AN ALGORITHM FOR EXACT SUPER-RESOLUTION AND PHASE RETRIEVAL

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ABSTRACT

We explore a fundamental problem of super-resolving a signal of interest from a few measurements of its low-pass magnitudes. We propose a 2-stage tractable algorithm that, in the absence of noise, admits perfect super-resolution of an r-sparse signal from $2r^2 - 2r + 2$ low-pass magnitude measurements. The spike locations of the signal can assume any value over a continuous disk, without increasing the required sample size. The proposed algorithm first employs a conventional super-resolution algorithm (e.g. the matrix pencil approach) to recover *unlabeled* sets of signal correlation coefficients, and then applies a simple sorting algorithm to disentangle and retrieve the true parameters in a deterministic manner. Our approach can be adapted to multi-dimensional spike models and random Fourier sampling by replacing its first step with other harmonic retrieval algorithms.

Index Terms— Super-resolution, Low-pass Frequencies, Phase Retrieval, Matrix Pencil, Quadratic Measurements, Hankel matrix, sorting

1. INTRODUCTION

Recovering fine-grained details of an object from its coarse-scale measurements, often termed "super-resolution", is a fundamental scientific problem that arises in many signal processing problems, e.g. direction of arrival analysis [1], wireless channel estimation [2], medical imaging [3], and optics [4], to name just a few. Due to physical limitations (e.g. diffraction limits) and hardware constraints, it is often difficult (and sometimes impossible) to obtain accurate measurements of the high-end spectrum of a signal. It is thus of significant interest to super-resolve a signal from its low-pass signal components.

Perfect super-resolution is in general impossible unless the object of interest has a parsimonious structural representation. Many parametric methods have been proposed to exploit the underlying harmonic structure, including MUSIC [5], ESPRIT [1], and the matrix pencil method [6]. These methods are typically based on the eigen-decomposition of a matrix constructed from low-pass samples, which can recover a signal with infinite precision in the absence of noise. Inspired by the success in sparse recovery, Gazit et. al. [7] developed an iterative method called Nonlocal Hard Thresholding (NLHT) for empirical super-resolution. Candès et. al. [8, 9] have recently proposed an efficient non-parametric approach based on semidefinite programming which, under certain separation conditions, enables provably exact and stable recovery.

The super-resolution task is more challenging in the high-frequency regime (the regime where the carrier frequency itself is ultra-high). Due to hardware limitations, it might be very difficult to measure and record the phase information from low-pass magnitude measurements in a reliable manner. This issue arises in diverse applications including X-ray crystallography [10], optics [11]. and diffraction imaging [4]. For many applications, including the examples just stated, recovering the ground truth in an efficient fashion without phase information is by nature very difficult and oftentimes ill-posed.

Most conventional methods (e.g. the Gerchberg-Saxton algorithm [12]) to recover the phase information from magnitude measurements (termed "phase retrieval") are based on strong prior information on the signal, and are unable to generate provably accurate signal recovery. A recent line of work [13–15] has approached this problem from a different angle by converting the phase retrieval problem to completion of a rank-1 lifted matrix. In particular, Candès et. al. [15, 16] deliver the encouraging performance guarantees that phase information of any N-dimensional signal can be perfectly recovered from $O(N)$ random amplitude samples via efficient semidefinite programming. Stability and uniqueness have also been studied by Eldar et. al. [17]. This early success has inspired a recent explosion of work in phase retrieval [18–23], from both theoretical and algorithmic perspectives.

Nevertheless, most performance guarantees for *tractable* algorithms are established for Gaussian sampling [15, 16, 18, 24] or sub-Gaussian sampling [23]. Phase retrieval from Fourier intensity measurements – which is the most practically demanding problem – has not been fully explored. Recent work by Jaganathan et. al. [20] proposed a tractable algorithm that, in the presence of a *full discrete* Fourier ensemble, allows provably exact recovery for signals up to sparsity $O\left(n^{1/3}\right)$ and empirical recovery for signals up to sparsity $O(\sqrt{n})$. Uniqueness has also been investigated in [25]. However, these works do not provide provably accurate algorithms that allow efficient recovery from the intensities of *unmasked low-pass* Fourier coefficients.

