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RELIABLE ANALYSIS  
OF  
SPEECH RELATED FMRI DATA  
USING ICA

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# 1 Introduction

The purpose of the work was to analyze functional Magnetic Resonance Imaging data using Independent Component Analysis. To identify interesting signals including stimulation related and other physiologically originated signals, but also artifacts.

Functional Magnetic Resonance Imaging provides a virtually non-invasive method for studying brain functions. It is based on the differing magnetic properties of oxygenated and deoxygenated blood. These changes can be detected in the MRI process, yet relatively low signal-to-noise ratio, head movement artifacts and other physiological vascular changes make detection of signals difficult.

The traditional methods for analyzing fMRI are based on finding statistically significant similarities with known reference signals in the data. The usage of these signals restricts the analysis, since they are usually simple estimates derived from the stimulus. Also, these methods usually focus only on the temporal changes in the data.

Using Independent Component Analysis for studying fMRI data can be useful, because ICA does not need a predefined model to work and it can also find interesting spatially distributed brain networks.

Section 2.1 gives a general overview of the human brain. Sections 2.2 and 2.3 describe the basics of functional Magnetic Resonance Imaging and section 2.4 the basics of Independent Component Analysis. The data and ICA experiments are described in section 2.5 and the results of those experiments in section 3. The article ends with conclusions in section 4.

The special assignment was done under the supervision of Dr. Ricardo Vigário in the [Laboratory of Computer and Information Science](#) at [Helsinki University of Technology](#). I would also like to thank the people of the [Brain Research Unit](#) in the [Low Temperature Laboratory](#) for providing the data and for useful insights and comments.

## 2 Methods

### 2.1 The Human Brain

The basic anatomical structure of the human brain, as depicted in figure 1, has been known for a long time and has been studied extensively using traditional medical methods.

Newer studies, *e.g.* on patients with brain injuries, have revealed that the different brain functions, like auditory, visual, somatosensory and motion, are performed on different parts of the brain. This has led to the widely accepted view of figure 2, which shows how the primary brain functions are spatially distributed on the cerebral cortex of the brain, *e.g.* auditory processing is done mainly on the superior temporal gyrus.

Recently, the development of more advanced methods for studying the living brain has verified the earlier results and also provided further knowledge of the functioning of the brain. The primary areas are tightly connected with other areas involved in higher processing of data. Figure 3 shows additional areas of auditory processing, which are

