Visual proteomics using whole-lamella 2D template matching

Authors

- **Johannes Elferich**
  ⓘD [XXXX-XXXX-XXXX-XXXX](#) · ⓖ [jojoelfe](#)
  RNA Therapeutic INstitute, UMass Chan Medical SChool; HHMI

- **Nikolaus Grigorieff**
  ⓘD [XXXX-XXXX-XXXX-XXXX](#) · ⓖ [nikogrigorieff](#)
  RNA Therapeutic INstitute, UMass Chan Medical SChool; HHMI

Abstract

Localization and characterization of biomolecules inside a cell is the fundamental quest of all biological imaging. Fluoresence microscopy can localize biomolecules inside whole cells and tissues, but its ability to count biomolecules and accuracy of the spatial coordinates is limited by the wavelength of visible light. Cryo-electron microscopy on the other hand provides highly accurate position and orientation information of biomolecules but is often limited to small fields of view inside a cell, providing only limited biological context. In this study we use a data-acquisition scheme called "Fast Observation of Whole Lamella" (FOWL) to collect cryo-electron microscopy data over thin central sections, representing roughly 1% of the total cellular volume, of neutrophil-ile mouse cells. We use 2D-template matching to determinine localization and orientation of the large subunit of the ribosome in . We furthermore use 2D-template matching to test for complex formation with the small ribosomal subunit and used relative orientations of ribosome to assign ribosomes to polysomes. Overall these results provide a "map" of translational activity in whole crosssections of mammalian cells. We envision that using these high-throughput cryo-EM data collection and 2D tempalting matching approaches will advance visual proteomics approaches that can complement other single-cell "omics" techniques, such as flow-cytometry and single-cell sequencing.

Introduction

References