

Compressive auto-indexing in femtosecond nanocrystallography

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Ultrafast nanocrystallography has the potential to revolutionize biology by enabling structural elucidation of proteins for which it is possible to grow crystals with 10 or fewer unit cells on the side. The success of nanocrystallography depends on robust orientation-determination procedures that allow us to average diffraction data from multiple nanocrystals to produce a three dimensional (3D) diffraction data volume with a high signal-to-noise ratio. Such a 3D diffraction volume can then be phased using standard crystallographic techniques. "Indexing" algorithms used in crystallography enable orientation determination of diffraction data from a single crystal when a relatively large number of reflections are recorded. Here we show that it is possible to obtain the exact lattice geometry from a smaller number of measurements than standard approaches using a basis pursuit solver.

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