Public data sets of *Arabidopsis thaliana( )* and *Oryza sativa(SRR1328237)* were downloaded from the National Center for Biotechnology Information (NCBI) database (https://www.ncbi.nlm.nih.gov) database used for the benchmarking study. Datasets were sequenced on the Illumina HiSeq 2000 platform and consisted of paired end reads with a read length of respectively 150 bp and 151 bp.

Reference genomes were retrieved from the NCBI. GenBank entry AP000423.1 was selected for the *Arabidopsis thaliana* assemblies, KM103369.1 for data set SRR1328237 of *Oryza sativa* as a reference genomes.

The three data sets were used for a benchmarking study comparing three selected assemblies. All tested assemblers were evaluated for execution time, memory usage, CPU usage, genome coverage and assembly accuracy. Comparing speed and system requirements was straightforward, since each assembler ran on the same servers and made use of the same input data set.

The quality indicators were measured relative to the corresponding reference as mentioned above.

Runtime, memory, cpu usage and accuracy given for different datasets

Data Set	Assembly Tool	Aiken Server			Tesla Server			Accuracy	
		Run Time	Memory Usage	CPU Usage	Run Time	Memory Usage	CPU Usage	Genome fraction	Missassemblies
Arabidopsis Thaliana (17 Mb)	Get-Organelle	4m 5s	0.276	6	3m 26s	0.26	12.0	100	0
	NOVO Plasty	23m 33s	0.100	99.40	28m 29s	0.10	102.0		
	Fast-Plast	9m 48s	0.100	99.6	18m 33s	0.1	60.7	100	0
Cinnamon (20 Gb)	Get-Organelle	469m 54s	1.100	99.8	405m 31	1.1	99.9	100	0
	NOVO Plasty	45m 32s	0.600	99.60	28m 29s	0.1	102.0		
	Fast-Plast	92m 35s	3.900	0.7	468m 48s	0.2	100.0	80.575	0

Only GetOrganalle gives the facility to user to change the number of threads. Other tools determine the number of threads by the tool itself and they use threads from a thread pool automatically according to their requirements.

Runtime, memory, cpu usage and accuracy given for different number of threads for GetOrganelle

Data Set	Assembly Tool	Num of threads	Aiken Server			Tesla Server			Accuracy	
			Run Time	Memory Usage	CPU Usage	Run Time	Memory Usage	CPU Usage	Genome fraction	Missassemblies
Arabidopsis Thaliana	Get-Organelle	1	4m 5s	0.276	6	3m 26s	0.260	12	100	0
		2	4m 36s	0.277	6	4m 55s	0.261	12	100	0
		3	3m 16s	0.276	5	2m 58s	0.260	14	100	0
		4	2m 2s	0.100	3	2m 5s	0.300	18	100	0
		5	2m 49s	0.100	5	3m 25s	0.200	21	100	0
		10	4m 5s	0.276	6	4m 59s	0.260	13	100	0

Comparison between reference based and DeNOVO assembly

Results for the assembly of the Oryza sativa chloroplast (dataset SRR1328237)

Performance	Without Ref	With Ref
Duration (min)	3m39.511s	3m10.811s
System+user time (min)	3m39.460s + 0m0.360s	0m0.694s + 3m8.376s
Memory %	0.10%	0.10%
CPU%	99.70%	99.01%
Total contigs	3	1
Average insert size	480 bp	480 bp
Total reads	279568	279568
Aligned reads	273234	268650
Assembled reads	248700	243944
Organelle genome %	97.73 %	96.09 %
Average organelle coverage	307	302