SIGNAL SAMPLING FOR EFFICIENT SPARSE REPRESENTATION OF RESTING STATE FMRI DATA

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ABSTRACT

As brain imaging data such as fMRI is growing explosively, how to reduce its size but not to lose much information becomes a pressing problem. To address this problem, this work aims to represent resting state fMRI (rs-fMRI) signals of a whole brain via a statistical sampling based sparse representation. Specifically, we improve the online dictionary learning and sparse coding algorithm by adding a sampling step before the whole-brain sparse representation. Our comparison experiments demonstrated that this sampling-enabled sparse representation method can speed-up by ten times without losing much information. In particular, our results showed that anatomical landmark-guided sampling is substantially better than statistical random sampling in reconstructing concurrent functional brain networks from the Human Connectome Project (HCP) rs-fMRI data.

Index Terms— DTI, resting state fMRI, sampling, DICCCOL, resting state networks.

1. INTRODUCTION

With the advancement of neuroimaging technologies, the spatial and temporal resolution of brain imaging data has become higher and higher. For instance, the ongoing Human Connectome Project (HCP) [1] released its rs-fMRI data with around 240,000 signals of 1200 time points. This fMRI big-data imposes significant challenges on the extraction and representation of meaningful information for brain mapping. In response to this need, recently, sparse representation has been explored to represent whole-brain fMRI signals [2, 3] and to reconstruct concurrent network activities, e.g., the recently developed holistic atlases of functional networks and interactions (HAFNI) system [3], and promising results have been reported [3]. However, these methods still cost significant amount of time and memory space to learn a dictionary for one brain's single fMRI scan because the input is a huge 4-D matrix with a number of over 10^6 voxels (several Giga bytes). The computing time cost thus would significantly hamper the wider application of sparse representation method to larger scale fMRI datasets. Therefore, this motivates us to investigate efficient data reduction methods, that is, sampling methods in this paper, to extract the representative signals without losing much information but can significantly speed-up.

In this paper, we examined two rs-fMRI signal sampling methods: one is anatomical landmark-guided sampling by using the dense individualized and common connectivity-based cortical landmarks (DICCCOL) system [5], and another is statistical random sampling. Experimental results showed that DICCCOL-guided sampling is substantially better than statistical random sampling in reconstructing concurrent functional brain networks from the HCP rs-fMRI data. In general, sampling 2% out of the 240,000 whole-brain signals is sufficient to learn an accurate dictionary (in comparison with that using all of the whole brain signals) for sparse representation and 10 times speed-up can be achieved.

2. METHODS

2.1. Overview

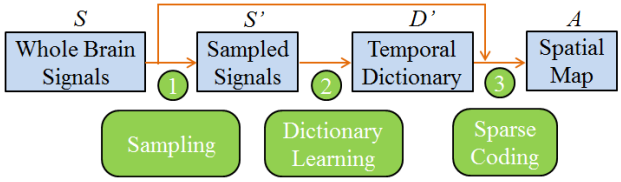

Fig.1. The overview of our computational framework. The sampling step (step 1) could include DICCCOL-based sampling, statistical random sampling, or no sampling. In any of these sampling methods, the whole brain signals (S) will be used for sparse representation (Step 3).

Our framework of signal sampling for sparse representation of resting state fMRI data is summarized in Fig.1. First, we sampled the rs-fMRI signal of the whole brain based on DICCCOL [5] which includes a set of consistent landmarks

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of the brain. For the purpose of comparison and evaluation, we also sampled randomly and used the whole brain's signals (no sampling). Then the sampled signals were used as an input matrix to learn an over-complete dictionary for sparse representation of whole brain's signals, based on which we can identify the RSNs. We described the theory in detail about why we designed these three steps in Section 2.3 and Fig.2(b). Furthermore, we compared and evaluated the temporal dictionary atoms and their spatial maps generated by the DICCCOL-guided sampling, random sampling, and no sampling, respectively. The details of the dataset and preprocessing are referred to [1, 3, 5, 6].

