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Multivariate Matching Pursuit in the Analysis of Single-trial Latency of the Auditory M100 Acquired with MEG

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Abstract. A multivariate version of the matching pursuit algorithm (MP) was used in the analysis of auditory evoked fields (AEFs) acquired by means of magnetoencephalography (MEG). Single-trial evoked brain responses were modelled with Gabor functions of certain time of occurrence, temporal width, frequency, and either fixed or varying phase. In particular, trial-to-trial variation of the auditory M100 component was addressed in terms of the phase parameter, with emphasis on the trial dependent amplitude and latency of the M100. The constrained or unconstrained phase turns out to play a significant role in modelling the single-trial M100 wave.

Keywords: Auditory Evoked Magnetic Fields; M100; Magnetoencephalography (MEG); Matching Pursuit; Single Trials

1. Introduction

The classical approach to the analysis of evoked brain responses in electroencephalography (EEG) and magnetoencephalography (MEG) is based on the so-called signal-plus-noise (SPN) model, in which the brain response to a particular repeatedly presented stimulus is assumed to be a deterministic process which does not vary across repetitive stimulations. Frequent repetition of the stimulus aims at minimizing the background noise, which is assumed to be a stochastic process of zero mean, and thus expected to vanish, or, more specifically, to diminish during averaging of the measured brain responses originating from repeated stimulation.

This averaging process constitutes the backbone in EEG and MEG data analysis, and its application is very plausible in many experiments; however, it completely ignores the variability of the stimulus-evoked response across single trials. Various approaches have been proposed over the last decades by numerous authors in order to estimate single-trial responses. The main problem in such single-trial analyses is to disentangle the actual stimulus-evoked brain activation from the ongoing noise, which is considered to represent any other activation not related to the actual stimulus.

We propose to use an extension of an adaptive approximation technique, the matching pursuit algorithm [Mallat and Zhang, 1993], to model evoked single-trial brain responses. In a previous study [Sielużycki et al., 2009], we have shown the feasibility of using a multivariate version of the matching pursuit algorithm (MMP) in the single-trial analysis of the auditory evoked M100 component. In the current work, we introduce a new quality to the single-trial analysis by releasing the constraint on the phase parameter of the Gabor functions used to parameterize the M100. As a consequence, the single-trial variation of the M100 latency is already reflected in the first iteration of the MMP decomposition of the MEG signal.

2. Material and Methods

2.1. Material

The algorithm was tested using the auditory evoked responses of an exemplary subject who was exposed to 224 sinusoidal 1-kHz tones of 0.5-s duration, delivered to both ears at a sound pressure level of 90 dB. The inter-stimulus interval was 1.5 s, and the auditory evoked magnetic fields (AEFs)

were acquired by means of a whole-head 148-channel magnetometer system (4-D Neuroimaging, USA). Artefact rejection reduced the number of trials to 190. The results presented are derived from the channel with the strongest M100 amplitude.

2.2. Methods

Matching pursuit (MP) provides a suboptimal solution to the problem of signal representation by means of an iterative procedure, in which the elements (atoms) of a redundant set of functions (typically Gabor functions), the so-called dictionary *D*, are used to explain the content of the analysed signal. In the first step, MP is searching the dictionary for the function *g* that best matches the signal *x*. In each consecutive step, another function is matched to the signal that is the residual left after subtracting the result of a previous iteration, i.e. the properly weighted atom in the previous iteration. For a complete dictionary, the procedure converges to *x*, but in practice, finite expansions are used:

$$x \approx \sum_{n=0}^{N-1} \left\langle R^n x, g_{\gamma_n} \right\rangle g_{\gamma_n}, \tag{1}$$

where *g* denotes the atom that is matched in the *n*th iteration, and γ represents the following parameters of the atom: translation (position in time), scale (temporal span), frequency of the underlying sine, and phase which reflects the temporal relation between the sine and the modulating Gaussian envelope [Durka, 2007]. The dot product between the signal of a current iteration *n* and the atom that best matches that signal (the match being rated in terms of the value of this dot product) is a scalar weight by which the selected atom must be multiplied prior to its subtraction from the signal in order to best explain the part of the signal coherent with the atom. This is because all atoms in the dictionary are normalized with respect to their norm, so that they all have equal chance in the search for the optimal match.

