

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>

How to avoid this in the future

- ▶ Namespace is the most common issue: write `dplyr::mutate()` rather than `mutate()`. Especially when mixing BioC and tidyverse.
- ▶ Always think about how to use `testthat` to check the correctness of the functions on the spot, not at the end before you package is about to be submitted.
- ▶ Read Hadley's books or consult your friend (aka Mark/Weichang) on C++.
- ▶ Don't build your package in a Dropbox folder.