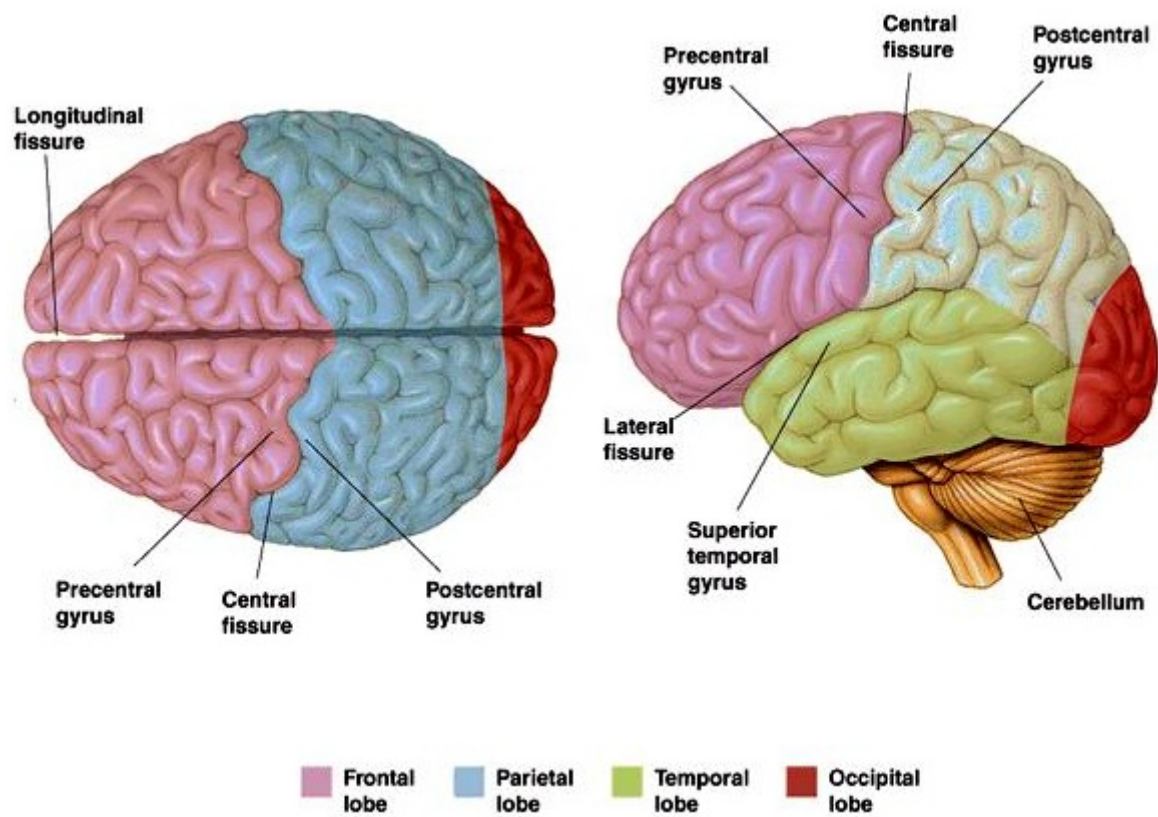


Figure 1: The structure of the human brain.

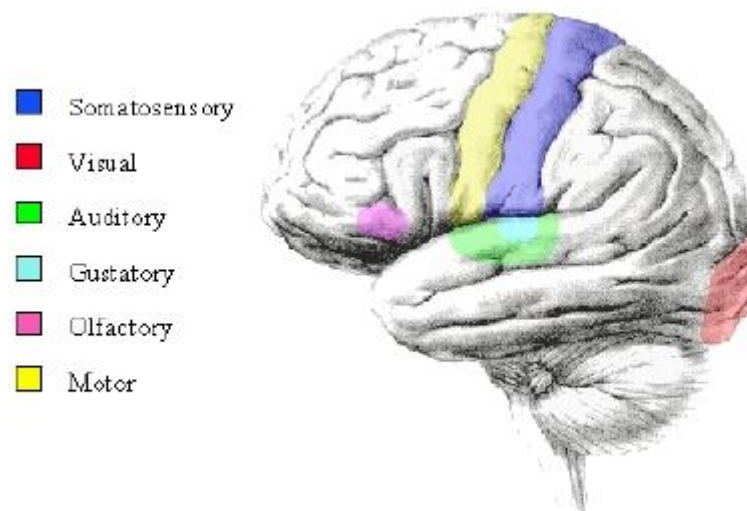


Figure 2: Distribution of functions on the cerebral cortex.

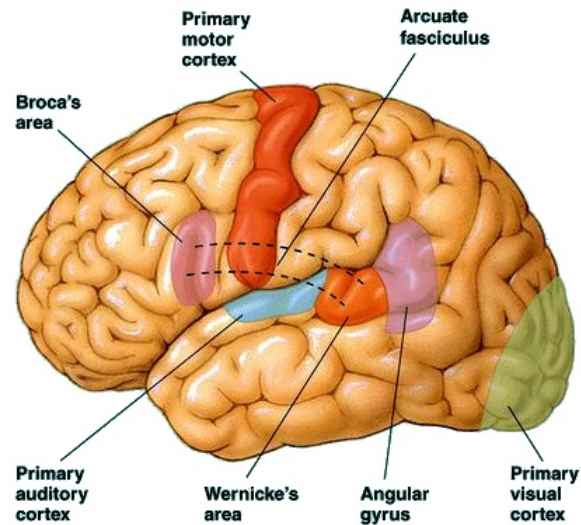


Figure 3: Additional auditory areas on the cerebral cortex.

usually more active on the left hemisphere. These areas are strongly involved in speech processing and act upon sentence forming and understanding speech.

For more details of the basic structure and function of the human brain turn to *e.g.* chapter 3 of [1] or any basic neuroscience textbook.

## 2.2 Magnetic Resonance Imaging

As magnetic resonance is a quantum mechanical phenomenon, the physics involved are quite complex and thus, are not discussed in detail here. For a detailed explanation of the physics of MRI see *e.g.* [1]. Yet, because of its importance in understanding the results, a quick overview of the main concepts is given.

Fundamentally, all MR-imaging is based on the interaction between the imaged tissue, externally applied strong magnetic fields and radio frequency pulses. Elementary particles have a magnetic property called *spin*, which behaves much like an ordinary dipole-magnet. The imaging is usually based on detecting hydrogen nuclei because of their abundance and since in bigger molecules the spins can cancel each other out.

These spins are first aligned coherently using a strong magnetic field and additional magnetic fields are used to focus the imaging on a planar slice. Next, with the application of radio frequency pulses the spins on the focused slice are caused to lose their alignment. After the radio pulses the spins will regain their coherent alignment with the main magnetic field and create detectable and characteristic magnetic resonances.

Using signal processing techniques, these measured resonances can be turned into an image of the focused slice, see *e.g.* figure 4. The scanning is continued by using the magnets to focus on another slice near the previous one and repeating the process. This produces a high-resolution volumetric image, whose *voxels* contain a kind of a density measure.

