

Off-the-grid Blind Deconvolution and Demixing

Sajad Daei

November 26, 2026

Session Chair: Mikael Skoglund

Acknowledgements

Research in collaboration with

- Saeed Razavikia, PhD student, KTH, Division of Network and Systems Engineering
- Mohammad Mahdi Kamjoo, Master student, SUT, Electrical Engineering
- Prof. Mikael Skoglund, KTH, Division of Information Science and Engineering
- Prof. Gabor Fordor, KTH, Division of Decision and Control Systems
- Prof. Carlo Fischione, KTH, Division of Network and Systems Engineering

This work is sponsored by



digital futures



SCANIA

Outline

1. Introduction and Motivations
2. Applications (ISAC+STORM+Neuroscience+Biology)
3. Proposed mathematical approach
4. Simulations
5. Future research directions

Introduction and Motivations

What is Blind Deconvolution and Demixing?

Suppose we observe a superposition of returns from multiple transmitters, each of which consists of the convolution of two unknown functions.

$$y(t) = \sum_{i=1}^{r} x_i(t) * g_i(t) \tag{1}$$

- Much more difficult than ordinary blind deconvolution problem but has more important applications in various fields.
- Solvability? What conditions on $x_i(t)$ and $g_i(t)$ make this problem solvable?
- How? What algorithms shall we use to recover $x_i(t)$ and $g_i(t)$?
- The goal is to recover the continuous parameters of $x_i(t)$s and $g_i(t)$s by observing $y(t)$ over a limited time.
- Remark: Phase retrieval is a special case if $g_i(-t) = \overline{x_i(t)}$ (applications in CCD cameras, electron microscopy and astronomy)

Assumptions for solvability

One of the possible conditions for solvability

- $x_i(t)$ is a sparse spike signal, i.e. $x_i(t) = \sum_{l=1}^{s_i} c_l^i \delta(t - \tau_l^i)$
- $g_i(t)$ lies in a low-dimensional subspace.
- Let $\{g_i(t)\}_{i=1}^r$ be the blurring PSFs whose spectrum lie in the interval $[-B_{\max}, B_{\max}]$
- Taking Fourier transform and uniformly sampling in the frequency domain with rate $\frac{2M}{B_{\max}} \geq T_{\max}$ leads to

$$\boldsymbol{y} = \sum_{i=1}^{r} \widehat{\boldsymbol{x}}_i \odot \widehat{\boldsymbol{g}}_i \in \mathbb{C}^N \tag{2}$$

where $\widehat{\boldsymbol{x}}_i(n) = \sum_{l=1}^{s_i} c_k^i \mathrm{e}^{-j2\pi n \tau_l^i \frac{B_{\max} T_{\max}}{2M}}$ and $N = 2M + 1$.

- Subspace assumption : $\widehat{\boldsymbol{g}}_i = \boldsymbol{B}_i \boldsymbol{h}_i$ and $\boldsymbol{h}_i \in \mathbb{C}^{k_i}$ is an unknown vector

Applications: Integrated Sensing and Communications (ISAC)

$$x_i^R(t) = \sum_{l=1}^{s_R} \beta_l^R \delta(t - \tau_l^R) e^{-j2\pi\nu_l^R t}$$

$$x_i^C(t) = \sum_{l=1}^{s_C} \beta_l^C \delta(t - \tau_l^C) e^{-j2\pi\nu_l^C t}$$

- Mutual interference of radar and communication working in the same band
- Erroneous data for both radar and communications tasks
- Can make autonomous cars take inaccurate decisions
- Can make misdiagnosis in heart beat rate monitoring
- Distinguish target echos from communication messages at the common receiver

