity [39- 41]. It is not only the accuracy reported increases markedly but also later transfer-learning tests with [42-45] achieving some 96% on a three-class benchmark and transfer-learning tests of better than 97% [46-49].

$$S_i^{(b,t)} = \sum_{z=1}^E p_{iz}^{(b)} J_z^{(b-1,t)} + \sum_{i'}^y x_{ii'}^{(b)} J_{i'}^{(b,t-1)} \quad \text{Eq (9)}$$

Attention introduced by the fourth/last family. Transformer-based models such as transformer encoders have encoded each region of each image into all the other images, without requiring any locality constraint, unlike the convolutional models. Hybrids combine a convolutional backbone with a transformer-based encoder to preserve the local texture attribute, while also providing global context to the model [50-53].

$$J_i^{(b,t)} = \beta^{(b)}(S_i^{(b,t)}) \quad \text{Eq (10)}$$

$$o_t = \sigma(W_o x_t + W_o h_{t-1} + b_o) \quad \text{Eq (11)}$$

Conceptually, sequence based variants get the same recognition success from [54-55] who reported 98.90% recognition success on a time-distributed CNN-LSTM and [56-59] got 88.3% recognition success of brain tumor classification using firefly-optimised hybrid classifier [60].

$$\tilde{c}_t = \tanh(W_c x_t + W_c h_{t-1} + b_c) \quad \text{Eq (12)}$$

This literature is an exception of variability with regard to explainability. Most of the studies listed above do not offer a technique for giving credit to the study; those that do describe one based on a single gradient computation discussed qualitatively, with a few heatmaps displayed next to the corresponding image and the reader asked to notice that the area of interest on the image and the area of interest on the heatmap seem congruent [61-65].

$$y = f\left(\sum_{k=1}^K h^k * w^k + c^k\right) \quad \text{Eq (13)}$$

Notably, there are no previous studies that have tested two or more attribution methodologies together on the same model or had the differences quantified, and there is no validation of the fidelity of attribution to a control model. This difference is where the present research study comes from [66-69].

$$f_t = \sigma(W_f x_t + W_f h_{t-1} + b_f) \quad \text{Eq (14)}$$

$$i_t = \sigma(W_i x_t + W_i h_{t-1} + b_i)$$

Eq (15)

### 3. Materials and Methods

#### 3.1 Dataset

The experiments are carried out on the public brain tumor MRI data set which is available online [16] having total images as 10,417 with four classes of diagnosis. As opposed to classification of only tumors, the addition of a class of no tumor is more representative of the real-world clinical problem as it facilitates sorting of pathological from healthy tissue and discriminates between the different classes of tumors. The distribution of classes is found in Table 1.

**Table 1. Class distribution of the Mendeley brain tumor MRI dataset.**

| Class        | Images        | Share (%)     |
|--------------|---------------|---------------|
| Glioma       | 2,547         | 24.45         |
| Meningioma   | 2,712         | 26.04         |
| Pituitary    | 2,658         | 25.52         |
| No-tumor     | 2,500         | 24.00         |
| <b>Total</b> | <b>10,417</b> | <b>100.00</b> |

The classes are nearly equally-sized, thus, accuracy, on a large scale, is an accurate summary measure and resampling or rebalancing is not required. In addition, there are metrics that are reported at a micro-averaged level but this does not diminish the visibility of per-class behaviour.

#### 3.2 Leakage-Safe Partitioning

The key characteristic of this data set for the purposes of the current work is that each author split it up into four subsets (client\_1, client\_2, client\_3, and client\_4), based on patients, with the same images assigned to the same subset per patient. We know how to utilise this here, precisely. By random splitting the images as in a standard approach, one would obtain images of the patient's anatomy, but not of the morphology of the tumour, and overestimate the classification. In our study, stratified group k-fold cross validation with k=4 is used, meaning: each group will not only have images on both sides of a fold but the distribution of 4 groups over the 4 folds will not differ as well. For 0, unfold the whole client\_2 (2,600 images), and the rest 7,817, is a train/valid 85%/15% (6,644 images respectively). The validation set is not used in any testing metric, but only to be used as checkpoints for the selection.

