



Contents lists available at ScienceDirect

Applied and Computational Harmonic Analysis

www.elsevier.com/locate/acha

Stable separation and super-resolution of mixture models [☆]Yuanxin Li, Yuejie Chi ^{*}

Department of Electrical and Computer Engineering, The Ohio State University, Columbus, OH 43210, United States

ARTICLE INFO

Article history:

Received 24 June 2015

Received in revised form 20 March 2017

Accepted 28 March 2017

Available online xxxx

Communicated by Charles K. Chui

Keywords:

Super-resolution

Parameter estimation

Atomic norm minimization

Mixture models

ABSTRACT

We consider simultaneously identifying the membership and locations of point sources that are convolved with different band-limited point spread functions, from the observation of their superpositions. This problem arises in three-dimensional super-resolution single-molecule imaging, neural spike sorting, multi-user channel identification, among other applications. We propose a novel algorithm, based on convex programming, and establish its near-optimal performance guarantee for exact recovery in the noise-free setting by exploiting the spectral sparsity of the point source models as well as the incoherence between point spread functions. Furthermore, robustness of the recovery algorithm in the presence of bounded noise is also established. Numerical examples are provided to demonstrate the effectiveness of the proposed approach.

© 2017 Elsevier Inc. All rights reserved.

1. Introduction

In many emerging applications in applied science and engineering, the acquired signal at the sensor can be regarded as a noisy superposition of returns from multiple *modalities*, where the return from each modality is a band-limited observation of a point source signal captured through a low-pass point spread function, governed by either the underlying physical field or the system design. Mathematically, we consider the following *parametric mixture model* of the acquired signal, $y(t)$, given as

$$y(t) = \sum_{i=1}^I x_i(t) * g_i(t) + w(t) = \sum_{i=1}^I \left(\sum_{k=1}^{K_i} a_{ik} g_i(t - \tau_{ik}) \right) + w(t), \quad (1)$$

where $*$ denotes the convolution operator, $w(t)$ is an additive noise, and I is the total number of modalities. Moreover,

[☆] This paper has been presented in part at 2015 International Symposium on Information Theory (ISIT) and 2015 International Conference on Sampling Theory and Applications (SampTA).

^{*} Corresponding author.

E-mail addresses: li.3822@osu.edu (Y. Li), chi.97@osu.edu (Y. Chi).

$$x_i(t) = \sum_{k=1}^{K_i} a_{ik} \delta(t - \tau_{ik})$$

is the point source signal observed from the i th modality, and $g_i(t)$ is the corresponding point spread function. For the i th modality, let $\tau_{ik} \in [0, 1)$ and $a_{ik} \in \mathbb{C}$ be the location and the amplitude of the k th point source, $1 \leq k \leq K_i$, respectively, where the locations of point sources τ_{ik} 's are continuous-valued and can lie anywhere in the parameter space, at nature's will. The point source model can be used to model a variety of physical phenomena occurring in a wide range of practical problems, such as the activation pattern of fluorescence in single-molecule imaging [1], sparse channel impulse response in multi-path fading environments, the locations of pollution plants in urban areas, firing times of neurons, and many more.

Our goal is to *stably invert* for the field parameters, i.e. the parameters of the point source models, of each modality from the acquired signal reflecting the ensemble behavior of all modalities, even in the presence of noise. This allows us to *separate* the contributions of each modality to the acquired signal. Moreover, typically we are interested in super-resolution, i.e. resolving the parameters at a resolution much higher than the native resolution of the acquired signal, determined by the Rayleigh limit, or in other words, the reciprocal of the bandwidth of the point spread functions.

1.1. Motivating applications

The mixture model (1) is motivated by the modeling and analysis of many practical problems, such as three-dimensional super-resolution single-molecule imaging [2,3], spike sorting in neural recording [4,5], multi-user multi-path channel identification [6,7], and blind calibration of time-interleaved analog-to-digital converters [8,9]. We describe several example applications below.

Three-dimensional super-resolution single-molecule imaging: By employing photoswitchable fluorescent molecules, the imaging process of single-molecule microscopies (Stochastic Optical Reconstruction Microscopy (STORM) [1] or Photo Activated Localization Microscopy (PALM) [10]) is divided into many frames, where in each frame, a *sparse* number of fluorophores (point sources) are randomly activated, localized at a resolution below the diffraction limit, and deactivated. The final image is thus obtained by superimposing the localization outcomes of all the frames. This principle can be extended to reconstruct a 3-D object from 2-D image frames, for example, by introducing a cylindrical lens to modulate the ellipticity of the point spread function based on the depth of the fluorescent object in 3-D STORM [2]. Therefore, the acquired image in each frame can be regarded as a *superposition* of returns from multiple depth layers, where the return from each layer corresponds to the convolution outcome of the fluorophores in that depth layer with the depth-dependent point spread function, as modeled in (1). The goal is thus to recover the locations and depth membership of each point source given the image frame.

Spike sorting for neural recording: Neurons in the brain communicate by firing action potentials, i.e. spikes, and it is possible to capture their communications through the use of a microelectrode, which records simultaneous activities of multiple neurons within a local neighborhood. Spike sorting [11], thus, refers to the grouping of spikes according to each neuron, from the recording of the microelectrode. Interestingly, it is possible to model the spike fired by each neuron with a *characteristic* shape [12]. The neural recording can thus be modeled as a *superposition* of returns from multiple neurons, as in (1), where the return from each neuron corresponds to the convolution of its characteristic spike shape with the sequence of its firing times. A similar problem also arises in DNA sequencing, please refer to [13].

Multi-path identification in random-access channels: In multi-user multiple access model [7], each active user transmits a signature waveform modulated via a signature sequence, which can be designed to optimize performance and the base station receives a *superposition* of returns from active users, as in (1), where the received signal from each active user corresponds to the convolution of its signature waveform with the

Download English Version:

<https://daneshyari.com/en/article/11010173>

Download Persian Version:

<https://daneshyari.com/article/11010173>

[Daneshyari.com](https://daneshyari.com)