In this paper, we design an algorithm that, in the absence of noise, allows us to retrieve the fine-scale structure of an object from the intensities of its low-end spectrum. Our algorithm operates under a very general setting, and enables perfect super-resolution of an r-sparse signal from $m \geq 2r^2 - 2r + 2$ magnitude measurements in an efficient and deterministic manner. The proposed algorithm is a 2-step method that involves a matrix pencil approach followed by a simple sorting algorithm. Its computational complexity is no greater than the complexity of performing elementary inversion and eigen-decomposition of an $\left(\frac{m}{2} - 1\right) \times \left(\frac{m}{2} - 1\right)$ Hankel matrix. The signal of interest can be an arbitrary *continuous-time* sparse signal, i.e. the positions of the time-domain spike of the signal can assume any value over a continuous region.

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2. PROBLEM FORMULATION: 1-D MODEL

2.1. Continuous-Time Model

Assume that the continuous-time signal of interest $x(t)$ ($t \in [0,1]$) can be modeled as a weighted superposition of spikes at r distinct positions t_l ($1 \le l \le r$) as follows

$$x(t) = \sum_{l=1}^{r} a_l \delta(t - t_l), \tag{1}$$

where a_l's represent the complex amplitudes. The positions t_l can assume any value within the continuous interval $[0, 0.5)$. The restriction is in order to avoid ambiguity, as discussed in Section 3.1. Expanding $x(t)$ in a Fourier series over the interval $[0,1]$ results in the Fourier coefficients

$$\forall k \in \mathbb{Z}: \quad \hat{x}[k] = \sum_{l=1}^{r} a_l e^{-j2\pi k t_l}. \tag{2}$$

Suppose that we obtain magnitude information of a few frequency samples of $x(t)$ in the low end of its spectrum, i.e. we observe

$$y[k] := |\hat{x}[k]|^2, \qquad -m_c \le k < m_c. \tag{3}$$

The question is how to recover the true signal $x(t)$ from the magnitude of these $m = 2m_c$ low-end Fourier coefficients.

2.2. Discrete-Time Model

The model presented in (1) and (2) has a counterpart in the discrete-time setting as follows. Suppose that a discrete-time signal $x[n]$ of length N is a weighted sum of r spikes as follows

$$x[n] = \sum_{l=1}^{r} a_l \delta[n - n_l], \tag{4}$$

where $n_l \in \{0, 1, \cdots, \lfloor \frac{N-1}{2} \rfloor\}$. The discrete Fourier transform (DFT) coefficients of $x[n]$ is given by

$$\hat{x}[k] = \sum_{l=1}^{r} a_l e^{-j2\pi k \frac{n_l}{N}}, \quad 0 \le k < N. \tag{5}$$

Therefore, the discrete-time setting (5) can be treated as a special case of the continuous-time model (2) by restricting the spike positions to a fine grid $\{\frac{l}{N} : 0 \le l < \frac{N-1}{2N}\}$. For this reason, we restrict our analysis and results to continuous-time models, which is more general. As we will show, our method results in recovery from the same sample complexity as for the discrete-time model.

3. METHODOLOGY

We propose a 2-step algorithm that allows perfect super-resolution to within infinite precision, provided that the number m of samples obeys $m \ge 2r^2 - 2r + 2$. The proposed algorithm works under the following fairly general conditions:

1. $|a_i| \ne |a_l|$ for all $i \ne l$;
2. $t_{i_1} - t_{l_1} \ne t_{i_2} - t_{l_2}$ for any $(i_1, l_1) \ne (i_2, l_2)$.

Without loss of generality, we assume that

$$|a_1| > |a_2| > \cdots > |a_r| > 0. \tag{6}$$

Our algorithm first recovers *unlabeled* sets of correlation coefficients $\{a_i a_l^* \mid i \ne l\}$ and $\{t_i - t_l\}$ using a matrix pencil approach, and then retrieves the a_i's and t_i's via a simple sorting algorithm. These two steps are described in more details in the following subsections.

