

Forest Rohwer shared his work on uncultured marine viruses that typically occur at 10^7 /ml in the surface seawater. Most of these are eating bacteria – bacteriophage. They play a major role in global carbon cycles and can affect microbial diversity by killing off particular strains of microbes. Forest detailed some of the methods his lab is using to study viruses in the sea. He presented the concept of a “metagenomic species” as being defined by assembly parameters of metagenomic data. He has been using Monte Carlo Analysis to predict the numbers and relatedness of viral genomes. For example, a marine sediment sample has around 10,000 viral genotypes for 1 kg of sediment and 200 liters of seawater contains 5,000 genotypes. Forest has been working on making dynamical programming available to everyone. He has also been exploring how the Power Law appears to be a better predictor of the number species in a sample than other models. Forest concluded by sharing some his work on corals where he has discovered a lot of host-specific microbial populations.