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Single-trial evoked brain responses modeled by multichannel matching pursuit

Jiang Haiteng[1] Lu Qing[1] Han Yinglin[2] Yao Zhijian[2] Liu Gang[1]

([1]Research Center for Learning Science, Southeast University, Nanjing 210096, China)
([2]Nanjing Brain Hospital Affiliated to Nanjing Medical University, Nanjing 210029, China)

Abstract: A multichannel matching pursuit (MMP) algorithm is proposed to decompose the one-dimensional multichannel non-stationary magnetoencephalography (MEG) signal at a single-trial level. The single-channel matching pursuit (MP) linearly decomposes the signal into a set of Gabor atoms, which are adaptively chosen from an overcomplete dictionary with good time-frequency characters. The MMP is the extension of the MP, which represents multichannel signals using linear combination of Gabor atoms with the same occurrence, frequency, phase, and time width, but varying amplitude in all channels. The results demonstrate that the MMP can optimally reconstruct the original signal and automatically remove artifact noises. Moreover, the coherence between the 3D source reconstruction and the prior knowledge of psychology further suggests that the MMP is effective in MEG single-trial processing.

Key words: magnetoencephalography (MEG); single trial; multichannel matching pursuit; source reconstruction

The traditional approach to dealing with evoked magnetic fields in the MEG, or electrical potentials in EEG is to apply the well-known and widely accepted repeated-stimulus paradigm followed by averaging the measured fields or potentials across repetitions. Frequent repetition of the stimulus aims to reduce the contributions from non-stimulus-locked and non-phase-locked activity. Although the averaging method reduces the contribution of background brain activity on the order of the square root of the number of trials, it completely loses the trial-to-trial variation in the averaging procedure.

Many approaches have been taken to address the problems of estimating single-trial responses over the last decades[1]. The main problem in such single-trial analyses is to extract the actual stimulus-evoked brain activation from the ongoing noise, which is considered to represent any other activations not related to the actual stimulus. In addition, single-trial analysis has not been sufficiently validated by studies of source localization on either simulated or empirical MEG data.

In this paper, we propose to use an adaptive algorithm MMP[2] for the Stroop word color interface single-trial analyses. The MMP is a relatively new signal decomposition method, where the MEG data are decomposed into a sum of waveforms (usually termed atoms) chosen from an overcomplete dictionary of atoms each being defined in time, frequency, and space. The parameterized atom allows the extraction of a certain part of a signal within given time and frequency intervals [3]. Removal of artifacts or the extraction of signal components of interest can be accomplished in the MEG single-trial multichannel analysis. Furthermore, in order to validate the algorithm, the distributed source reconstruction technique is applied to estimate the source location, and it is compared with the professional physiological opinion.

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Biographies: Jiang Haiteng (1985—), male, graduate; Lu Qing (corresponding author), female, doctor, associate professor, luq@seu.edu.cn.
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1 Materials and Method

1.1 Materials

The subject under study is a healthy female with the age of twenty years. The data is recorded using an Omega 2000 (VSM Med Tech Inc., Port Coquitlam, Canada) 275-channel device placed in a magnetically shielded room, which provides a considerable amount of shielding from noise and interference. The Stroop stimuli are the color words, "red", "blue" and "green", printed in red, blue or green ink. The color words are presented in an incongruent (e.g., "red" is displayed in blue color) or a congruent color (e.g., "red" is displayed in red). The stimuli of the task consist of 48 incongruent and 48 congruent stimuli, which are pseudo-randomly presented. Each stimulus consists of an eye fixation cross of 500 ms and an incongruent/congruent stimulus of 1 000 ms. The subject is asked to name the color quickly and accurately in a very small voice. These MEG data are sampled at 1 200 Hz and filtered from 1 to 48 Hz. 120 samples of pre-stimulus data and 720 samples of post stimulus data are included as well for each trial. The individual MRI data is collected using a GE 1.5T Signa system. In this paper, only the incongruent data is analyzed.

1.2 Method

The single-channel matching pursuit (MP) is an adaptive algorithm that finds a suboptimal solution to the problem of an optimal representation of a signal in a redundant dictionary of functions[4]. We use a dictionary composed of Gabor functions, which are built of cosines modulated by Gaussian envelopes:

$$g_\gamma(t) = k(\gamma)\, e^{-\pi((t-u)/s))^2} \cos\left(2\pi \frac{v}{N}(t-u) + w\right) \quad (1)$$

where $\gamma = \{s, u, v, w\}$; s is the scale; u is the translation; v

is the modulation frequency; and w is the phase. N represents the signal's length.