The multivariate algorithm used to parameterize the evoked brain responses in single trials of one selected channel is technically similar to the multichannel matching pursuit (MMP) algorithm used to parameterize the averaged signal in multiple channels, as proposed in [Durka et al., 2005] as a preprocessing stage for EEG inverse solutions (see also [Sielużycki et al., 2009]). In this version of the algorithm, the criterion for selecting the optimal atom in each iteration *n* is such that the maximum of the module of the sum of its products with the signals of the consecutive single trials is obtained:

$$g_{\gamma_n} = \arg\max_{g_{\gamma_i} \in D} \left| \sum_{k=1}^{K} \left\langle R^n x^k, g_{\gamma_i} \right\rangle \right|, \tag{2}$$

where *k* enumerates trials *1*…*K*.

Provided the parameters of the Gabor function *g*, i.e. its translation, scale, frequency and phase, are constrained not to vary across trials *k*, only those signal features (or patterns) that consistently appear across single trials should be represented by the selected atom (Gabor function). This consistency will be reflected by constant translation, scale, frequency, and phase across all trials. However, the trial-dependent amplitude, weighted by the values of the products of the selected atom with the signals of the individual single trials, enables distinguishing between different response amplitudes in individual trials [Sielużycki et al., 2009]. Superposition of the atoms of a few consecutive MMP iterations can be used to explain the trial-to-trial variation of the peak latency of the so obtained reconstructions modelling the single-trial evoked response [Sielużycki et al., 2009]. This is because each of those fixed-phase atoms has its own profile of trial-to-trial amplitude variation.

Here, we propose a more advanced alternative approach, in which we released the constraint of a constant phase. As a consequence, it turned out that the atom obtained already in the first iteration of the MMP algorithm was sufficient to efficiently model the single-trial M100. We compare the findings with those obtained with the approach in which the phase was kept fixed (constant) across all trials. Note that in both approaches no parameter was set to a particular value a priori.

3. Results

Figure 1 shows the time course of the magnetic field of a selection of 16 single trials acquired in the aforementioned auditory experiment. The measured signal is depicted in grey. The black dashed curves show the waveforms of the Gabor function of the first iteration of the MMP algorithm, in which the phase of the atoms was kept fixed across consecutive trials (MMP_{fp}) resulting in identical M100-peak latencies across all trials. However, since the amplitude of that atom was allowed to vary, trial-to-trial variations of the response strength can be observed.