3.1. Step 1: Recovering unlabeled sets of correlation coefficients via a matrix pencil approach

The key observation underlying our algorithm is that

$$y[k] := |\hat{x}(k)|^2 = \sum_{i=1}^{r}\sum_{l=1}^{r} \underbrace{a_i a_l^*}_{a_{i,l}} \exp\Big(-j2\pi \underbrace{(t_i - t_l)}_{t_{i,l}} k\Big). \tag{7}$$

Therefore, $y[k]$ corresponds to a weighted superposition of no more than $r^2 - r + 1$ spikes in the time domain[1]. Recall our assumption that $t_i \in [0, 0.5)$, which implies that $t_i - t_j \in (-0.5, 0.5)$. Since we can only observe $y[k]$ at integer values $k \in \mathbb{Z}$, restricting $t_i - t_j$ to within $(-0.5, 0.5)$ is necessary to avoid ambiguity.

The form (7) allows us to apply the matrix pencil method [6, 26] to retrieve $\{a_i a_l^* \mid i \ne l\}$ and $\{t_i - t_l \mid i \ne l\}$, which we briefly summarize as follows. Arrange $\boldsymbol{y} := [y[-m_c], \cdots, y[m_c - 1]]$ into an enhanced $(m_c + 1) \times m_c$ Hankel matrix

$$\boldsymbol{Y} := \begin{bmatrix} y[-m_c] & y[1-m_c] & \cdots & y[-1] \\ y[1-m_c] & y[2-m_c] & \cdots & y[0] \\ \vdots & \vdots & \ddots & \vdots \\ y[0] & y[1] & \cdots & y[m_c - 1] \end{bmatrix}. \tag{8}$$

The analysis framework of [6, 26] suggests that

$$\operatorname{rank}(\boldsymbol{Y}) \le \min\{r^2 - r + 1, m_c\}. \tag{9}$$

Let $\boldsymbol{Y}_1$ and $\boldsymbol{Y}_2$ represent the first m_c rows and the last m_c rows of $\boldsymbol{Y}$, respectively, then both $\boldsymbol{Y}_1$ and $\boldsymbol{Y}_2$ have rank at most $r^2 - r + 1$. The matrix pencil method for super-resolution then proceeds as follows:

- Calculate the eigenvalues $\{\lambda_i \mid 1 \le i \le r^2 - r + 1\}$ of $\boldsymbol{Y}_1^\dagger \boldsymbol{Y}_2$, where $\boldsymbol{Y}_1^\dagger$ represents the pseudo-inverse of $\boldsymbol{Y}_1$;
- Let $\tilde{t}_k := \frac{1}{2\pi} \arg\lambda_k$. One can verify that

$$\{\tilde{t}_k\} = \{0\} \cup \{t_i - t_l \mid i \ne l\}. \tag{10}$$

  Note that we can only derive the above set in an unlabeled manner, i.e. we are unable to link each value $\tilde{t}_k$ with a pair of indices (i, l) such that $\tilde{t}_k = t_i - t_l$.

- By substituting all values $\tilde{t}_k$ (or, equivalently, $\{0\} \cup \{t_i - t_l \mid i \ne l\}$) into (7), one can derive the set of complex amplitudes associated with each value $t_i - t_l$. In particular, one can easily see that this amplitude set contains the values $\sum_{i=1}^{r} |a_i|^2$ and $a_i a_l^*$ for all $i \ne l$. Since $\sum_{i=1}^{r} |a_i|^2$ has the largest amplitude among the whole set, we are able to separate out the *unlabeled* correlation set $\{a_i a_l^* \mid i \ne l\}$.

Note that the matrix pencil approach is only one method to recover $\{a_i a_l^* \mid i \ne l\}$ and $\{t_i - t_l\}$ from a mixture of sinusoids (7). Since the spikes at positions $t_i - t_l$ and $t_l - t_i$ always arise in pairs in (7), we essentially only obtain $\{|t_i - t_l|\}$.

