



Single cell RNA sequencing data analysis, 12 Feb – 16 Feb, 2024

Åsa Björklund, Roy Francis & Susanne Reinsbach

National Bioinformatics Infrastructure Sweden (NBIS)

Consultations



Future compute infrastructure



Compute projects
Software and databases



Training



Data publishing and open science
Secure sharing of sensitive data



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



Roy Francis



Susanne Reinsbach



Åsa Björklund

TAs



Fariba Roshanzamir



Rasool Saghaleyni



Yuan Li



Stefan Ebmeyer



Massimiliano Volpe

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

Practical information

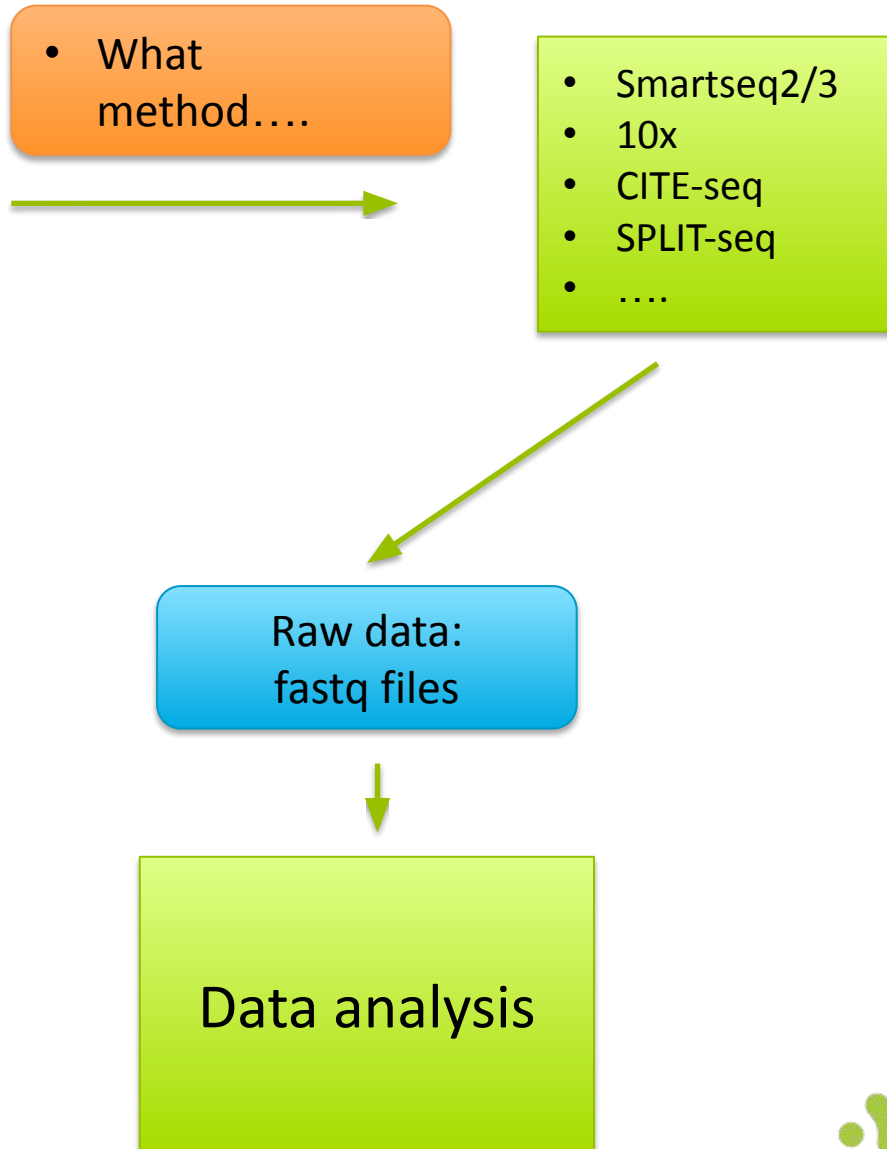
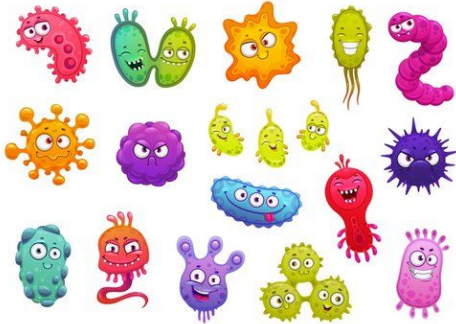
- All code and links to lectures etc. via our github page: <https://github.com/NBISweden/workshop-scRNAseq>
- Lunches at [Bikupan](#) on campus – we have reserved tables. Buffet. Just queue up and say that you are from the course.
- Course Dinner on Tuesday – [Restaurant Meze](#). Please fill in in the attendance sheet today if you are joining the dinner or not.
- Building map: <https://link.mazemap.com/zZ7Vt1cP>