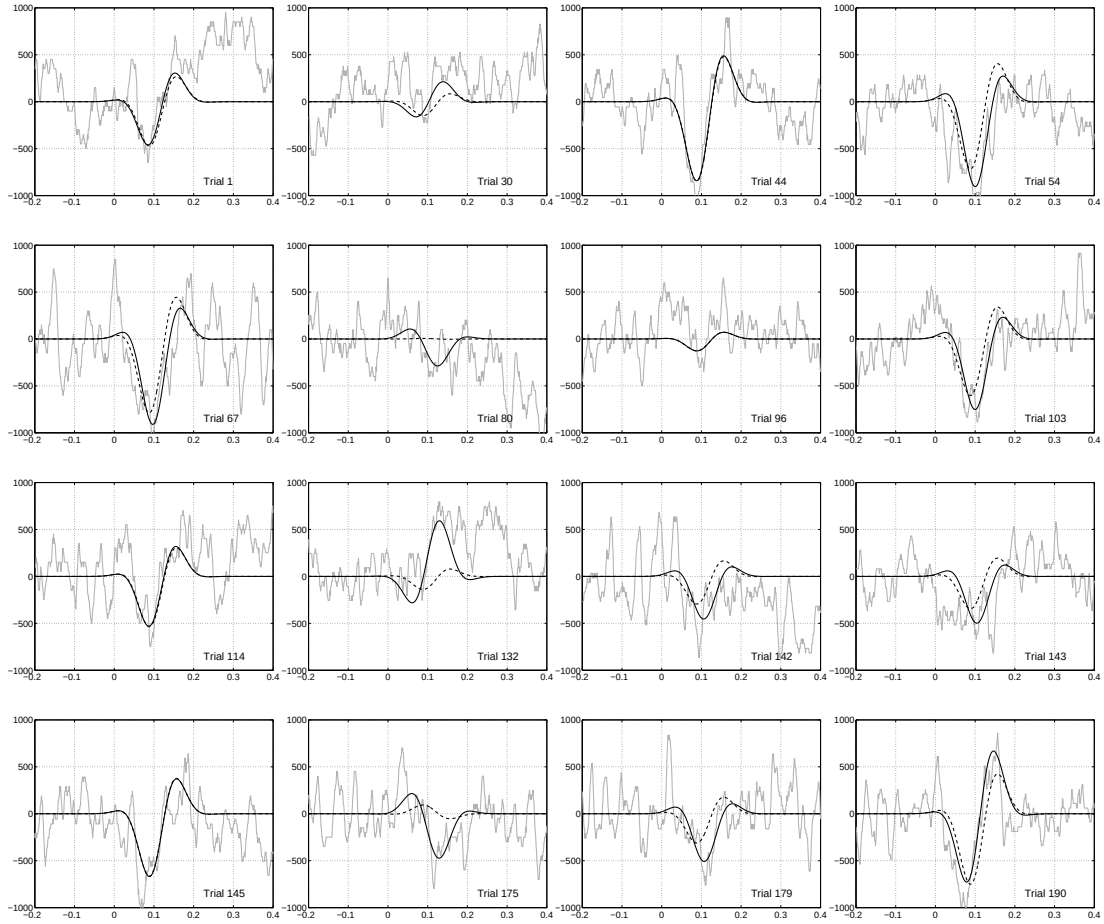

Figure 1. *Selected single trials with the signal (grey line) recorded from the channel with the strongest M100 deflection over the right hemisphere, and the Gabor function fitted in the first iteration of the fixed-phase MMP (black dashed line) and of the variable-phase MMP (black solid line). Ordinate: B [fT], abscissa: t [s]. t = 0 corresponds to the stimulus onset. The selection criterion for the trials displayed in this figure was to provide an overview on characteristic patterns reflecting the relationship between MMP_{fp} and MMP_{vp} solutions.*

However, single-trial responses are believed to vary from trial to trial not only in their peak amplitude but also in the corresponding peak latency. The solid lines in the 16 insets of Fig. 1 visualize the Gabor function obtained in the first iteration of the MMP, in which there was no constraint on the phase of the Gabor functions (variable-phase MMP_{vp}). Consequently, the peak latencies of such a single-atom M100 reconstruction vary from trial to trial.

The temporal relations between the fixed-phase waveform and its corresponding variable-phase counterpart display several different characteristics. Apart from some trials where no difference between the parameterization of the two approaches was found (see, e.g., Trials 44, 96, 145 in Fig. 1), the majority of the trials shows some moderate differences (shifts) between the resulting waveform of the two approaches (Trials 1, 54, 67, 103, 114, 190). In only a few trials (Trials 80, 132, 175) strong differences were observed.

Figure 2 shows an overlay plot of the single-trial M100 reconstructions using the atom of the first iteration only, for the fixed-phase MMP (left) and the variable-phase MMP (right). The substantial difference between the two approaches discussed above is particularly clear here. The vertical lines depict the average M100-peak latency (88 ms), which is identical in both cases and stems from the inherent properties of the MMP algorithm.

Figure 3 (left) shows the trial-dependent peak amplitude of the reconstructed M100 obtained by means of the fixed-phase MMP versus the corresponding values obtained with the variable-phase algorithm. Interestingly, the amplitudes in the varying-phase approach tend to exceed those in the alternative model, which means that the adaptive phase fits the peaks of the single-trial signals better.

