Python AND R

- **be pragmatic!!**
- use a suitable tool you feel comfortable with and will work with dataset your size

- **read documentation!!**
- in scRNAseq it is normal that you go in circles
  qc→normalise→dimred→cluster→qc→dimred→cluster
  qc→normalise→dimred→cluster→split into subsets→ dimred→cluster

- for repeated analyses build/adapt workflows (snakemake, nextflow)

(many already available, for example https://github.com/wtsi-hgi/yascp - documentation in a separate branch)

“Constant improvement is better than delayed perfection” (Mark Twain)