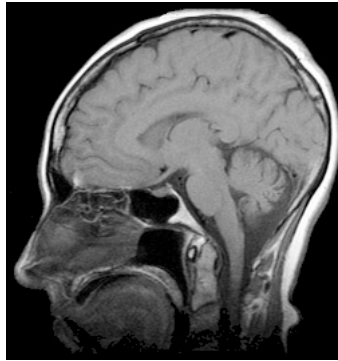


Figure 4: An example of one Magnetic Resonance Imaging slice.

### 2.3 Functional Magnetic Resonance Imaging

The goal of fMRI is to detect hemodynamic changes in the brain due to activity. Thus, the fact that it is relatively non-invasive makes it highly attractive as a research method, since usually other functional imaging methods involve using *e.g.* radioactive markers injected to a subject's bloodstream. fMRI tries to detect the temporal changes due to neural activation. It is based on the differing magnetic properties of oxygenated (*diamagnetic*) and deoxygenated (*paramagnetic*) hemoglobin molecules.

Activation of neurons results in a localized change in blood flow and oxygenation level which can be detected in the MRI process. These *vascular* or *hemodynamic* changes are related to the electrical activity of the neurons in a complex and delayed way. It is not possible to completely recover the electrical process from the vascular one, but local changes in the level of oxygenation remain a good measure of changes in the corresponding electrical activity of the neurons.

The presence of artifacts, such as head movement, and relatively low signal-to-noise ratio of the hemodynamic effect as well as other physiological vascular changes, makes the analysis of activations difficult. Therefore, the data is usually preprocessed, *e.g.* using the following methods:

- Realigning the volumes to account for head movement.
- Normalizing the volumes to allow comparison of different volumes.
- Smoothing, or low-pass filtering, to reduce high frequency noise and to increase local voxel correlations.

Usually, under controlled stimulus a subject is scanned multiple times with a certain interval. Shorter intervals and faster scanning speed are made possible by lowering the spatial resolution used in the fMRI. The most common method for analyzing this time-series of volumes is to form a reference signal of the known stimulus and to statistically compare this signal to the different voxels in the volumes. Thus, the voxels with the most significant similarity to the reference signal would reveal the areas of the brain with stimulus related activation.

## 2.4 Independent Component Analysis

*Independent Component Analysis*, or *ICA*, is a high-order statistics method for *Blind Source Separation*, whose goal is to express a set of random variables as a linear combination of statistically independent components. In the simplest form of ICA we observe  $m$  random variables  $\mathbf{x} = (x_1, x_2, \dots, x_m)^T$  which are assumed to be linear combinations of  $n$  unknown (*latent*) components  $\mathbf{s} = (s_1, s_2, \dots, s_n)^T$  and  $n \leq m$ . Then, the independent component analysis model can be expressed as

$$\mathbf{x} = \mathbf{A}\mathbf{s}. \quad (1)$$

Here,  $\mathbf{A}$  is an unknown  $m \times n$  full-rank matrix. The problem is then to estimate the original components  $s_i$  from the mixtures  $x_i$ , or equivalently, to estimate matrix  $\mathbf{A}$ .

Any additive noise has been omitted in equation 1 for simplicity. The independent components  $\mathbf{s}$  can only be estimated up to sign and magnitude because any constant multiplier in  $\mathbf{s}$  can be counter-weighted in  $\mathbf{A}$ . Also, no specific ordering of the components is forced. It is further assumed that the distributions of the random variables  $\mathbf{s}$  are not known, but that they are either all nongaussian or only one of them is gaussian.

To simplify the estimation of matrix  $\mathbf{A}$  in equation 1, it can be assumed without any loss of generality that the observed random variables  $\mathbf{x}$  are zero-mean, have unit variances and are uncorrelated. It is always possible to construct such a transformation that would produce a new set of random variables with these characteristics. One such method is called Principal Component Analysis or PCA, see *e.g.* [2]. An additional benefit of using PCA is that the dimension of the observed random variables  $m$  can be reduced to  $n$  while preserving as much of the original power of the variables as possible. Therefore, instead of having to estimate a full-rank matrix  $\mathbf{A}$  we only need to find an orthogonal matrix. If we define  $\mathbf{W} = \hat{\mathbf{A}}^T$  then the latent variables become simply

$$\hat{\mathbf{s}} = \mathbf{W}\mathbf{x}. \quad (2)$$

Intuitively, according to *central limit theory*, the distribution of a sum of  $n$  nongaussian random variables approaches gaussian as  $n$  approaches infinity. Therefore, the less gaussian the distribution of the linear combination is the more independent the latent variable will be. This gives a method for estimating  $\mathbf{A}$  and  $\mathbf{s}$  by minimizing gaussianity, or equivalently, by maximizing a measure of nongaussianity. For a more theoretical foundation of ICA, based on mutual information and negentropy concepts see *e.g.* [3].

