

Crutchfield Information Metric for Quantifying the Inter-sequence Relationship of Multiparametric MRI Data

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Abstract: A plethora of different MRI sequences exists. To automatically structure this 'zoo' of available sequences we propose the usage of a framework rooted in information theory. In this paper we show that the Crutchfield information metric is a suitable distance measure for this purpose. It is demonstrated that the physical relationship can be inferred with this metric solely based on the voxel intensities. As future applications we envisage MRI sequence quality control and standardization.

1 INTRODUCTION

The necessity of multiparametric magnetic resonance imaging (MRI) for diagnosis and therapy monitoring of diseases is undoubted. However, in general there are no standardized protocols specified (Cornfeld and Sprengle, 2013). In the clinical routine workup it is not feasible to acquire every available sequence deposited at the scanner. This would result in an unreasonable long scanning time, very likely making the patient feel uncomfortable. Secondly, the images acquired at the end of a long scanning session tend to suffer from motion artifacts which impair their diagnostic value. Needless to say that this approach is economically unacceptable.

To shed light on the zoo of available MRI sequences we try to establish a framework that is rooted in information theory and allows us to capture and quantify the relative information content between MRI sequences. The current work should be seen as a proof of concept which in the future can be an aid for standardizing MRI protocols and possibly also be used to optimize MRI sequence parameters.

Historically, information theory investigated the transmission between a sender and a receiver (Shannon and Weaver, 1949) but it has also been extended to theoretical measures that capture the information integration (Tononi et al., 1998) and information distances of information sources (Kullback, 1968). A not well known but still very important information distance was introduced by Crutchfield (Crutchfield,

1990). He showed that a proper metric space (in a mathematical sense) of information sources can be defined. Given physically or functionally related sources, i.e. different MRI sequences, that are activated by an identical localized stimulus, in our case a patient that is examined, the information distance between those sources can be determined using this metric. In turn, due to the fact that it is a proper metric we can exploit the discovered relationship geometrically.

To the best of our knowledge no comparable approach has been examined for multiparametric MRI data previously. We were inspired by robotic experiments where the Crutchfield information metric has been used to determine the informational topology of a set of robot sensors, that consecutively was exploited for simple visually guided movements (Olsson et al., 2006) or unsupervised activity classification (Kaplan and Hafner, 2006).

2 MATERIALS AND METHODS

2.1 Theory

Each MRI sequence can be interpreted as an information source with the voxel intensities as the respective measurements. Given two different information sources X and Y , e.g. corresponding T1- and T2-weighted data sets, it is possible to compute the *conditional entropy* of the two sources:

$$H(X|Y) = -\sum_x \sum_y p(x,y) \log_2 p(x|y). \quad (1)$$

Consecutively, given $H(X|Y)$ and the entropy $H(X)$ allows to determine the *joint entropy*:

$$\begin{aligned} H(X,Y) &= H(X) + H(Y|X) \\ &= \sum_x p(x) \log_2 p(x) + H(Y|X). \end{aligned} \quad (2)$$

After calculating these quantities the distance between the two information sources can be computed in the form of the Crutchfield information metric (Crutchfield, 1990):

$$d_C(X,Y) = \frac{H(Y|X) + H(X|Y)}{H(X,Y)}. \quad (3)$$

This metric is related to the mutual information (MI). However, MI measures what two random variables have in common, whereas the Crutchfield information metric quantifies what they do not have in common (Olsson et al., 2006). In Addition, in contrast to the MI the Crutchfield distance is a proper metric fulfilling the properties of:

1. *symmetry*: $d_C(X,Y) = d_C(Y,X)$,
2. *equivalence*: $d_C(X,Y) = 0$ **iff** X and Y are recoding-equivalent (as defined by Crutchfield (Crutchfield, 1990)), $d_C(X,Y) = 1$ states that the two sources are independent,
3. *triangle inequality*: $d_C(X,Z) \leq d_C(X,Y) + d_C(Y,Z)$.

Being a metric implies that the information space has a structure that can be exploited geometrically. The first experiment is a proof of concept. In the second experiment we computed the metric for all combinations ($D = 171$) of sequences within a private multiparametric MRI data set (see Sec. 2.2) and interpreted the resulting matrix as a distance (dissimilarity) matrix and as a graph adjacency matrix. In the former case we used non-linear dimensional-reduction methods like *Isomap* (Tenenbaum et al., 2000) and *local linear embedding* (Roweis and Saul, 2000) to embed the data in a 2D geometric space, in the latter case we used Kruskal's algorithm (Kruskal, 1956) to obtain the minimum spanning tree (MST). In a third experiment we computed the distance matrices ($N = 216$, $D = 6$) for a publicly available multiparametric MRI data set (see Sec. 2.2) and used the low dimensional embedding to identify impaired images.

