
scMerge

- ▶ C++ performance issues + speeding up SVD
- ▶ Majority of the functions (exported or otherwise) does not have testthat checks.
- ▶ Documentations of the package, inconsistent naming.
- ▶ Fixing namespaces, especially with R-devel and BioC-devel.
 - ▶ kBET is only a GitHub package.
 - ▶ M3Drop changed their output in the BioC-devel branch.
- ▶ Check time limit and data size issue as required by BioC.

Of course, none of these matters if God hates you

Matrix multiplication of a 20000 by 100 matrix

Machine	%*%	RcppEigen
MacBook	755ms	442ms
Verona	730ms	457ms
Savona	389ms	415ms*

- ▶ You are at the cutting edge of R and BioC development. Anything that could go wrong will go wrong.
- ▶ GitHub issues are your only hope, forget about textbooks.
- ▶ This performance issue can be resolved by running `devtools::load_all()` and then Clean & Rebuild in RStudio. Don't ask me why.

<https://github-history.netlify.com/SydneyBioX/scMerge/blob/master/docs/articles/scMerge.html>