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Matched signal detection on graphs: Theory and application to brain imaging data classification

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ABSTRACT

Motivated by recent progress in signal processing on graphs, we have developed a matched signal detection (MSD) theory for signals with intrinsic structures described by weighted graphs. First, we regard graph Laplacian eigenvalues as frequencies of graph-signals and assume that the signal is in a subspace spanned by the first few graph Laplacian eigenvectors associated with lower eigenvalues. The conventional matched subspace detector can be applied to this case. Furthermore, we study signals that may not merely live in a subspace. Concretely, we consider signals with bounded variation on graphs and more general signals that are randomly drawn from a prior distribution. For bounded variation signals, the test is a weighted energy detector. For the random signals, the test statistic is the difference of signal variations on associated graphs, if a degenerate Gaussian distribution specified by the graph Laplacian is adopted. We evaluate the effectiveness of the MSD on graphs both with simulated and real data sets. Specifically, we apply MSD to the brain imaging data classification problem of Alzheimer's disease (AD) based on two independent data sets: 1) positron emission tomography data with Pittsburgh compound-B tracer of 30 AD and 40 normal control (NC) subjects, and 2) resting-state functional magnetic resonance imaging (R-fMRI) data of 30 early mild cognitive impairment and 20 NC subjects. Our results demonstrate that the MSD approach is able to outperform the traditional methods and help detect AD at an early stage, probably due to the success of exploiting the manifold structure of the data.

Introduction

Matched subspace detection is a classic tool that determines whether a multidimensional signal lies in a given linear subspace or not (Scharf and Friedlander, 1994). It has achieved great success in applications such as radar, hyperspectral imaging (Manolakis and Shaw, 2002) and medical imaging (Li et al., 2009). The subspace is either known from the physical system that generates the signal, or can be inferred from training data. Subspace learning is a natural way of data dimension reduction and can be achieved by principal component analysis (PCA), which projects the original data to a linear subspace spanned by the leading eigenvectors of the covariance matrix (Jolliffe, 2005). While a common assumption of PCA is that the data come from a linear subspace, many real data are lying in or close to a nonlinear *manifold*, which is a topological space that resembles Euclidean space around each point (Belkin and Niyogi, 2003). Examples of the latter case include brain images (Liu et al., 2013), genetic data (Lee et al., 2008), social network records, and sensor network measurements. In this setting, the low-dimensional subspace that best preserves the intrinsic geometry of the data can be effectively learned by graph spectral methods, e.g., isomap, locality linear embedding (LLE), Laplacian eigenmaps (Belkin and Niyogi, 2003; Roweis and Saul, 2000; Saul et al., 2006; Tenenbaum et al., 2000).

In neuroimaging, as more and more nonlinear data are collected by multiple imaging modalities, there is a need for classifying data with complex intrinsic structures. For instance, the analysis and classification of positron emission tomography (PET) images or functional magnetic resonance imaging (fMRI) data may facilitate the prediction and early detection of Alzheimer's disease (AD). Concurrently, an emerging area of signal processing on graphs is developed for handling these challenging data through the combination of algebraic and spectral graph theoretic concepts with computational harmonic analysis (Shuman et al., 2013). Signals are assumed to reside on vertices of weighted graphs which are often naturally defined by the application. The weight associated with a certain edge in the graph represents the similarity between the two vertices joined by the edge. We refer to graph supported data as *graph-signals*, to differentiate them from conventional signals in Euclidean spaces. In the brain imaging classification, we could view the PET/fMRI data as graph-signals on weighted graphs describing the affinity between each pair of brain regions.

Motivated by the above data classification requirement, we are interested in developing a detection framework for graph-signals.