2.2 Data

2.2.1 Data Set 1

In total $N = 17$ multiparametric MRI data sets with $C = 19$ channels each were acquired in a clinical routine workup of patients using two different 3 Tesla MR system from the same manufacturer (Magnetom Tim Trio ($N = 9$) and Magnetom Verio ($N = 8$), Siemens Healthcare, Erlangen, Germany).

All patients were suffering from a *glioblastoma multiforme* (WHO grade IV). The data was anonymized. The reasoning for taken data from diseased subjects is motivated by the fact that patients suffering from this disease are scanned with a more detailed protocol that comprises more MRI sequences.

The following MRI images were acquired: native (T1) and contrast enhanced (T1CE) T1-weighted images with $TE = 4.04$ ms and $TR = 1710$ ms; T2-weighted TSE imaging (T2) with $TE = 85$ ms and $TR = 5500$ ms; T2-weighted fluid attenuated inversion recovery images (FLAIR) with $TE = 135$ ms and $TR = 8500$ ms; diffusion-weighted images with $TE = 90$ ms and $TR = 5300$ ms comprising a $b = 0$ (DWI.b0), a $b = 1200$ (DWI.b1200t) as well as an apparent diffusion coefficient (ADC) map; native (SWI) and contrast enhanced (SWICE) susceptibility weighted images with $TE = 19.7$ ms and $TR = 27$ ms, this set of sequences also includes a magnitude (SWI[CE].MAG) and phase (SWI[CE].PHA) image as well as a minimum intensity projection (SWI[CE].MIP); dynamic susceptibility contrast perfusion images with $TE = 37$ ms and $TR = 2220$ ms yielding the relative cerebral blood flow (PWI.CBF) and volume (PWI.CBV), the mean transit time (PWI.MTT) and the time to peak (PWI.TTP).

2.2.2 Data Set 2

For the third experiment we use the publicly available BraTS 2014 training data set provided via the Virtual Skeleton Database (VSD) (Kistler et al., 2013). It comprises $N = 216$ co-registered native and contrast enhanced T1-weighted images, as well as T2-weighted and T2-FLAIR images ($C = 4$). The data was acquired with MR scanners of different vendors, at different field strengths and using non-uniform protocols (i.e. physical parameters). The images contain low grade as well as high grade tumors.

2.3 Preprocessing

2.3.1 Experiment 1 and 2

All sequences of the multiparametric data set 1 were co-registered intra-individually to the respective native T1-weighted images. A rigid 6-DOF registration was performed using the BRAINSFit (Johnson et al., 2007) command line interface of 3D-Slicer (3D Slicer v4.3). The registration accuracy was confirmed by a board-certified neuroradiologist. In the next step we used FMRIB’s brain extraction tool (BET) (Smith, 2002), which is part of FSL (FMRIBs Software Library FSL v5.0), for deskulling of the T1-weighted images. The obtained mask was applied to all channels. Finally, all data was rescaled to be in the range $[0, 1024]$. To estimate the probabilities we used a standard frequency count method, after we confirmed that histogram equalization methods do not alter the results.

2.3.2 Experiment 3

Data set 2 was rescaled to be in the range $[0, 1024]$ and the same standard frequency count method as in the first two experiments was applied.

2.4 Data Manipulation

For the first experiment we manipulated the data. We added increasing levels of noise to the images using a normal distribution $\mathcal{N}(\mu = 0, \sigma^2)$ centered at zero but with varying values of sigma. Further, we generated an artificial sequence Z by combining two recorded sequences X and Y with a weighted sum:

$$Z = (1 - \alpha)X + \alpha Y . \quad (4)$$

Finally, we applied a 6-DOF rigid transformation T that allows for separately rotating around an axis or translating along an axis.

2.5 Implementation

Except the two tools (BRAINSFit (Johnson et al., 2007) and BET (Smith, 2002)) noted above, all algorithms were implemented in custom python scripts (Python v2.7.6). For analyzing the distance matrices we adapted functions implemented in scikit-learn (Pedregosa et al., 2011) and NetworkX (Hagberg et al., 2008).

