Databases containing the coding sequences of thousands of genomes as well as the atomic resolution 3D structures of tens of thousands of proteins are transforming phylogenomics as well as refreshing the ways that cellular evolution is studied. Although gene trees based on nucleotide substitution frequencies are useful to study the evolution of genes, phylogeny, which is the equivalent of species evolution, is reconstructed with genome content data. This consists of genomic content of proteins or protein domains that represent the tertiary folds in proteins. Rooted phylogeny based on protein domains shows two complex lineages consisting of akaryotes and eukarytes, respectively diverging from a common ancestor. Surprisingly, the common ancestor is complex and is neither an archaeon, nor a bacterium nor a eukaryote. These data and more are transforming phylogenomics as well as refreshing the ways that cellular evolution is studied. Genome evolution takes precedence over gene trees as the guiding theme in the molecular evolution of organisms.

C. G. Kurland (SE) (Chair), Julian Gough (UK), Ajith Harish (SE), and Lars Nordenskiöld are facilitating this meeting.

We welcome all interested participants to register. For more information, please visit GD @ NTU website at http://global.ntu.edu.sg/GDI/ME18