The constant $k(\gamma)$ is adjusted such that $\| g_\gamma(t) \| = 1$. Gabor dictionary $D = \{g_\gamma\}$ is composed of all $\gamma = (a^j, pa^j\Delta u, ka^{-j}v)$ with $a = 2$, $u = 1/2$, $v = \pi$, $0 < j \leqslant \log_2 N$, $0 \leqslant p \leqslant 2^{-j+1}N$, $0 \leqslant k < 2^{j+1}$. The phase parameter is optimized separately in numerical implementations.

The multichannel matching pursuit is the extension of the single-channel MP algorithm, which linearly decomposes a multichannel signal $f = (f^1, f^2, \ldots, f^n)$ of n single channels into atoms of the form $(g_\gamma, \ldots, g_\gamma) \in D$. Let $R^0 f^l = f^l$ be the 0th-order residual of channel l. A multichannel matching pursuit is an iterative algorithm that subdecomposes each channel's residue Rf by projecting it on a vector of D that matches Rf almost at best. The procedure is repeated each time on the following obtained residue. The selection of a Gabor atom is not random. It is defined by the choice function, which associates with the summation of all channels' inner products between each channel's residue Rf and each Gabor atom in D. For a given residual $R^k f^l$ of iteration $k \geqslant 0$, we select the best atom g_{γ_k} using the following criterion:

$$\sum_{l=1}^{n} |\langle R^k f^l, g_{\gamma_k}\rangle|^2 \geqslant \alpha \sup_{g_\gamma \in D} \sum_{l=1}^{n} |\langle R^k f^l, g_\gamma\rangle|^2 \quad (2)$$

where $\langle R^k f^l, g_{\gamma_k}\rangle$ defines the correlation coefficient computed by the inner product of $(R^k f^l, g_{\gamma_k})$; $\alpha \in (0, 1]$ is an optimized parameter[5]. Phase parameter w_γ is defined as

$$w_\gamma = \arg \max_{w \in [0, 2\pi)} \sum_{l=1}^{n} |\langle R^k f^l, g_{(\gamma, w)}\rangle|^2 \quad (3)$$

Then the new standard of selecting the best atom g_{γ_k} in the k-th iteration is updated as follows:

$$\sum_{l=1}^{n} |\langle R^k f^l, g_{(\gamma_k, w_\gamma)}\rangle|^2 = \arg \max_{g_\gamma \in D_k} \sum_{l=1}^{n} |\langle R^k f^l, g_{(\gamma, w_\gamma)}\rangle|^2 \quad (4)$$

where D_k denotes the set of atoms that satisfy Eq. (2).

After M iterations, the component f^l finally leads to the following expansion formula:

$$f^l = \sum_{k=0}^{M-1} \langle R^n f^l, g_{(\gamma_k, w_\gamma)}\rangle g_{(\gamma_k, w_\gamma)} + R^M f^l \quad (5)$$

However, the atoms selected by the above MMP algorithm are not all useful components. The frequency parameters of relative long atoms (high scale value) are more resistant to noise than those of relative short ones, whereas the translation parameters of relative short atoms (small scale value) are more resistant to noise than those of relative long ones. It has also been shown that the EEG consists of subsecond epochs with stable spatial configuration (microstates) lasting about 100 ms and separated by rapid topographical changes [6]. Those atoms, which are less than 1.5 periods [7] of the cosine modulation falling within half-width of the Gabor envelope and lasting less than 100 ms, or bigger than 5 periods of the cosine modulation falling within half-width of the Gabor envelope and sustaining over the entire time interval, in this study are treated as noises.

2 Results

2.1 MMP reconstruction results

Results for the first incongruent Stroop trial using the MMP algorithm is shown in Fig. 1 with the reconstructed sensor signals by every 60th channels. We set $\alpha = 0.9$ according to experiences. The search stops at the 32nd iteration when the energy changing rate is smaller than 10^{-3}. 89.56% of the data energy is approximated in this iteration. From Fig. 1, we find that the MMP extracts the main features of all the channels and reconstructs the signals basically fitted to the original signals. Moreover, the residual signal, which may be directly related to the background noise, is obtained when the algorithm stops iterating.

