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ChloroExtractor: A fully automated plastid assembly pipeline reveals dozens of novel plastid genomes

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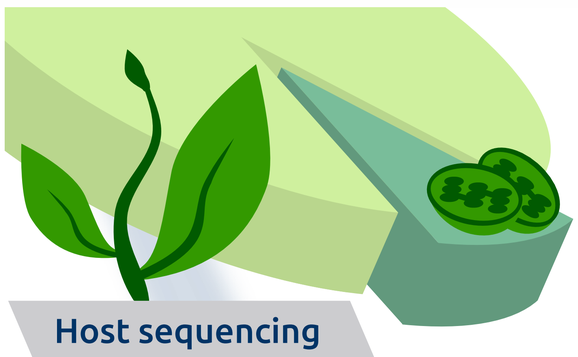
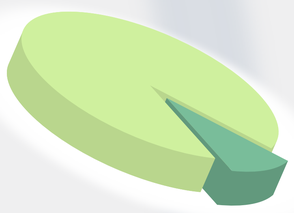
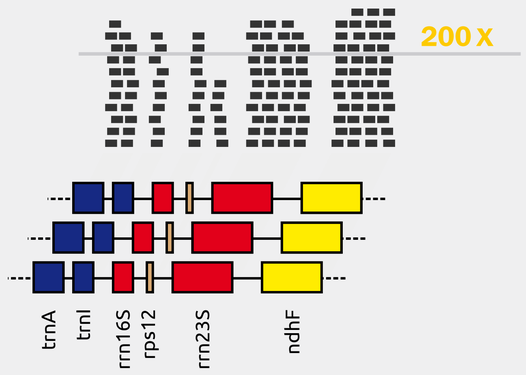
In times of large scale high troughput sequencing, novel plastid genomes mostly emerge from host genome sequencing projects. Here we present **ChloroExtractor**, a fully automated pipeline designed to generate high quality plastid assemblies from heterogeneous short read data. By applying our software to 100 publicly available plant sequencing libraries, we salvaged **27 novel and complete plastid genomes** across a wide range of plant taxa. Thus, we consider ChloroExtractor a valuable tool in the process of further unraveling plastid biology and evolution.



