SPATIAL AND TEMPORAL CRYOEM OF MOLECULAR GELS AND 1-DIMENSIONAL STRUCTURES

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Understanding the structure and structure-property-function relationship is key for the development of new functional materials. Structural analysis of multiscale soft systems may, however, be limited due to the 'invisible' complexity of the structures. Cryo-electron microscopy (CryoEM) techniques which comprises cryo-TEM and cryo-SEM are non-invasive methods that enable direct detection of soft suprastructures in solution at their hydrated state, at multiple length scales, and at high resolution. Additionally , analysis is done directly, i.e., without the need for a pre-determined model or post-imaging analysis. Cryo-TEM, for example, is highly effective for resolving the coexistence of multiple nanostructures and short-lived intermediates [1], thus providing particle-specific unique data that cannot be obtained from techniques such as scattering or rheology that probe bulk properties. Cryo-SEM covers a wide scale of structures and can readily be applied to highly visocus systems. Combined with another CryoEM method, Cryo-Tomography, one can resolve the detailed spatial organization in 3 dimensions.

This talk will focus on characterization of soft molecular matter systems by CryoEM techniques, and will emphasize analysis of molecular gels and 1-dimensional sturtcures, with examples from our recent works with surfactants, lipids, peptides and proteins.

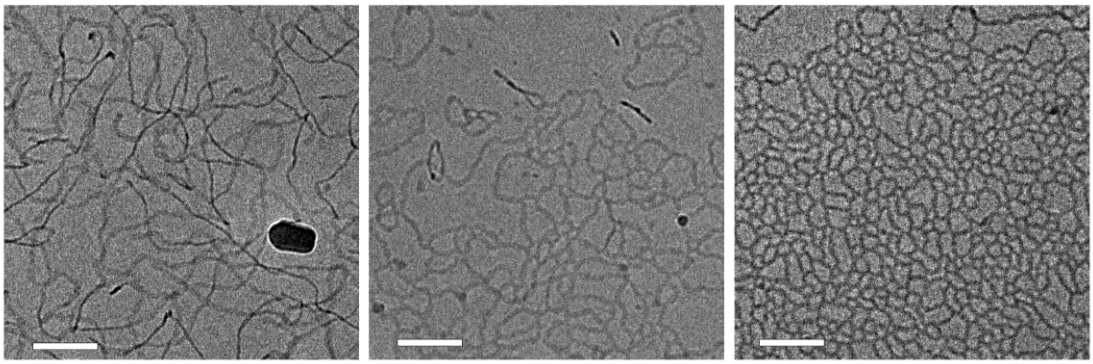

Figure 1. Cryo-TEM analysis of entangled and branched micellar netwworks

References:

1. Danino D, Cryo-TEM of Soft Molecular Assemblies, Curr Opin Colloid In 17(6), 316–329 (2012).
2. Danino et al., From Discs to Ribbons Networks: The Second Critical Micelle Concentration in Nonionic Sterol Solutions J Phys Chem Lett 7, 1434–1439 (2016).