



Single cell RNA sequencing data analysis, 25-29 January 2021

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Who are we?

Main:



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Lectureres:



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Leiden U

TAs:



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Jonathan Robinson
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NBIS/LU

National Bioinformatics Infrastructure Sweden (NBIS)

Future compute infrastructure



Consultations





Compute projects
Software and databases







Data publishing and open science
Secure sharing of sensitive data





Research support

Efficient tools and workflows

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NATIONAL BIOINFORMATICS
INFRASTRUCTURE SWEDEN



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 center

www.nbis.se

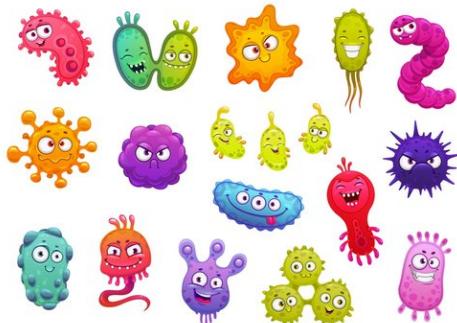
Practical information

- All lectures/exercises will be held on this zoom link.
- We ask all participants to keep their camera on, but please mute unless you have some questions.
- If you have questions:
 - Just unmute and ask directly.
 - Raise your hand in zoom
 - Ask the question in the zoom chat / slack channel
#questions
- We have included many breaks – take the chance to stretch your legs to avoid zoom fatigue!

Practical information - Slack

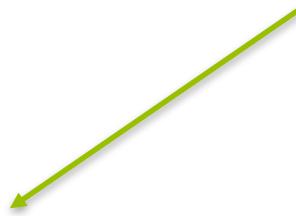
- Communication around the course will be handled via slack.
- Please add picture and brief description
- Channels:
 - #general – general information about the course
 - #exercises – questions during exercises
 - #installation_issues – questions about the installations
 - #group1,2,3,4,5, a for each group to communicate
 - #questions – post any question regarding the course content.

scRNA-seq overview



- What method....

