

Cryo-electron Microscopy of the Ribosome: Methods of Fitting, and Inference of Dynamics

Joachim Frank^a, Haixiao Gao^a, Wen Li^b, Jayati Sengupta^a, ^a*HHMI, HRI*. ^b*Wadsworth Center, Empire State Plaza, Albany, New York*. E-mail: joachim@wadsworth.org

Cryo-electron microscopy yields “three-dimensional snapshots” of the ribosome and its interaction with ligands at time points determined by the use of antibiotics or GTP analogs. If several such snapshots are available for one of the functional processes, how can we obtain a seamless picture of its dynamics? We address the two aspects of this problem: the interpretation of medium-resolution cryo-EM density in terms of published coordinates of structural components, and the means of “interpolating” between subsequent structures inferred from the snapshots. This problem is exemplified by the investigation of the decoding process, for which four 3D snapshots are available [1,2].

[1] Valle M. et al., *Nat. Struct. Biol.*, 2003, **10**, 899. [2] Frank J., Sengupta J., Gao H., Li W., Valle M., Zavialov A., Ehrenberg M., *FEBS Lett.*, 2005, **579**, 959.

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