3 RESULTS

3.1 Experiment 1 – Proof of Concept

In the first experiment (Fig. 1) we confirmed that the Crutchfield information distance is a valid metric for our purposes. On this account we manipulated the MRI image data (data set 1) in several ways. The average course as well as the standard deviation (gray shaded area) are plotted for all experiments.

Initially we added an increasing level of gaussian noise to the data. This manipulation was repeated for each T1 sequence of MRI data set 1 ($N = 17$). In Fig. 1A left it can be seen that the Crutchfield distance increases monotonically with the amount of noise added. In Fig. 1A right an exemplary axial T1-weighted image is shown without noise and with a noise level corresponding to $\sigma = 30$.

Secondly, we generated artificial MRI data by blending the T1-weighted and T2-weighted images of the same, co-registered data set using varying weighting factors (Eq. 4). We then computed the Crutchfield distance between the T1 sequence and the artificial images. This was repeated for all images of MRI data set 1. In Fig. 1B left it can be seen that, as expected, with an increasing T2-fraction of the artificial image also the Crutchfield distance to the T1 image increases. In Fig. 1B right an exemplary axial T1 slice as well as a mixed T1- and T2-weighted image using a factor of $\alpha = 0.3$ are shown.

Next, we used a rigid transformation to selectively rotate a data set around an axis. We measured the Crutchfield distance of an unmodified reference sequence to the identical, but rotated data set in the interval of $[-2, 2]$ degrees. This is shown for the pitch movement in Fig. 1C left. It clearly can be seen that there is a well defined minimum at 0 degrees with an almost symmetrically increasing information distance in both rotation directions. As an example, an unrotated sagittal T1-weighted image as well as an image pitched by 2 degrees is presented in Fig. 1C right.

3.2 Experiment 2 – Application to Multiparametric MRI Data

Fig. 2A shows the Crutchfield information distance for all combinations ($D = 171$) of sequences from data set 1. Note the symmetry of the matrix. We depicted the average of all $N = 17$ multiparametric MRI data sets. However, the structure that can be seen is also present at the individual level. This is also supported by the small standard deviation of the distances, which is on average 0.0035.