- Smartseq2/3
- 10x
- CITE-seq
- SPLIT-seq
-



Raw data:
fastq files



Data analysis

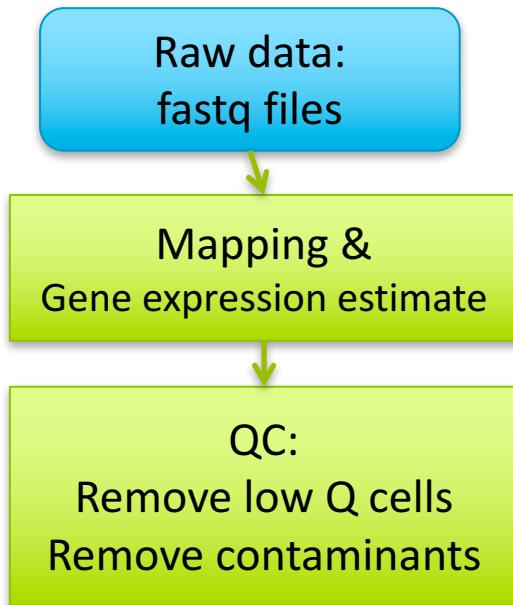
Raw data:
fastq files

Mapping &
Gene expression estimate

scRNA-seq analysis overview

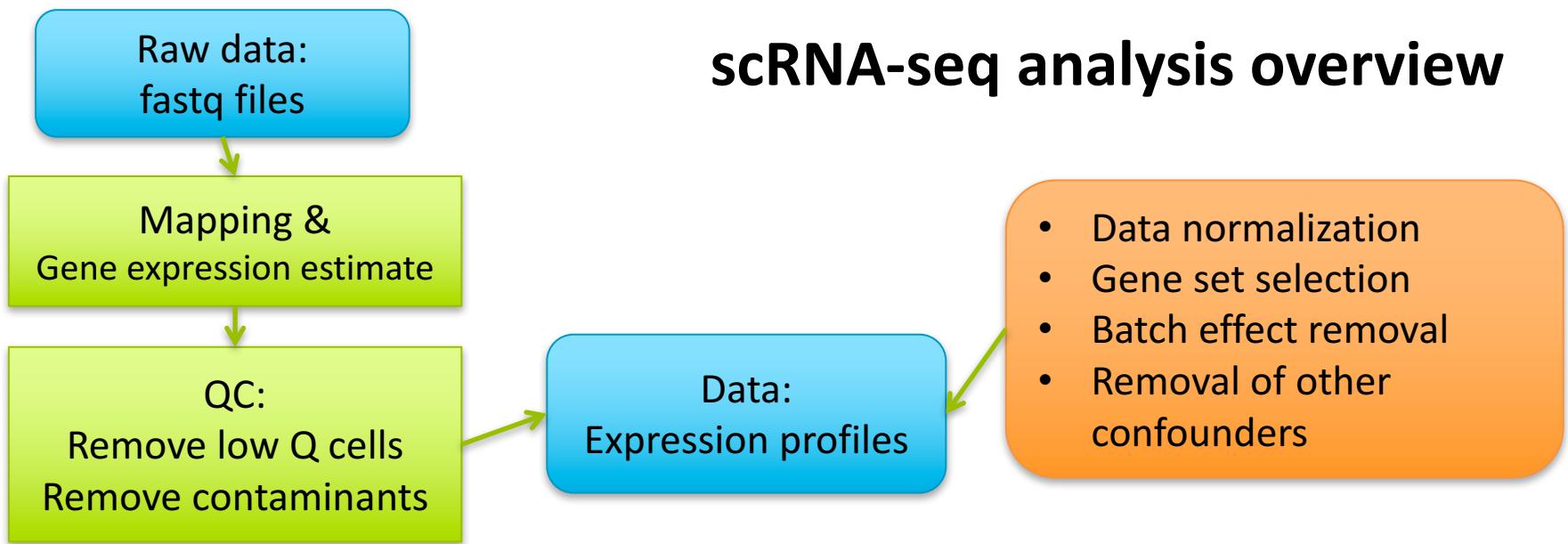
- Cellranger (10x)
- Dropseq - Alevin/Kallisto Bustools
(transcriptome only)
- Dropletutils
- nf-core/scrnaseq
-

