

Qlucore Omics Explorer calculation benchmarks

Qlucore Omics Explorer is much faster than other bioinformatic software solutions. Below are two benchmarks presented. They are static comparisons. In real life data analysis, the difference is even greater since changes to for instance filter levels which changes the input requires full recalculation in R where Qlucore Omics Explorer (QOE) only will recalculate as little as possible. Hence, the dynamic behavior of QOE will be many times faster than the already impressive static performance.

STATIC PCA CALCULATIONS:

30k features and 150 samples.

Set-up in R:

```
X = matrix(rnorm(30000*150),30000)

df = as.data.frame(X)

system.time({ F = prcomp(df, scale=TRUE, rank=3) })
```

The same calculation in Qlucore is **77 times faster**.

STATIC T-SNE CALCULATIONS

30k features and 150 samples.

Set-up in R:

```
X = matrix(rnorm(30000*150),150)

system.time({ T = Rtsne(X, dims=2, pca_scale = TRUE, perplexity = 30, exaggeration_factor = 1) })
```

The same calculation in Qlucore is **13 times faster**.

BACKGROUND

The tests are run on the same computer. Qlucore Omics Explorer version 3.6