Course credit

NBIS as an organization cannot give out course credits only 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

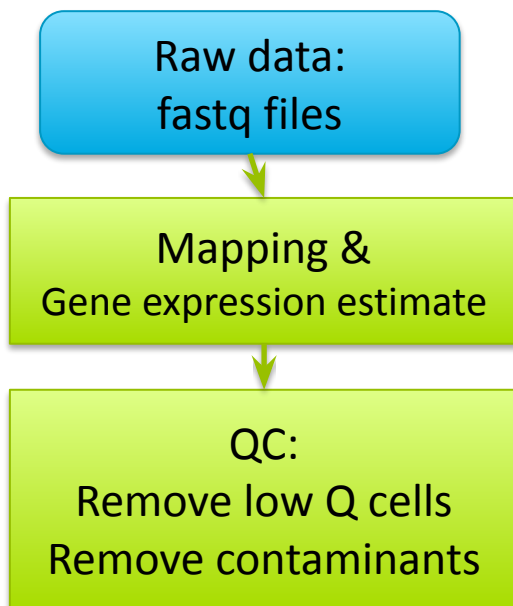
Raw data:
fastq files



Mapping &
Gene expression estimate

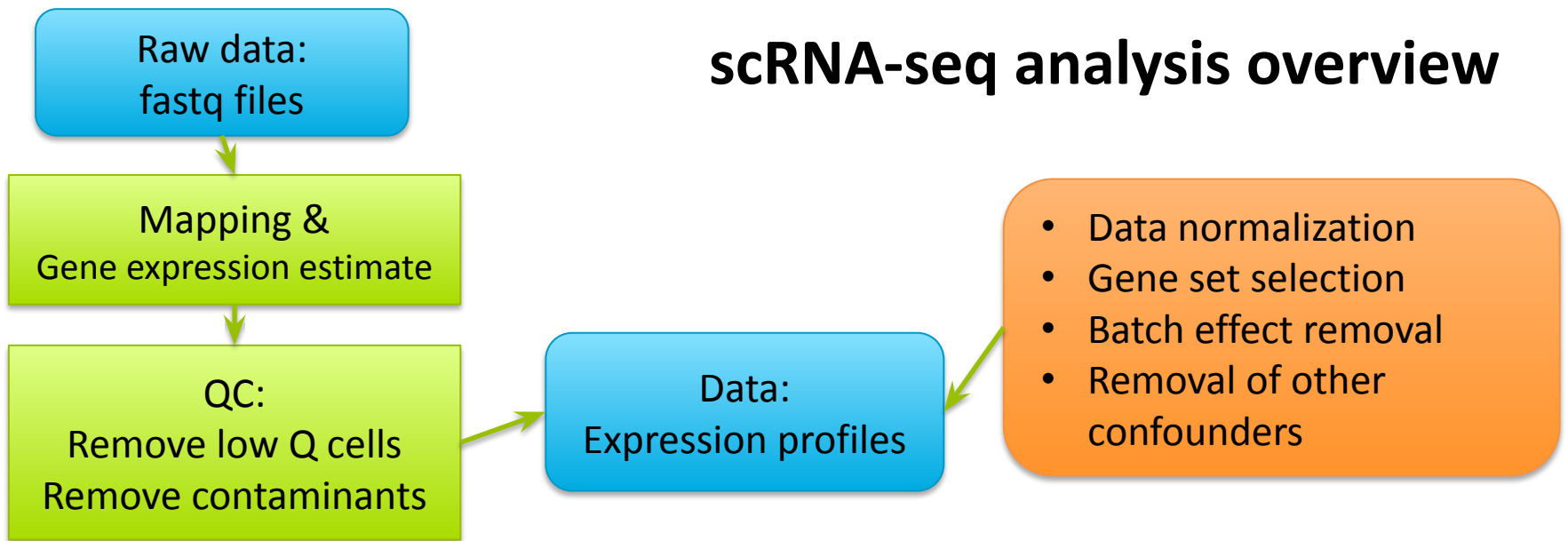
- Cellranger (10x)
- Dropseq - Alevin/Kallisto Bustools (transcriptome only)
- Dropletutils
- nf-core/scrnaseq
-