Theoretically, a good measure of nongaussianity is *kurtosis*, which is based on fourth order statistics. It is zero for gaussian, negative for sub-gaussian and positive for super-gaussian distributions. The mathematical simplicity and relatively good discrimination make it computationally attractive. The solution to estimation by maximizing kurtosis is a gradient descent algorithm with a nonlinear term in its cost function. The two most used nonlinearities are *cubic power* and *hyperbolic tangent*. Also, the algorithm can work by estimating either one latent variable at a time or all at the same time.

Using Independent Component Analysis for studying fMRI data can be useful for several reasons. The temporal dynamics of fMRI experiments are difficult to analyze due

to the lack of a complete brain-activation model. But ICA can reveal temporally coherent brain regions without constraining to a temporal model and it can also find interesting spatial distributions. For a more in-depth discussion on the benefits of both spatial and temporal ICA and even on using them at the same time see *e.g.* [4]. An overview of other methods for applying ICA in analysis of fMRI data can be found in *e.g.* [5].

The implementation of ICA used in the experiments is a particularly fast and robust variant called Fast fixed-point ICA or simply FastICA [6]. It was selected because it is widely popular and can cope well with the vast amounts of data used in the experiments.

## 2.5 Data and Preprocessing

The data was acquired by subjecting a person to an on-off type of auditory stimulus using speech, *i.e.*, the subject listened to speech for a while followed by a moment of silence. This was repeated 4 times, resulting in 4 interleaved sets of speech and silence. During each phase of sound and silence the subject was scanned 10 times. The resulting stimulus reference signal typically looks much like the ideal one in figure 5. In practice the hemodynamic effect makes the signal smoother.

The data consisted of 80 fMRI volumes of the whole human brain. The volumes were scanned with an interval of approximately 3 seconds and preprocessed with the usual methods in fMRI scanning as explained in section 2.3. The voxel resolution of each volume after preprocessing was  $128 \times 128 \times 68$ .

In order to use this volumetric data with ICA it is necessary to vectorize it (see equation 1). This is accomplished by reshaping each of the 3 dimensional volumes into a single vector, but since the temporal resolution of the data might not be adequate to explain all the structures in the huge amount of volumetric data and since we do not want to restrict our analysis to a subset of the whole brain, a simple method of thresholding and masking was used to exclude the outside of the brain from the volumes. This method works well, since the majority of these voxels contain only ambient noise originating outside the brain, which is of no interest anyway.

Also, as mentioned earlier in section 2.4, the ICA estimation can be improved by whitening the data. Therefore, the resulting vectorized data was whitened using PCA and selecting the 30 most powerful components. However, it is important to note that in this case the reduction of dimensionality during whitening actually means compression of

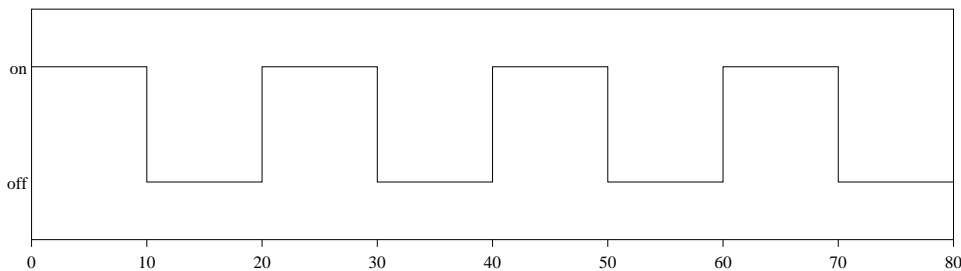


Figure 5: An ideal on-off type stimulus reference signal.

temporal data, since our data vectors are the volumes scanned at different times. And as the sampling frequency of the scanning was quite slow to begin with, one has to be very careful not to compress the data too much. Additionally, the most powerful component in the data is quite likely the structural image of the brain, since it is present at all the volumes. It does not change with time and is much more apparent than the hemodynamic changes. Thus, surprisingly, it might be beneficial to leave out the most powerful PCA component from the data.

After the data is well prepared for the actual application of ICA, it is quite straightforward to do so, especially with the used FastICA. The selectable options in FastICA are:

- Number of estimated independent components.
- Deflation or symmetric mode.
- Used nonlinearity (cubic power, hyperbolic tangent or gaussian).