No clear relation between the peak amplitude and the corresponding peak latency of the M100

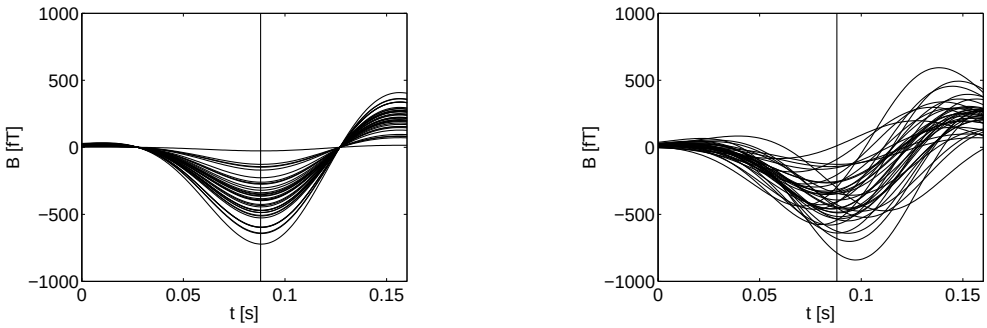

Figure 2. *Single-trial M100 waveforms reconstructed with the first atoms of the fixed-phase MMP (left), and of the variable-phase MMP (right). For clarity, only every 5th trial is shown. The vertical solid lines display the mean value of the M100-peak latency.*

reconstructions for the variable-phase approach was observed (Fig. 3 (right)), which may indicate that the algorithm is free from a systematic and cumulative bias.

Figure 4 depicts the time course of the M100-peak amplitudes (left) and the corresponding peak latencies (right) of the variable-phase reconstructions across all but seven single trials (the latter were spoiled by severe noise and were removed from further analysis). The solid lines reflect first degree polynomials fitted to the data in order to reveal a general tendency in the trial-to-trial variability. A habituation effect is clearly observable for the peak amplitudes with a value for the slope coefficient of –0.7849 fT/trial, which is comparable to the findings of the fixed-phase approach (slope coefficient: –0.8585 fT/trial). The slope coefficient for the corresponding polynomial fitted to the peak latencies equalled $-1.3284 \cdot 10^{-5}$ s/trial.

4. Discussion

We parameterized the single-trial brain responses to an auditory stimulation with simple sinusoidal 1-kHz tones, and compared the results of two alternative approaches of modelling the single-trial M100. Two distinct variants of the MMP algorithm were applied to parameterize the MEG signal with one Gabor function only—the *fixed-phase* version versus the *variable-phase* approach. It was common to both strategies that the single-trial estimates revealed trial-to-trial variation of the response amplitude. In addition, the MMP_{vp} algorithm, due to its inherent properties, enabled estimation of the trial dependent peak latency of the M100 as well. Because of the different approaches to phase, the two algorithms did not only differ in terms of the estimated M100-peak amplitude and latency values of the single-trial responses but also as the morphology (waveform) of the estimates is concerned.

An open question remains as to which of the two approaches provides better estimates of the "real" single-trial responses. Most researchers would rather tend to skip the first strategy, which assumes constant latency of the modelled M100 across the entire course of the multi-trial measurement; the MMP_{vp} approach seems to be more intriguing. However, it is not unambiguously clear whether the adaptive phase of the variable-phase approach indeed reflects the "real" trial-to-trial variation of the

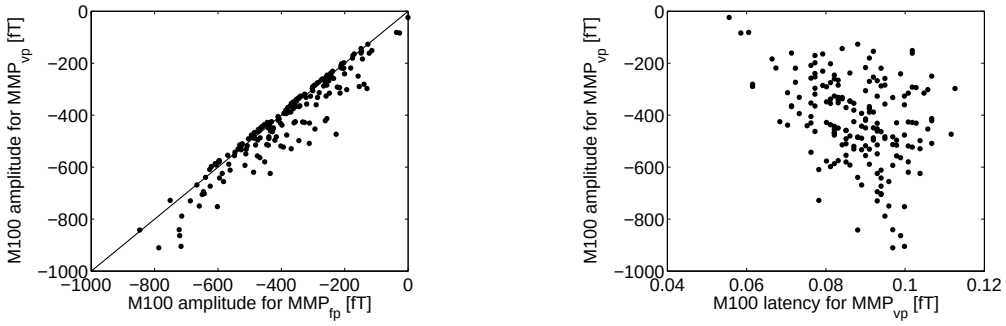

Figure 3. *Left: Trial-dependent peak amplitude of the reconstructed M100 obtained by means of the fixed-phase MMP (abscissa) versus the variable-phase MMP (ordinate). Right: Peak amplitude versus latency of the M100 reconstructed with the variable-phase MMP.*