scRNA-seq analysis overview

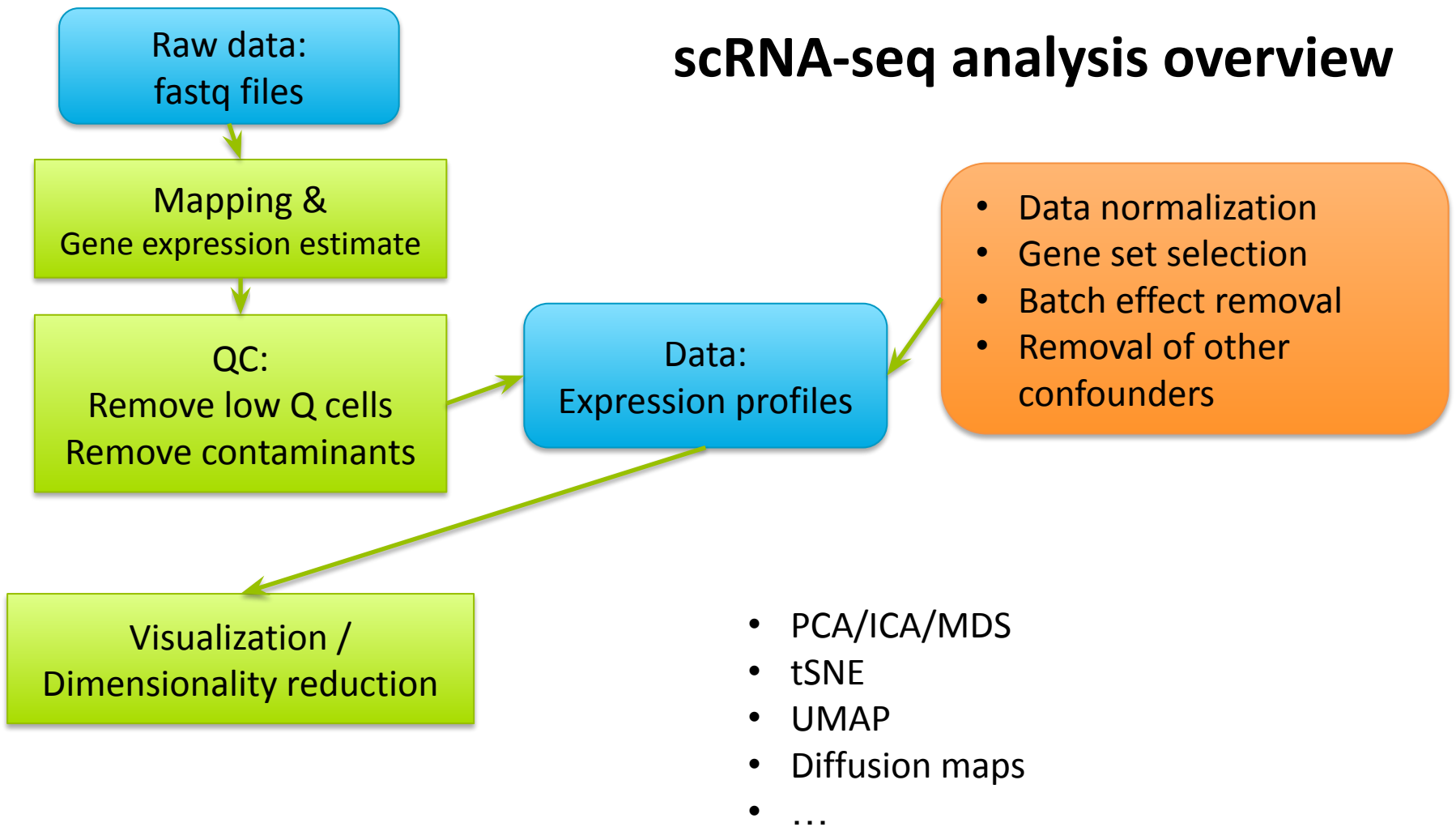


- Low/high number of reads
- Low/high number of genes
- Intronic reads
- Mitochondrial content
- Mapping stats
- ...

