## scMerge package review

## **NAMESPACE**

 It's easier to import specific functions in the NAMESPACE of large packages like BiocParallel.

Thank you for this comment. We have implemented this.

## R

- Don't use "print" as an end user message in your code.
- End-User messages
- •
- message() communicates diagnostic messages (e.g., progress during lengthy computations) during code evaluation.
- warning() communicates unusual situations handled by your code.
- stop() indicates an error condition.
- <u>cat()</u> or print() are used only when displaying an object to the user, e.g., in a show method.

Thank you for this comment. We have implemented a verbose option to capture most intermediate print outs. Where critical information is needed for diagnose the <a href="scMerge">scMerge</a> procedure, we invoked the <a href="mailto:message">message</a>() option.

- The recommended length of a function in BioC is 50 lines. This has the advantage of easy tests and maintenance.
- The package reviewer was 10 times easier than any paper reviewer.
- Kevin's Daily Ranks are genuine issues that I ran into. You will have your own and I can't help you.

## testthat

- A "tests" folder is set up with a collection of test scripts.
- The hardest part is to make sure your tests does not take too long to run, because BioC enforces 10 minutes check time and 5 minutes build time.

```
context("Test fastRUVIII")
set.seed(12345)
L = ruvSimulate(m = 400, n = 500, nc = 400, nCelltypes = 3, nBatch = 2, lambda = 0.1, sce = FALSE)
Y = L$Y
M = L$M
ctl = L$ctl

old = ruv::RUVIII(Y = Y, M = M, ctl = ctl, k = 20)
improved1 = scMerge::fastRUVIII(Y = Y, M = M, ctl = ctl, k = 20, fast_svd = FALSE)
improved2 = scMerge::fastRUVIII(Y = Y, M = M, ctl = ctl, k = 20, fast_svd = TRUE, rsvd_prop = 0.3)
expect_equal(old, improved1)
expect_equal(improved1, improved2, tol = 0.01)
```