Single cell RNA sequencing data analysis,
31 March – 3 April, 10 April, 2025

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National Bioinformatics Infrastructure Sweden (NBIS)

Consultations

Future compute infrastructure

Compute projects
Software and databases

Data publishing and open science
Secure sharing of sensitive data

Training

Efficient tools and workflows

Research support

Need help from NBIS?

- Drop-in sessions at all universities (now online) 14.00 Tuesdays
- Consultations
- Courses
- Support:
  - Long-term support (Peer reviewed)
  - Fee-for-service support, hourly fee
  - Partner projects
- Data management
- Advisory program

www.nbis.se

Who are we?

Course leaders

Jennifer Fransson

Susanne Reinsbach

Åsa Björklund

TAs

Teachers

Fariba Roshanzamir

Nima Rafati

Yuan Li

Henrik Gezelius

Nikolay Oskolkov

Stefan Ebmeyer

Aditya Singh

Snaevar Sigurdsson

Paulo Czarnewski

Jakub Westholm

Jason Hill

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SciLifeLab

Practical information - Zoom

- Please keep your cameras on unless you are having severe network issues
  - Both for lectures and exercises.
- Ask questions:
  - Feel free to unmute and interrupt during lectures!
  - Or by raising your hand in Zoom.
  - Or write in the slack channel #lectures.
- We will be recording the lectures for future reference, your voice may be included.
  - If you do not want your voice to be public, let us know and we can cut it out.

Practical information - Zoom

- For exercises we will have 4-5 people in each breakout room.
- We will post a survey on slack where we want to know which toolkit you wish to practise on to create the groups.

Practical information - Slack

- Communication around the course will be handled via slack.

- Please add picture and brief description

- Channels:
  - #general – general information about the course
  - #lectures - questions about lectures
  - #exercises – questions during exercises
  - #precourse – questions about the installations
  - #roomX - one for each breakout room for exercises.

Practical information

- All code via our github page:
  https://github.com/NBISweden/workshop-scRNAseq
  Use folder compiled/labs!!

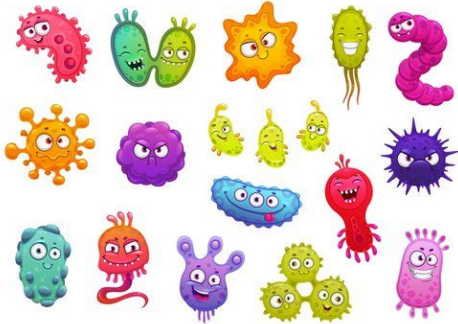- Lunches and coffee breaks - please take a minute to step away from the screen!

Course credits

NBIS as an organization cannot give out course credits, only the Universities can.

With your course certificate you should contact the person responsible at your department and usually there is no problem getting credits for the course.
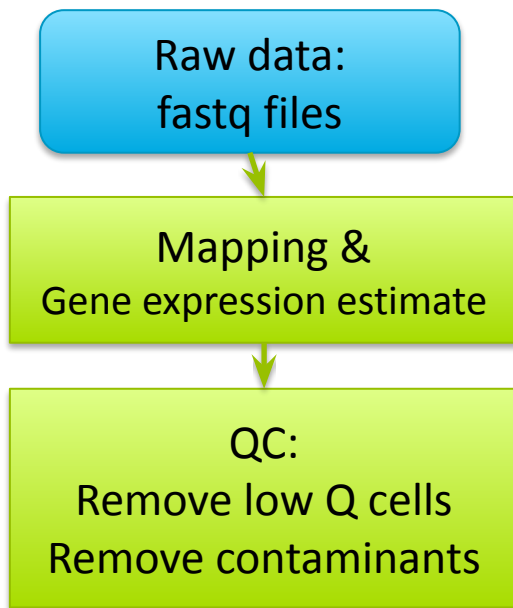
scRNA-seq overview