Even after successful application of ICA, we are still left with the problem of ambiguity. Not only are we free to choose a sign and scale for each estimated independent component, but the estimates from any single run of ICA differ from each other. Mainly the order of the components might differ, but the whole set of components might also differ, since we are only estimating a certain amount of components out of an unknown set. Additionally, the ICA algorithms always start from a random initial condition and try to converge to the global minimum or maximum of the specified cost function. Now, even the best algorithm can be caught in a local minimum or maximum, causing poor estimation of the independent components. Even if the algorithm converges into the global minimum or maximum, the random initial condition will introduce a variable noise into the estimates. Also, there is another kind of a problem, namely over-learning, resulting from strong low frequency content of the smoothed fMRI data. Thus, the estimation algorithm can quite easily over-fit the data.

To overcome such difficulties and to generally improve the independent component estimates, the ICA algorithm can be run multiple times, resulting in different sets of components with varying noise. These components can be packed by correlation, *i.e.* calculate the average of all estimated components, which exceed a certain amount of correlation with each other. An additional benefit of doing correlation packing is obtaining a kind of consistency measure for the components in the form of the amount of averaged components and the correlation coefficients of those components. This can be used *e.g.* to order the resulting components in a consistent manner and to spot over-learning. An algorithm archiving this consist of the following steps:

1. Estimate the correlation coefficients (correlation matrix) of all the estimated components.
2. Threshold the correlation matrix with a specified limit to exclude too small and unmeaningful correlations.

3. Raise the thresholded correlation matrix to a specified power in order to identify and include long chains of small correlations.
4. Calculate the averaged components based on the resulting packing matrix.

### 3 Results

Detailed results from an experiment, where the following steps of analysis were applied:

1. PCA whitening, retaining the 30 most powerful dimensions.
2. 200 randomly initiated runs of FastICA, with 15 estimated independent components in symmetric mode and using nonlinearity *tanh*.
3. Correlation packing the  $200 \times 15$  components, with a threshold of 85% and a power of 16.

It is important to remember, as was explained in section 2.4, the ambiguity of sign and scale of the independent components, while interpreting the results.

#### 3.1 Overview

The resulting 17 correlation packed independent components are shown in figures 6 and 7. Figure 6 shows the activation time-courses of the components, which are the columns of the estimated matrix  $\mathbf{A}$ . They are plotted in blue over the gray-scale distributions of all the packed components. Also shown in the figure above the time-courses are the number of packed components and lowest correlation coefficient. Figure 7 shows example slices from the volumes corresponding to the time courses. They are the actual estimated independent components  $\mathbf{s}$ . The upper example slice contains the highest voxel value and the lower is from a fixed position roughly crossing the superior temporal gyrus, or just above the ears.

For example, component 15 is a result of correlation packing 6 independent components, with the lowest correlation coefficient being 93.22%. Clearly, the time-course is an arc shaped signal and there is some, though quite dense, variance in those 6 packed components. Also, the corresponding example slices contain mostly low values *i.e.* are relatively dark.

The variance present in the first three components is clearly different than in the rest. It seems to be caused by phase shifts in the correlation packed estimates.

#### 3.2 Closeup visualization

As the three-dimensional volumes are by nature images, it is helpful to visualize them as such. And since modern computers are quite good at drawing three-dimensional graphics, the following improved visualization was used to allow closer inspection.