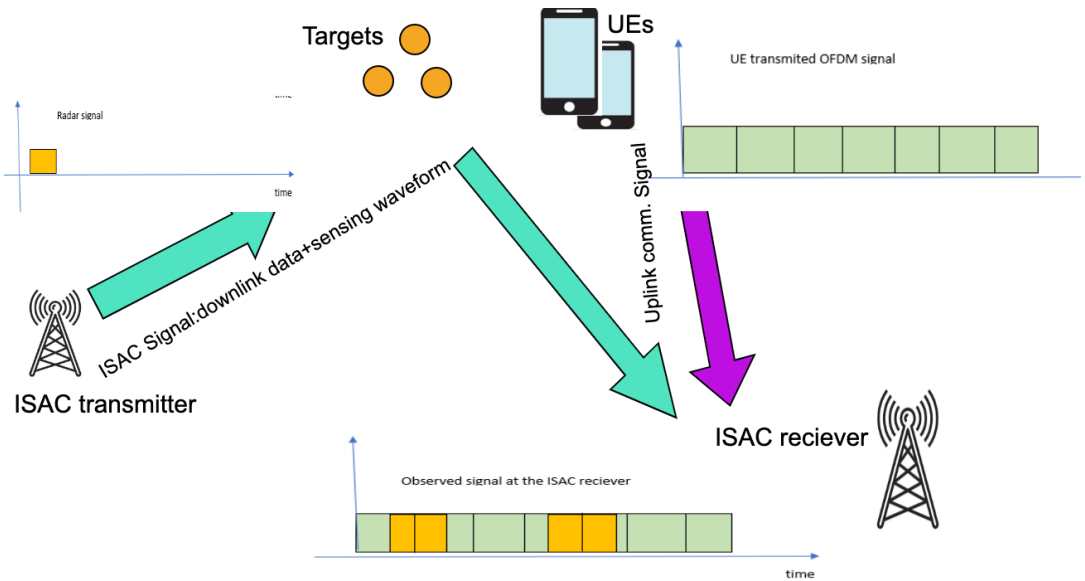


Figure 2: ISAC receiver observes signals coming from radar only, communications only and ISAC transmitters.