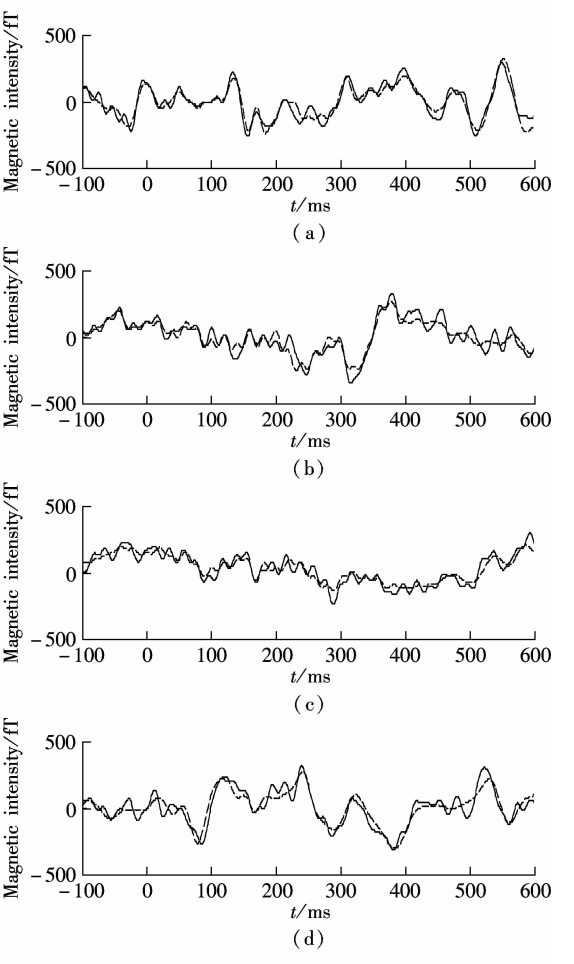

Fig. 1 Comparison between the reconstructed signal using MMP and the original signal. (a) Channel 60; (b) Channel 120; (c) Channel 180; (d) Channel 240

2.2 Artifact rejection results

The MEG sensor data can be described in terms of unobserved evoked and background factors with additive sensor noise. After the MMP is applied to the noisy multichannel data, some of the selected atoms will correspond with such activities (e.g., eye blink, background activity, etc.). Artifacts can be detected in the given space of scale and modulation. Using this feature, the algorithm cleans the stimulus-evoked data by removing the interference from

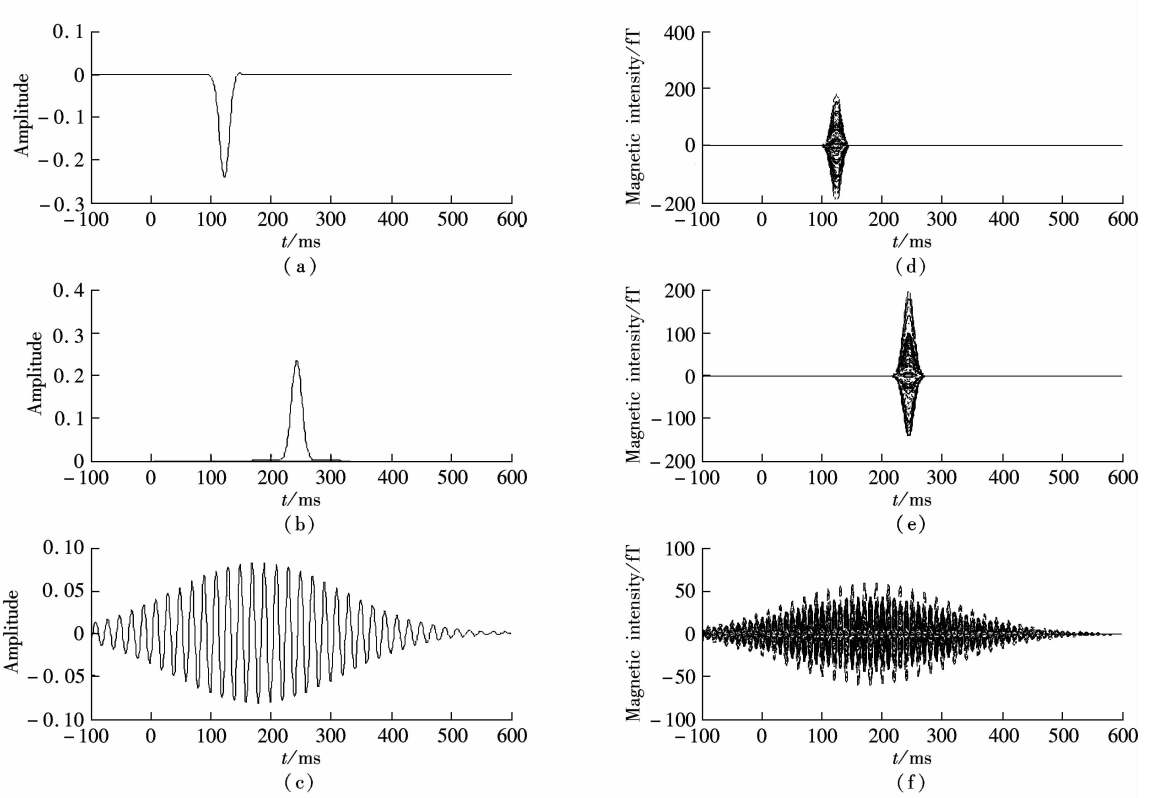

Fig. 2 Artifact atoms and their topographic approximation. (a) to (c) Artifact atoms selected from iteration 25, 29 and 31, respectively; (d) to (f) Their corresponding topographic approximations