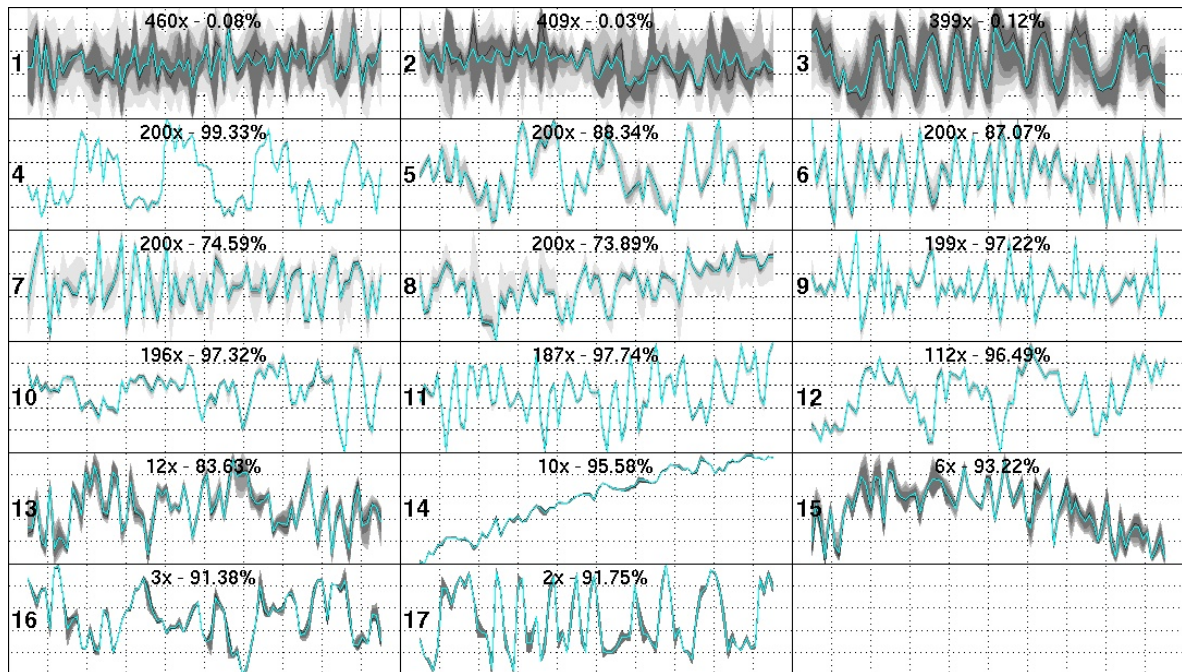


Figure 6: Activation time-courses of the correlation packed ICA components.

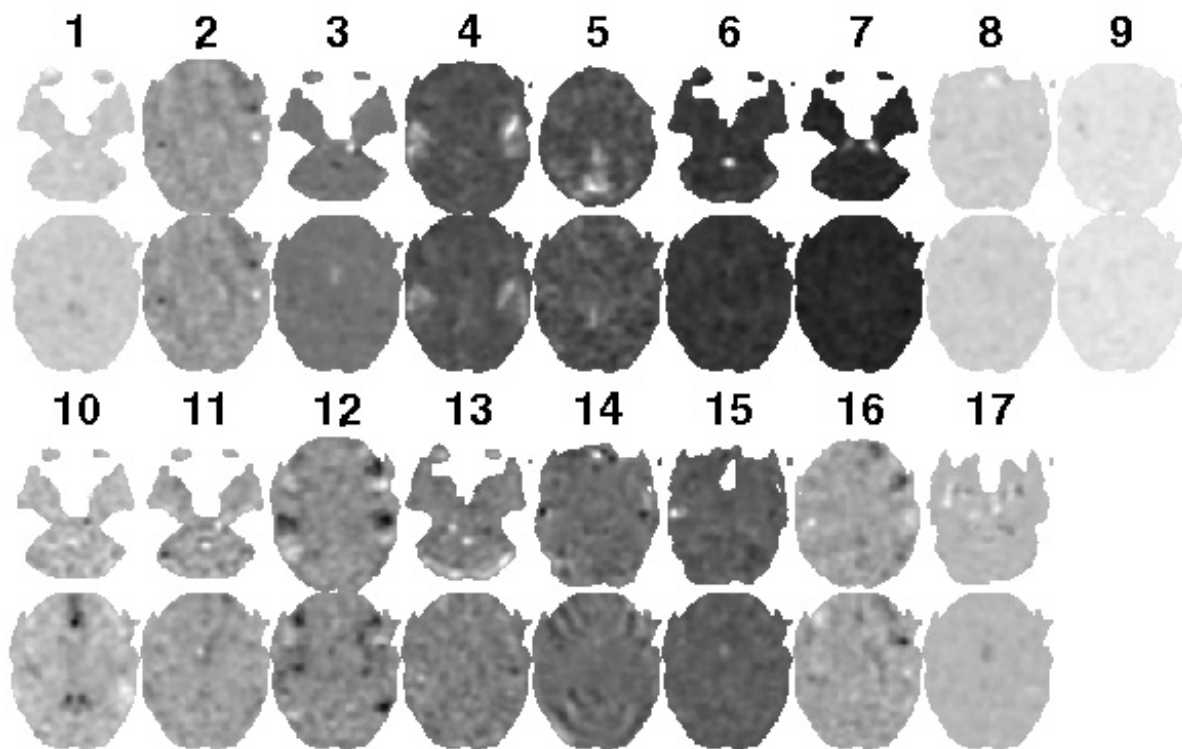


Figure 7: Example slices of the correlation packed ICA components.

The volumes can be visualized three-dimensionally from any direction and the view can be focused on any point within the volume. To improve the contrast in the interesting regions, the histogram of a volume can be calculated. Then, the highest and lowest values of the histogram can be thresholded and the corresponding voxels can be highlighted using artificial coloring. In figures 8, 9, 10 and 11 the volumes are viewed from all three main axes of the brain simultaneously. The lowest values in the volume are highlighted in red and the highest in green. Also present in the figures are histograms of the volumes and the corresponding activation time-courses.

Additionally, the overall activity in a volume can be visualized by summing the highlighted voxels through the whole volume. This results in a single image per direction, which is a kind of a virtual x-ray of the activity. These images help to visualize the locations of the activated sub-volumes. Figure 12 shows such x-rays with yellow highlighting.