scRNA-seq analysis overview

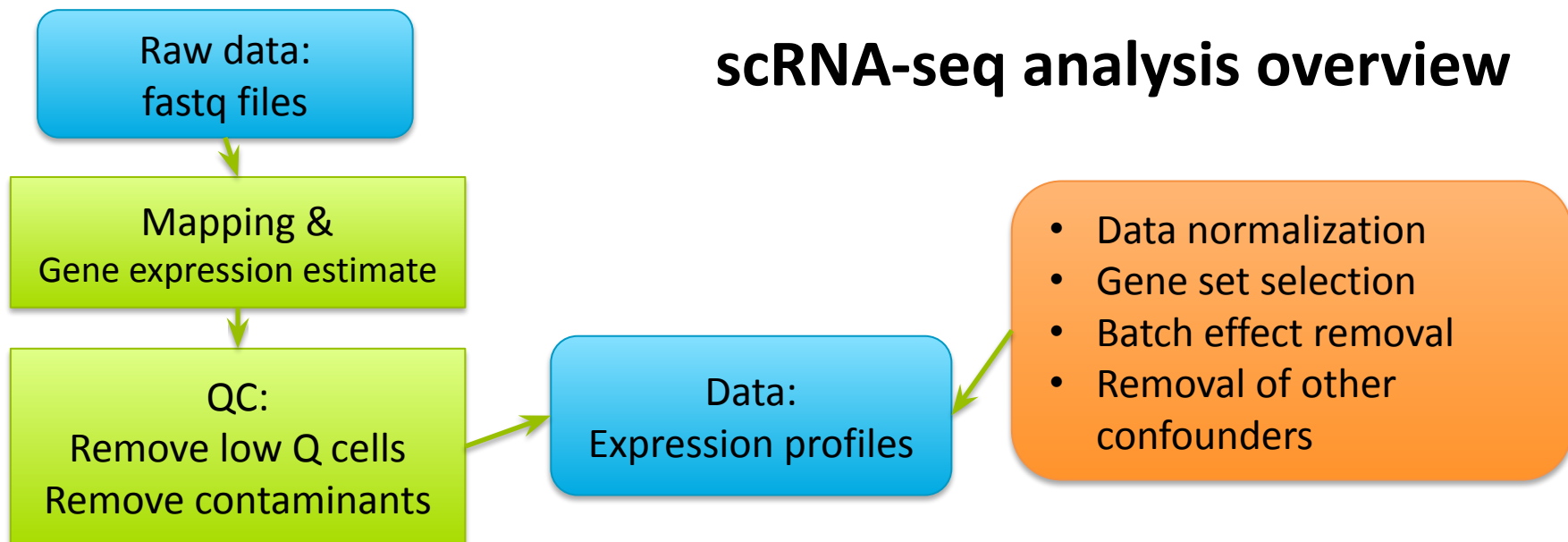Raw data:
fastq files

↓

Mapping &
Gene expression estimate

- Cellranger (10x)
- Dropseq - Alevin/Kallisto Bustools (transcriptome only)
- Dropletutils
- nf-core/scrnaseq
- zUMIs
- ….