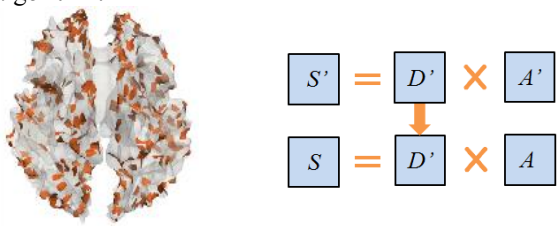
2.2. Dictionary learning and sparse representation

To map the resting state networks (RSN) of human brain, we adopt a dictionary learning and sparse coding method [2, 3] from the machine learning and pattern recognition fields. Briefly, it can be considered as a matrix factorization problem, given the rs-fMRI signal matrix of whole brain $S \epsilon \mathbb{R}^{t \times n}$. Here, each column represents an rs-fMRI signal time series and S can be factorized as $S=D \times A$, where $D \epsilon \mathbb{R}^{t \times m}$ is the dictionary, and $A \epsilon \mathbb{R}^{m \times n}$ is called coefficient matrix. Each column in D is an atom of a learned basis dictionary D, and each rs-fMRI time series S_i can be represented as a linear combination of atoms of dictionary, that is, $S_i = D \times A_i$, where A_i is a coefficient column in A which gives the sparse weights for the combination. Meanwhile, each row of the A matrix represents the spatial volumetric distributions that have references to certain dictionary atoms. In this work, the factorization problem was resolved by the publicly available effective online dictionary learning and sparse coding method [4], which aims to learn a meaningful and over-complete dictionary of functional bases $D \epsilon \mathbb{R}^{t \times m}$ (m>t, m<<n) for the sparse representation of S, and then learn an optimized A matrix for spare representation of rs-fMRI time signal using the obtained dictionary D. More details are referred to [2-4].

Finally, the fMRI signal matrix from a single subject's whole brain (named no sampling method in this paper) will be represented by a learned dictionary matrix and a sparse coefficient matrix. Here, we also assume, as in previous studies [2, 3], that the atoms of each voxel's fMRI signal are sparse and the neural integration of those atoms is linear [7].

2.3. DICCCOL-based sampling for sparse representation

It has been shown that DICCCOL [5] provided a set of consistent cortical landmarks which have corresponding structural and functional features across subjects. Based on these landmarks, first, we extracted the *2*-ring surface neighborhood of all DICCCOL landmarks (shown in Fig.2(a)), and then picked up the rs-fMRI signals on these neighborhood voxels and aggregated them into a signal matrix *S'*. In the second step, as similarly done in Section 2.2, we employed the online dictionary learning and sparse coding method [4] to learn the dictionary *D'* and the corresponding coefficient matrix *A'*, that is *S'=D'×A'*. Finally, to obtain the sparse representation of whole brain signals, we performed the sparse coding method again on the whole brain signals matrix *S* using the learned *D'* in this step, that is *S=D' ×A*, as shown in Fig.2(b). Because learning D and A are two separate processes in the online dictionary learning and sparse coding algorithm [4], we can combine the last two steps as one-time dictionary learning (obtaining D') and one-time sparse coding (obtaining A), as shown in Fig.1. So it does not add additional computation in the algorithm.



(a) (b)

Fig.2. (a) 2-ring neighborhood of DICCCOL (orange patches). (b) Dictionary learning based on sampled signals (top row) and separate sparse representation of whole-brain signals (bottom row).

In addition to DICCCOL-based sampling, we also performed no sampling (using whole-brain signals, that is, *S=D×A*) and statistical random sampling (now *S'* denotes the randomly sampled signals in Fig.2 (b)) for the purpose of comparison. To conduct a fair comparison, we selected the same parameters for all of these three sampling methods, that is, the number of dictionary atom is 400, the sparsity regularization parameter λ=0.07, and set the batch size times iteration divided by the number of signals equals 4, and etc.