#### 3.3 Model Architecture

The backbone of the classifier is made up of a combination of convolutional backbone and transformer encoder. One benefit of this is the complementary weakness of the two families: max pooling performs well on local texture; it's only connected to the other two points in the array via depth, but the transformer relates each point with each other point in one pass, with no sense of locality, so much data makes a difference.

Another example of an initialised backbone is ResNet50 trained with ImageNet-pretrained weights which produces a  $7 \times 7 \times 2048$  feature map of an input size of  $224 \times 224$ . This is made in a  $1 \times 1$  convolution that outputs an embedding (ours) of 512, which is flattening the 2D spatial grid into tokens of size 49, pairing the flattening with a learnable prepended classification token, and a learnable pos embedding added as a post effect. Scaled dot-product

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attention applies the attention with a pair of eight-layer eight-head transformer encoders.

$$\text{Attention}(Q, K, V) = \text{softmax}(Q K^T / \sqrt{d_k}) V \quad \text{Eq (16)}$$

For an important dimension  $d_k$ . The classification token is gone through a linear layer after the final state of the classification token is layer-normalised. The full model has a total number of trainable parameters of 30,891,076.

### 3.4 Training Protocol

The pre-processing follows as follows with the main trick being the use of image net based normalisation values for the components: intentionally, very simple pre-processing, performed by converting to three colour channels rgb and then resizing to 224 x 224 and applying image net based normalisation values for each of the three colour channels. Two Flipped Label Preserving Augmentations (horizontal only) and Random Rotation in Training Partition (by 10 degree/ -10 degree). Intensity distortion is not allowed since it would change diagnostic content, particularly vertical flipping.

We use stochastic gradient descent with momentum (SGD-mu 0.9, initial learning rate 0.01, weight decay  $5 \times 10^{-4}$ , cosine annealer) schedule [20] for 120 epochs and a batch size of 10. The best validation accuracy (along with the associated date and learning rate) is stored when the validation performance is best in a validation accuracy checkpoint. A partition-free baseline is trained with the same partitions and the same ResNet50 backbone with global average pooling with a linear-classifier (23,516,228 parameters) to isolate the contribution of the self-attention component.

### 3.5 Triple-XAI Framework

Explanations are computed from a held out test dataset with a proportionate number of images per class (6 images/24 for 6 classes, class balance is programmed): The description is only about the class if the explicit stratification is required not incidentally: If it is required to be on the file path, then a subset of the file path may be described by an "explicit" stratum of that file path class, achieving a 'good appearance' of statistics about the file path, but describing only that class.

Finally, Grad-CAM is employed at the last residual block, SHAP is taken in a gradient-based form, using an 8-image set for the use of background images, and LIME, together with superpixel segmentation and 400 perturbed samples per image. All the relative maps of attributions are normalised within the ranges [0,1] prior to comparing.

There is no single dimension that gets it right, so pairwise disagreement is used – where two maps may consider the same pixels as important, but be unable to agree on the importance level for those pixels when thresholded. For computing spatial overlap, both maps are binarised at the highest 20% of the attribution values, for which the Dice coefficient is computed.

$$\text{DSC}(A, B) = 2 |A \cap B| / (|A| + |B|) \quad \text{Eq (17)}$$

How good an ROASE Against the Inverse Value and the Stricter Intersection over Union. The Spearman and Kendall correlations on the attribution values are used for rank agreement and SSIM [21] is used for structural similarity. It should be noted here that the two attribution maps are compared to each other; to a 'ground-truth' boundary, the dataset doesn't contain a reference boundary.