scRNA-seq analysis overview

Raw data:
fastq files

Mapping &
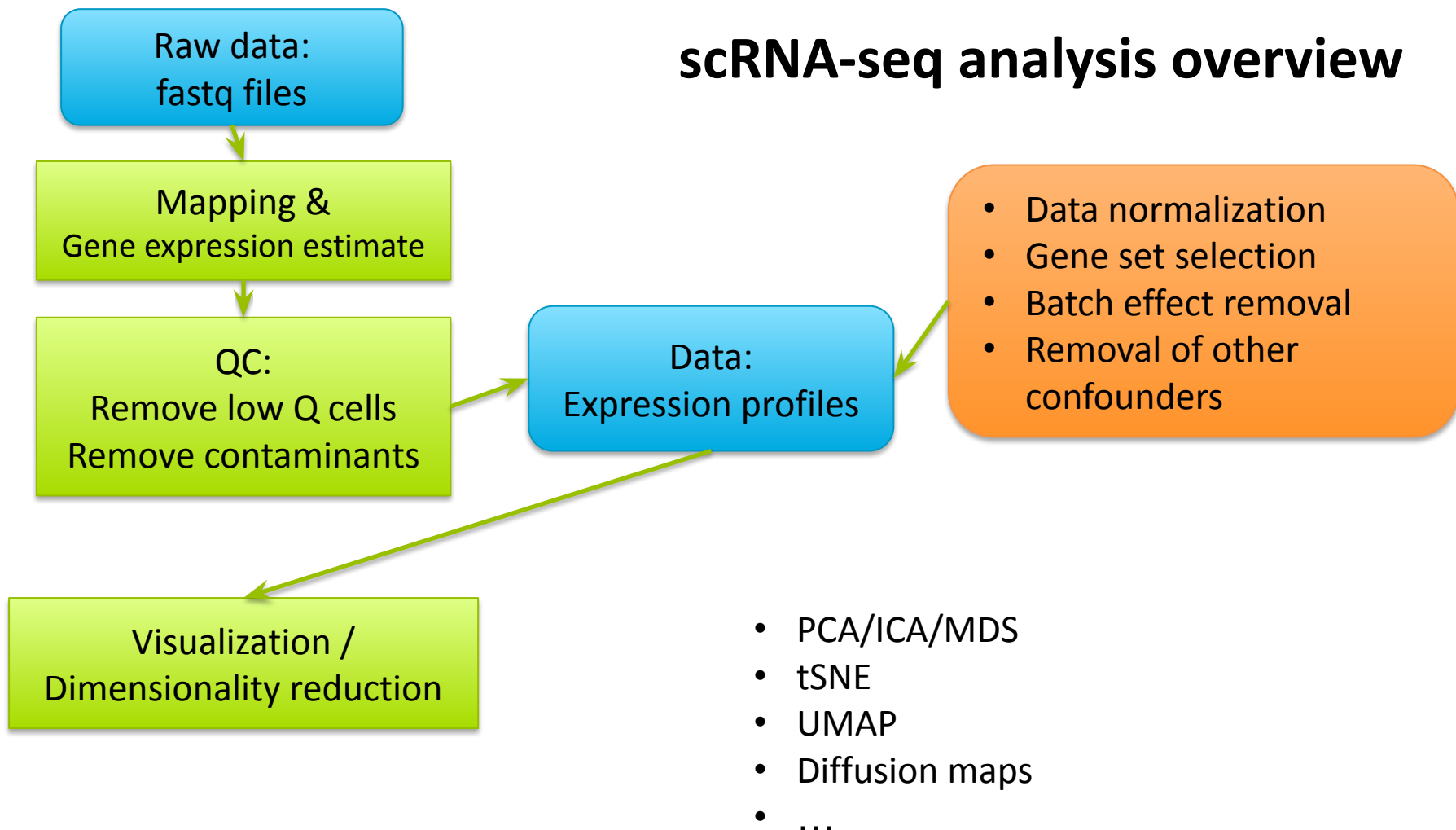Gene expression estimate

QC:
Remove low Q cells
Remove contaminants

- Low/high number of reads
- Low/high number of genes
- Intronic reads
- Mitochondrial content
- Mapping stats
- Filter genes
- …