In the absence of noise, the matrix pencil approach allows recovery to within arbitrary precision without additional assumptions on the spike locations. Another alternative is the total variation minimization method recently proposed by Candès et. al. [8, 9], which often improves stability in the presence of noise.

[1] Note that there are r terms (i.e. all terms with $i = l$) in (7) leading to spikes at $t = 0$.

Algorithm 1 Sorting algorithm to recover $\{|a_i| : 1 \le i \le r\}$ from $\{|a_i a_l| : i \ne l\}$ and $|a_1|$.

1. Sort $\mathcal{A} = \{|a_i a_l| \mid i \ne l\}$.
2. **for** $2 \le i \le r$:
3. Set $|a_i| = \frac{1}{|a_1|} \max_{\tilde{a} \in \mathcal{A}} \tilde{a}$.
4. **for** $1 \le l < i$:
5. $\mathcal{A} \leftarrow \mathcal{A} \backslash \{|a_l a_i|\}$
6. **end**
7. **end**

3.2. Step 2: Recovering the a_i's and t_i's from the sets of correlation coefficients via sorting

We now consider how to retrieve t_i and a_i in order to recover $x(t)$. Note that knowledge of $\{ a_i a_l^* | \, i \ne l\}$ gives us the information on

$$\{|a_i a_l| : i \ne l\}. \tag{11}$$

Suppose first that we are able to identify $|a_1|$. When one knows the whole (unlabeled) set of pairwise products, various tractable methods have been proposed to perfectly recover all $|a_i|$'s (e.g. [27]). Here, we employ a simple sorting algorithm as presented in Algorithm 1. This method is based on the simple observation that the largest element in $\{|a_i a_l| : l \ge k\}$ is necessarily equal to $|a_1 a_k|$.

Recovering $|a_i|$ is a crucial step since it allows us to label the whole set $\{|t_i - t_l| \mid i \ne l\}$. In fact, from now on we not only have information on the set $\{|a_i a_l| : i \ne l\}$ but also the labels (i.e. (i,l)) associated with all elements in it. This immediately reveals information[2] on all $|t_i - t_l|$. Recovering t_i from all pairwise absolute differences $|t_i - t_l|$ is now a special case of the classical graph realization problem from Euclidean distance [28, 29], which can be easily solved. Specifically, let us define $\boldsymbol{t} = [t_1, \cdots, t_r]^T$, an $r \times r$ distance matrix $\boldsymbol{D}$ such that

$$\boldsymbol{D}_{il} = (t_i - t_l)^2, \quad 1 \le i, l \le r, \tag{12}$$

an $r \times r$ Gram matrix $\boldsymbol{G} = \boldsymbol{t}\boldsymbol{t}^T$, and a geometric centering matrix $\boldsymbol{V} = \boldsymbol{I} - \frac{1}{r}\boldsymbol{1}\boldsymbol{1}^T$. Since $\boldsymbol{D}$ is now given, one can show that (see [28])

$$\boldsymbol{V}\boldsymbol{G}\boldsymbol{V} = -\boldsymbol{V}\boldsymbol{D}\boldsymbol{V}/2.$$

The goal is to recover $\boldsymbol{G}$, which in turn allows us to produce $\boldsymbol{t}$. However, it has been pointed out in [29] that for any two Gram matrices $\boldsymbol{G}$ and $\tilde{\boldsymbol{G}}$ associated with $\{t_1, \cdots, t_r\}$ and $\{\tilde{t}_1, \cdots, \tilde{t}_r\}$ respectively, the identity $\boldsymbol{V}\boldsymbol{G}\boldsymbol{V} = \boldsymbol{V}\tilde{\boldsymbol{G}}\boldsymbol{V}$ implies that $\{t_1, \cdots, t_r\}$ is equivalent to $\{\tilde{t}_1, \cdots, \tilde{t}_r\}$ up to rigid transform (i.e. rotation and translation, see [29] for these definitions). Note that in our case, the rigid transform corresponds to the global phase information that is impossible to recover from the magnitude information.

