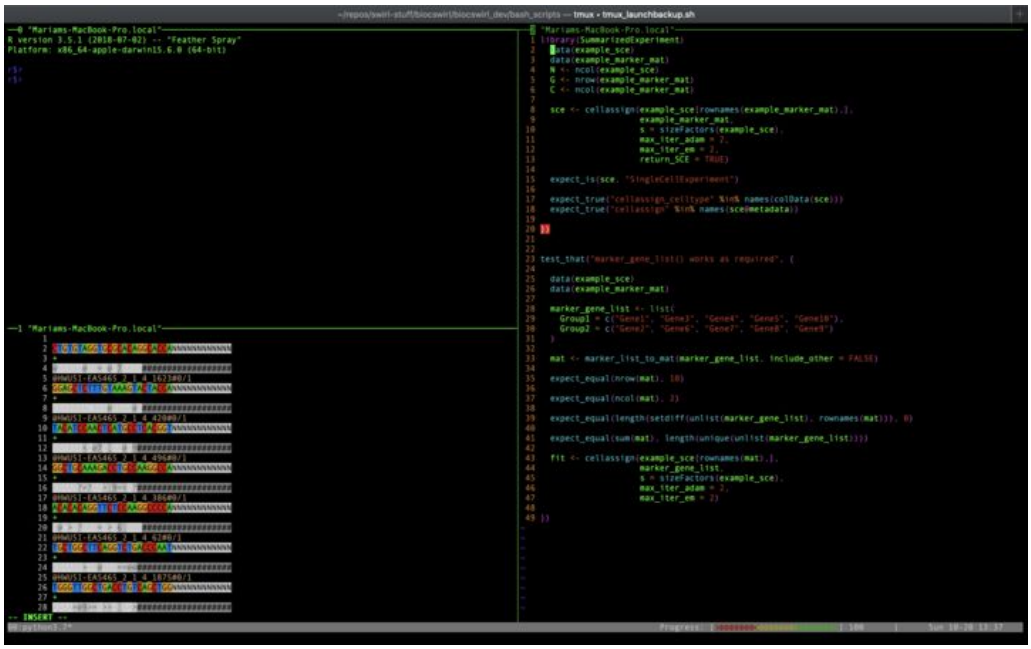
BIOINFORMATICS TUTORIALS & TOOLS

The interface (BiocTerm) and R package (BiocSwirl) can be used independently of each other but are best used together for people who are interested in making the most of their learning experience.

BiocTerm

BiocTerm is a standalone terminal application that acts as the ideal interface for those conducting bioinformatics as it integrates our custom editor, biovim (a vim installation bundled with bio plugins), radian (an r console), and tmux (our customized terminal wrapper) in a contained instance. Our interface supports R, Bash, and vim. It is ideal for multi language workflows.