Applications: Super-resolution Fluorescence Microscopy

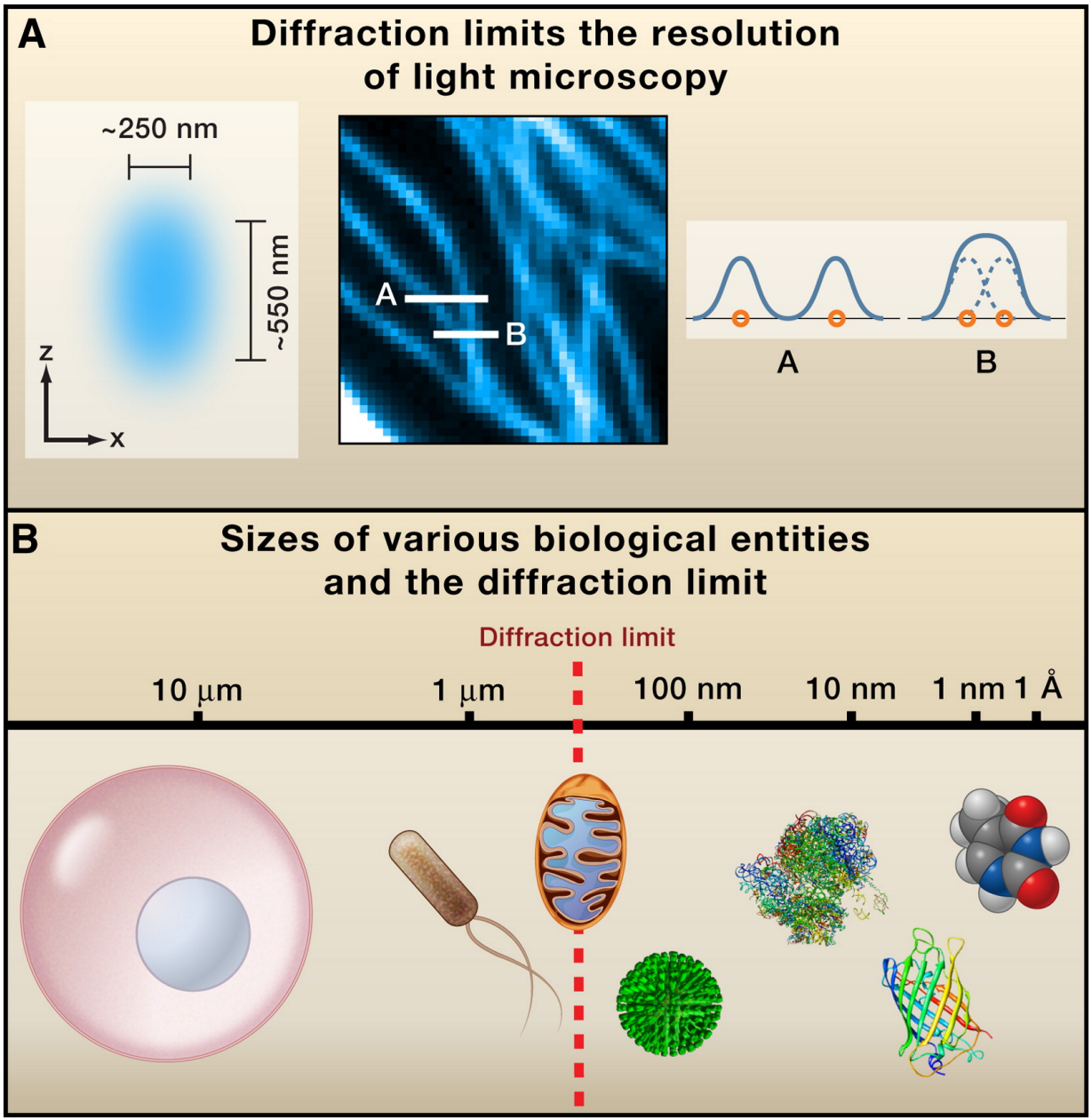


Figure 3: Diffraction-Limited Resolution of Conventional Light Microscopy

Applications: Super-resolution Fluorescence Microscopy

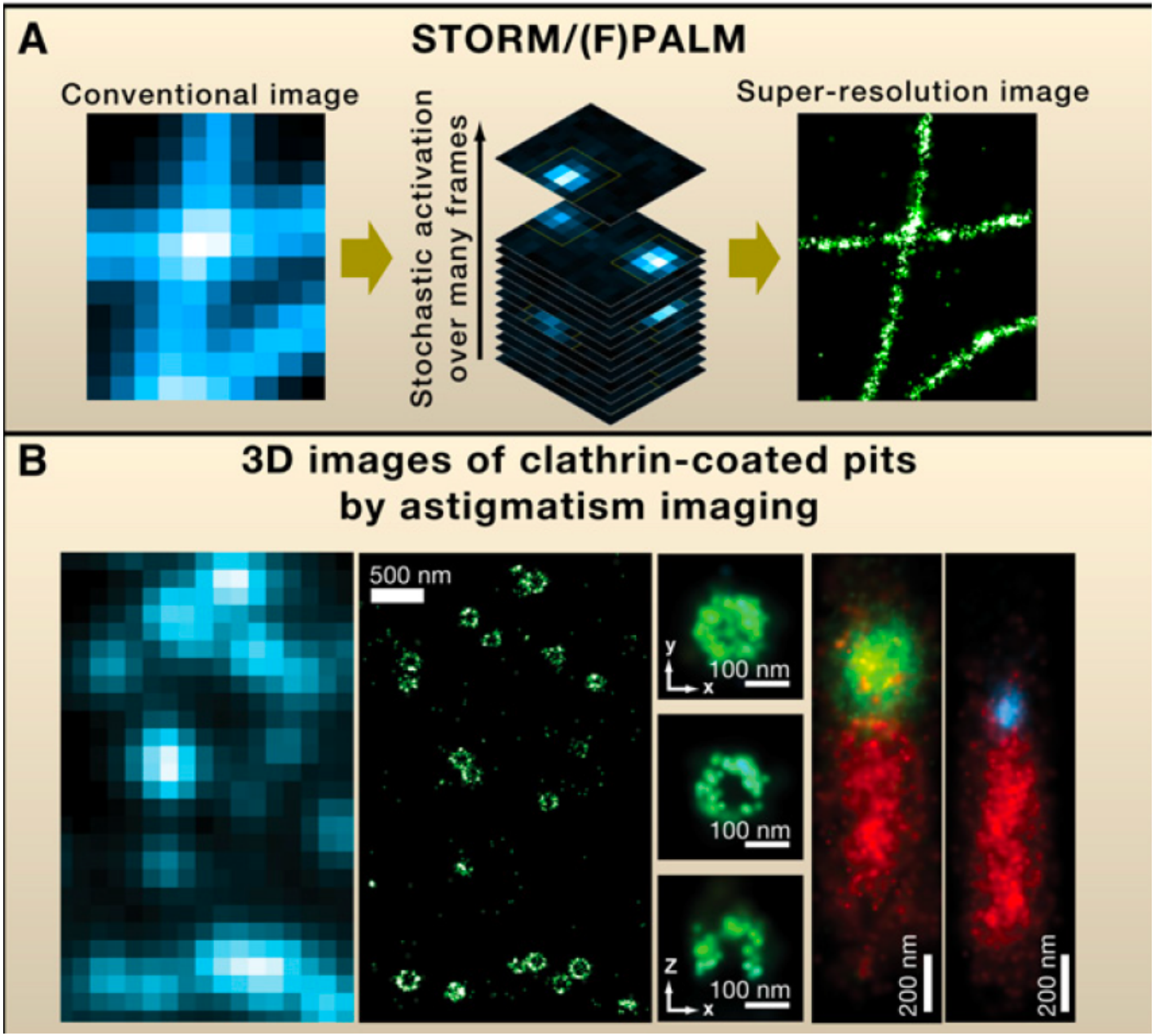
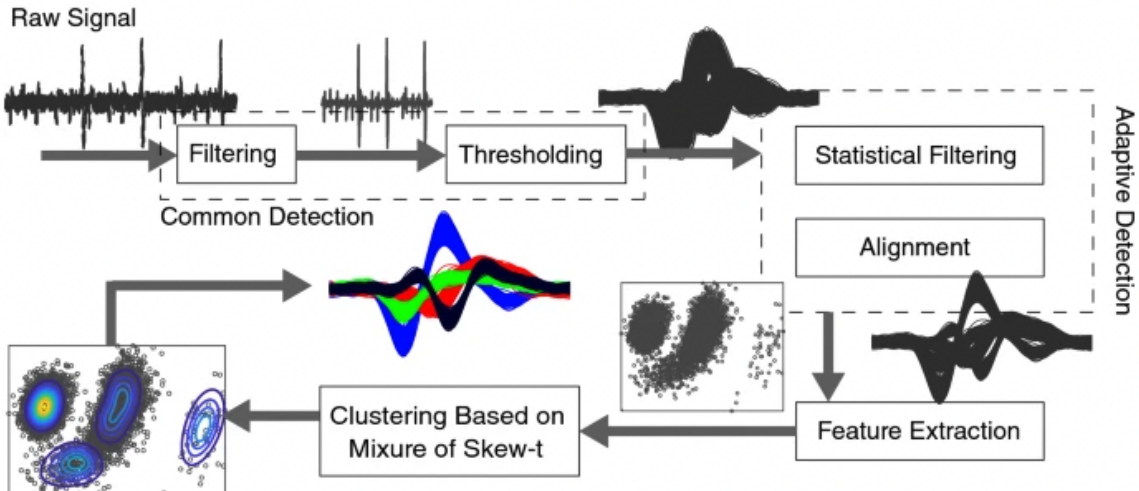