To provide reliability a fidelity measure based on deletion is used, and pixels are deleted in order of their importance and average reduction in the total true-class predicted probability of each of the lists recorded as the deletion progresses. Importantly this is also accomplished in the case of the random attribution maps, but averaged over 5 random drawings per image, in order to establish a control floor. For Grad-CAM, the stability of the explanation under

horizontal flipping is evaluated by calculating the explanation from the horizontally flipped input, flipping horizontally to the output and comparing using SSIM [22]. Finally the 3 maps are blended based on their individual measured fidelity.

$$A^* = \text{Normalise}(\sum_m (r_m / \sum_j r_j) \cdot A_m) \quad \text{Eq (18)}$$

The deletion- fidelity for method  $m$  is  $r_m$  and the fusion being evaluated is of the same fidelity used for the fused map, for a fair comparison between the fusion of the best single method.

### 3.6 Evaluation and Statistical Analysis

The classification performance is evaluated in terms of an AUC curve (one versus rest), a confusion matrix, the accuracy, macro-averaged precision, recall, F1 score and specificity. Four-fold patient-disjoint cross validation, leaving one patient out at a time, provides stability for the estimate that is computed as its mean, the standard deviation and a 95% confidence interval to be computed using the student t-distribution. As the two classifiers are applied to the same samples, the results of the two classifiers are thus paired, hence the hybrid model is compared with the baseline by McNemar's exact test [23] was used. Experiments have been conducted with a fixed seed (23) using a single NVIDIA Tesla T4 GPU, PyTorch [24] and metrics from scikit-learn [25] with partitioning.

## 4. Results

### 4.1 Classification Performance

The proposed model achieved 99.88% accuracy on the held-out client\_2 partition of 2,600 images of patient disjunction, 99.89% macro precision, 99.88% macro recall, 99.88% macro F1-score, 99.96% macro specificity and 99.99% macro AUC. These figures can be summarised in the table below (Table 2) and are presented in a confusion matrix below (Table 3).

**Table 2. Overall classification performance on the held-out test partition.**

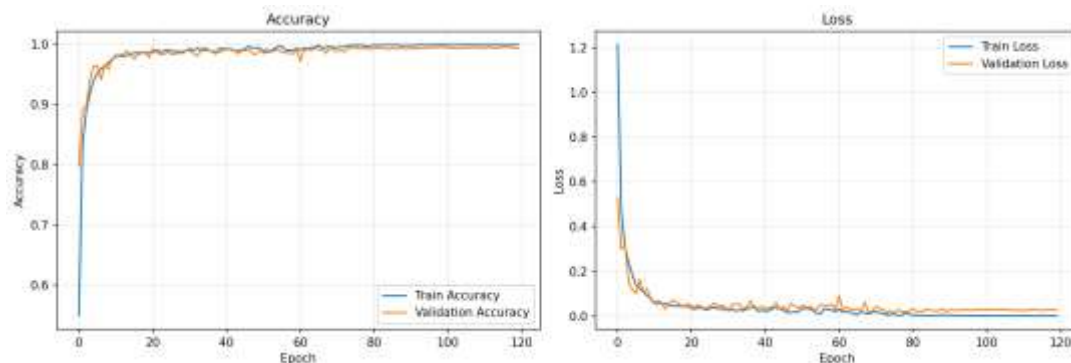
| Metric            | Value (%) | Metric              | Value (%) |
|-------------------|-----------|---------------------|-----------|
| Accuracy          | 99.88     | F1-score (macro)    | 99.88     |
| Precision (macro) | 99.89     | Specificity (macro) | 99.96     |
| Recall (macro)    | 99.88     | AUC (one-vs-rest)   | 99.99     |

**Table 3. Confusion matrix (rows: true class; columns: predicted class).**

| True \ Predicted | Glioma | Meningioma | Pituitary | No-tumor | Support |
|------------------|--------|------------|-----------|----------|---------|
| Glioma           | 634    | 1          | 0         | 1        | 636     |
| Meningioma       | 0      | 677        | 0         | 0        | 677     |
| Pituitary        | 0      | 1          | 662       | 0        | 663     |
| No-tumor         | 0      | 0          | 0         | 624      | 624     |

Only three of 2,600 test images are misclassified. These are mainly within the two most similar classes on one slice (e.g. within the slice of glioma and meningioma, where the discrimination is most likely to be easy). There are no confusions between no tumor vs pituitary cases, as these are the most visually distinguishable cases, and any error would have indicated a flaw in learned representation as opposed to a real visual confusion.