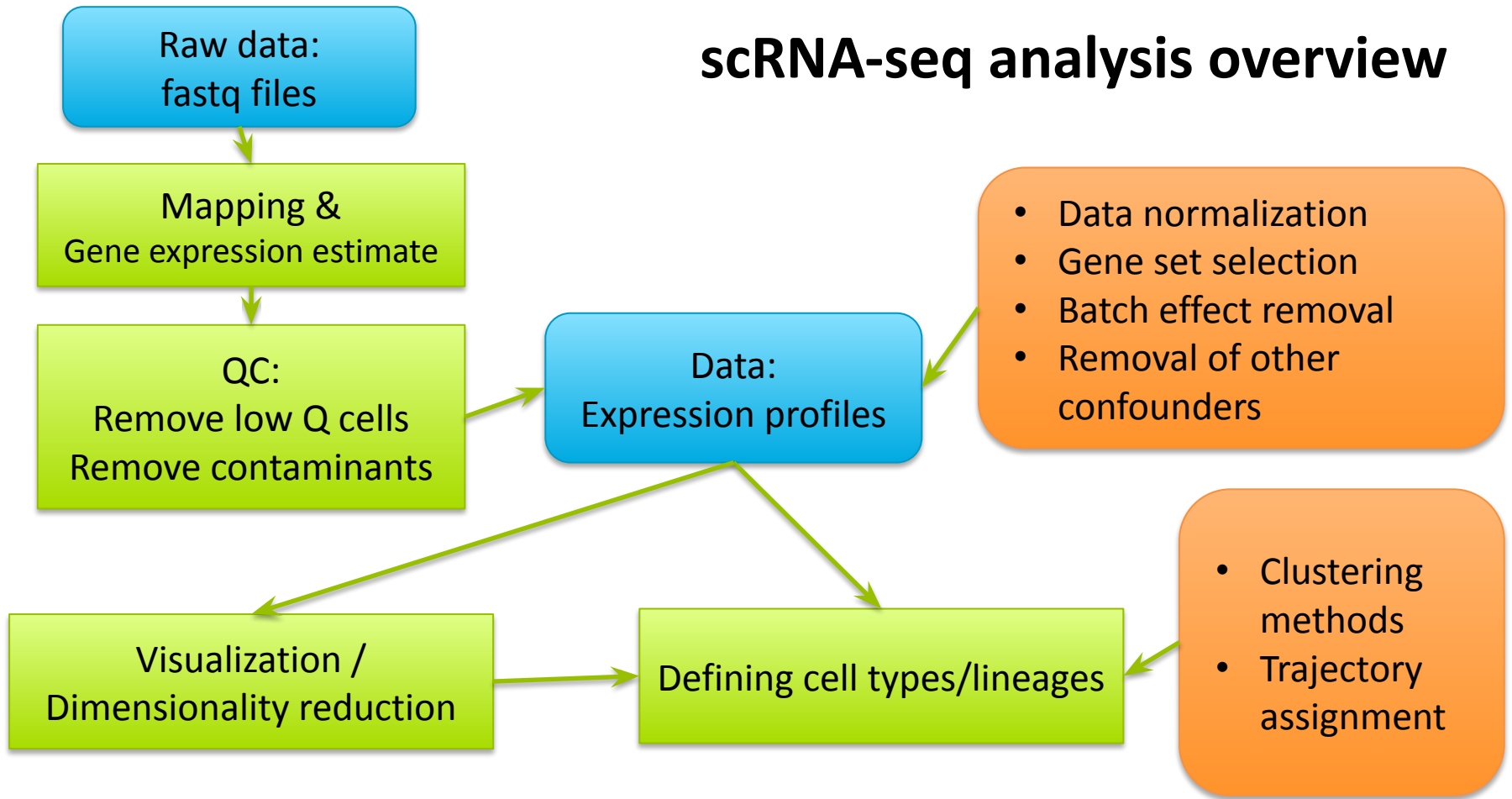
scRNA-seq analysis overview



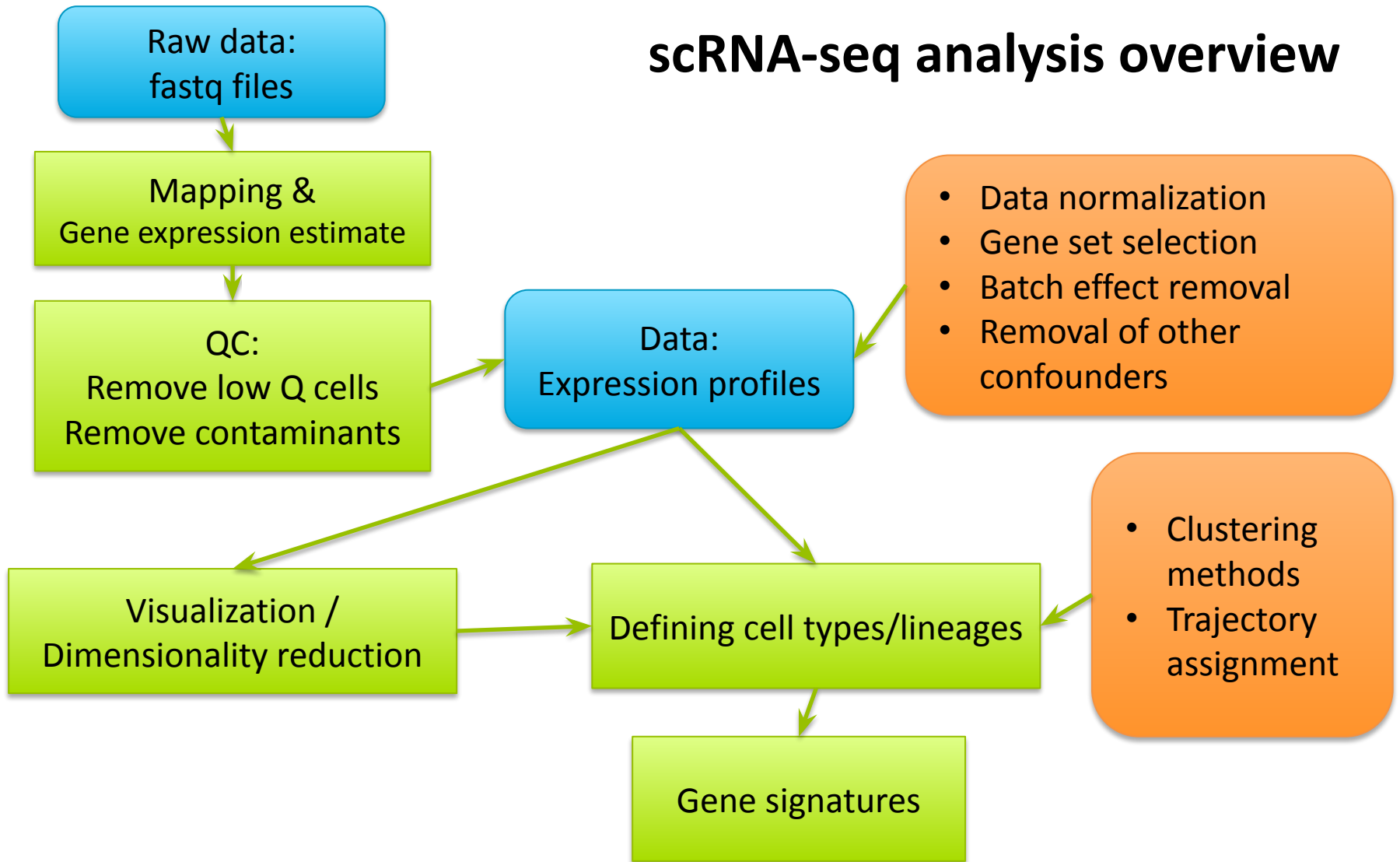
scRNA-seq analysis overview



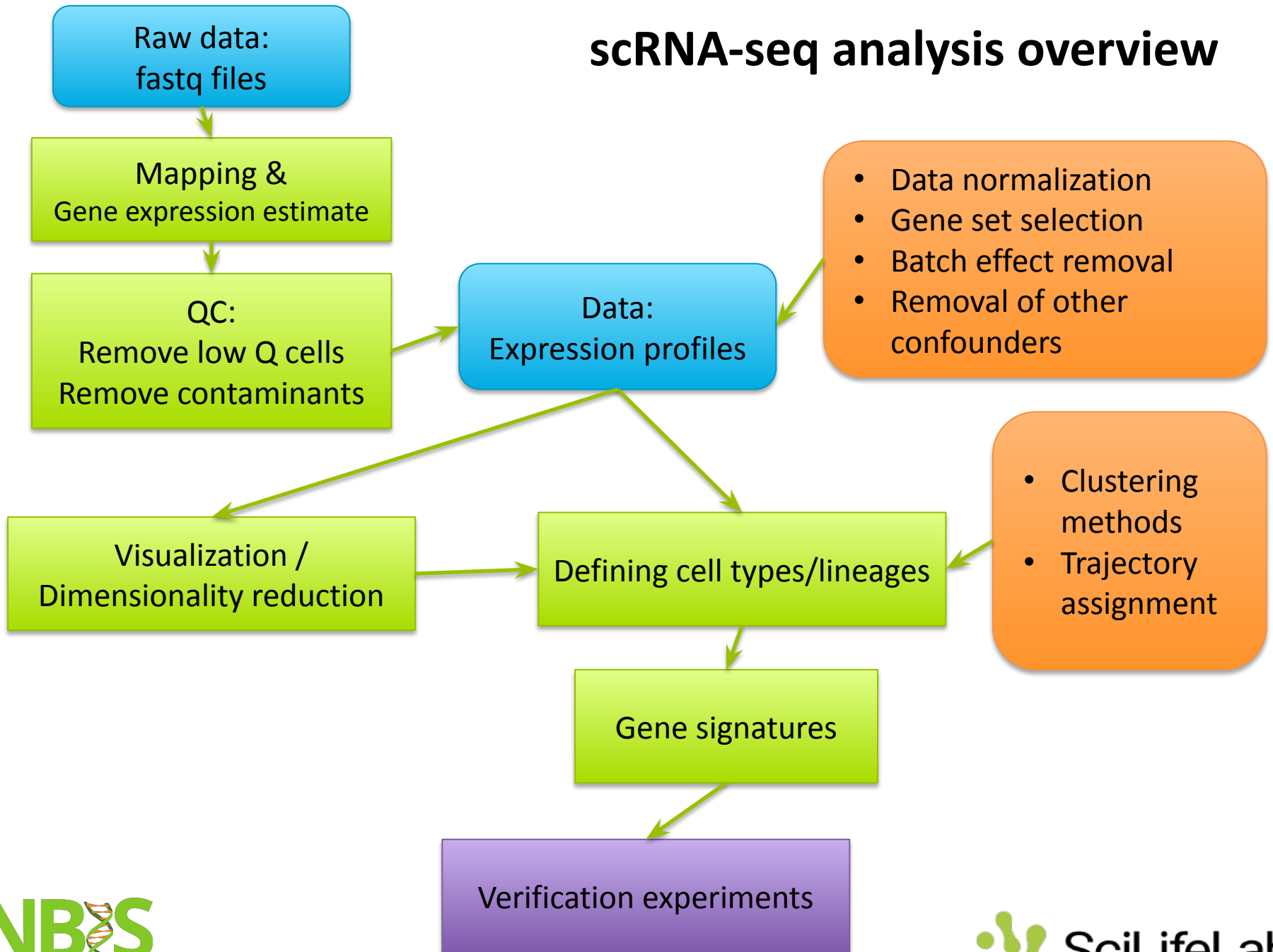
scRNA-seq analysis overview