Figure 4: Single-Molecule Switching

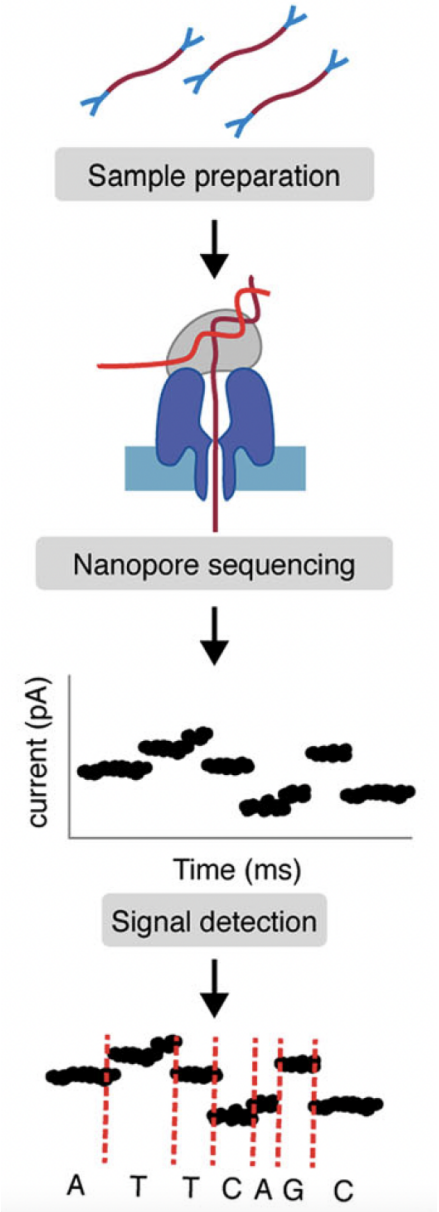
Applications: Spike sorting for neural recording

- Neurons in the brain communicate by firing action potentials, i.e. spikes.
- Each neuron has spikes of a characteristic shape, which is mainly determined by the morphology of their dendritic trees and the distance and orientation relative to the recording electrode.
- Spike sorting refers to the grouping of spikes according to each neuron, from the recording of the micro-electrode.
- The neural recording can thus be modeled as a superposition of returns from multiple neurons, where the return from each neuron corresponds to the convolution of its characteristic spike shape $(g_i(t))$ with the sequence of its firing times $(x_i(t))$.