Figure 1 shows the training dynamics over the full 120-epoch run.



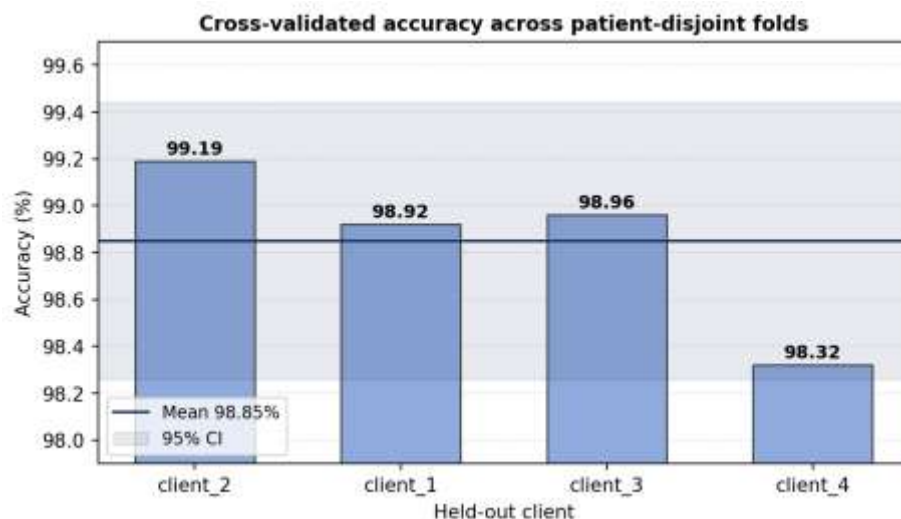
**Figure 1. Training and validation accuracy (left) and loss (right) over 120 epochs.**

As can be seen in the accuracy curves of figure 1, the accuracy improves quickly at the beginning of the 10th epoch, and reaches or surpasses 0.99 at the 20th epoch, while the loss curves remain very close to zero at the 20th epoch and have not begun to deviate in the process from the training loss curve. If the explicit growing gap over all 120 epochs were there, it would mean that the model started overfitting the training partition. To achieve the 99.38% the same protocol was repeated independently and a similar result was obtained within the same performance range, as known floating point non-determinism for GPU's exists.

## 4.2 Cross-Validated Stability

One single split calls into question the result, on the basis of which patients were excluded. The first thing that comes to mind is 4-fold cross validation.

Figure 2 plots the accuracy obtained on each fold.



**Figure 2. Accuracy across the four patient-disjoint folds, with mean and 95% confidence interval.**

The accuracy of the Mean is 98.85% with 95% confidence interval ranging from 98.26 – 99.44%, and the standard deviation is 0.37 points. The range between the weakest and strongest folds was less than one point – from 98.32 to 99.19, or less than onefold apart. This set of fixed partitions is a good testament to transferable model learning features. Additionally, it also does proportionate its headline 99.88%, which is made up of primary 120 epochs, whereas cross validation's much smaller 25 epochs budget is done with more reasonable proportions of mean score.

### 4.3 Ablation: Contribution of the Transformer

The backbone used for the baseline is the same with the removal of the transformer and input vector configuration, with an identical backbone but different partitions for train and test, which should also result in differences if any, due to the attention component only.

Figure 3 compares the two configurations and Table 4 reports the significance test.