The recovery procedure then proceeds as follows. By computing the largest eigenvalue λ_1 of $\boldsymbol{V}\boldsymbol{G}\boldsymbol{V}$ and its associated eigenvector $\boldsymbol{u}_1$, we obtain the entire family of candidate solutions for $\boldsymbol{t} = [t_1, \cdots, t_l]^T$ that yield the same $\boldsymbol{V}\boldsymbol{G}\boldsymbol{V}$ as follows

$$\tilde{\boldsymbol{t}} = \sqrt{\lambda_1}\boldsymbol{u}_1 + c_1\boldsymbol{1}, \quad \text{or} \quad \tilde{\boldsymbol{t}} = -\sqrt{\lambda_1}\boldsymbol{u}_1 + c_2\boldsymbol{1}. \tag{13}$$

Here, c_1, c_2 are arbitrary scalars that encode the global shift of spike positions. Note that all of these candidates satisfying $\tilde{\boldsymbol{t}} \in [0, 0.5)^r$ are valid solutions compatible with the measurements. In practice, the solutions can be refined with the aid of information on a few (two or more) reference / anchor spikes.

After we retrieve the t_i's, we equivalently derive all labels for $\arg(a_i a_l^*) = \arg(a_i) - \arg(a_l)$. Since we have knowledge on all values of $\arg(a_i) - \arg(a_l)$, recovering $\arg(a_i)$ can then be easily solved by elementary linear algebra, except for a global phase on the a_i's.

It remains to determine $|a_1|$. Observe that

$$\forall (i,l) \notin \{(1,2),(1,3)\} : \quad |a_1 a_2| \ge |a_1 a_3| \ge |a_i a_l|$$

and

$$\forall i \ge 2, l \ge 3, \quad |a_2 a_3| \ge |a_i a_l|.$$

Therefore, $|a_2 a_3|$ can only take place within the largest $r-2$ elements of the set $\{|a_i a_l| : i \ne l\}$ (i.e. $\{|a_1 a_l| \mid 4 \le l \le r\} \cup \{|a_2 a_3|\}$). For each value of $|a_2 a_3|$, we can easily determine $|a_1|$ as follows

$$|a_1| = \sqrt{|a_1 a_2|\,|a_1 a_3|} / |a_2 a_3|.$$

An exhaustive search over all $r-2$ choices and checking compatibility for each choice allow us to solve the problem exactly.

In summary, our algorithm is able to return all solutions compatible with the measurements. In the cases where uniqueness is not guaranteed, our algorithm can discover all possible solutions.

3.3. Discussion

Complexity. The proposed solution is summarized in Algorithm 2. One can see that the bottleneck lies in the matrix pencil approach, which involves inversion and eigen-decomposition of an $m_c \times m_c$ matrix. Therefore, our algorithm has computational complexity no greater than elementary inversion and eigen-decomposition of a Hankel matrix, and it is capable of recovering *all* signals that are compatible with the magnitude samples. That said, we do not need the uniqueness condition (e.g. [25,30]) in order to perform recovery. The algorithm works as soon as the number m of measurements exceeds $2r^2 - 2r + 2$. In other words, our algorithm admits perfect super-resolution up to sparsity $O(\sqrt{m})$.

Comparison with [20]. When a full N-dimensional discrete Fourier ensemble is present, the algorithm proposed in [20] can provably work for signals up to sparsity $O(\sqrt{N})$, and numerically work for signals up to sparsity $O(N^{1/3})$. The complexity of the algorithms therein is a polynomial function of the size of the grid in which the discrete-time signal lies, and the recovery guarantee can only be stated in a probabilistic sense. In contrast, our algorithm can recover any continuous-time spike with infinite precision *deterministically*, and the computational complexity depends only on the signal sparsity r.