Finally, we mapped each row in the *A* matrix back to the brain volume, thus functional network components can be visualized and characterized on brain volumes. These network components are then identified as the known RSNs in the following section.

2.4. Identifying and evaluating RSNs by matching with templates

To determine and evaluate the resting state networks, we defined a metric named as Spatial Matching Ratio for checking the spatial similarity between the identified RSNs and the RSN template. In this work, we adopted the ten well-defined RSN templates provided in the literature [8]. For the rs-fMRI data of each subject, we identified each RSN by matching its spatial weight map with each specific RSN template. Those network components with the maximum Spatial Matching Ratio (SMR) were selected as RSNs. The Spatial Matching Ratio is defined as follows:

$$SMR(X,T) = \frac{|X \cap T|}{|X \cup T|}$$

where X is the spatial map of network component and T is that of the RSN template. $|X \cap T|$ and $|X \cup T|$ are the numbers of voxels in both X and T and in X or T, respectively. Notably, before the comparison of X and T, we registered all X images to T via the linear registration method of FSL FLIRT.

3. RESULTS

By applying the DICCCOL sampling, random sampling and no sampling [3] on ten randomly selected subjects from the HCP datasets according to the procedure shown in Fig.1, we generated their atomic dictionaries and corresponding coefficient matrices. For random sampling, we sampled the same number of points as DICCCOL-based sampling for the fairness of comparison and evaluation. Their results are as follows.

3.1 Comparison of temporal dictionary atoms

We identified the RSNs by matching them with the ten well-defined RSN templates [8]. Those with the highest spatial matching ratio were selected out of the 400 network components as the RSNs. For the DICCCOL-based sampling, random sampling and whole brain signal without sampling, we performed the same identification procedure to find the most matched RSNs with the templates. Then we traced back to find the ten corresponding dictionary atoms associated with the ten identified RSNs. Thus we can compare the time series differences of the derived dictionaries by different sampling methods, as shown in Fig.3. We quantitatively computed the Pearson correlation coefficients between the dictionaries by these sampling methods, as listed as in Table 1(a).

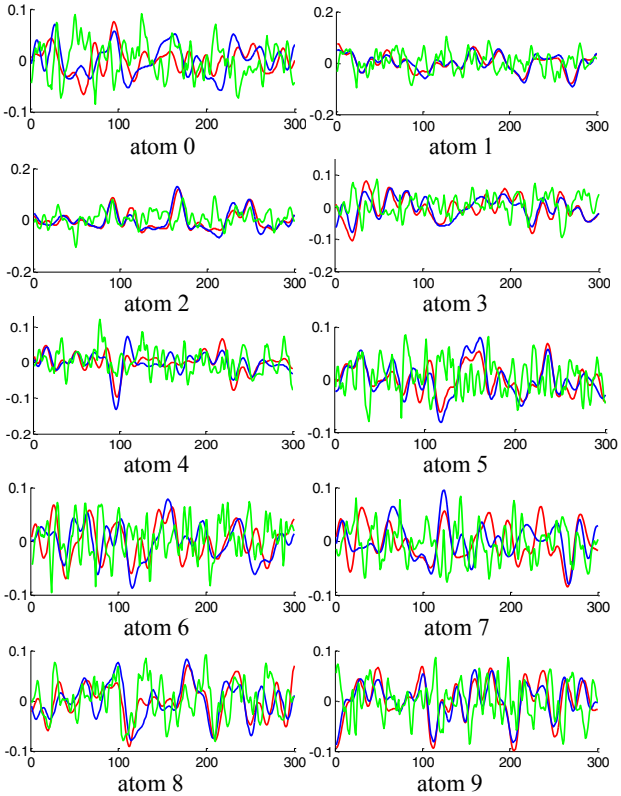


Fig.3. The time series signals of the 10 dictionary atoms from DICCCOL-based sampling (blue curve), random sampling (green curve) and no sampling methods (red curve, as a baseline for comparison) for a randomly selected subject. The blue curve represents the time series signal generated by 2-ring neighborhood of DICCCOL. The green curve represents the time signals generated by random sampling with the same number of points as DICCCOL sampling. It is clear that the blue curve is more similar to the red curve than the green one. For the reason of limit space, only 300 time points are shown here as examples.

