**What to expect from *de novo* assembly of eukaryotic metagenome skimming data: A test case for lichens**

Lichens, an association of a filamentous fungus and one to several green algal or cyanobacterial photobionts, are a hallmark for the success of symbiotic associations involving eukaryotes. They colonize extreme ecological niches, frequently act as pioneering organisms, and are a promising source for novel bioactive substances. Yet, the full potential of lichens for evolutionary and biotechnological research has not been tapped. This is mainly because generating comprehensive genomic data is not trivial, since separate cultivation and sequencing of the symbionts is often not possible. Metagenome skimming of lichens is a cost-effective and rapid way to broaden the data basis. We systematically investigate the performance and pitfalls of different assembly strategies applied to metagenome skims of eukaryotic species mixtures. Using genomic data of the lichenized fungus *Cladonia grayi* and its green algal photobiont *Asterochloris sp*., we simulated 11 data sets of different fungal-to-algal coverage ratios (twin sets). These were used for benchmarking a diverse set of assemblers, representing Overlap-graph (OLG) based methods, *de Bruijn Graph* based (DBG) methods anddedicated metagenome assemblers. Our results show that DBG methods, suffer most from uneven coverages, generating highly fragmented assemblies when compared to OLG based ones. Moreover, the common practice of empirically choosing assembly parameters to maximize the N50 value can interfere with completeness of genome reconstructions from metagenome skimming data, even precluding an entire genome from the assembly. For our data, we showed that, independent of the coverage ratio, the best assemblies allow the identification of almost all genes annotated in the original data.