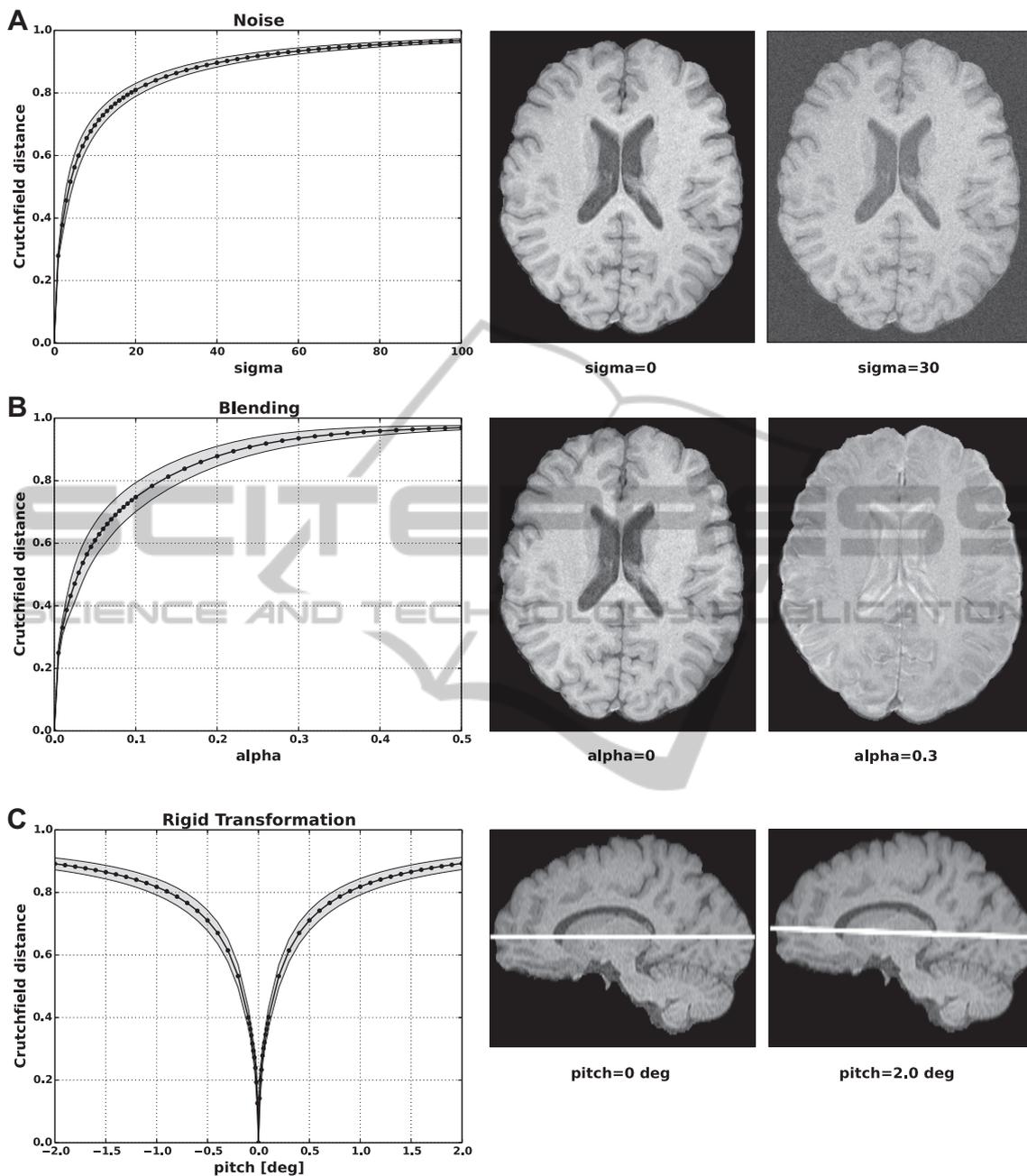


Figure 1: **Data manipulation.** A) Increasing levels of gaussian noise were added to a T1-weighted image and the Crutchfield distance to the original sequence was determined (left). Exemplary axial T1 image with ($\sigma = 30$) and without noise (right). B) Crutchfield distance between a T1-weighted image and artificially generated images (left). The artificial images were obtained by blending co-registered T1- and T2-weighted images. Exemplary axial T1 image as well as a mixed T1- and T2-weighted image using a factor of $\alpha = 0.3$ (right). C) Crutchfield distance of an unmodified reference sequence to the identical, but in the interval of $[-2, 2]$ degrees rotated data set (left). Unrotated sagittal T1 image as well as an image pitched by 2 degrees (right). The average course for all data sets $N = 17$ as well as the standard deviation (gray shaded area) are plotted.

First, we interpreted the distance matrix as a dis-similarity matrix. We used the *Isomap* algorithm (Tenenbaum et al., 2000) to perform a 2D embedding of the data (Fig. 2B). Comparable results

were obtained, when we employed *local linear embedding* (Roweis and Saul, 2000) to reduce the dimensionality of the data (not shown). It clearly can be seen that related sequences cluster in close proxim-