scRNA-seq analysis overview

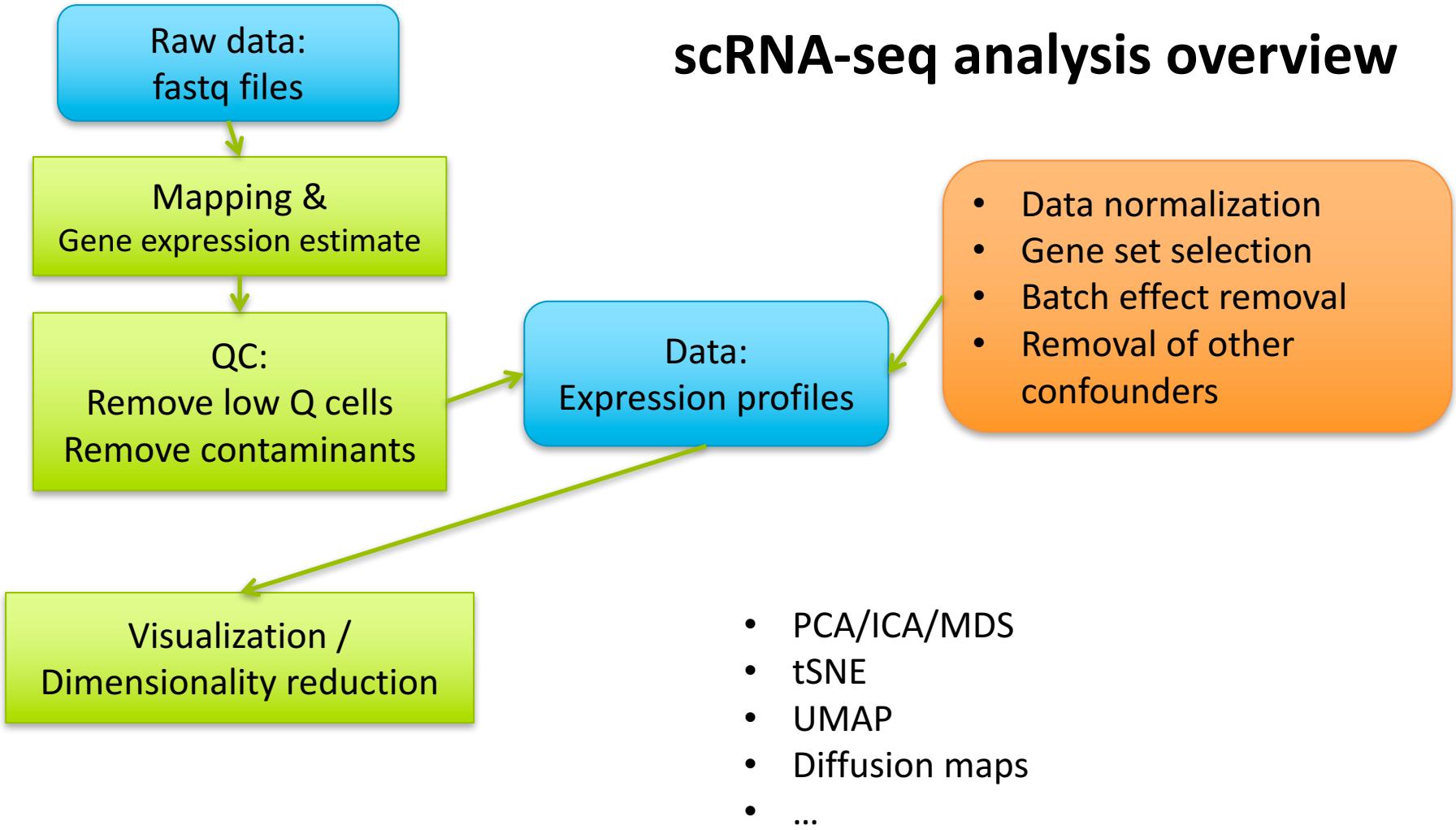


- Low/high number of reads
- Low/high number of genes
- Intronic reads
- Mitochondrial content
- Mapping stats
- ...