4. EXTENSIONS

4.1. Multi-dimensional Spikes

Our method immediately extends to multi-dimensional spike models. Suppose that $x(\boldsymbol{t})$ is a mixture of K-dimensional spikes at r distinct locations $\boldsymbol{t}_i \in [0, 0.5)^K$ $(1 \le i \le r)$. If we let $\hat{x}[\boldsymbol{k}]$ denote the K-dimensional Fourier series coefficients of $x(\boldsymbol{t})$, then we can write

$$y[\boldsymbol{k}] := |\hat{x}(\boldsymbol{k})|^2 = \sum\nolimits_{i,l=1}^{r} a_i a_l^* \exp\left(-j2\pi \langle \boldsymbol{t}_i - \boldsymbol{t}_l, \boldsymbol{k} \rangle\right).$$

Recovering the unlabeled sets $\{a_i a_l^* \mid i \ne l\}$ and $\{\boldsymbol{t}_i - \boldsymbol{t}_l \mid i \ne l\}$ can be done by multi-dimensional matrix pencil methods (e.g. [26]).

[2] Note that we are only able to recover the absolute value of each difference. This arises because for any $i \ne l$, the values $t_i - t_l$ (resp. $a_i a_l^*$) and $t_l - t_i$ (resp. $a_l a_i^*$) always come up in pairs in (7).

Algorithm 2 Super-Resolution and Phase Retrieval Algorithm

1. Using the matrix pencil approach to retrieve the sets $\{ a_i a_l^* \mid i \neq l\}$ and $\{t_i - t_l \mid i \neq l\}$.
   (a) Calculate the eigenvalues $\{\lambda_i\}$ of $\boldsymbol{Y}_1^\dagger \boldsymbol{Y}_2$, where $\boldsymbol{Y}_1$ and $\boldsymbol{Y}_2$ are the first and the last m_c rows of $\boldsymbol{Y}$ of (8), respectively.
   (b) Let $\tilde{t}_i := \frac{1}{2\pi} \arg \lambda_i$. Then the set $\{t_i - t_l\} = \{\tilde{t}_i\}$.
   (c) Substitute $\{t_i - t_l\}$ into (7) to obtain $\{ a_i a_l^* \mid i \neq l\}$.

2. **Initialize** $\mathcal{S} = \{|a_i a_l| : i \neq l\}$, and set $|a_1 a_2|$ and $|a_1 a_3|$ to be the largest 2 elements of S. $\mathcal{S} \leftarrow \mathcal{S} \backslash \{|a_1 a_2|, |a_1 a_3|\}$.
   for $i = 1 : r-2$
      let $s^* = \max_{s \in \mathcal{S}} \mathcal{S}$, and let $\mathcal{S} \leftarrow \mathcal{S} \backslash \{s^*\}$
      set $|a_1| \leftarrow \sqrt{|a_1 a_2|\,|a_1 a_3|}/\sqrt{s^*}$.
      Perform Algorithm 1 to identify $\{|a_i|\}$, which in turn allows us to retrieve $|t_i - t_l|$ for all $i \neq l$.
      Let $\boldsymbol{D} := [(t_i - t_l)^2]_{1 \leq i,l \leq r}$ and $\boldsymbol{V} := \boldsymbol{I} - \frac{1}{r}\mathbf{1}\mathbf{1}^T$. Set $\boldsymbol{G}_{\boldsymbol{V}} := -\boldsymbol{V}\boldsymbol{D}\boldsymbol{V}/2$, and compute its largest eigenvalue λ_1 and the associated eigenvector $\boldsymbol{u}_1$.
      Obtain candidate solutions for $\boldsymbol{t} := \{t_1, \cdots, t_r\}$ are given by $\boldsymbol{t} = \sqrt{\lambda_1}\boldsymbol{u}_1 + c_1\mathbf{1}$ or $\boldsymbol{t} = -\sqrt{\lambda_1}\boldsymbol{u}_1 + c_2\mathbf{1}$ for any c_1 and c_2 that encode the global shift.
      Compute $\arg a_i$ (up to a global phase) using all values $\arg a_i - \arg a_l$.
      if this iteration yields a valid solution (i.e. obeying $\boldsymbol{t} \in [0, 0.5)^r$ and (3)):
         report this solution;
      end
   end

Note that the matrix pencil form for K-dimensional spike models is no longer a Hankel matrix, but instead an enhanced K-fold Hankel matrix, as discussed in [31].