DNA Sequencing

- The primary purpose of sequencing one's genome is to obtain information of medical value for future care.
- DNA sequencing can provide information on genetic variants that can lead to disease or can increase the risk of disease development,
- It includes any method or technology that is used to determine the order of the four bases (A, T, C, and G).
- In Nanopore sequencing, an electrical signal is generated from DNA passing through a nanopore channel.
- The goal is to determine which rectangular pulses ($g_i(t)$) correspond to which bases ($r = 4$).



Mathematical approaches

Non-convex continuous optimization?

One may try to solve the following optimization:

$$\min_{\substack{\boldsymbol{h}_i,\tau_k^i,c_k^i \\ i=1,\ldots,r}} \sum_{n=-2M}^{2M} \left| y(n) - \sum_{i=1}^{r} \sum_{k=1}^{s_i} c_k^i \mathrm{e}^{-j2\pi n\tau_k^i} \boldsymbol{b}_n^{i\,\mathrm{T}} \boldsymbol{h}_i \right|^2 \tag{3}$$

- May get stuck in local minima.
- By exploiting some additional prior information, we can have some recovery guaranty in the discrete case.

Convex approach

- Lifting trick: Transforming nonlinear relations to linear in higher dimensions
- Atomic norm minimization: Exploiting the features inherent in the system.

Proposed Approach

Lifting

$$y_n = \sum_{i=1}^{r}\sum_{k=1}^{s_i} c_k^i \mathrm{e}^{-j2\pi n\tau_k^i} \boldsymbol{b}_n^{i\,\mathrm{T}} \boldsymbol{h}_i = \sum_{i=1}^{r}\sum_{k=1}^{s_i} c_k^i \boldsymbol{e}_n^{\mathrm{T}} \boldsymbol{a}(\tau_k^i) \boldsymbol{b}_n^{i\,\mathrm{T}} \boldsymbol{h}_i =$$

$$\sum_{i=1}^{r} \left\langle \boldsymbol{X}_i, \boldsymbol{b}_n^i \boldsymbol{e}_n^{\mathrm{T}} \right\rangle_F \tag{4}$$

where $\boldsymbol{X}_i = \sum_{k=1}^{s_i} c_k^i \boldsymbol{h}_i \boldsymbol{a}(\tau_k^i)^{\mathrm{T}} \in \mathbb{C}^{k_i \times N}$.

$$\boldsymbol{y} = \mathcal{B}(\boldsymbol{\mathcal{X}}) \in \mathbb{C}^N, \tag{5}$$

Continuous sparsity in the atomic domain

Each $\boldsymbol{X}_i$ is sparse in the atomic domain with the atoms defined by

$$\mathcal{A}_i = \left\{ \boldsymbol{h}\boldsymbol{a}(\tau)^{\mathrm{T}} : \tau \in [0,1), \|\boldsymbol{h}\|_2 = 1, \boldsymbol{h} \in \mathbb{C}^{k_i} \right\}, \; i = 1, ..., r. \tag{6}$$

Atomic norm minimization

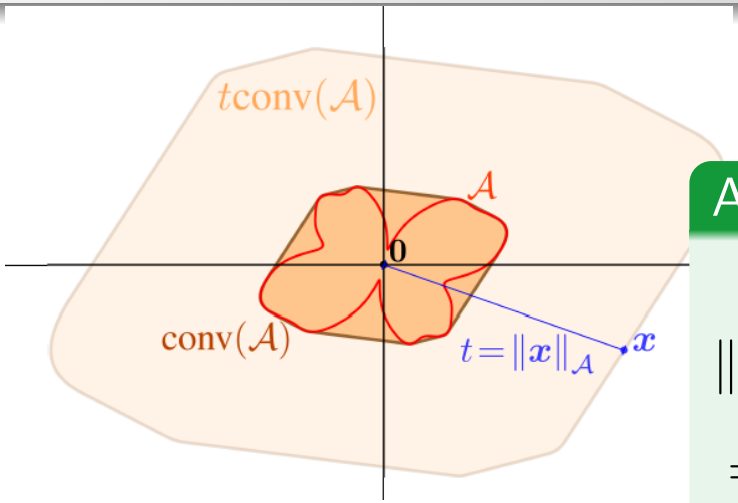


Figure 5: An atomic set $\mathcal{A}$ and its convex hull $conv(\mathcal{A})$. The atomic norm of $\boldsymbol{x}$ is the smallest scaling t such that t $conv(\mathcal{A})$ touches x.