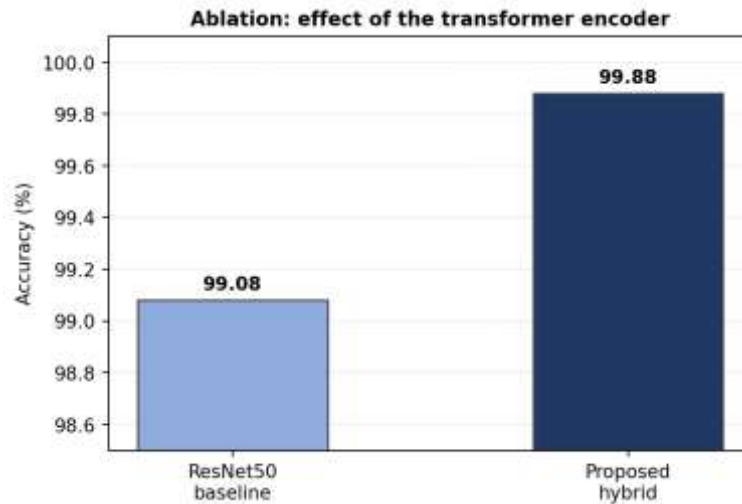


Figure 3. Ablation comparing the hybrid model against the transformer-free baseline.

Table 4. Ablation results and significance test.

| Configuration                | Accuracy (%) | F1 (%)       | Parameters | McNemar outcome                                   |
|------------------------------|--------------|--------------|------------|---------------------------------------------------|
| ResNet50 baseline (CNN only) | 99.08        | 99.08        | 23,516,228 | reference                                         |
| <b>Proposed hybrid model</b> | <b>99.88</b> | <b>99.88</b> | 30,891,076 | <b>21-0, <math>p = 9.54 \times 10^{-7}</math></b> |

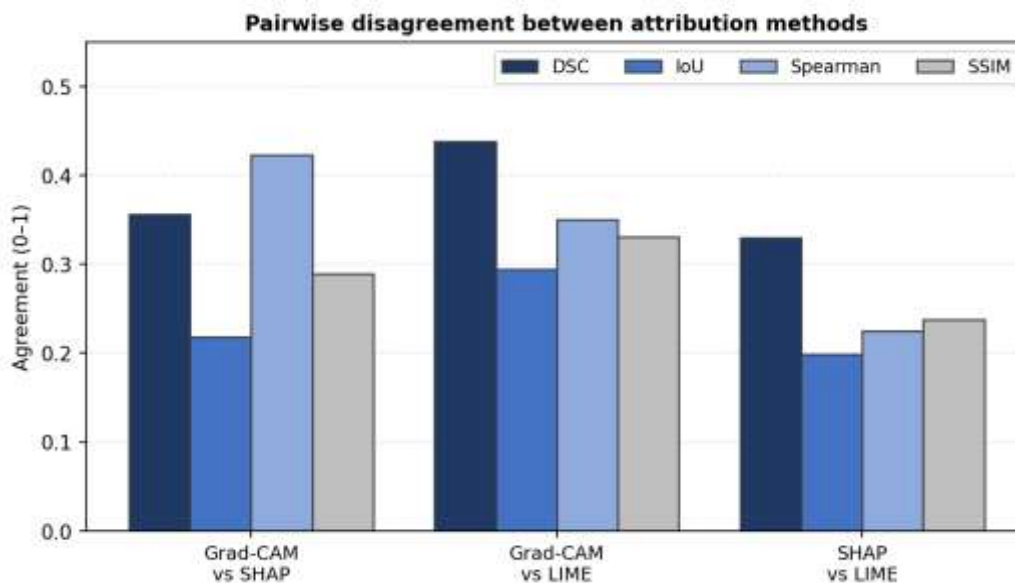
The margin is 0.80 percentage points but the size of the test set is small, too. McNemar's test rules them out! The 2,600 images held out of the total data set that the two models did not agree on resulted by the two models in one case of 21 where the baseline was the inaccurate model, and in none of the 21 where the hybrid was the inaccurate model. It is not a one-way disagreement which would indicate random variation at  $p = 9.54 \times 10^{-7}$ .

