Single cell RNA sequencing data analysis
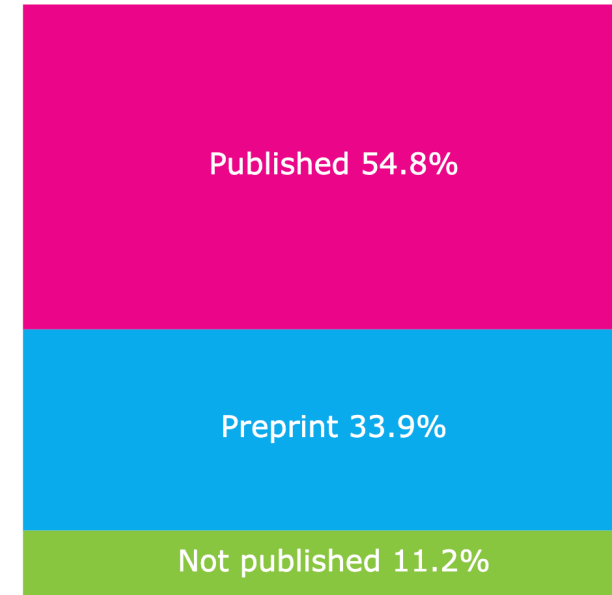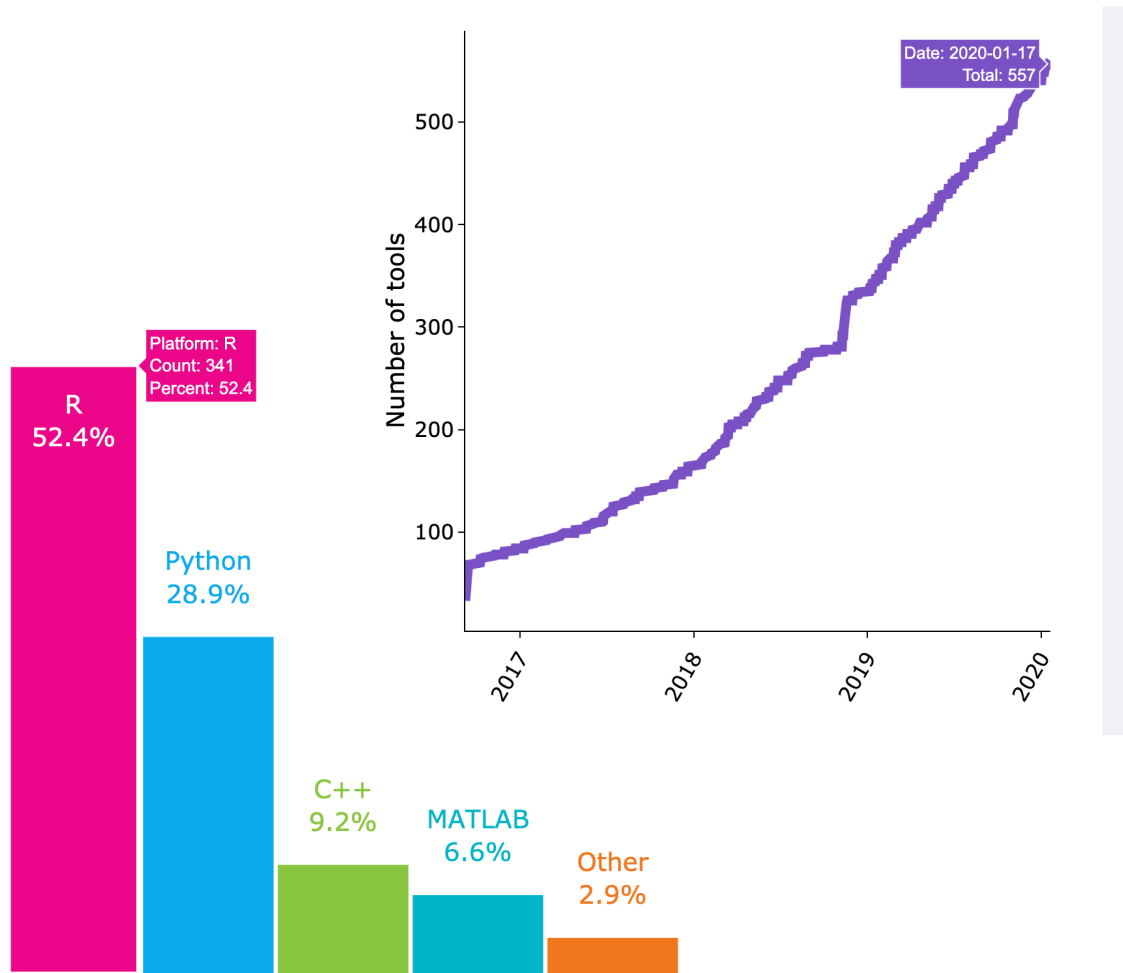# Practical exercises
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Many available tools for analysis

https://www.scrna-tools.org/

Three main pipelines for analysing single cell data:

- ## Seurat:
  - R based, centered around Seurat objects.
  - Mainly developed for droplet based data
  - Easy to use, recommended for R beginners

- ## Scran:
  - R based, sentered around SingleCellExperiment objects
  - Has more different statistical methods

- ## Scanpy:
  - Python based
  - Does not yet have all the functionality of the R based tools
  - Handles large datasets better.

The exercises

Tutorial	![R] Seurat	![R] Scater/Scran	![Python] Scanpy
Quality Control	Seurat_qc	Scater_qc	ScanPY_qc
Dimensionality reduction	Seurat_dr	Scater_dr	Scanpy_dr
Data integration	Seurat_integr	Scater_integr	Scanpy_integr
Clustering	Seurat_clust	Scater_clust	Scanpy_clust
Differential expression	Seurat_dge	Scater_dge	Scanpy_dge
Trajectory inference	Slingshot_ti		PAGA_ti

https://nbisweden.github.io/workshop-scRNAseq/exercises

The datasets

- Periferal blood mononuclated cells (PBMC) with 10x Genomics
  - One dataset with version2 chemistry
  - One dataset with version3 chemistry
  - One dataset with version3 chemistry combined with protein detection (we will only analyse the expression data)

- Should contain the main immune celltypes: T-cells, B-cells, NK-cells, monocytes and dendritic cells

Installation of all packages

- We have created a conda environment for the course that should contain all packages you need for the exercises

- However, for slingshot trajectory inference lab, there is an additional conda environment that needs to be installed.

- If you chose to instead work with standard R installations, you can use the list of required packages in the environment file and install them on your own.

The code:

- All code for the exercises is available as R-markdown documents, or jupyter notebooks in the folder:

  workshop-scRNAseq/labs/compiled/

- Please report to us if you find any errors in the code!

Practical exercises

- Everyone works in very different pace. Focus on one of the pipelines first. If you have time left over, you can also try out the other ones.

- Hopefully everyone will have time to finish the labs in the allocated time, if not, there is extra time on Thursday to also finish labs and get help with that.

Troubleshooting

- We have put up a FAQ page where we will try to put up common problems & questions

- It is important that you learn how to troubleshoot yourselves.
  - Look at your error messages, perhaps the answer is there?
  - If not – Google is your best friend! Forums like Seqanswers, Stackexchange, Bioconductor support forum and some specific forums for each package may have the answer.

- TAs are there to answer any questions and give suggestions, but we may not always have the answer.