Clearly, component 4 (see figure 8) shows a strong stimulus related on-off type of activation, which seems to be located in the primary auditory cortex. Also, components 12 (see figure 9) and 16 (see figures 6 and 7) show stimulus related activations around the usual locations of the Broca's and Wernicke's areas, as illustrated in figure 3, which is supported by the fact that the stimulus is speech.

One interesting component is 14 (see figure 10), which clearly does not relate to the stimulus at all. Instead it seems to be a scanning or preprocessing artifact related to filtering. This is further supported by the periodic waveform visible in the corresponding volume.

Additionally, components 1 and 3 (see figures 11 and 12) show strong activations apparently in the thalamus. These activations seem to have frequency changes somewhat related to the stimulus.

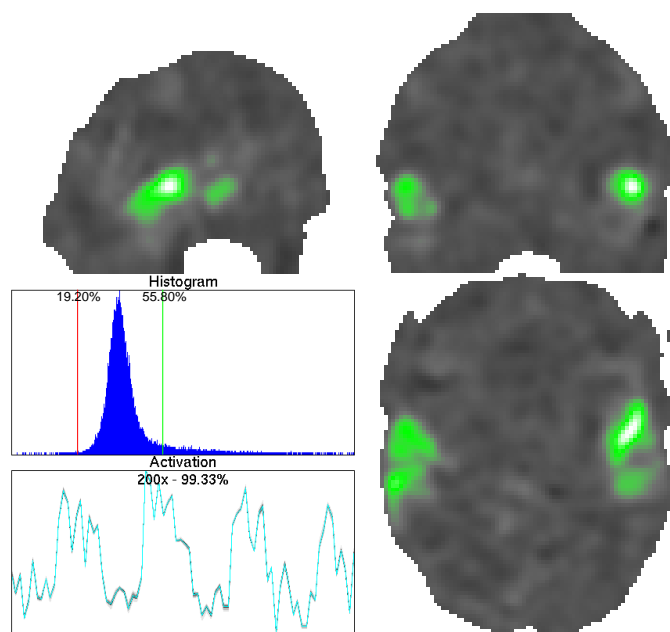


Figure 8: Closeup of independent component 4.

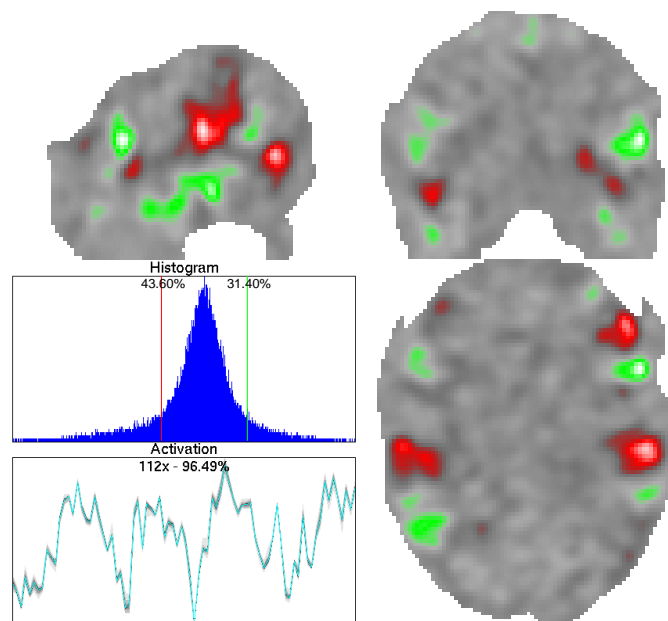


Figure 9: Closeup of independent component 12.

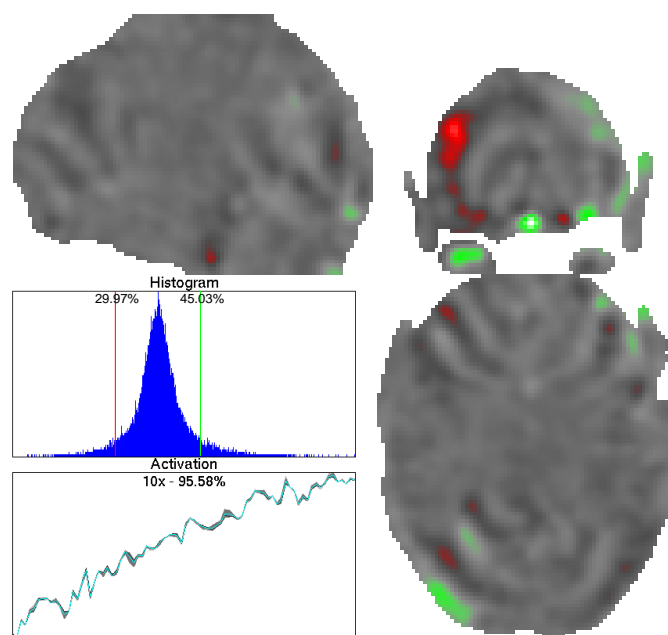


Figure 10: Closeup of independent component 14.