Atomic norm

$$\|\boldsymbol{Z}\|_{\mathcal{A}_i} := \inf\{t > 0 : \boldsymbol{X} \in t\mathrm{conv}(\mathcal{A}_i)\}$$
$$= \inf_{\substack{c_k, \tau_k \\ \|\boldsymbol{h}_k\|_2 = 1}} \left\{ \sum_k |c_k| : \ \boldsymbol{Z} = \sum_k c_k \boldsymbol{h}_k \boldsymbol{a}(\tau_k)^T \in \mathbb{C}^{k_i \times N} \right\} \tag{7}$$

Atomic norm minimization

$$\min_{\mathcal{Z}=(\boldsymbol{Z}_i)_{i=1}^r} \sum_{i=1}^r \|\boldsymbol{Z}_i\|_{\mathcal{A}_i}$$
$$\boldsymbol{y}_{N\times 1} = \mathcal{B}(\mathcal{Z}). \tag{8}$$

Dual formulation

$$\max_{\substack{\boldsymbol{\lambda}\in\mathbb{C}^N \\ \tau^i \in [0,1)}} \ \mathrm{Re}\,\langle \boldsymbol{\lambda}, \boldsymbol{y} \rangle$$
$$\text{s.t.} \ \ \|(\mathcal{B}^*\boldsymbol{\lambda})_i \boldsymbol{a}^*(\tau^i)\|_2 \le 1$$
$$\tau^i \in [0,1), \ \ i = 1, ..., r, \tag{9}$$

Semi-definite programming (SDP)

Theorem

The infinite number of constraints in the dual formulations are equivalent to saying that there exists some matrices Q_i satisfying

$$\begin{bmatrix} \boldsymbol{Q}_i & (\mathcal{B}^*\boldsymbol{\lambda})_i^H \\ (\mathcal{B}^*\boldsymbol{\lambda})_i & \boldsymbol{I}_{k_i} \end{bmatrix} \succeq \mathbf{0}, \langle \boldsymbol{\Theta}_q, \boldsymbol{Q}_i \rangle = 1_{q=0},$$
$$q = -N+1, ..., N-1, i = 1, ..., r \tag{10}$$

where $\boldsymbol{\Theta}_q$ is the elementary Toeplitz matrix with ones on the q-th diagonal and zero elsewhere.

Continuous parameter estimation

Once we obtain $\boldsymbol{\lambda}$, we form the ℓ_2 norm of the dual polynomial $\boldsymbol{q}_i(\tau) = (\mathcal{B}^*\boldsymbol{\lambda})_i \boldsymbol{a}^*(\tau) = \sum_{n=-2M}^{2M} \lambda_n e^{j2\pi n\tau} \boldsymbol{b}_n^i$ and find the parameters τ that achieves the maximum.

Least square solution

$$\begin{bmatrix} \boldsymbol{e}_{-2M}^T \boldsymbol{a}(\hat{\tau}_1^1) \boldsymbol{b}_{-2M}^1{}^T & \dots & \boldsymbol{e}_{-2M}^T \boldsymbol{a}(\hat{\tau}_{s_r}^r) \boldsymbol{b}_{-2M}^r{}^T \\ \vdots & \ddots & \vdots \\ \boldsymbol{e}_{2M}^T \boldsymbol{a}(\hat{\tau}_1^1) \boldsymbol{b}_{2M}^1{}^T & \dots & \boldsymbol{e}_{2M}^T \boldsymbol{a}(\hat{\tau}_{s_r}^r) \boldsymbol{b}_{2M}^r{}^T \end{bmatrix} \begin{bmatrix} c_1^1 \boldsymbol{h}_1 \\ \vdots \\ c_{s_1}^1 \boldsymbol{h}_1 \\ \vdots \\ c_1^r \boldsymbol{h}_r \\ \vdots \\ c_{s_r}^r \boldsymbol{h}_r \end{bmatrix} = \begin{bmatrix} y(-2M) \\ \vdots \\ y(2M) \end{bmatrix} \tag{11}$$

Assumptions for solvability

- The messages are ℓ_2 unit normalized.
- First, we obtain $|c_l^i|$. Then, we can find $|h_i(p)| \forall p = 1, ..., k_i$.

Performance Guarantees

Key question: When and under which conditions the estimated parameters are exact?

