GENFIRE: from Precisely Localizing Single Atoms in Materials to High Resolution 3D Imaging of Cellular Structures

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Tomography has made a radical impact on diverse fields ranging from the study of 3D atomic arrangements in matter to the study of human health in medicine. Despite its very diverse applications, the core of tomography remains the same, that is, a mathematical method must be implemented to reconstruct the 3D structure of an object from a number of 2D projections. Here, we present the mathematical implementation of a tomographic algorithm, termed GENeralized Fourier Iterative REconstruction (GENFIRE) [1], for high-resolution 3D reconstruction from a limited number of 2D projections. GENFIRE, like equal slope tomography [2-6], first assembles a 3D Fourier grid with oversampling and then iterates between real and reciprocal space to search for a global solution that is concurrently consistent with the measured data and general physical constraints. The algorithm requires minimal human intervention and also incorporates angular refinement to reduce the tilt angle error. We demonstrate that GENFIRE can produce superior results relative to several other popular tomographic reconstruction techniques through numerical simulations and by experimentally determining the 3D atomic positions in materials and imaging frozen-hydrated cellular structures at high resolution [1,7]. Equipped with a graphical user interface, GENFIRE is freely available from our website and is expected to find broad applications across different disciplines (http://genfire-em.com).

References:

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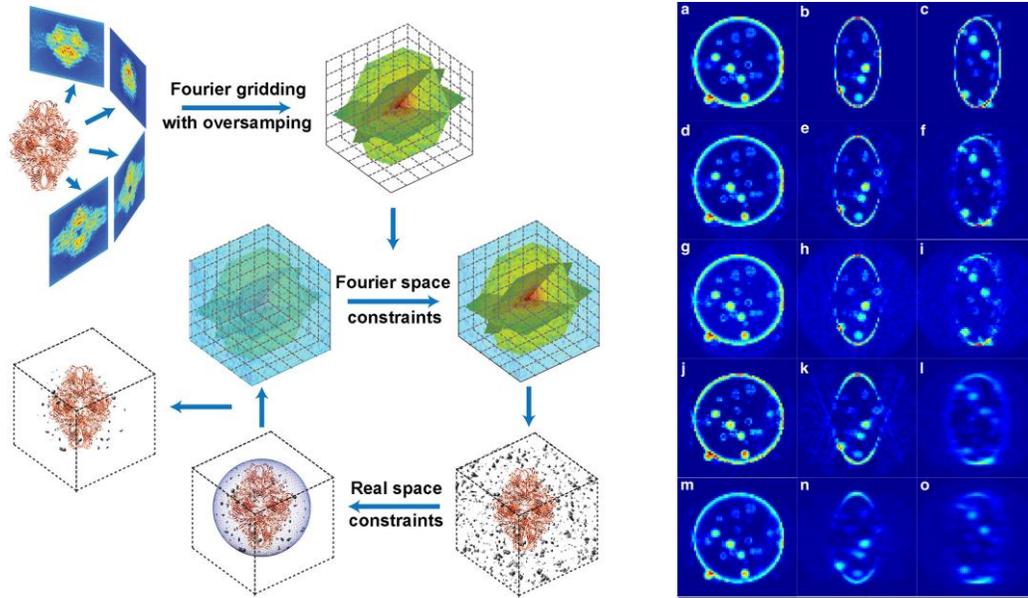
Figure 1. (Left) The GENFIRE algorithm. (Right) Numerical simulations on the 3D reconstruction of a 64×64×64 voxel vesicle model from 71 noisy projections using GENFIRE, EST, FBP and SIRT. (a–c) Three 10-voxel-thick central slices of the vesicle model in the XY, ZX and ZY planes, respectively. The corresponding three reconstructed slices with GENFIRE (d–f), EST (g–i), FBP (j–l), and SIRT (m–o), where the missing wedge axis is along the z-axis.
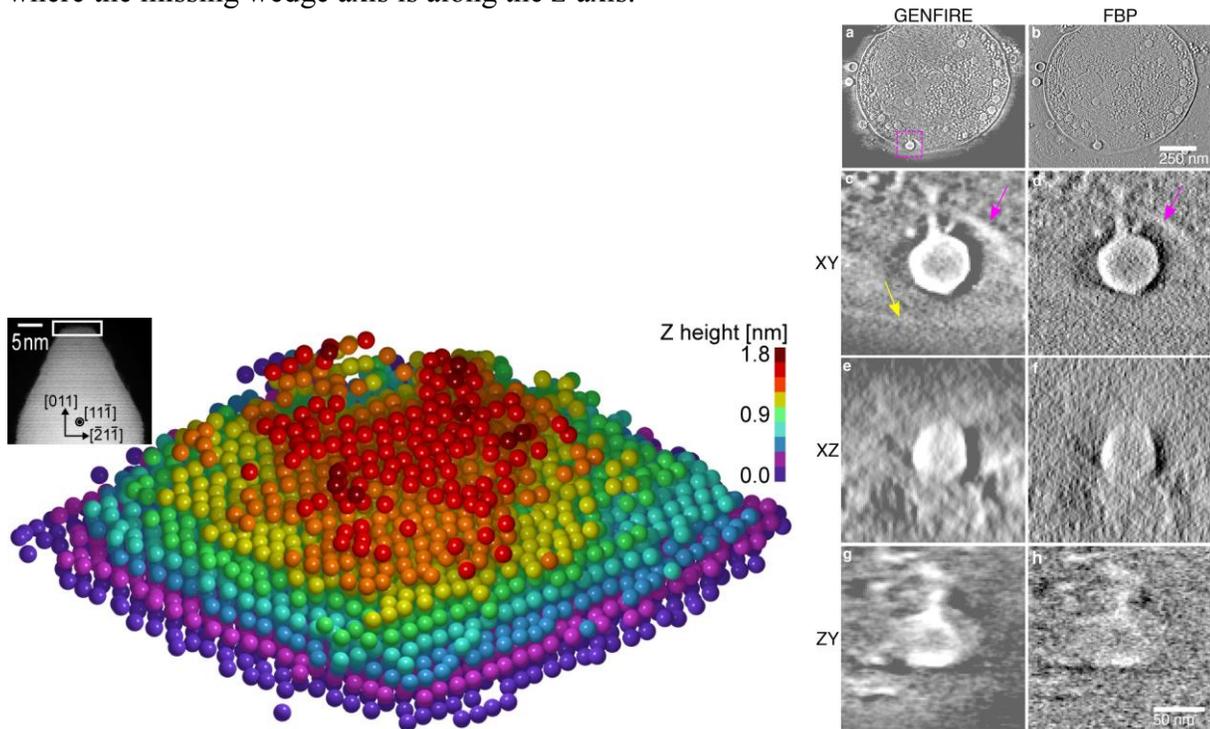

Figure 2. (Left) 3D positions of individual atoms in a tungsten needle sample revealed by atomic electron tomography with a 3D precision of 19 picometers. (Right) 3D structure of a frozen-hydrated marine cyanobacterium. (a, b) 5.4-nm-thick slices of the cell in the XY plane reconstructed by GENFIRE and FBP, respectively, Magnified views of the penetration of a cyanophage for the GENFIRE and FBP reconstructions in the XY (c, d), XZ (e, f), and ZY (g, h) planes, respectively.