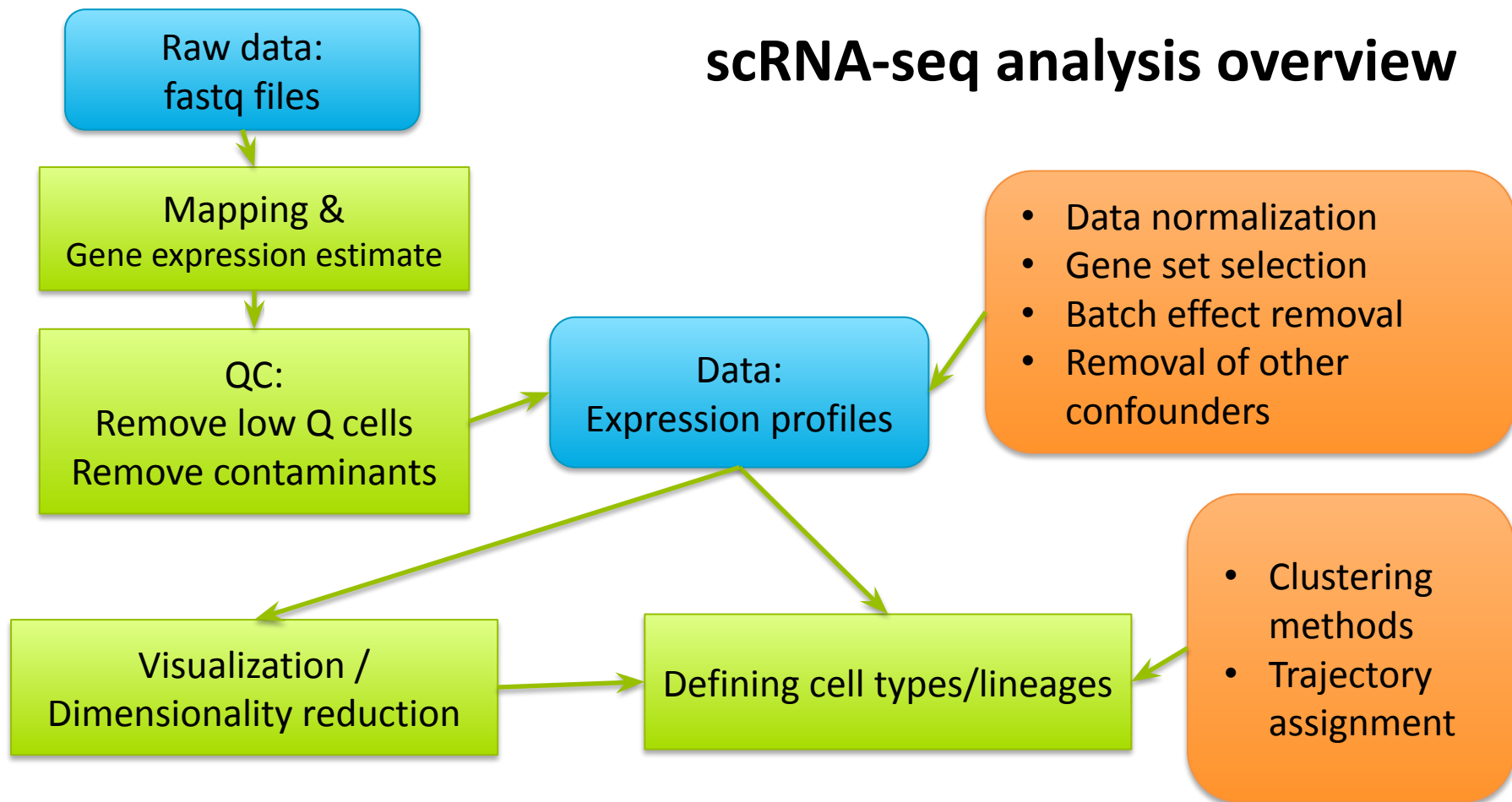# scRNA-seq analysis overview
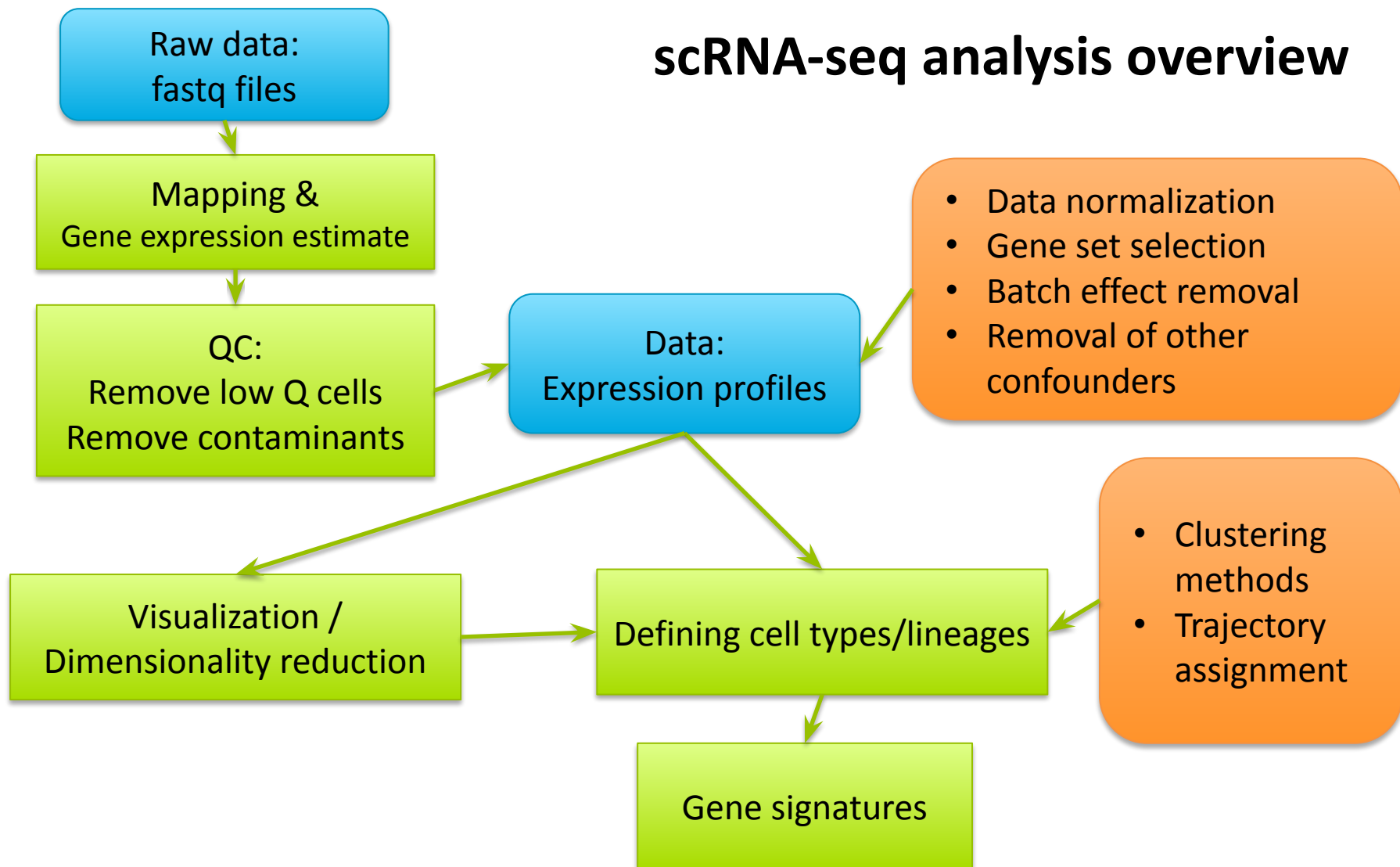
- Raw data: fastq files
- Mapping & Gene expression estimate
- QC: Remove low Q cells / Remove contaminants
- Data: Expression profiles
- Data normalization
- Gene set selection
- Batch effect removal
- Removal of other confounders