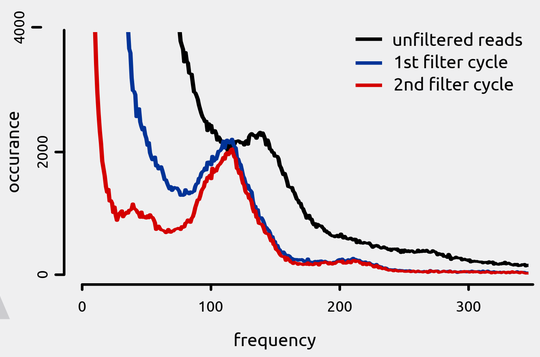
Host sequencing short read data

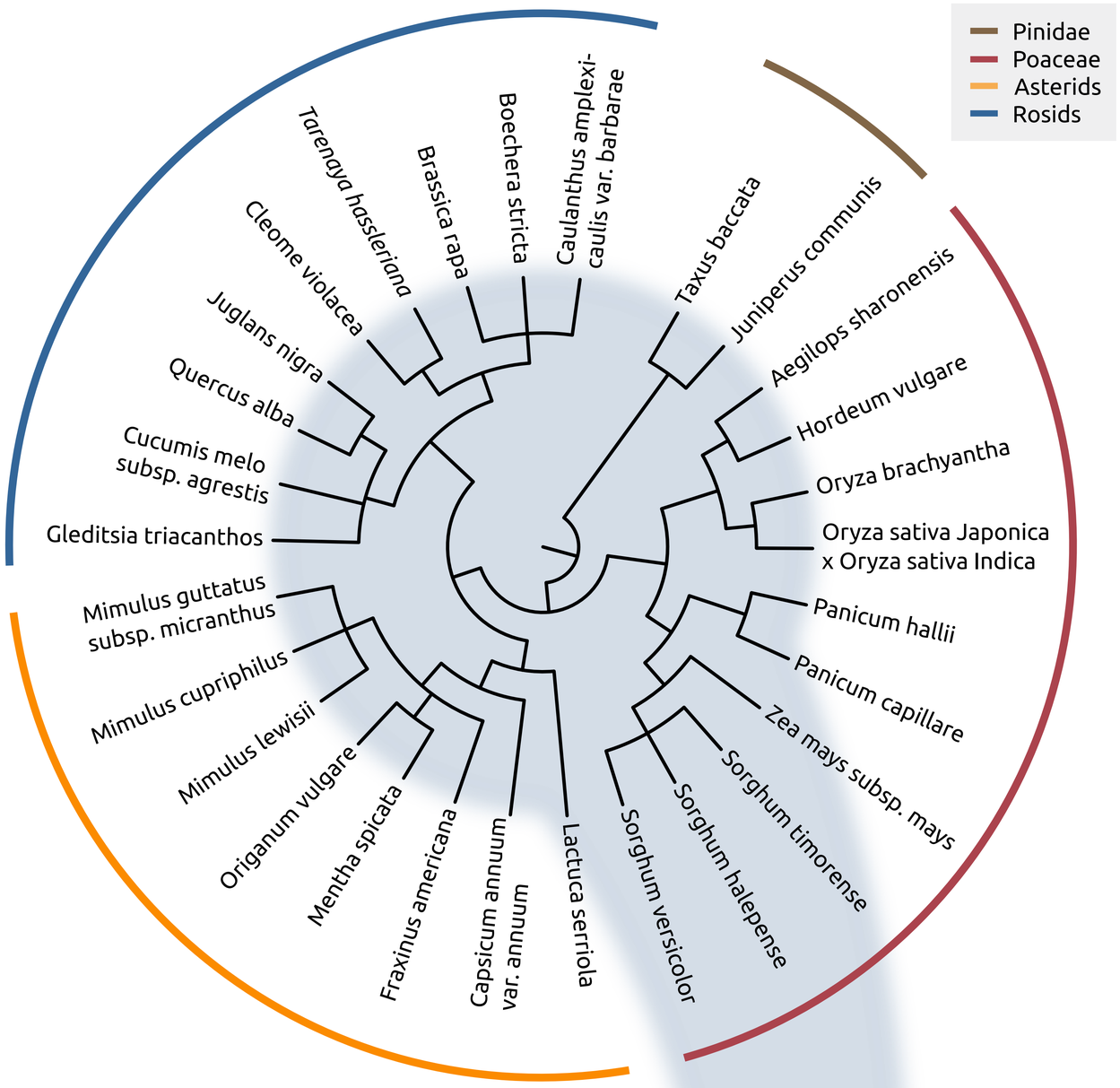


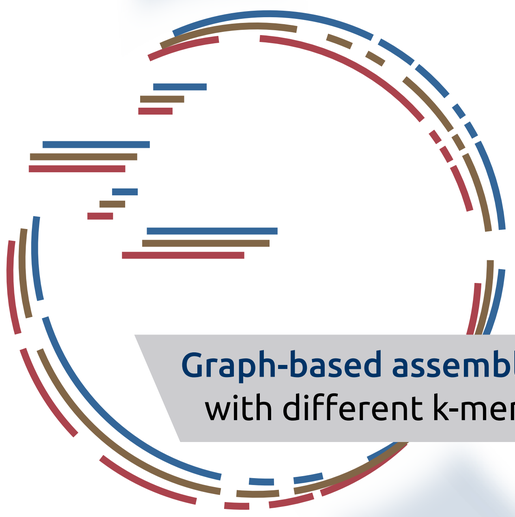
Scaling of data set based on **CDS cluster** coverage



