· Development of network-based methods to display 'evolution as it happened' including reticulation (LGT, endosymbiosis, hybrid species etc) up to the limits of what can be discerned from extant data.

· Phylogenetic approaches for handling patchy taxon coverage and analyzing large numbers of short reads from next generation sequencing.

· Phylogenetic approaches to early life using non-stationary models and protein structural constraints

· Statistical approaches for analyzing non-aligned sequence data.

· More realistic models of speciation and extinction that better describe the shape of 'real' phylogenies.