scRNA-seq analysis overview

Raw data:
fastq files

Mapping &
Gene expression estimate

QC:
Remove low Q cells
Remove contaminants

Data:
Expression profiles

- Data normalization
- Gene set selection
- Batch effect removal
- Removal of other confounders

Visualization /
Dimensionality reduction

- PCA/ICA/MDS
- tSNE
- UMAP
- Diffusion maps
- …

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scRNA-seq analysis overview

Raw data: fastq files

Mapping & Gene expression estimate

QC: Remove low Q cells Remove contaminants

Data: Expression profiles

- Data normalization
- Gene set selection
- Batch effect removal
- Removal of other confounders

Visualization / Dimensionality reduction

Defining cell types/lineages

- Clustering methods
- Trajectory assignment

Many available tools for analysis

2025

2021

https://www.scrna-tools.org/
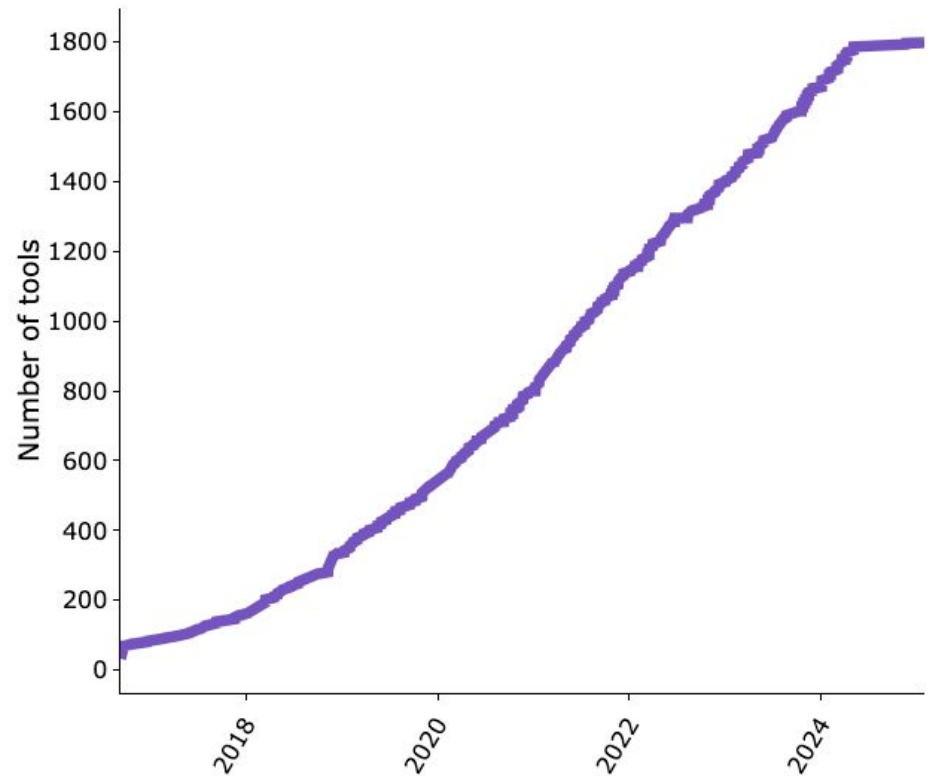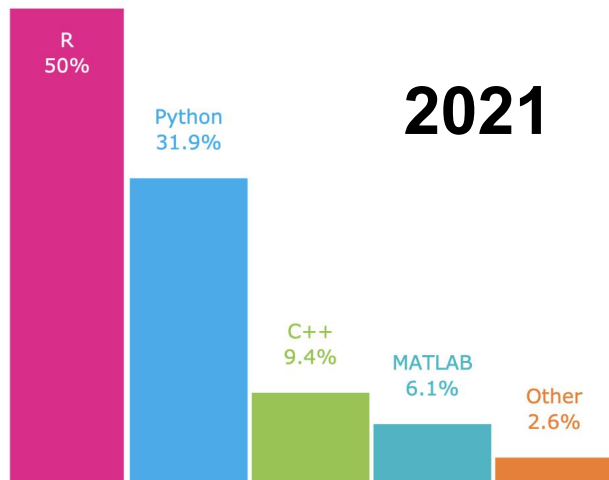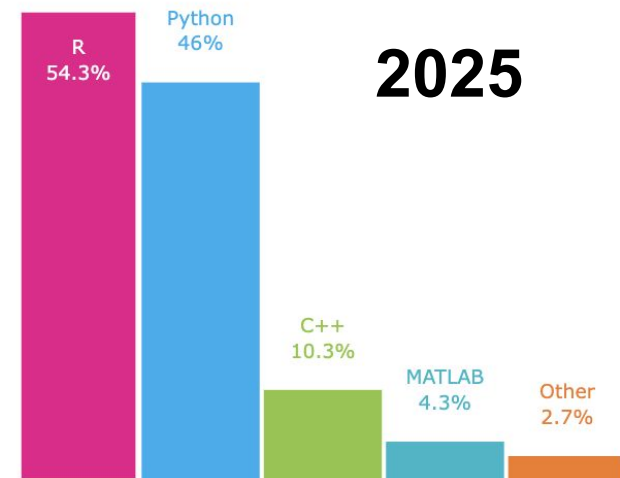
In this course

- We have selected a set of tools/pipelines that we think are relevant for most cases.

- Cannot cover all tools that are out there.

- Use your common sense to select methods for your problem.

Bring your own data - Thursday April 10th

You can work on any dataset of your choice - your own or a public dataset from a tissue that is relevant to your research.

Try out some of the methods you have worked with in the exercises and we will be there to guide you through.

More detailed information will come on the April 3rd.

Schedule

https://nbisweden.github.io/workshop-scRNAseq/home_schedule.html

Have links to pdfs with slides, but some are from last year and will be updated as we give the lectures.

Scilifelab serve account

If you have not requested an account yet, please let us know immediately via slack and we can inform the Serve staff to speed up the process.

Also, Serve is still in beta testing mode, so we want everyone to have Docker installed as an emergency backup solution.

For BYOD the allocated resources may not be enough