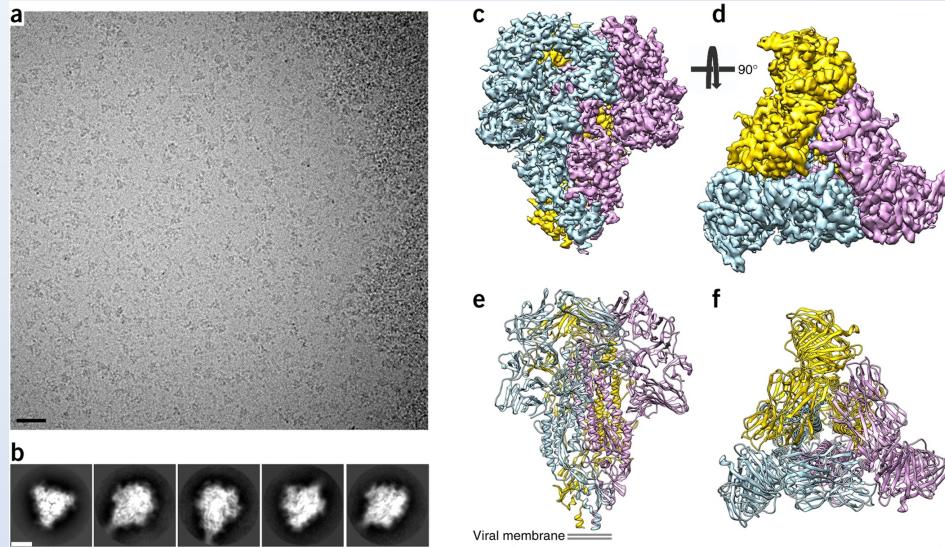
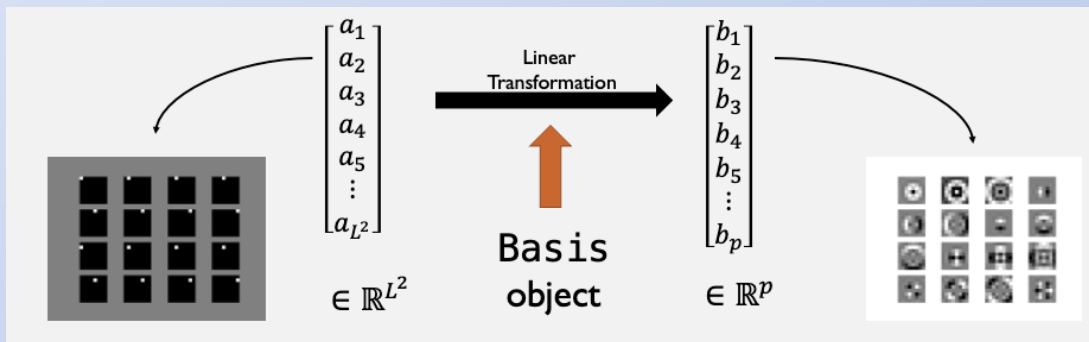


Representing Steerable Bases for cryo-EM in ASPIRE

Christopher Langfield, Joshua Carmichael, Garrett Wright, Joakim Andén, Amit Singer



Cryo-EM Reconstruction of Covid-19 spike protein. Walls et al (2016)
Nature Structural and Molecular Biology



- Cryo-EM is a method for reconstructing the 3D structure of biomolecules from hundreds of thousands of noisy 2D projections (the creators of the technique won the 2017 Nobel Prize in Chemistry)
- ASPIRE is an open-source Python package developed at Princeton University for performing these reconstructions from raw particle images
- Particles are class-averaged according to their 3D orientation in the frozen sample, but images in the same class may be rotated in the imaging plane relative to one another, making identification a challenge
- We represent these images using different “steerable” Fourier-Bessel bases which allow for rapid rotation of images in the plane
- In the code, these bases are organized according to a flexible class hierarchy involving inheritance and mixins.