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Specifically, we formulate several hypotheses to decide which graph structure is more likely to match a given signal. Moreover, we exploit the matched subspace detection technique and propose different types of graph-signal models to make our framework generic to deal with a variety of real situations. The subspace for graph-signal is formed by eigenvectors of the *Laplacian matrix* $\boldsymbol{L}$ of the graph. The graph Laplacian matrix encodes the structure of the graph concisely. From a graph signal processing point-of-view, eigenvectors of $\boldsymbol{L}$ could be treated as the generalization of the basis of conventional Fourier transform (Agaskar and Lu, 2013; Sandryhaila and Moura, 2013; Shuman et al., 2013). Based on spectral graph theory, we can define the variation of graph-signals. It follows that the variation of an eigenvector of $\boldsymbol{L}$ is equal to the associated eigenvalue (Hu et al., 2015a). When we decompose a signal containing instantaneous fMRI measurements into linear combination of eigenvectors of Laplacian matrix associated with the brain-region-affinity graph, we might deem that the components in those eigenvectors with larger eigenvalues as being noisier if the true fMRI signal is assumed to be bandlimited on the graph (Gadde et al., 2013; Kim et al., 2013; Meyer and Shen, 2014).

Our first hypothesis test model simply assumes that the signal lies in a subspace spanned by the first few Laplacian eigenvectors corresponding to smaller eigenvalues. The traditional matched subspace detection could be applied directly to this case. Furthermore, we consider two categories of graph-signal models: *deterministic signals* with constraints and *probabilistic signals* with prior distributions. For deterministic signals, we impose a bounded variation on the signal with respect to the graph. The penalized maximum likelihood estimator (MLE) of the true signal is derived by solving a constrained optimization problem. We find that the test is a weighted energy detector. For probabilistic signals, when we choose a certain degenerate Gaussian distribution as the prior of the projection coefficients of the signal onto the graph Laplacian eigenvectors, the decision ends up comparing the signal variations on the two hypothetic graphs in a noise-free case.

We evaluate the effectiveness of the matched signal detection (MSD) theory on both synthetic and real data sets. Simulations based on randomly generated graphs demonstrate the feasibility of our approaches even if we do not know the exact probability distributions of the testing signals. Then, we apply the proposed detection algorithms to brain imaging classification tasks of AD. As one of the most prevalent forms of dementia, AD is believed to be a brain network associated disease (Gomez-Ramirez and Wu, 2014; Raj et al., 2012; Sepulcre et al., 2013), and is characterized by progressive impairment of memory and other cognitive capacity. It affects nearly 36 million people worldwide with an expected number of cases to be 65.7 million by 2030 (Brookmeyer et al., 2007). The development of neuroimaging classification techniques may enable us to monitor the functional and anatomical changes of the brain in vivo and discover reliable biomarkers for identifying AD at an early stage. In this study, we have compared a novel MSD approach with other widely used methods including principle component analysis (PCA), support vector machine (SVM) and linear discriminant analysis (LDA) on two data sets: one is PET imaging of brain amyloid using Pittsburgh compound-B (PIB) tracer of AD and normal control (NC) subjects; the other contains resting-state fMRI (R-fMRI) images of early mild cognitive impairment (EMCI) and NC subjects in the Alzheimer's Disease Neuroimaging Initiative (ADNI) database. For the MSD, we compute the similarity between each of two brain regions with the Gaussian radial basis function (RBF) kernel. This simple way of building brain networks avoids estimating network structures by solving inverse problems, which often requires more data; yet the weighted graphs associated with the networks approximate the data manifolds. Experimental results show that when using the MSD on graphs, we can achieve significantly better classification performance than the compared algorithms. The results indicate that our method provides an effective way for brain imaging classification, probably due to the capability of exploiting the manifold structure of the data.

Our contributions in this paper are three-fold: first, we have developed a matched signal detection theory for graph-signals which are ubiquitous in medical imaging applications; second, we keep the framework generic and simple by proposing a variety of signal models and using simple similarity metrics to construct graphs; third, we demonstrate that the detection theory is particularly suitable for neuroimaging classifications.