Table 1. (a) The Pearson correlations of 10 corresponding dictionary atoms between the two sampling methods and no sampling method. (b) The SMR of 10 corresponding identified RSNs from the two sampling methods and no sampling method. "D2" represents 2-ring DICCCOL sampling and "R2" represents sampling randomly the same number of points as the 2-ring DICCCOL sampling. "W" in (b) means using whole brain's signals (no sampling).

(a)

	D2	R2
atom0	0.79	0.23
atom1	0.64	0.22
atom2	0.74	0.23
atom3	0.74	0.25
atom4	0.52	0.23
atom5	0.77	0.23
atom6	0.66	0.25
atom7	0.57	0.24
atom8	0.64	0.23
atom9	0.72	0.25
mean	0.678	0.236

(b)

	W	D2	R2
RSN0	0.52	0.54	0.22
RSN1	0.35	0.30	0.17
RSN2	0.35	0.34	0.15
RSN3	0.36	0.31	0.16
RSN4	0.35	0.19	0.13
RSN5	0.35	0.29	0.15
RSN6	0.37	0.34	0.17
RSN7	0.26	0.24	0.20
RSN8	0.29	0.27	0.14
RSN9	0.33	0.32	0.24
mean	0.356	0.318	0.174

From Fig.3 and Table 1(a), we can see that the dictionaries from DICCCOL-based sampling have substantially higher similarity with those of no sampling, compared with statistical random sampling. It is 0.678 vs 0.236 for the averaged 10 dictionary atoms. Therefore we can conclude that the dictionaries obtained by DICCCOL-based sampling are much more representative of the whole brain's functional activities information. This result also suggests the DICCCOLs cover key functional areas of the brains, offering supporting evidence of the effectiveness and validity of the DICCCOL system [5].

3.2 Comparison of spatial RSNs

We identified 10 RSNs by matching each network component with that of 10 RSN templates, and performed this same step for the three sampling methods, respectively. Then we compared their spatial maps of the RSNs and the SMRs with 10 templates, as shown in Fig.4 and Table 1(b). Due to space limit, we did not show the results from the random sampling because we already know its less effectiveness from Table 1(a). Instead, we listed its SMRs with templates in Table 1(b). We can see from Fig. 4 that the RSNs from whole brain's signals and DICCCOL-based sampling were identified very well. Also, the DICCCOL-based sampling has almost the same results as that by no sampling method, which demonstrates that the rs-fMRI signals of DICCCOL-based sampling can well represent the rs-fMRI signal of the whole brain in terms of learning sparse dictionaries. It has also been demonstrated in Table 1(b) that the SMR from DICCCOL-based sampling and whole brain's signals have very close values (0.318 vs 0.356).

However, the random sampling method only has the much lower SMR of 0.174. It should be noted that the SMR values in Table 1 are relatively low because we computed group-averaged RSNs from only 10 subjects, so it is reasonable to see that they have some differences with the templates.