A simple example: Structured Convex optimization

$$\min_{z} f(z)$$
$$s.t.\ \boldsymbol{A}\boldsymbol{x}^{\star} := \boldsymbol{y} = \boldsymbol{A}\boldsymbol{z} \tag{12}$$

Optimality condition

$\mathcal{D}(f, \boldsymbol{x}^{\star}) \bigcap \mathcal{N}(\boldsymbol{A}) = \{\boldsymbol{0}\}$ or $\exists \boldsymbol{\lambda} \neq \boldsymbol{0} : \boldsymbol{A}^{H}\boldsymbol{\lambda} \in \partial f(\boldsymbol{x}^{\star})$

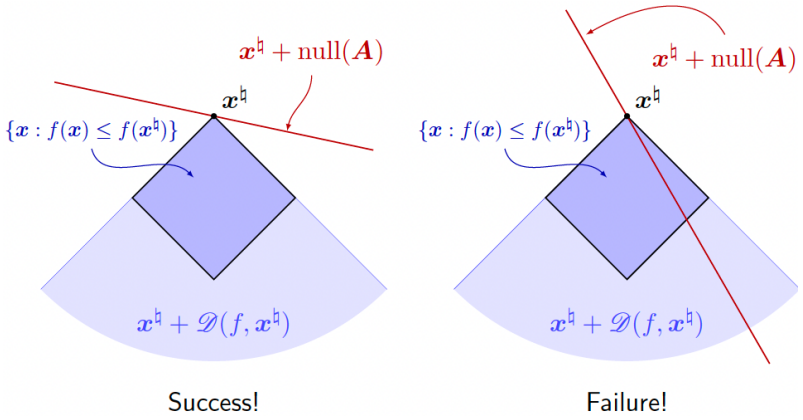


Figure 6: Optimality condition

Required sample complexity

Theorem

Denote the set of spike locations of $x_i(t)$ as $\mathcal{S}_i := \{\tau_k^i\}_{k=1}^{s_i}$. The solution $\widehat{\boldsymbol{\mathcal{X}}} = (\widehat{\boldsymbol{X}}_i)_{i=1}^r$ of (8) is unique if there exists a vector $\boldsymbol{\lambda} = [\lambda_{-2M}, ..., \lambda_{2M}]^T \in \mathbb{C}^N$ such that the vector-valued dual polynomials

$$\boldsymbol{q}_i(\tau) = (\mathcal{B}^*\boldsymbol{\lambda})_i \overline{\boldsymbol{a}(\tau)} \qquad i = 1, ..., r, \tag{13}$$

satisfy the conditions

$$\boldsymbol{q}_i(\tau_k) = \operatorname{sgn}(c_k^i)\boldsymbol{h}_i \ \forall \tau_k \in \mathcal{S}_i, \ \ i = 1, ..., r \tag{14}$$

$$\|\boldsymbol{q}_i(\tau)\|_2 < 1 \ \ \forall \tau \in [0, 1) \setminus \mathcal{S}_i, \ \ i = 1, ..., r \tag{15}$$