background components and noise artifacts. Three atoms in this single trial are identified as noisy sources. Fig. 2 shows artifact noisy atoms and their corresponding topographic approximations. According to the artifact removal criterion, the atoms in Figs. 2 (a) and (b) can be classified as peak artifacts while the atom in Fig. 2(c) can be regarded as background noise.

2.3 3D source reconstruction results

In order to further validate the algorithm, a distributed approach is applied to estimate the MEG source locations. This method results in a spatial projection of sensor data into a 3D brain space and considers brain activity as comprising a very large number of dipolar sources spread over the cortical sheet, with fixed locations and orientations. This renders the observation model linear, the unknown variables being the source amplitudes or power. It is implemented in SPM8[8], a toolbox developed using Matlab. SPM8 exploits hierarchical or empirical Bayes to solve the distributed source reconstruction problem in EEG and MEG, which rests on the automatic selection of multiple cortical sources with compact spatial supports that are specified in terms of empirical priors. This means that the approach automatically selects either a sparse or a distributed model depending on the data and obviates the need to use priors with a specific form (e.g., smoothness or minimum norm) or with a spatial structure [9]. Liotti et al. [10] pointed out that 350 to 500 ms post-stimulus is a critical time period in mediating the conflict involved in the Stroop color word interference. Fig. 3 shows the inverse reconstruction results in this time period using the MMP-preprocessed first trial's signals and the 48-trials-averaged signals respectively. The obtained reconstructed activities are shown in a 3D voxel space. Previous neuroimaging studies in healthy volunteers have shown that the anterior cingulated cortex (ACC) appears to be heavily involved in the Stroop color word interference, although other areas have been less consistently reported [11]. Obviously, ACC is significantly activated in both Figs. 3 (a) and (b), which is basically consistent with the prior knowledge. However, the activation strength of the ACC in Fig. 3(b) is lower than that in Fig. 3(a), which may be associated with habituation or fatigue.

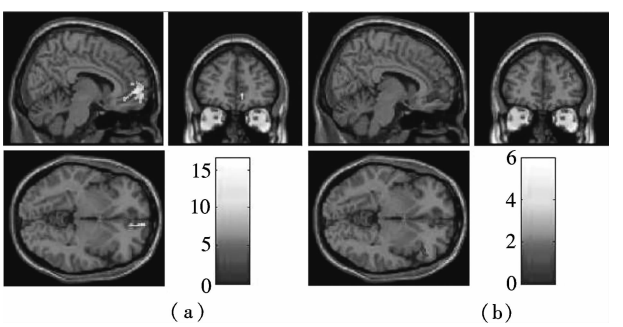

Fig. 3 Brain active map of Stroop word-color incongruent test during the period of 350 to 500 ms ($p < 0.005$ (uncorrected), cluster > 5). (a) With MMP-preprocessed first single-trial signals; (b) With 48-trials-averaged signals

3 Discussion

This paper introduces the MMP method to MEG single-trial analysis. It takes advantage of the fact that the multi-channel data may be decomposed into a sum of atoms localized in the time-frequency space of interest. The time-frequency characters of the chosen MMP atoms are described by their Gabor atoms and the spatial properties are represented by their correlation coefficients. The time-frequency

property enables the identification, extraction and description of atoms with biological meaning as well as the identification and removal of artifact atoms. In real signals, atoms with long time support may denote power supply noise or its higher harmonics; otherwise, they may represent artifacts peaks [3]. These kinds of unwanted atoms are removed from the signal approximation.

How to validate the reliability of results given by single-trial analysis remains an open question[2]. Although we do not have definitive proof that our results exactly reflect the real physical implication inside the data, there are two aspects of the method we can learn from for assessing the quality of results.