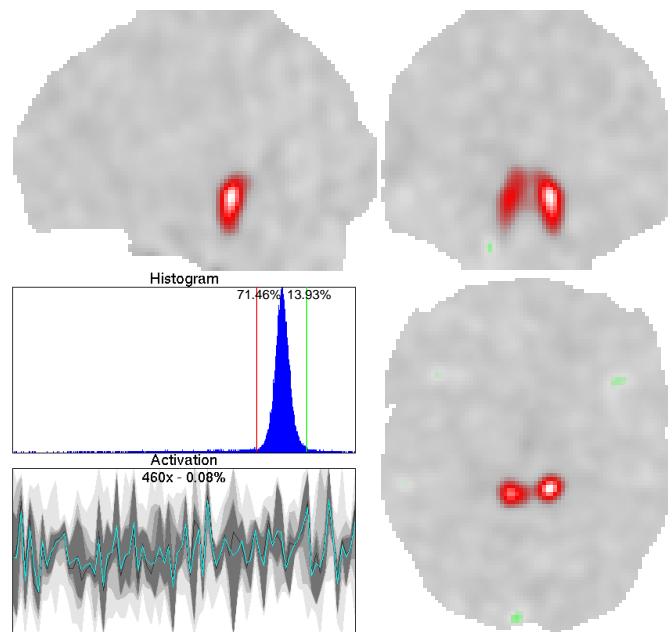


Figure 11: Closeup of independent component 1.

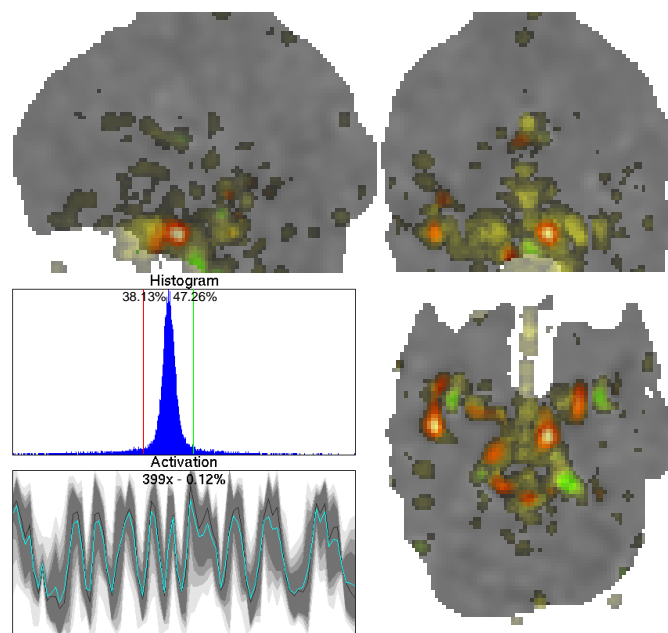


Figure 12: Closeup of independent component 3 with transparency.

## 4 Conclusions

Functions of the human brain can be studied using functional Magnetic Resonance Imaging. However, the complex nature of the data and contained artifacts make analysis difficult. In addition, the traditional methods of analysis are based on simple statistical models making crude assumptions and further restricting the analysis.

Independent Component Analysis is a relatively new high-order statistics method that does not need a predefined model. It can be used to reveal both temporal and spatial structure of the brain activations. The resulting independent components can be stimulus related or unrelated and even artifacts can be separated.

The experiments were done using fMRI data scanned under on-off type auditory stimulus and analyzed using FastICA. The ICA was applied multiple times and the results were then correlation packed. This resulted in improved estimates and additional consistency measures.

The results show multiple interesting stimulus related signals located around the auditory cortex. Additionally, interesting signals not clearly related to stimulus and artifacts were also revealed. Some of these interesting activation patterns seem to be located in the thalamus.

Thalamic activity is not yet fully understood in this context and is the subject of many ongoing research efforts. It is suggested that thalamic activity could be related to the level of awareness or concentration. Also, in auditory signal processing some frequency analysis could be done within the thalamus.

In addition, the experiments showed that ICA is relatively easy to apply without any *a priori* knowledge of the type of stimulus and without enforcing any specific hemodynamic model. ICA thus serves well for the purpose of hypothesis testing and helps in creation of new hypotheses for further analysis and testing.

Further research might improve the analysis of fMRI data more than the simple correlation packing does. Using the temporal data gained from the results of the spatial ICA, or iteratively repeating both spatial and temporal ICA, should improve the estimates of the independent components and thus, allow more accurate conclusions to be made from the data.

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