After we identify $\{a_i a_l^* \mid i \neq l\}$ and $\{\boldsymbol{t}_i - \boldsymbol{t}_l \mid i \neq l\}$, then $\boldsymbol{t}_i$ can be retrieved in a coordinate-wise manner, i.e. we apply the second step of Algorithm 2 for each coordinate and retrieve it. This generates all signals compatible with the measurements.

4.2. Random Fourier Sampling

Our algorithms can also be adapted to accommodate random Fourier magnitude samples, by replacing Step 1 with more appropriate harmonic retrieval algorithms. For example, when the underlying spikes lie on a fine grid, one can attempt recovery via a compressed sensing algorithm (e.g. ℓ_1 minimization in [32]), MUSIC, or NLHT [7]. When the spike locations can assume any value over a continuous region, more complicated convex optimization methods are needed to address the basis mismatch issue [33]. Examples include the atomic norm minimization [34] for the 1-D model and Hankel matrix completion [31] for multi-dimensional models.

More broadly, Step 2 of Algorithm 2 is quite general and can build on top of any method that can retrieve the sets $\{a_i a_l^* \mid i \neq l\}$ and $\{\boldsymbol{t}_i - \boldsymbol{t}_l \mid i \neq l\}$ from the obtained measurements, regardless of the pattern of the obtained intensity measurements.

5. NUMERICAL EXAMPLE

We conduct the following numerical example to illustrate the correctness of our algorithm. Generate a signal $x(t)$ of $r = 5$ random spikes lying in $(0, 0.5)$. The amplitudes associated with the spikes are independently drawn from $\mathcal{N}(0, 1)$. Suppose we observe

$$y[k] := |\hat{x}[k]|^2 \quad (-m_c \leq k < m_c)$$

for various choices of m_c. To avoid numerical issues, the spike positions t_i's are generated such that

$$\min \{|\alpha - \beta| \,|\alpha, \beta \in \mathcal{T}_{\text{diff}}\} \geq 0.02, \tag{14}$$

where $\mathcal{T}_{\text{diff}} := \{|t_i - t_l| : 1 \leq i, l \leq r\}$. Condition (14) is some separation condition typically required to ensure numerical stability. In fact, we observe that if the separation condition is violated, then the matrix pencil approach is often numerically unstable as well.

Under the above model, the algorithm works perfectly in recovering the underlying frequencies whenever $m \geq 2r^2 - 2r + 2$. For example, when the spikes are defined by

$$\boldsymbol{t} = [0.0092, 0.1411, 0.3435, 0.3735, 0.4463]$$

$$\text{and} \quad \boldsymbol{a} = [0.4296, 0.5160, 0.9052, -0.0785, -2.2056]\,,$$

the recovery on both $\boldsymbol{a}$ and $\boldsymbol{t}$ is exact (with inaccuracy 1.2385×10^{-8}) except for the global phase, whenever $m \geq 42$.

6. CONCLUSION AND FUTURE WORK

We present an efficient 2-stage algorithm that allows us to super-resolve a signal from a few Fourier intensity measurements in its low-end spectrum. We demonstrate that for almost all signals with sparsity r, the algorithm admits perfect signal recovery from as few as $2r^2 - 2r + 2$ magnitude samples. The signal spikes are not required to lie on a fine grid, and the algorithm can be extended to accommodate multi-dimensional spike models and random Fourier samples.

It remains to be seen whether efficient algorithms can be found to accurately recover a sparse signal from even fewer magnitude samples. In addition, the success of the proposed super-resolution algorithm highly relies on the sorting algorithm, which is not very stable in the presence of noise. An algorithm more robust to noise might need to retrieve t_i and a_i simultaneously to improve stability. It would also be interesting to explore whether there is a non-parametric method for Step 2, i.e. to (approximately) retrieve t_i's and a_i's from the unlabeled correlation sets without prior information on the model order.

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