melt

Benchmarking computational efficiency of microbiome data containers

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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)
- SongQAData Song et al. (2016)
- GrieneisenTSData Grieneisen et al. (2021) baboon data set

Data characteristics

Full sample sizes by data set:

Dataset	N
AsnicarF_2021	1098
SongQAData	1522
GrieneisenTSData	16234

Feature counts by data set:

Rank	AsnicarF_2021	SongQAData	GrieneisenTSData
Phylum	15	39	12
Class	27	92	18
Order	42	167	24
Family	84	271	40
Genus	200	583	92
Species	639	375	0

Relative differences in execution time by sample size

Relative difference in execution times

Execution time ratio by samples (TreeSE/phyloseq): melt
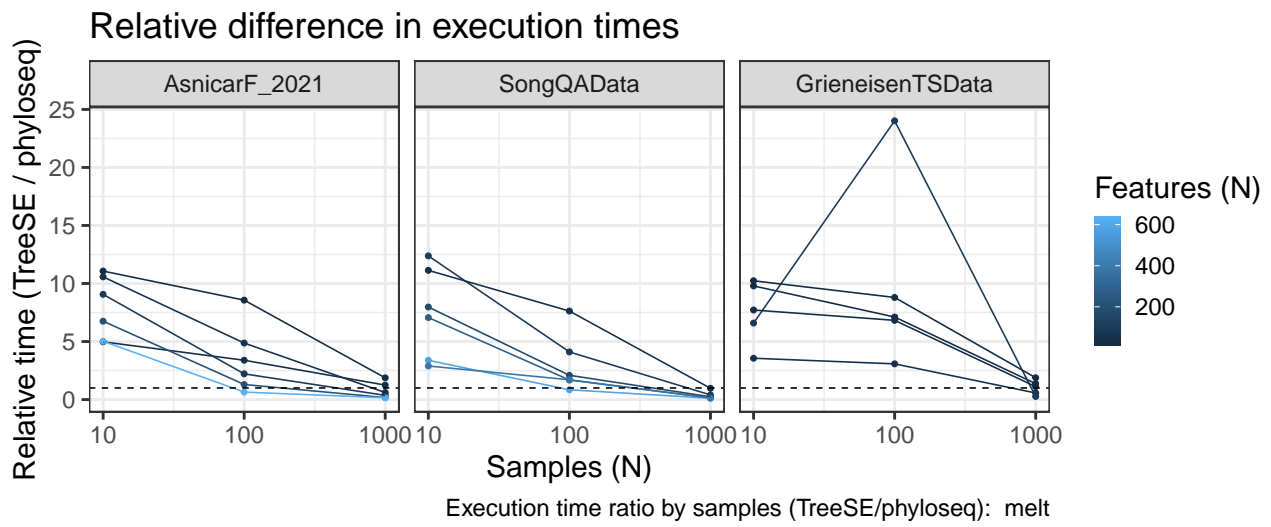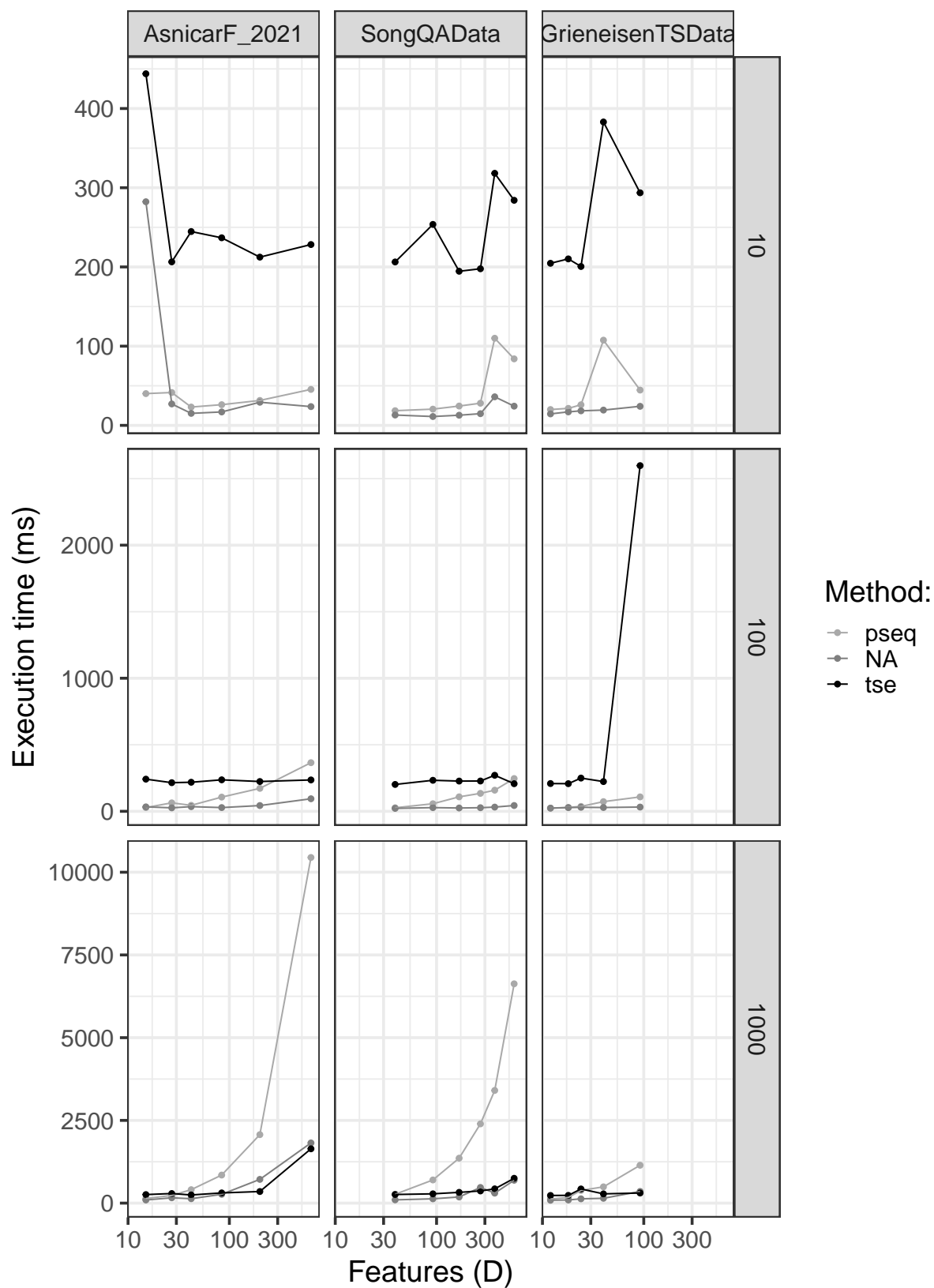
Absolute times
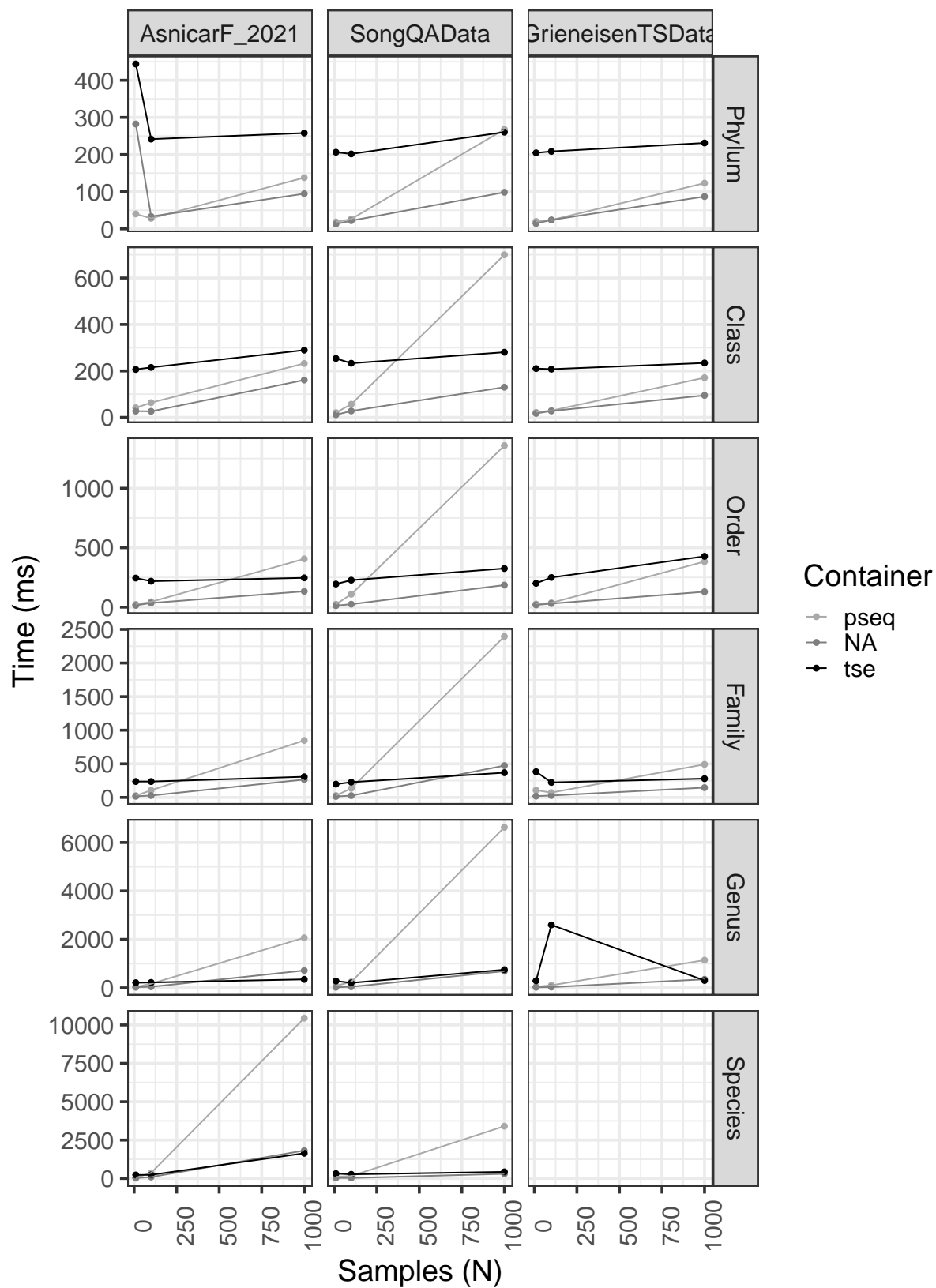
Execution time by sample size: melt

Execution times vs number of features

Feature count vs. execution time

Execution time by feature count: melt