

Choices

You've already got your data.

- you've chosen the sequencing platform
- I wouldn't choose 454 anyways ;)
- ... where to go from here?

Let's start with hardware.

- own desktop
- own server
- own cluster
- shared cluster or grid
- cloud
- SaaS (Galaxy)

Operating systems.

- MS Windows (can get UNIX;)
- Linux
- Mac OS X
- OS specific tools (Adobe, ...)

Tools.

- commercial vs. open source
- GUI vs. CLI
- size of community vs. organism specificity
- active development

Own code.

- R / Perl / Python / C++
- general readability
- documentation culture
- publish vs. keep for yourself
(GitHub, GNU, Linux)

My setup.

- MS Windows as a desktop
- Linux for work, shared folder to MS Win
- MetaCentrum for demanding tasks
- Win+Linux: Python, bash
- Win: Total Commander, Cygwin
- Win: R + RStudio + ggplot2 for graphs
- Win: Tableau for quick graphs
- Win: Adobe for DTP
- Win: Zotero for all literature