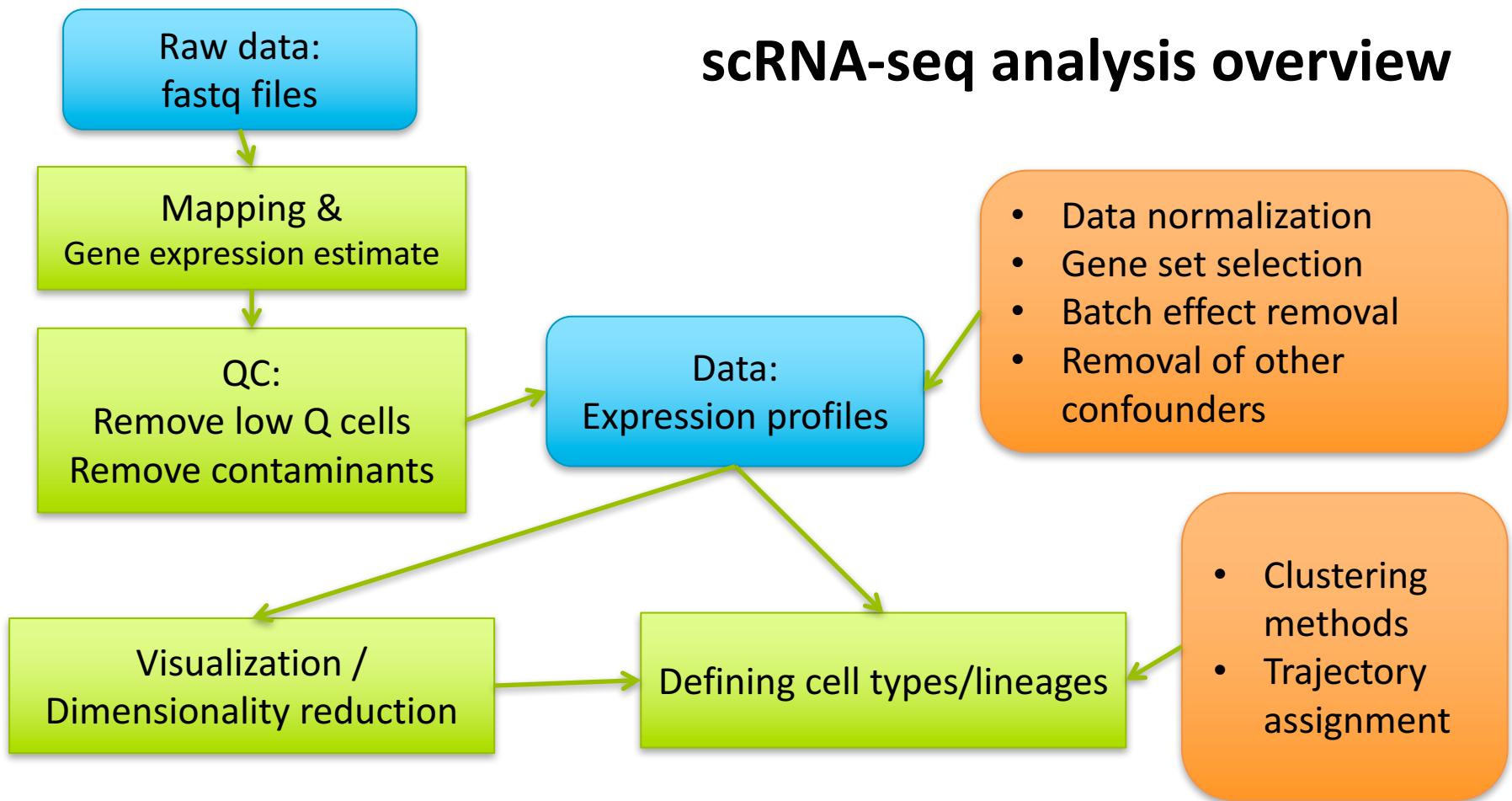
scRNA-seq analysis overview



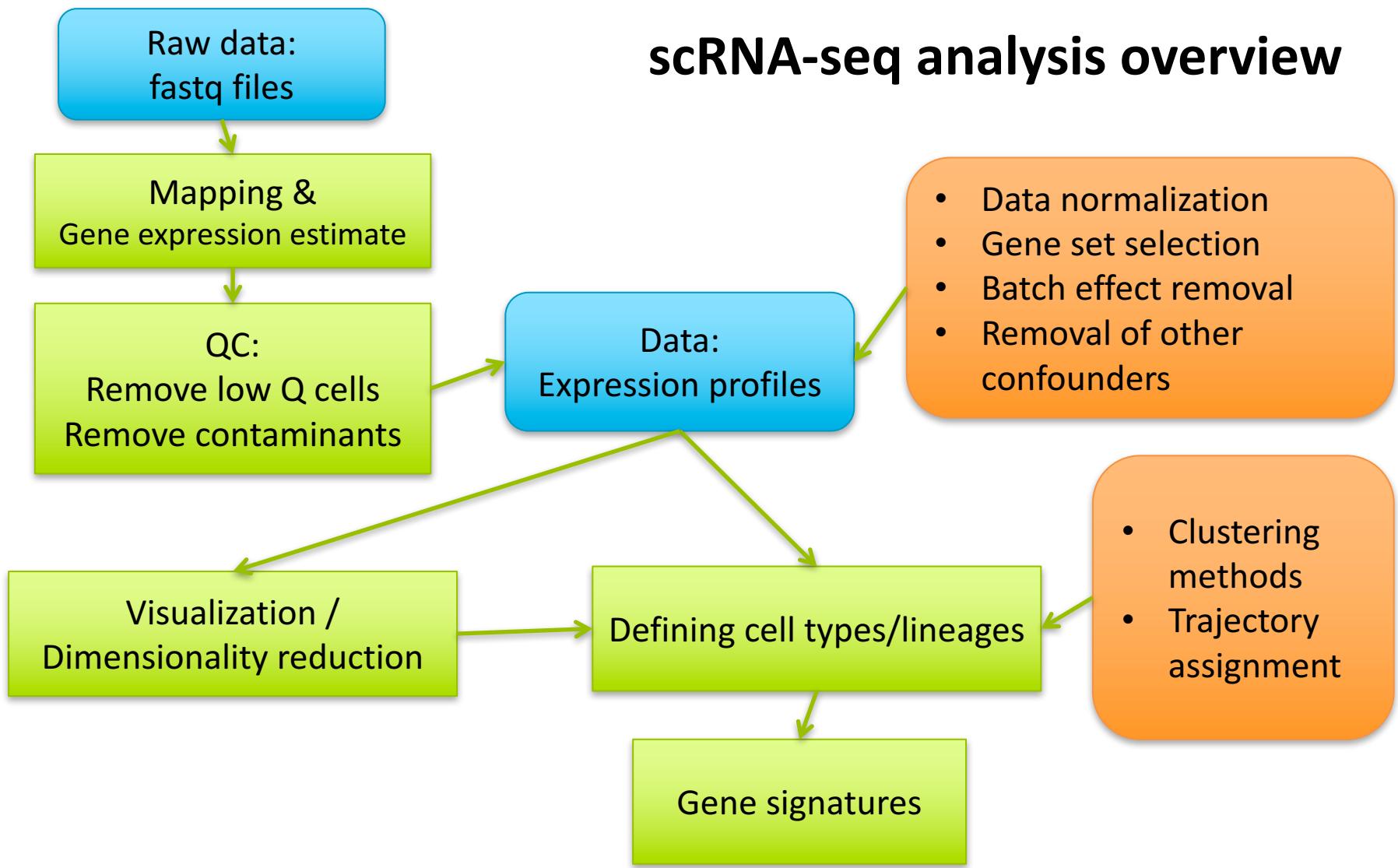
scRNA-seq analysis overview



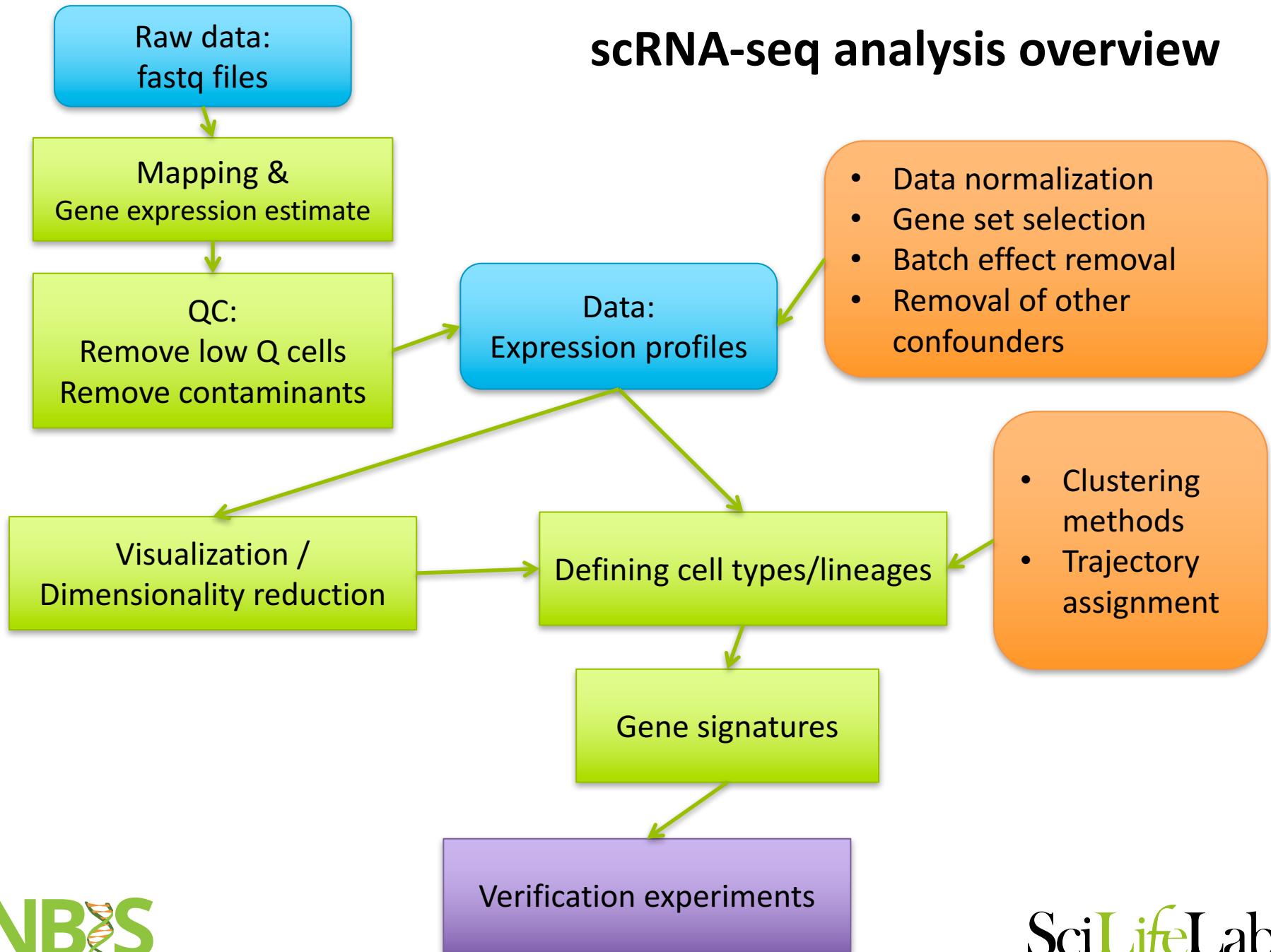
scRNA-seq analysis overview