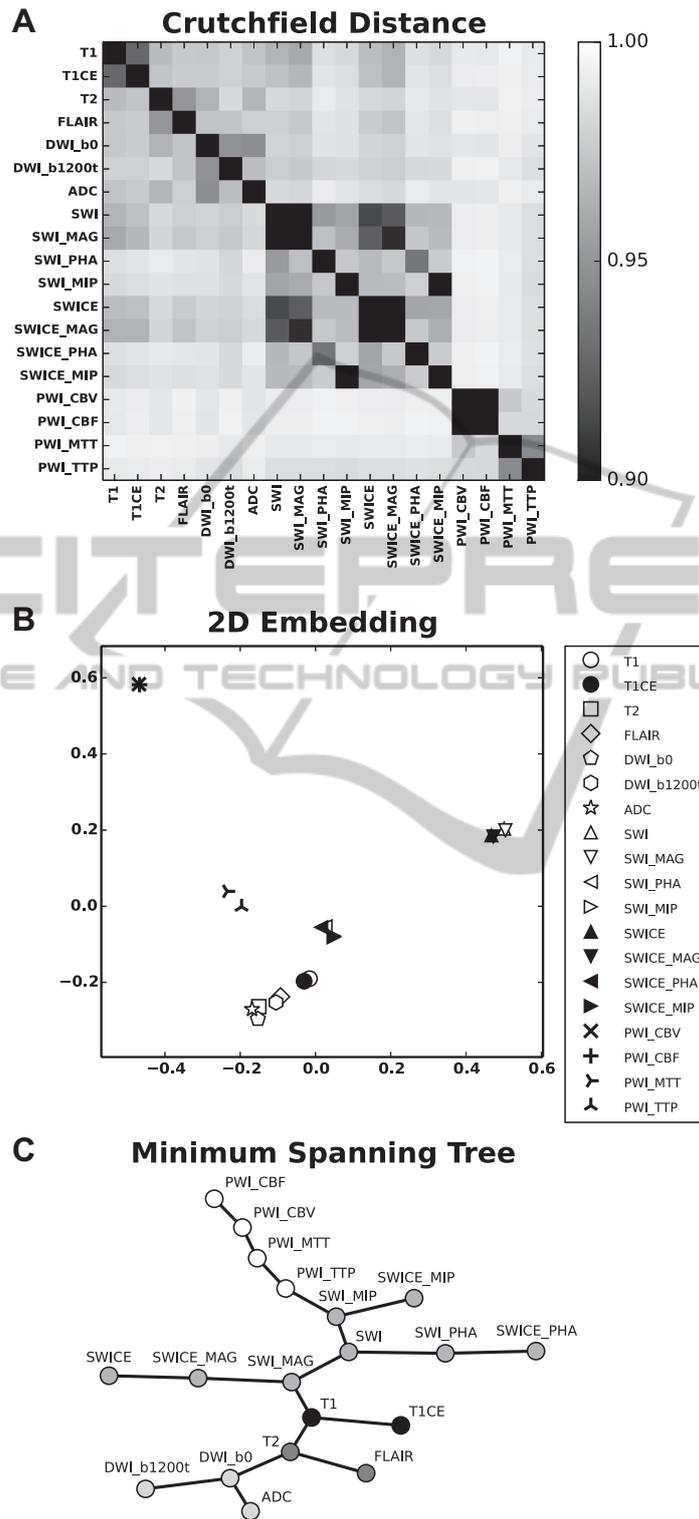


Figure 2: **Crutchfield Matrix.** A) Average Crutchfield information distance between all combinations of the multiparametric MRI data of data set 1. The scaling ($[0.9, 1.0]$) was chosen to better emphasize the structure. B) 2D geometric embedding of the distance matrix depicted in A using the *Isomap* algorithm. C) MST computed from the distance matrix depicted in A using Kruskal's algorithm. For the embedding we used the graphviz "spring model" layout (Graphviz). For the abbreviations of the MRI sequences please refer to Sec. 2.2.

ity. In a second approach we used the distance matrix as an adjacency matrix of a fully connected graph and applied Kruskal's algorithm (Kruskal, 1956) to obtain the MST (Fig. 2C). Also this method allows to discover physically related sequences by grouping them at neighboring leaves in the tree.

3.3 Experiment 3 – Automatic Quality Control

To demonstrate a potential application of the proposed framework we compute the distance matrices for $N = 216$ data sets from the BraTS 2014 training data (data set 2) and use the *Isomap* algorithm (Tenenbaum et al., 2000) to perform a 2D embedding (Fig. 3A). Based on the distance to the cluster centers we were able to identify outliers. This is shown for four cases (numbered 1 to 4 in Fig. 3A). To confirm our hypothesis that the outliers correspond to impaired data sets that do not meet quality standards, we manually inspected them. Case 1 corresponds to data set *brats_tcia_pat313_1*. This data set contains no native T1 - instead the T2-FLAIR image was enclosed twice. Case 2 (*brats_tcia_pat216_1*) misses again a native T1 weighted image. Instead a contrast enhanced image with spherical artifacts was included (Fig. 3B left). Case 3 (*brats_tcia_pat230_2*) displays severe motion artifacts in T1 (Fig. 3B right). Case 4 corresponds to *brats_tcia_pat250_1* and does not contain a native T1, instead a T1CE was included twice.

Note, even if only one channel is corrupted this leads to changes of multiple entries in the distance matrix and thus can affect the position of (all) other channels in the low dimensional embedding.

4 DISCUSSION

We present an information theoretic framework that allows to infer the relationship of MRI sequences purely based on voxel intensities. It is shown that the Crutchfield information metric (Crutchfield, 1990) is a suitable distance measure for MRI sequences and is able to capture the following relationship: the greater the (physical) distance between two MRI sequences, the less information they share. We manipulated images by adding noise (Fig. 1A), blending two MRI sequences (Fig. 1B) and purposefully applying a rigid transform to them (Fig. 1C). In all cases the Crutchfield distance increased monotonically with the amount of manipulation and showed only a small standard deviation across data set 1 ($N = 17$). If we measure the information distance between all combinations of sequences ($D = 171$) of data set 1, we

can construct a distance matrix which already shows a structure that corresponds to the intrinsic physical relationship of the sequences (Fig. 2A). This relationship becomes more explicit if we perform a low dimensional (2D) embedding (Fig. 2B) or compute the MST (Fig. 2C).