First, the MMP is adapted in an overcomplete Gabor dictionary whose structure is randomized to avoid statistical bias. Compared with the Gabor atoms, the window Fourier transform atoms have a constant scale, while the wavelet family is built by fixing the frequency parameter[12]. Within a redundant dictionary, there are more free parameters than with an orthogonal wavelet basis. In particular, the amount of oscillation within an atom is free to change, allowing describing both transient waves and sustained oscillations. Secondly, we do 3D source reconstruction to identify where the signals originate. Source localization can help improve the understanding of the representation, and it can directly give information regarding the observed phenomena from the sources within the cortex. The coherence between the source locations and the prior knowledge gives additional evidence in this regard.

4 Conclusion

In this paper, an MMP algorithm is described to extract single-trial MEG evoked signals. From our results, we think that MMP atomic decomposition of the multichannel MEG can reliably extract meaningful and significant physiological activities, although this does not ensure that the results are in accord with the physical sources that generate the signals. Nevertheless, the proposed approach done before inverse modeling is an adequate way to noninvasively estimate brain activity to external stimuli. Further studies should use this algorithm to observe the trial-to-trial variation during long tests.

References

[1] Cao J T, Murata N, Cichocki A, et al. Independent component analysis for unaveraged single-trial MEG data decomposition and single-dipole source localization [J]. *Neurocomputing*, 2002, **49**(1/2/3/4): 255 - 277.

[2] Studer D, Hoffmann U, Koenig T. From EEG dependency multichannel matching pursuit to sparse topographic EEG decomposition [J]. *Journal of Neuroscience Methods*, 2006, **153**(2): 261 - 275.

[3] Gratkowski M, Haueisen J, Arendt-Nielsen L, et al. Time-frequency filtering of MEG signals with matching pursuit[J]. *Journal of Physiology-Paris*, 2006, **99**(1): 47 - 57.

[4] Durka P J, Ircha D, Blinowska K J. Matching pursuit [J]. *IEEE Transactions on Signal Processing*, 2001, **49**(3): 507 - 510.

[5] Gribonval R, Rauhut H, Schnass K, et al. Atoms of all channels, unite! Average case analysis of multi-channel sparse recovery using greedy algorithms [J]. *Journal of Fourier Analysis and Applications*, 2008, **14**(5/6): 655 - 687.

[6] Koenig T, Marti-Lopez F, Valdes-Sosa P. Topographic time-frequency decomposition of the EEG [J]. *NeuroImage*, 2001, **14**(2): 383 - 390.

[7] Durka P J. Adaptive time-frequency parametrization of epileptic spikes [J]. *Physical Review E*, 2004, **69**(5): 51914.

[8] Wellcome Trust Center for Neuroimaging. Statistical parametric mapping[EB/OL]. [2008-10-12]. http://www.fil.ion.ucl.ac.uk/spm.

[9] Friston K, Harrison L, Daunizeau J, et al. Multiple sparse priors for the M/EEG inverse problem [J]. *NeuroImage*, 2008, **39**(3): 1104 - 1120.

[10] Liotti M, Woldorff M G, Perez R, et al. An ERP study of the temporal course of the Stroop color-word interference effect [J]. *Neuropsychologia*, 2001, **38**(5): 701 - 711.

[11] Larson M J, Kaufman D A S, Perlstein W M. Neural time course of conflict adaptation effects on the Stroop task [J]. *Neuropsychologia*, 2009, **47**(3): 663 - 670.

[12] Mallat S G, Zhang Z F. Matching pursuit with time frequency dictionaries [J]. *IEEE Transactions on Signal Processing*, 1993, **41**(12): 3397 - 3415.

基于多通道匹配追踪算法的单次脑响应信号建模

江海腾[1] 卢 青[1] 韩颖琳[2] 姚志剑[2] 刘 刚[1]

([1]东南大学学习科学研究中心,南京 210096)

([2]南京医科大学附属脑科医院,南京 210029)

摘要:提出了一种基于多通道匹配追踪算法对一维多通道脑磁图非平稳信号进行单次分解的方法. 单通道匹配追踪算法通过在过完备的库中自适应地搜索匹配具有良好时频特性的 Gabor 原子,最终将信号表示为 Gabor 原子的线性组合. 多通道匹配追踪算法是单通道匹配追踪算法的延伸,即所有通道的信号是由发生时间、振荡频率、相位、持续时间相同,但振幅不同的 Gabor 原子线性叠加组成. 结果显示,多通道匹配追踪算法能较好地重建源信号,并且自动检测与分离伪迹噪声. 此外,3D 源重建结果和心理学先验知识一致,这进一步表明多通道匹配追踪算法应用于脑磁信号单次提取是有效的.

关键词:脑磁图;单次提取;多通道匹配追踪;源重建

中图分类号:Q64;TP301.4