

# Fourier inference for reconstruction problems in biophysics

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Cryo-electron microscopy is a powerful technique employed by biophysicists in order to build highly accurate structural models of macromolecular assemblies at very small dimensions (Angstrom dimension). The technique involves a variety of statistical issues that arise mainly from noise present due to the nature of the imaging technique, but also depending on the geometric structure of the sample (whether we are studying well ordered crystals or loose single particles). In this talk we explore these statistical issues adopting a Fourier approach. We take a look at a contribution of statistics in the crystal approach, and also introduce challenges associated with the single particle approach, along with a discussion of a lower dimensional analogue that is of interest in its own right.

## References

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