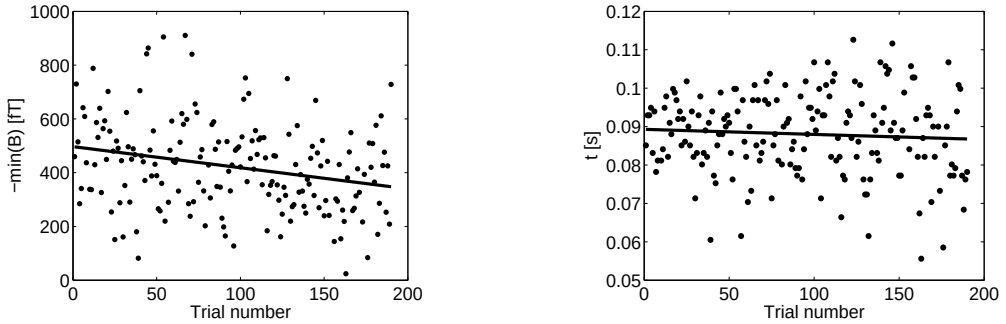

Figure 4. *M100 peak amplitudes (left) and corresponding peak latencies (right) of the reconstructed M100 obtained with the first atom of the variable-phase MMP. Note that the amplitudes depicted in the left inset were multiplied by –*1 *to account for the negative deflection of the M100 for the selected channel. The habituation of the peak amplitude as well as that of the corresponding peak latency is expressed by first-degree polynomials fitted to the data (solid lines).*

single responses or whether, alternatively, it simply tends to explain particular noise patterns. Furthermore, it is not obvious to which extent features of the single-trial signals are effectively addressed by the variable-phase model. In Fig. 1, Trial 80 provides a good example of a noisy signal, in which the solid trace representing MMP_{vp} may reflect noise rather than any brain response. The dashed MMP_{fp} curve is practically flat in this trial, which means that the contribution of this trial to the quasi-deterministic morphology modelled by the fixed-phase approach was negligible. However, this does not mean that there was no brain response at all in this trial; it could have simply been spoiled, or even cancelled, by a particularly "unfortunate" noise pattern, which led to a significantly diminished SNR.

One may also consider whether the fixed-phase approach possibly resulted in worse fits for the later trials, thus providing underestimated amplitudes, which may have resulted in the larger absolute value of the slope coefficient of the amplitude habituation. Some supporting evidence for this hypothesis is the finding that the standard deviation of the estimated latency obtained in the variable-phase approach increases with increasing trial number (see Fig. 4 (right)).

To date, no bullet-proof methodology for extracting the real single-trial response from its superposition with the contaminating noise exists, and, unfortunately, noise is inherent to any MEG or EEG measurement. Numerous groups have introduced various tools aimed at such an extraction over the last decades, and the ongoing discussion concerning evoked versus induced activity and their roles as to the generation of event-related magnetic fields or electric potentials does not head toward a promising solution. After all, the situation seems to be comparable with a checkmate, which is simply to be expected when using pure mathematical reasoning, as it is impossible to precisely disentangle any unknown components measured as their superposition. In this respect, an intelligent and diligent study was, for example, provided by Yeung et al. [Yeung et al., 2004]. Notwithstanding we expect that our proposed approach will be advantageous especially in studies which explicitly address the trial-to-trial variation of evoked magnetic fields. Beside habituation studies, possible examples for this are learning and memory experiments, or task-related studies involving, e.g., the discrimination of different stimuli.

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