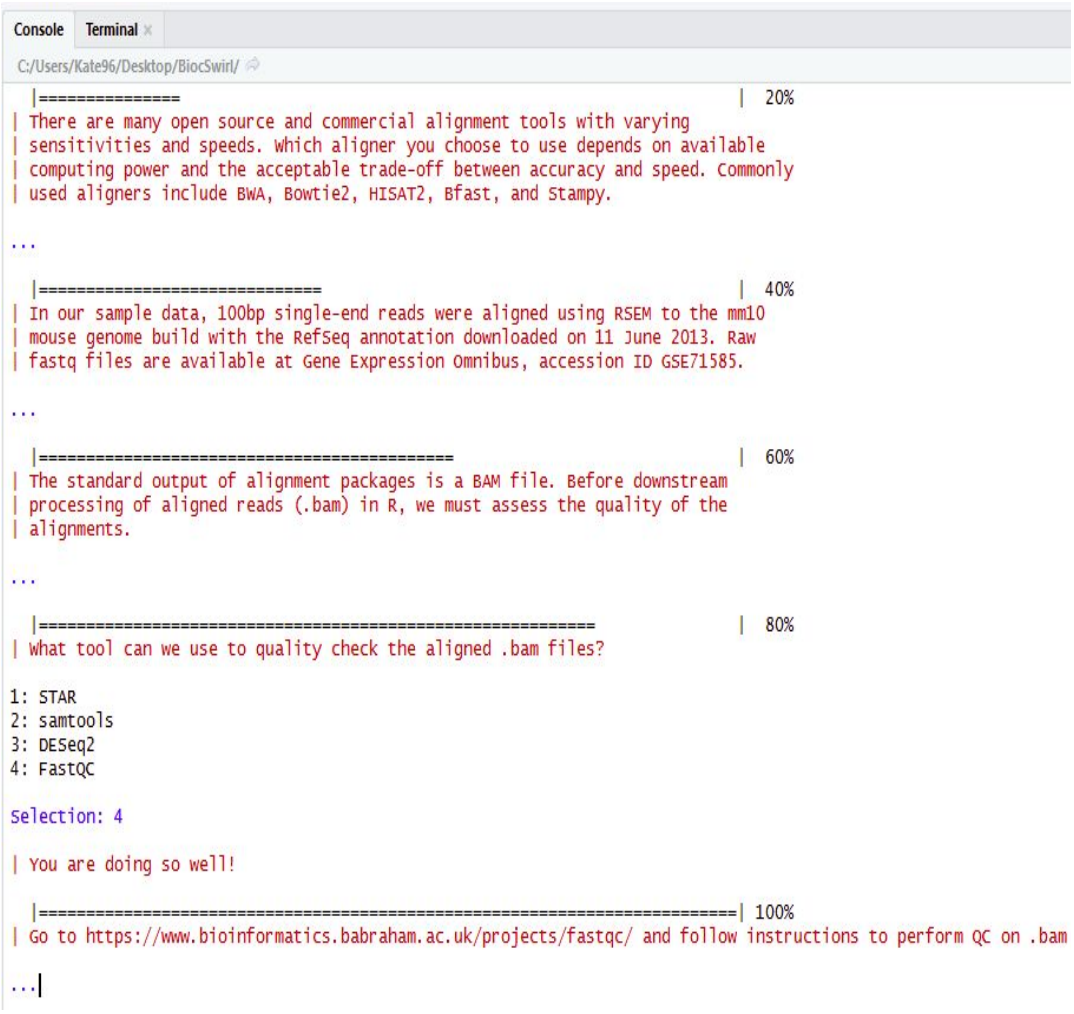
+ Automatically saves session info + restores and generates a log
+ Multiple panes for native file viewing, has robust syntax highlighting that is ideal for bioinformaticians such as BioSyntax or Radian
+ Tmux.conf file and plugin capabilities for vim and tmux allow for high configurability depending on what your needs are
+ Comes with our editor biovim, a powerful editor that makes reading gene files easy

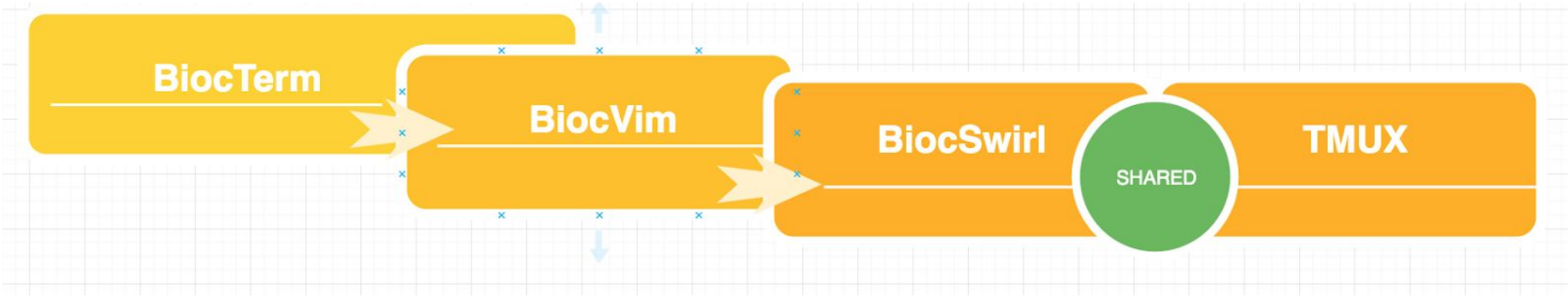


BiocSwirl

Our swirlify() R package and course installation client, used to deliver our interactive courses and can be run within R console. Biocswirl aims to make learning bioinformatics concepts hands on through the development of course material that takes you through the common bioinformatics workflows.

+ Is easily configurable and breaks down complex bioinformatics workflows into simple, easy to chew steps. Includes standardized datasets to work with and checks your work
+ Highly emphases good coding practices, open science, reproducibility, and
+ YAML file format and templates make it easy to update a workflow to match current best practices and create/communicate your own workflows for within lab




BiocTerm
BiocVim
BiocSwirl
SHARED
TMUX