

Benchmarking computational efficiency of microbiome data containers

melt

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Overview

This report contains benchmarking results for the melt operation with common microbiome data containers in R/Bioconductor for the melt operation.

The tests utilize the following publicly available data sets. We thank the original authors for making these valuable data resources openly available. Check the links for details and original references:

- hitchip1006 (Lahti et al. 2014)
- SongQADData Song et al. (2016)
- GrieneisenTSDData Grieneisen et al. (2021) baboon data set

Data characteristics

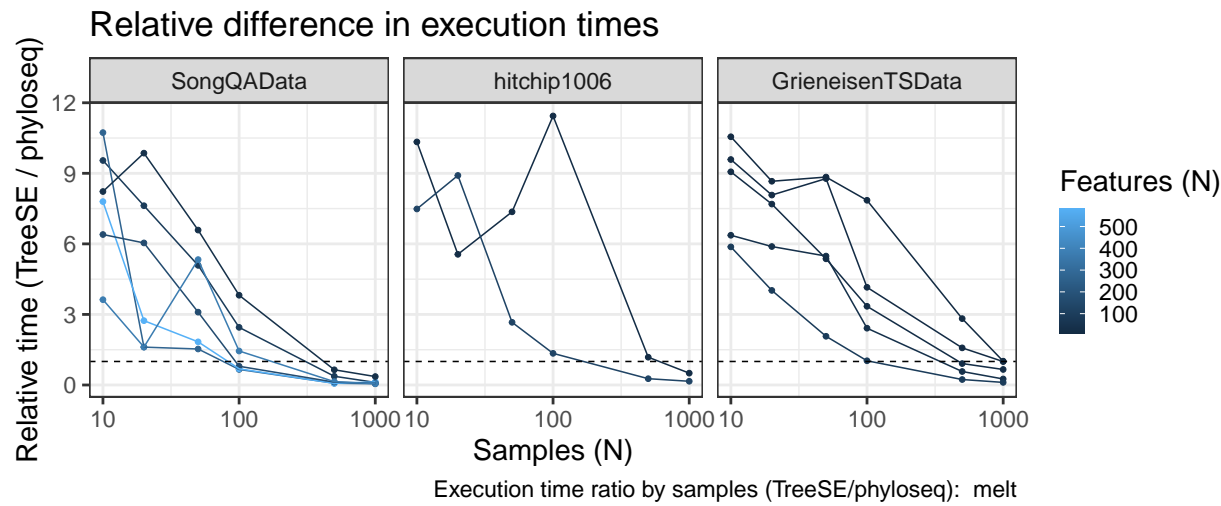
Full sample sizes by data set:

Dataset	N
hitchip1006	1151
SongQADData	1522
GrieneisenTSDData	16234

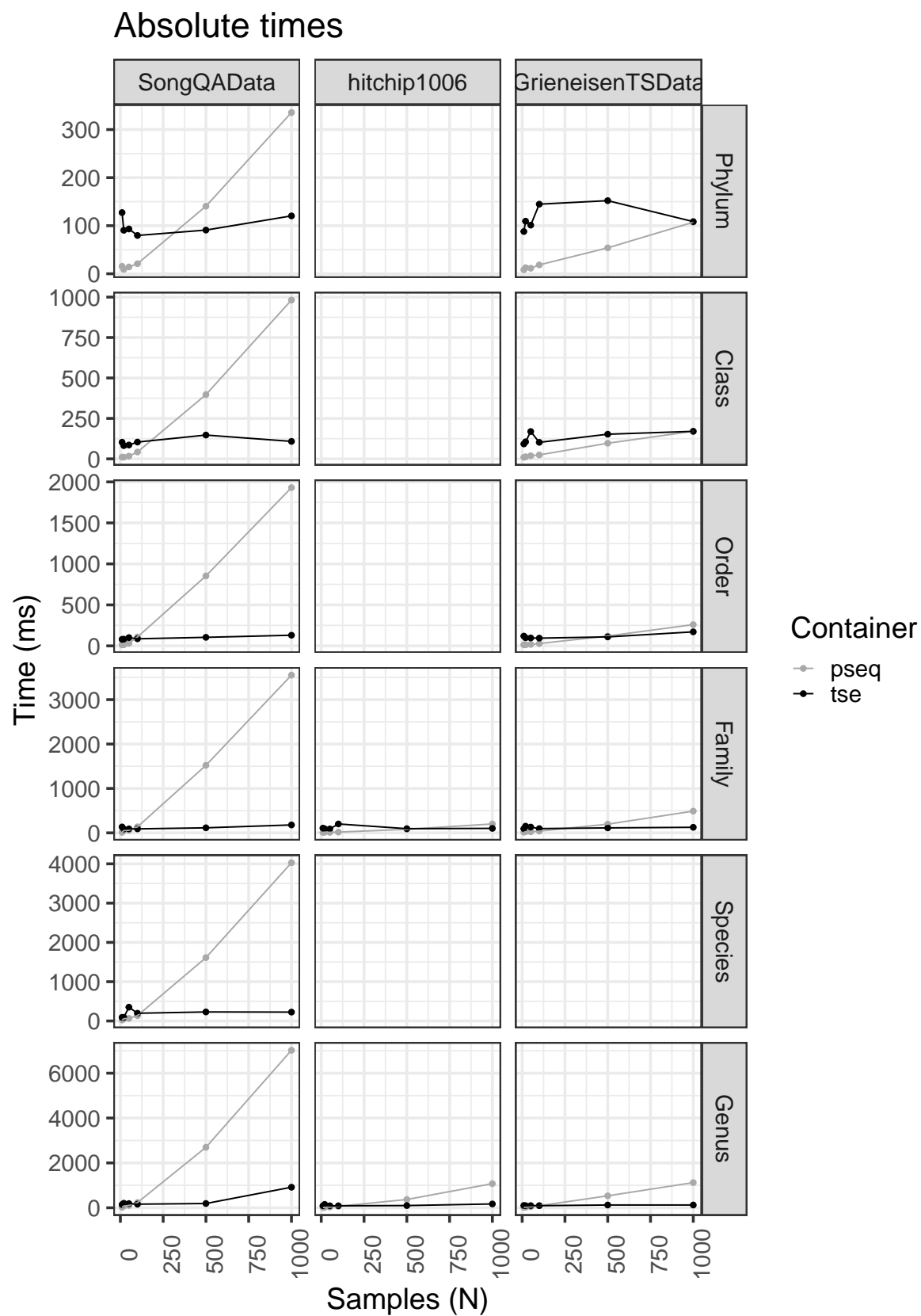
Feature counts by data set:

Rank	SongQADData	hitchip1006	GrieneisenTSDData
Phylum	39	0	12
Class	92	0	18
Order	167	0	24
Family	271	22	40
Species	375	0	0
Genus	583	130	92

Relative differences in execution time by sample size



Absolute execution time by sample size



Execution time by sample size: melt

Execution times vs number of features