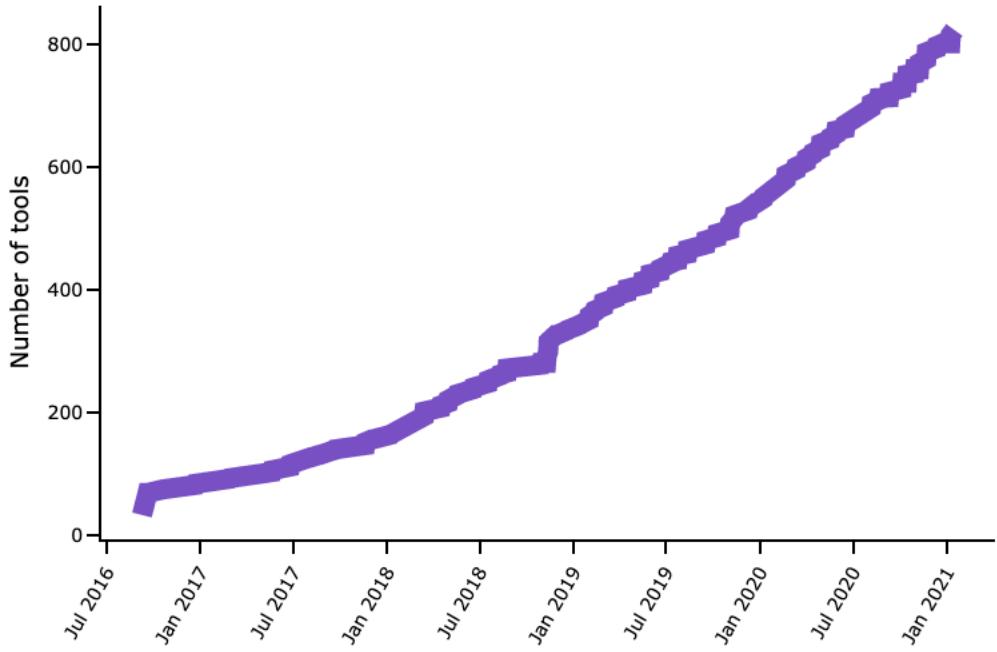
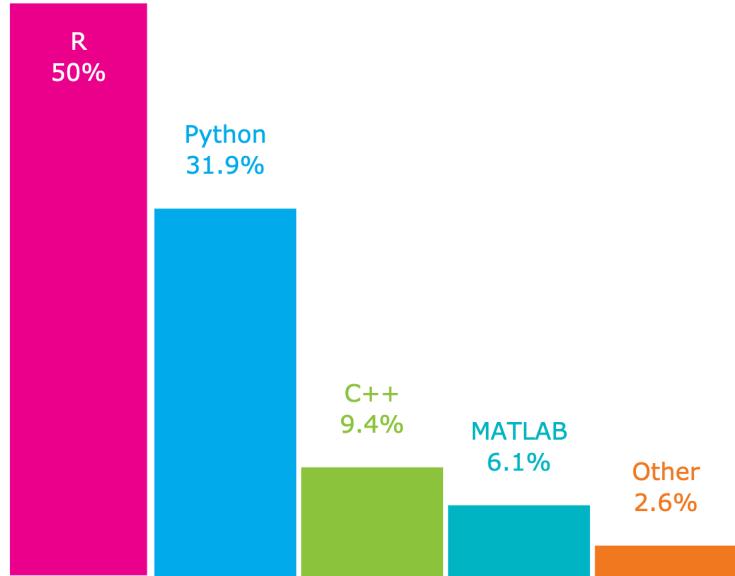
scRNA-seq analysis overview



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.

Course content

- Monday: scMethodology, QC
- Tuesday: Normalization, Dimensionality reduction, Batch correction
- Wednesday: Clustering, Differential expression
- Thursday: Trajectory inference, Spatial transcriptomics
- Friday: Celltype prediction, Multimodal omics.
Course summary.

PLEASE ASK QUESTIONS!