Theory

To formulate the framework of matched signal detection on graphs, we first introduce the concept of graph-signals. We extend the traditional Fourier transform to a graph Fourier transform and define a notion of graph-signal frequency based upon spectral graph theory. Then, to model different real data, we propose three classes of signal models on graphs. Finally, we derive the signal detection criterion under each signal model.

Weighted graphs and graph-signals

Many contemporary applications such as social, power grid, sensor, and brain networks involve high-dimensional data with natural structures defined by weighted graphs. To efficiently process such signals on graphs, an emerging field of signal processing on graphs integrates the graph spectral theory with computational harmonic analysis. Here we present basic concepts of signal processing on graphs in the context of neuroimaging data analysis.

A brain network can be represented by a *weighted graph* $\mathcal{G}(\mathcal{V}, \mathcal{E}, \boldsymbol{W})$ containing a vertex set $\mathcal{V}(|\mathcal{V}| = N)$, an edge set $\mathcal{E}$ and a weighted adjacency matrix $\boldsymbol{W}$. The vertices typically indicate a group of predefined brain regions or a set of image voxels (Stanley et al., 2013; Zalesky et al., 2010). If there is an edge between vertices i and j, then W_{ij} denotes the weight of the edge; otherwise, $W_{ij} = 0$. We assume the similarity metric is symmetric and non-negative, namely $W_{ij} = W_{ji} \geq 0$ for all i and j. Meanwhile, it is reasonable to assume that no brain region is isolated. Therefore, $\mathcal{G}$ should be undirected and connected. Physiologically, W_{ij} may quantify the similarity of two brain regions in terms of their biochemical measurements (such as the amyloid deposition revealed by PIB-PET) or anatomical properties (such as the number of fiber pathways connecting those regions). The exact formula of the weights could be chosen flexibly based on different applications.

In addition to the adjacency matrix, we introduce the *graph Laplacian* as another important graph associated matrix. We denote by $\boldsymbol{D}$ the degree matrix which is diagonal with $D_{ii} = \sum_{j=1}^{N} W_{ij}$. Then, the graph Laplacian is defined as $\boldsymbol{L} \stackrel{\text{def}}{=} \boldsymbol{D} - \boldsymbol{W}$. Because $\boldsymbol{L}$ is a real symmetric matrix, it has a complete set of orthonormal eigenvectors $\{\boldsymbol{f}_i\}_{i=1,\ldots,N}$. If $\mathcal{G}$ is connected, the associated eigenvalues $\{\lambda_i\}_{i=1,\ldots,N}$ are real non-negative with the unique smallest eigenvalue being zero (Chung, 1997). We assume that the eigenvalues are increasingly sorted as $0 = \lambda_1 \leq \lambda_2 \leq \ldots \leq \lambda_N$. By eigendecomposition, we can decompose the graph Laplacian into $\boldsymbol{L} = \boldsymbol{F}\boldsymbol{\Lambda}\boldsymbol{F}^T$, where $\boldsymbol{\Lambda}$ is diagonal with $\Lambda_{ii} = \lambda_i$ being the ith smallest eigenvalue of $\boldsymbol{L}$ and the ith column of $\boldsymbol{F}, \boldsymbol{f}_i$, is the associated eigenvector.

A signal x defined on the vertices of graph $\mathcal{G}$ is a function from $\mathcal{V}$ to $\mathbb{R}$. This *graph-signal* could be expressed as a vector in $\mathbb{R}^N$ with the ith element of the vector being a real value assigned to the ith vertex. We will also denote this vector by $\boldsymbol{x}$ and use $x(i)$ to indicate both the function value at the ith vertex and the ith element of the vector. Examples of the graph-signal are in Fig. 1. In practice, we could view PET scans or fMRI time series as graph-signals defined on vertices of the brain connectivity network that is constructed by connecting edges between different brain regions or image voxels. For a graph-signal $\boldsymbol{x}$, the graph Laplacian behaves as a difference operator on it:

$$(\boldsymbol{L}\boldsymbol{x})(i) = \sum_{j \sim i} W_{ij}[x(i) - x(j)], \tag{1}$$

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