### 4.4 Attribution Disagreement

The decision would be a convenience one if the results obtained are the same with either of the three explanation methods. As in this case, de-repression does not, as demonstrated in Table 5 and in Figure 4, cause the coincidence of the three elements.

Table 5. Pairwise agreement between attribution maps across five measures.

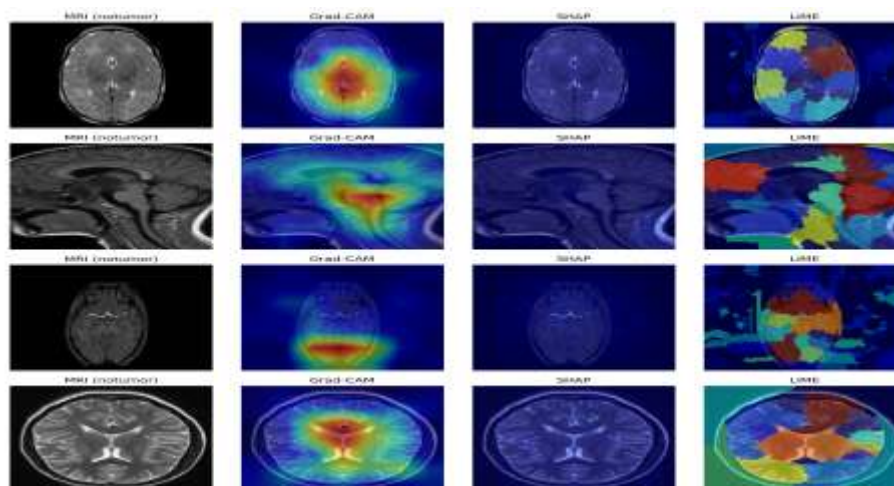
| Method pair      | DSC    | IoU    | Spearman | Kendall | SSIM   |
|------------------|--------|--------|----------|---------|--------|
| Grad-CAM vs SHAP | 0.3561 | 0.2180 | 0.4232   | 0.2941  | 0.2890 |
| Grad-CAM vs LIME | 0.4383 | 0.2941 | 0.3502   | 0.2555  | 0.3305 |
| SHAP vs LIME     | 0.3299 | 0.1991 | 0.2249   | 0.1571  | 0.2378 |



**Figure 4. Pairwise disagreement between Grad-CAM, SHAP and LIME.**

Depending on the model, the two values of dice coefficient - between 0.3299 and 0.4383, and IoU - between 0.1991 and 0.2941 - for the same prediction are in general only 5-30% identical. Ordering is the same for each of the 5 measures. The outputs as such, of course, show the outputs which make the closest match in non-comprehensible way - this is not surprising, since both output are coarse, spatially localised. Least agreement between SHAP and LIME is on all measures.

The pair (Grad-CAM, SHAP) together has the most information. It has the greatest rank correlation (Spearman 0.4232) and moderate degree of overlap with the regions (DSC 0.3561) of any combination. Many of the same pixels will then be marked as relevant using both of these methods, but different areas will be marked up after a certain threshold - as might be expected when comparing a method that returns smooth, contiguous heat, with a method that returns fine distributed attributions. This is really important to see that disagreement cannot be measured by a single overlap score since it falls into two separate "agreement" and "overlap" levels. There are three attribution maps for each sample prediction which can be seen from top to bottom in figure 5 and differences in the structures is immediately apparent.