Usually the physical relationship of the MRI sequences is known or can be obtained from the DICOM header. What is the benefit of the proposed method? This objection is certainly valid, however, consider for instance data from a multicenter study which is designated for an automatic evaluation. Even if the data sets are acquired with similar parameters (e.g. TE and TR) they still originate from different scanners and thus might not be located in the same informational space. It also is very likely, as known from clinical routine, that some of the channels are affected by motion artifacts, which would also alter the informational structure. We demonstrated for $N = 216$ data sets that the proposed framework indeed can be used as an automated screening method for impaired images (Fig. 3). Employing the Crutchfield metric for quality control allows to identify data sets which are not located in the same informational space, e.g. are affected by motion artifacts (Fig. 3B right). Admittedly, so far this is a very coarse approach and it still has to be validated on a finer level with controlled experiments that determine sensitivity and specificity of the method.

Another potential application is to utilize this method for the assembly of standardized multiparametric MRI sequences. The information distance can be used as guideline for radiologists to select optimal subsets of the available sequences by e.g. pruning the MST to minimize the acquisition of redundant information. Further applications include MRI sequence optimization by choosing parameters of a set of sequences to maximize the coverage in information space, i.e. reducing redundancy within the sequences. Yet, this still requires a thorough study of the dependence of the Crutchfield distance on the differences in physical parameters of MRI sequences.

5 CONCLUSIONS

We demonstrated that the Crutchfield information metric in combination with methods for dimensionality reduction or from graph theory are suitable for discovering the physical relationship of various MRI sequences solely based on their voxel intensities. Initial experiments confirm that the proposed framework can be used for automatic MRI sequence quality control. This has to be validated in future work.

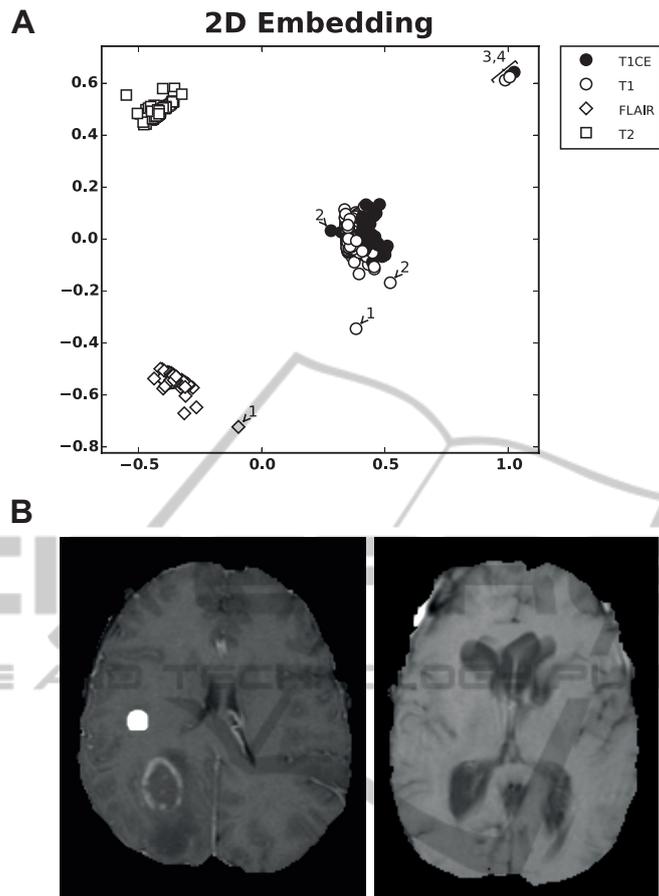


Figure 3: **2D Embedding of BraTS 2014 training data.** A) Using the *Isomap* algorithm we embedded all $N = 216$ data sets in 2D. This allowed us to identify outliers (e.g. numbered 1 to 4) which indeed corresponded to impaired data sets. The scatter of the embedded points can be explained by the fact that the data was acquired with MRI scanners of different vendors as well as with different field strengths and protocols. For the abbreviations of the MRI sequences please refer to Sec. 2.2. B) The left image corresponds to number 2 above and was labeled as a native T1 weighted image. Instead it is a contrast enhanced T1 image that contains multiple spherical hyperintense artifacts (a neuroradiologist confirmed that these do not correspond to hemorrhage). The image on the right side exhibits severe motion artifacts and corresponds to number 3 above.

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