Enrichment of plastid reads by **k-mer coverage**



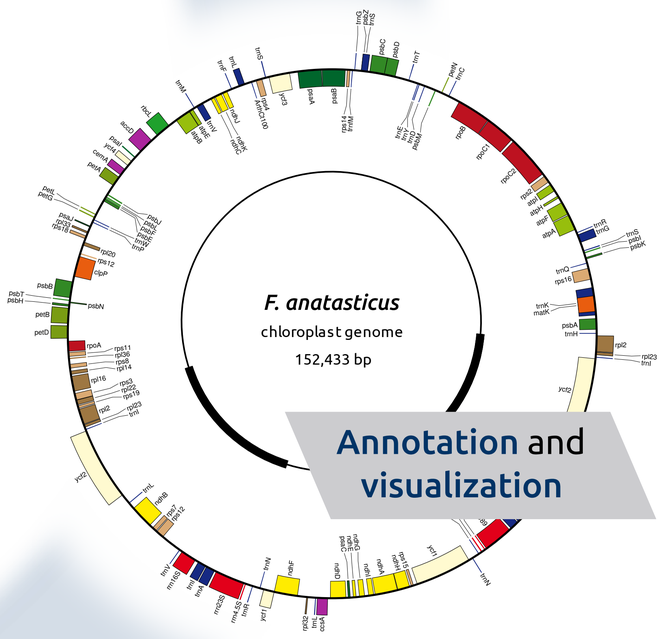




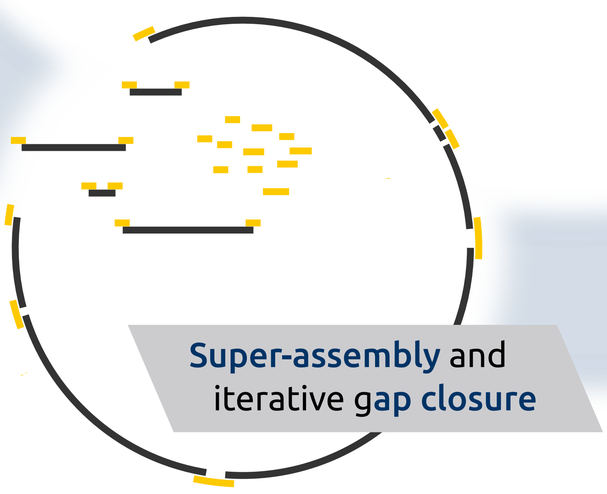
Graph-based assembly with different k-mer sizes

The relative content of plastid DNA is estimated from reads mapped with Bowtie2[1] onto clusters of plastid-gene coding sequences. The initial data set is scaled to an approximate 200-fold plastid coverage. Using k-mer frequencies counted with Jellyfish[2], the set is purged of host sequences by iterative removal of reads with low frequency k-mers.

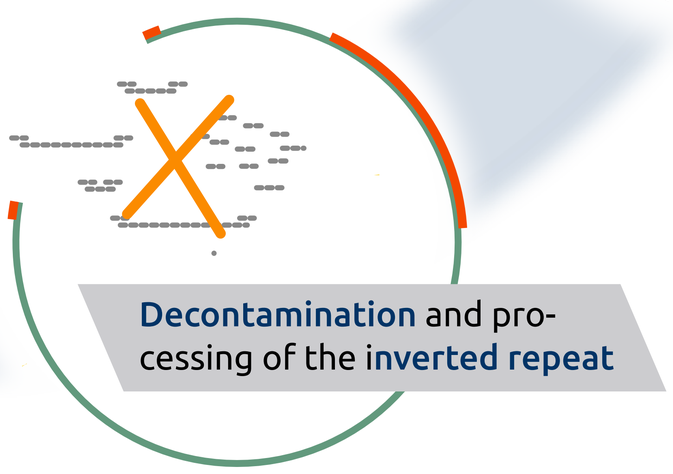
Primary assemblies are generated using Velvet[3] with k-mer sizes between 33 and 93. A contiguous super-assembly is calculated with Phrap[4]. Contig extensions and gap patches are obtained through a newly developed algorithm from paired end mapping information and local micro-assemblies. Contaminations are filtered by homology and the collapsed inverted repeat sequence is recovered. The final genome assembly is annotated with CpGAVAS[5] and visualized with OGDraw[6].



Annotation and **visualization**



Super-assembly and iterative g**ap closure**



Decontamination and pro-cessing of the i**nverted repeat**

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