**Figure 5. Grad-CAM, SHAP and LIME attribution maps for four sample predictions, beside the original slice.**

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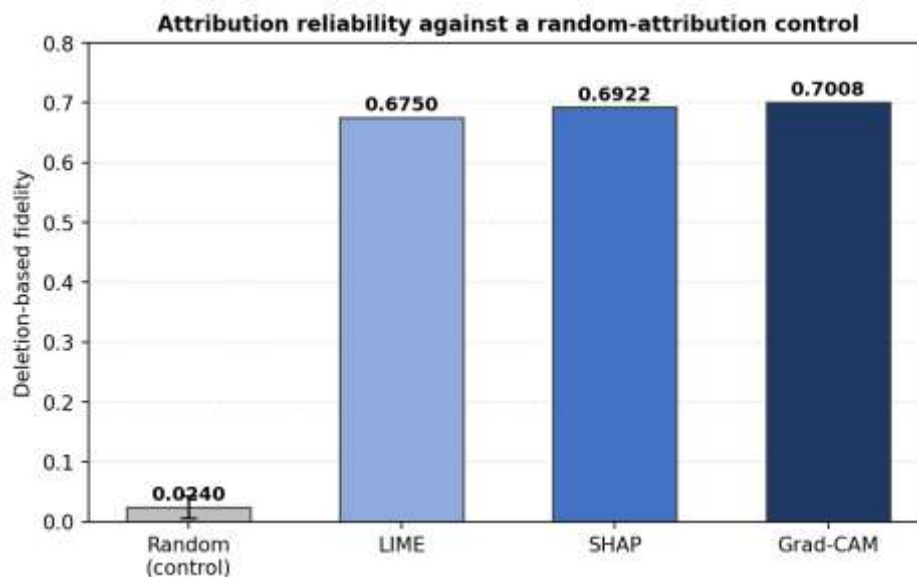
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#### 4.5 Attribution Reliability

Measuring disagreement gives us insight that their methods are different – it does not give any insight into which should be trusted as correct because two methods may agree, yet both be false. The latter is quite directly dealt with by the deletion-based fidelity, which forms what the measure looks like when the attribution contains no information, as is the random-attribution control.



**Figure 6. Deletion-based fidelity of each method against a random-attribution control.**

Grad-CAM scores 0.7008, SHAP 0.6922 and LIME 0.6750, against a random-attribution floor of  $0.0240 \pm 0.0187$ . All three then exceed chance by about 28-29 times, suggesting that as these three find evidence that is relevant to their class, rather than exploiting an artefact of the deletion procedure. This control is crucial for interpretation: with this, a fidelity of 0.70 is neither good nor bad to say the least. However, there is only a margin of 0.026 between the most and least faithful method. Unlike the most common strategy of using only Grad-CAM, any of the methods may not be the most reliable method on this dataset. Thus the flip-test evaluation of the stability of Grad-CAM is 0.5854 (moderate) close to 1.0, considered ideal for a good method, since the diagnosis remains intact when the data are horizontally flipped. The marked spot displayed in the map is only approximately oriented because it now faces more of an angle with the direction of input, and so this marked area must be viewed as an approximation: Where is the evidence coming from?

#### 4.6 Reliability-Weighted Fusion

The final experiment is testing the hypothesis as to whether the combined maps will give better understanding by using different degrees of reliability in maps. It does not. The unified map represents the result with the fidelity score of 0.6895, slightly lower than the score of 0.7008 obtained by Grad-CAM.

Table 6 collects the fidelity of every configuration evaluated, including the control.

**Table 6. Single best method against reliability-weighted fusion.**

| Configuration                | Deletion-based fidelity |
|------------------------------|-------------------------|
| Random attribution (control) | $0.0240 \pm 0.0187$     |
| LIME                         | 0.6750                  |

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| Configuration                            | Deletion-based fidelity |
|------------------------------------------|-------------------------|
| SHAP                                     | 0.6922                  |
| <b>Grad-CAM (best single method)</b>     | <b>0.7008</b>           |
| Reliability-weighted fusion of all three | 0.6895                  |

We do not try to gloss over the comparison, we don't look on the bright side of it; we look at it honestly. The slight reduction in fused fidelity was always going to be the case overall: logically, it could be either the highest or the lowest score - so the small drop was not due to fault, just due to fact the scores were so close. It might be called here reliability weighted fusion, legitimate to own that, as it's utilized here, it's not a method to attain maximum fidelity. It's interesting to note that the thing is to reconcile three accounts in conflict with one another and to arrive at a map, which is not the issue of faithfulness that fidelity takes up, but the issue of what it is to make three conflicting accounts converge.