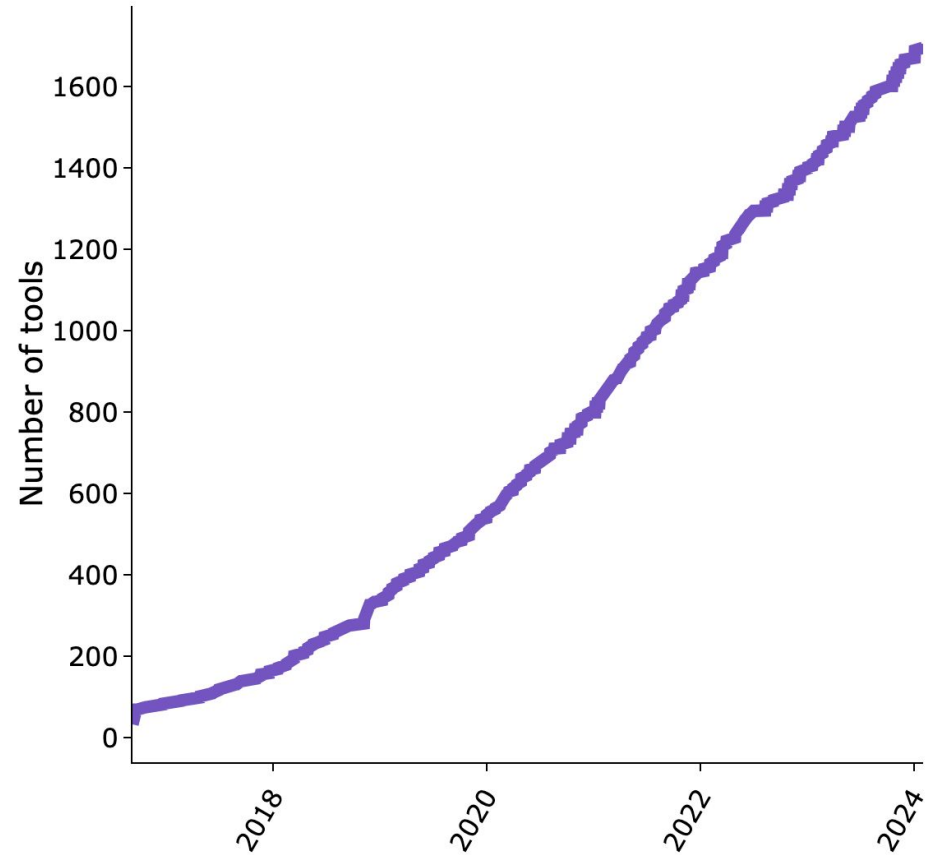
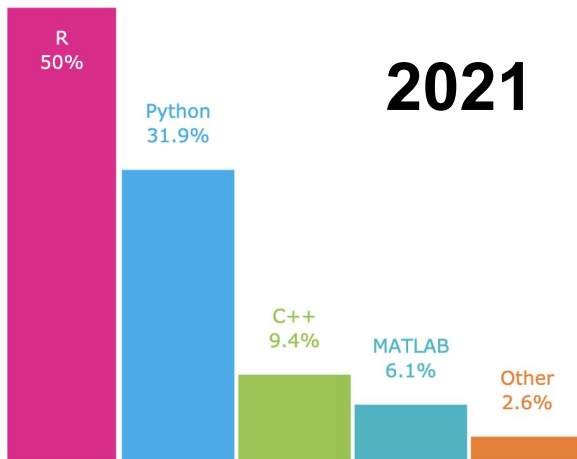
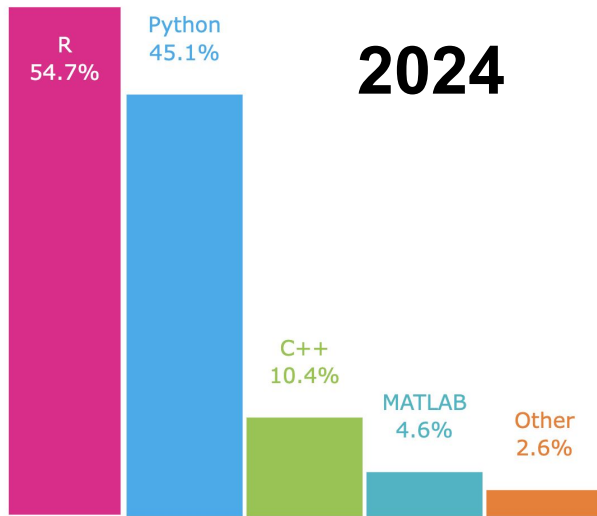
scRNA-seq analysis overview



scRNA-seq analysis overview



Many available tools for analysis



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 - Friday

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.

Schedule

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

Have links to pdfs with slides, but some are from 2023 course and will be updated as we give the lectures.

Uppmax project

If you have not requested access to the project yet,
please do so now!

PLEASE ASK QUESTIONS!

