Topology Representing Network Enables Highly-Accurate Classification of Protein Images Taken by Cryo Electron-Microscope

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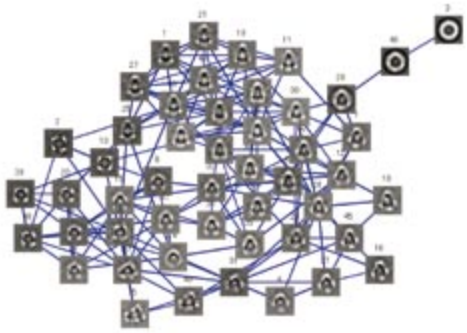
In single-particle analysis, a three-dimensional (3-D) structure of a protein is constructed using electron microscopy (EM). The primary process of this 3-D reconstruction is the classification of images according to their Euler angles, the images in each classified group then being averaged to reduce the noise level. In our newly developed strategy of classification, we introduce a topology representing network (TRN) method. It is a modified method of a growing neural gas network (GNG). In this system, a network structure is automatically determined in response to the images input through a growing process. The GNG creates clear averages of the inputs as unit coordinates in multi-dimensional space, which are then utilized for classification[1].

1) T. Ogura, K. Iwasaki & C. Sato, J. Struct. Biol., Vol. 143, 185-200 (2003).



Accuracy of the GNG, the SOM and the MSA to classify a mixed library composed of sodium channel taken by cryo-EM.

Direct Observation of Kinesin's Hand-over-Hand Motion

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A conventional kinesin molecule travels continuously along a microtubule, in discrete steps of 8 nm. This processive movement is generally explained by models in which the two heads of a kinesin move in a hand-over-hand fashion. In order to prove this model, we have constructed a heterodimeric kinesin in which the mechanochemical cycle rate of one of the heads is considerably slower than the other's. Optical trapping nanometry experiments showed that a single heterodimeric kinesin exhibits fast and slow, 8 nm-steps alternately. Our results provide the first, direct evidence for the hand-over-hand model.

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K. Kaseda, H. Higuchi, and K. Hirose : Proc. Natl. Acad. Sci., USA. 99 (25), 16058-16063 (2002).
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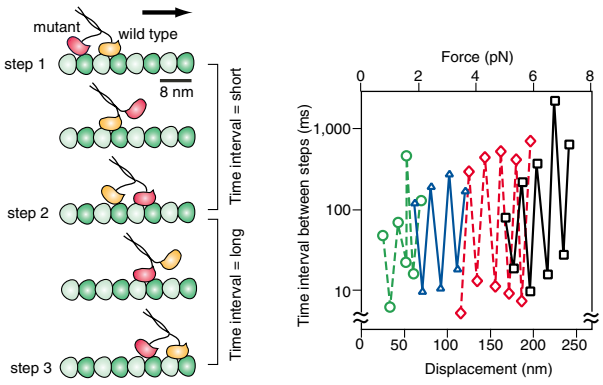

Alternate fast and slow steps of a heterodimer kinesin