#### 4.7 Computational Cost

The model consists of 30,891,076 parameters, can classify an image in 8.61ms and uses about 374.1MB of GPU memory during inference, that is about 116 images per second. Production of the three explanations (not separately profiled) is an easy expense to make when deploying onto regular clinical devices, but classification cost is not as prohibitive.

#### 5. Discussion

The results of the classification indicate that the model is on top of the literature reported, while, as stated above, it should be avoided assuming that it would be a rank. There are several different sets of data, several different numbers of classes, etc. etc. and the number you get in one study isn't the same as that you get in another study with a figure you find under a patient-disjoint evaluation versus the other evaluation. Not a minor gain in accuracy (as is the case in a number of other approaches, where accuracy is indeed satisfactory) but, competitive accuracy and a numerical estimate for the quality of explanations.

The findings from the disagreements have the most direct practical implications. Only 2/5 of the region shown was attributed in common between the two types of prediction made in this region. The explanation clinician receives is thus at least in part dependent on a methodological decision taken by the system designer, one which is "hidden" at point of care and unpublished in the literature. A single heatmap is misleading in its certainty of the conclusions it draws and one that is reporting the difference in distance between explanations to its conclusions provides a real sense of the ambiguity — it does not replace, but enhances, clinical judgement.

The reliabilities in line with the same warrant the same degree of caution. This is good as all three are a long way from random control and up-to date - not proven in this domain. The one that is more important is that they are almost identical; therefore, no general reason exists to use either one or the other. The moderate level of flip-stability of Grad-CAM, when combined with this, implies that one attribution map should not be viewed as a "localisation of a tumour" for itself; viewing multiple maps as a 'vote' implies that multiple maps may be combined for that purpose.

These conclusions were limited by a number of constraints. But is based on just one data set and the approach of dividing the patients up in the same way meant to ensure that these numbers are not boosted by "leakage" into the data? But cannot show this model working on images taken on another scanner or on another institution, and independent testing on an independent source remains most easily extendable extension of the evaluation. The reliability analysis is lacking: No segmentation mask is given with the dataset, something that

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is needed to calculate the alignment between the expert-drawn tumour boundaries and the attribution maps. Implementation is two dimensional everywhere – everywhere, everything is physically scaled according to the size of the data slice. Finally, the 24 image class-balanced subset was chosen because the computational time of LIME and SHAP would have been increased for a larger subset that would further narrow the estimate on the disagreements.

## 6. Conclusion

We suggested a hybrid CNN–Transformer based classifier for magnetic resonance imaging (MRI) classification of brain tumour types (4-class classification) and evaluated it by implementing a leakage-safe protocol of splitting the patient set, and using a systematic measurement of the disagreement and reliability of 3 alternative explanation techniques to the predictions of the proposed classifiers. The classifier classified a held-out set of patients with a held-out accuracy of 99.88%, with the fourfold cross validation average of 98.85% and the transformer had best been shown to offer a statistically meaningful improvement over an identical train/test convolutional baseline.

Explanation findings "show" the main thing of the study in the analysis. Grad-CAM and SHAP, and even LIME do not agree on 50% or more of the area that they show when they are used on the same prediction. Each displays a significant degree of fidelity which is not solely due to chance; no one is the most faithful obviously, but each exhibits fidelity to class appropriate evidence. It can be shown that it not only does it not compromise the fidelity of each individual method, but that it is possible to have a reliable method that combines the three methods without loss of fidelity, even though they are in conflict with each other.

Other studies should be able to test them on an independent dataset, independent of the current one, with the inclusion of volumetric data and move towards external validation where there would be the possibility of an independent measure of the quality of the expert – mask match presented here, as well as combine quality of the match presented here with disagreement between the expert explanation generation and how the explanation is used for validation. The general implication of the brain MRI statement: if one explanation is going to suffice in the absence of an alternative, it is testable, and as this example illustrates, it is not true, wherever there is a need to explain a phenomenon a posteriori in a high-stakes situation

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