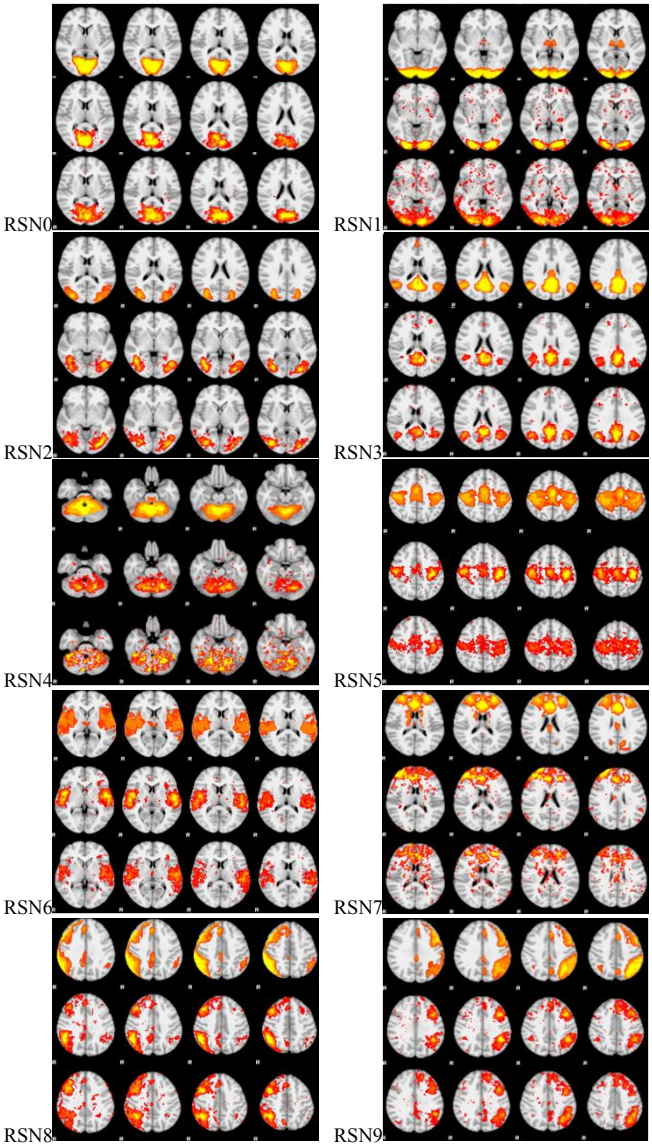


Fig.4. The spatial maps of RSNs by DICCCOL sampling, no sampling and the templates. In each panel of RSNs, the first row is the RSN template, the second row represents the RSNs identified from whole brain's signals and the third one represents those identified from 2-ring DICCCOL sampling. These RSNs are all group-averaged results from 10 randomly selected subjects.

3.3 Comparison of computing time

Additionally, we evaluated and compared the computing time cost for dictionary learning, which is the major part of the online dictionary learning and sparse coding [4]. The dictionary learning step costs more time than the sparse coding step (which is fixed), and the difference of time cost heavily depends on the number of rs-fMRI signals given that the size of dictionary is fixed as 400. So we just computed and compared the time cost of dictionary learning. Each whole brain has about 2.4×10^5 rs-fMRI signals, and a 2-ring DICCCOL-based sampling resulted in 4825 signals. The averaged time cost of no sampling, DICCCOL sampling and random sampling for 10 subjects are 321.9s, 31.7s and 82.1s, respectively. It is obvious that DICCCOL-based sampling is approximately 10 times faster than no sampling without sacrificing much accuracy for sparsely representing the whole brain's rs-fMRI signals.

4. DISCUSSION AND CONCLUSION

In this paper, we presented and evaluated a novel signal sampling strategy for efficient sparse representation of resting state fMRI data. We quantitatively and qualitatively compared three sampling schemes and experimental results demonstrated that the DICCCOL-based sampling signals exhibit much better performance than statistical random sampling for identifying RSNs, and have almost the same high performance as no sampling method. Also, the signal sampling method achieved around ten times speed-up. Thus, we can conclude that DICCCOL-based sampling is able to well represent the whole brain's rs-fMRI signals with low costs. In the future, we plan to apply and evaluate it on task-based fMRI datasets, and learn multiple task-evoked and resting state networks simultaneously from a group of subjects.

5. REFERENCES

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