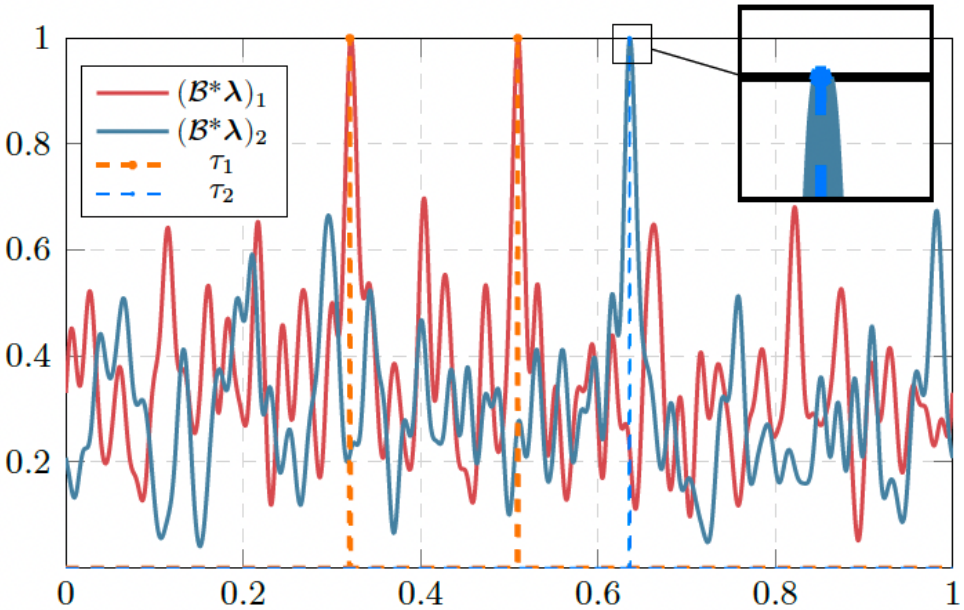
Theorem

If the sample complexity satisfies

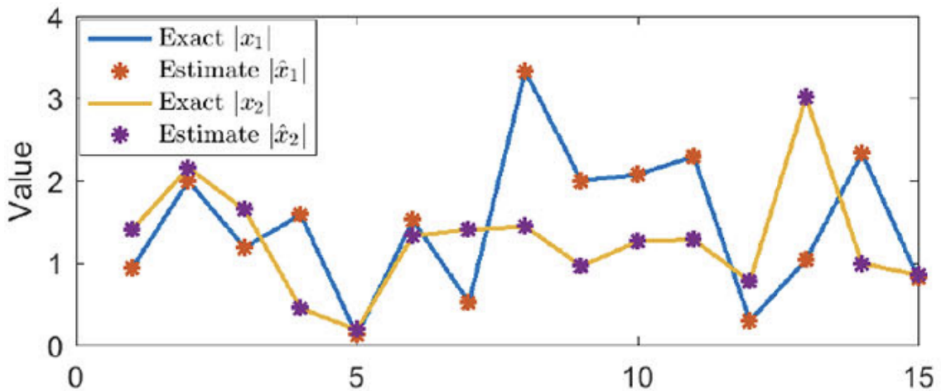
$$M \geq \frac{c_1 \mu_+ \sum_i s_i k_i}{\epsilon_1^2} \log\left(1 + \frac{c_2 \mu_+^2 \sum_i s_i k_i}{\mu_-}\right) \log\left(\frac{4 \sum_i s_i k_i}{\delta_1}\right) \tag{16}$$

then, with probability at least $1 - \delta_1$, the estimated parameters are exact.

Simulations



ℓ_2 norm of the dual polynomial



Waveform estimation

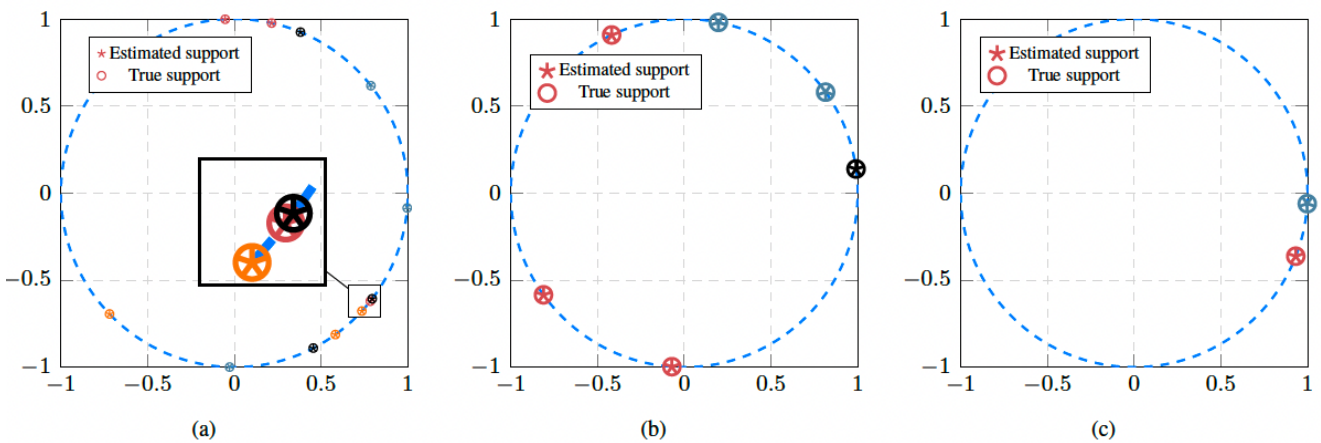


Figure 8: Polar representation of continuous parameters and their estimates.

Future Research directions

- Correlated transmitters?
- Improved resolution by using inherent non-convex optimization techniques?
- Design fast algorithms for off-the-grid blind deconvolution and demixing
- Develop a theoretical framework where $g_i(t)$ lives in a nonlinear subspace ?
- Develop Machine learning algorithms to solve this problem?
- Active transmitter identification when the number of transmitters are extremely large?
- Goal-oriented Blind deconvolution and demixing (needs far less resources but it is highly challenging)


Thank you
for your attention

Qr code

