# Benchmarking computational efficiency of TreeSE methods

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#### Data characteristics

Full sample sizes by data set:

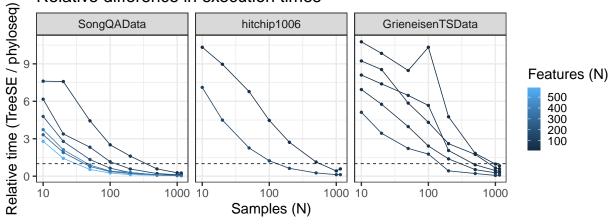
| Dataset                       | N     |
|-------------------------------|-------|
| hitchip1006                   | 1151  |
| SongQAData                    | 1522  |
| ${\bf Griene is en TSD at a}$ | 16234 |

Feature counts by data set:

| Rank    | SongQAData | hitchip1006 | GrieneisenTSData |
|---------|------------|-------------|------------------|
| Phylum  | 39         | 0           | 12               |
| Class   | 92         | 0           | 18               |
| Order   | 167        | 0           | 24               |
| Family  | 271        | 22          | 40               |
| Species | 375        | 0           | 0                |
| Genus   | 583        | 130         | 92               |

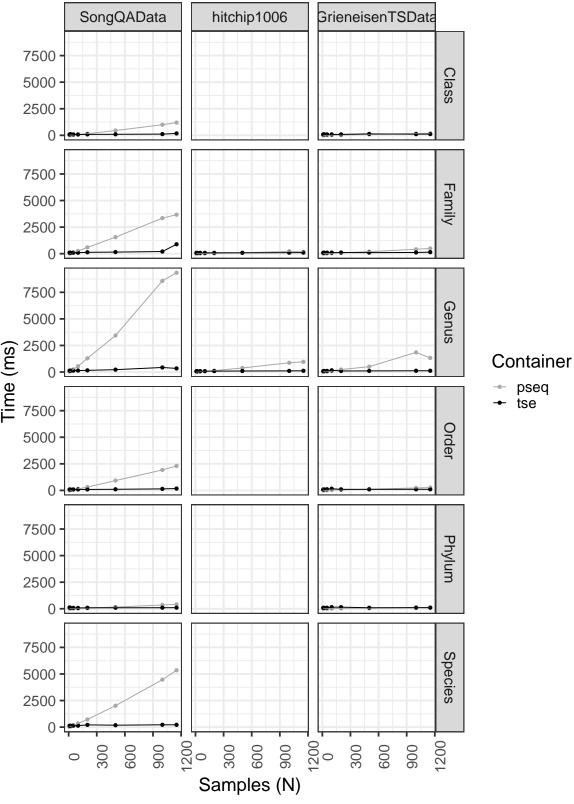
### Relative differences in execution time by sample size

#### Relative difference in execution times



### Absolute execution time by sample size

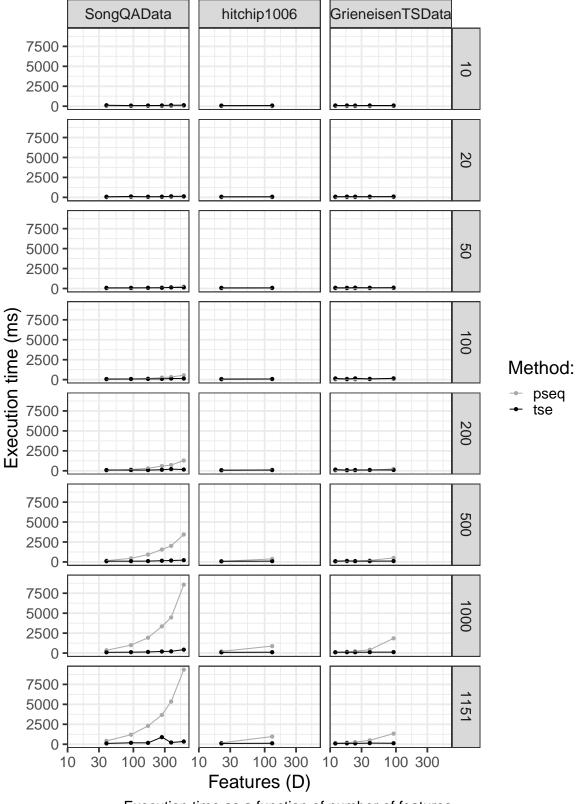
## Absolute times



Execution time comparison between TreeSE and phyloseq.

#### Execution times vs number of features

## Feature count vs. execution time



Execution time as a function of number of features