Algebraically Structured Models
Applications to Molecular Imaging

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This work aims to obtain non-asymptotic minimax rates of estimation of a vector $\theta \in \mathbb{R}^d$ in a class of algebraically structured models.

One of the most important applications to this problem is to answer to a question arising in molecular imaging : given many noisy images of a molecule taken from different angles, how can we reconstruct this molecule as accurately and quickly as possible?

In the class of algebraically structured models, n random rotations of θ are observed, up to a centered Gaussian noise with known variance $\sigma^2 > 0$. We assume that these rotations belong to some known compact subgroup G of $\mathcal{O}_d(\mathbb{R})$. We derive a lower bound for the minimax quadratic risk for the estimation of θ holding for general G. We show that this lower bound is optimal in the case $G = \{\mathrm{Id}, -\mathrm{Id}\}$, obtaining an upper bound fitting our lower bound, when the signal to noise ratio $\frac{\|\theta\|}{\sigma}$ is bounded by some universal constant c. We prove similar results when $G = \mathcal{O}_d(\mathbb{R})$, this time, without conditions on θ. In both of these configurations, we find that the optimal rate of estimation of θ is $\sigma \left(\frac{d}{n}\right)^{\frac{1}{4}}$. In addition, for general G, we give upper bounds for the estimation of $\|\theta\|$ and $\|\theta\|^2$ scaled respectively as $\sigma \left(\frac{d}{n}\right)^{\frac{1}{4}}$, and as $\sigma^2 \left(\frac{d}{n}\right)^{\frac{1}{2}}$.

Keywords: multi-reference alignment; Gaussian mixtures; minimax estimation, Cryo-Electron Microscopy.