

MS04-04 | AUTOMATED INTERPRETATION OF CRYO-EM DENSITY MAPS WITH CONVOLUTIONAL NEURAL NETWORKS

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In recent years, three-dimensional density maps reconstructed from single particle images obtained by electron cryo-microscopy (Cryo-EM maps) have reached unprecedented resolution. However, assigning a fold to map regions can be a challenge, in particular if the constituting macromolecules are unknown or mobile. Convolutional neural networks (CNNs) combine traditional image analysis with machine learning by cascading layers of trainable convolution filters and are exceptionally well suited for map annotation [1]. CNNs have been successfully applied to biological problems such as breast cancer mitosis recognition [2] and volumetric data segmentation [3].

Here, we will give a general perspective on the potential of CNNs for the interpretation of Cryo-EM maps and present a network which was trained on a carefully curated set of 293 experimentally derived reconstruction maps from the EMDB [4] to automatically annotate protein secondary structure as well as nucleotides. The network, named Haruspex, can be straightforwardly applied to predict structures in newly reconstructed maps to facilitate model building. It can also support domain placement, and due to its high median recall and precision rates of 94.2% and 79.2%, respectively (on an independent test set of 167 EMDB entries), it can be used for structure validation. The network and a plugin for COOT [5] will be available from our website.

[1] Cireşan et al. (2011). IJCNN, 1918

[2] Cireşan et al. (2013). MICCAI, 411

[3] Çiçek et al. (2016). MICCAI, 424

[4] Tagari et al. (2002). Trends Biochem. Sci. 27, 589

[5] Emsley et al. (2010). Acta Cryst. D66, 486