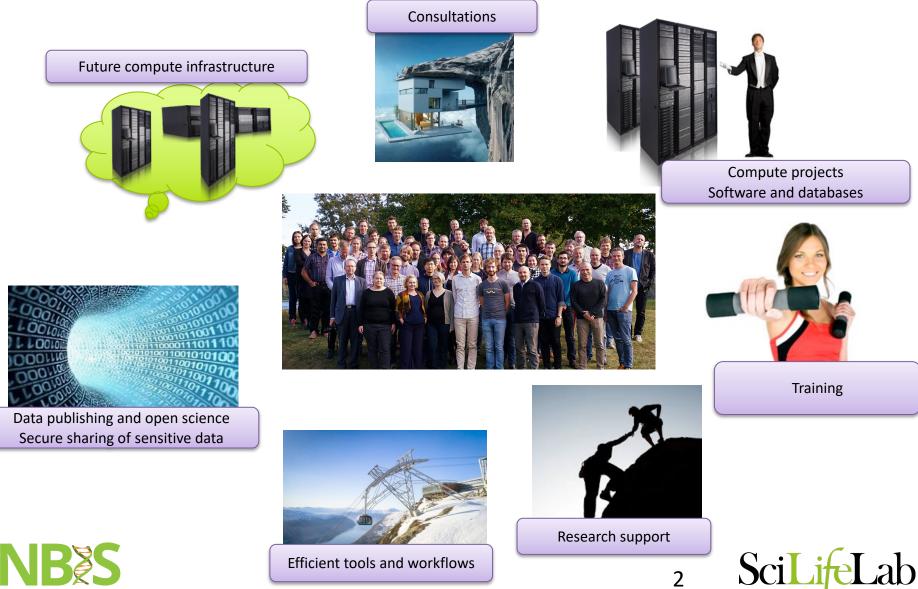
Single cell RNA sequencing data analysis, 30 Jan – 3 Feb, 2023

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National Bioinformatics Infrastructure Sweden (NBIS)



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 - 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





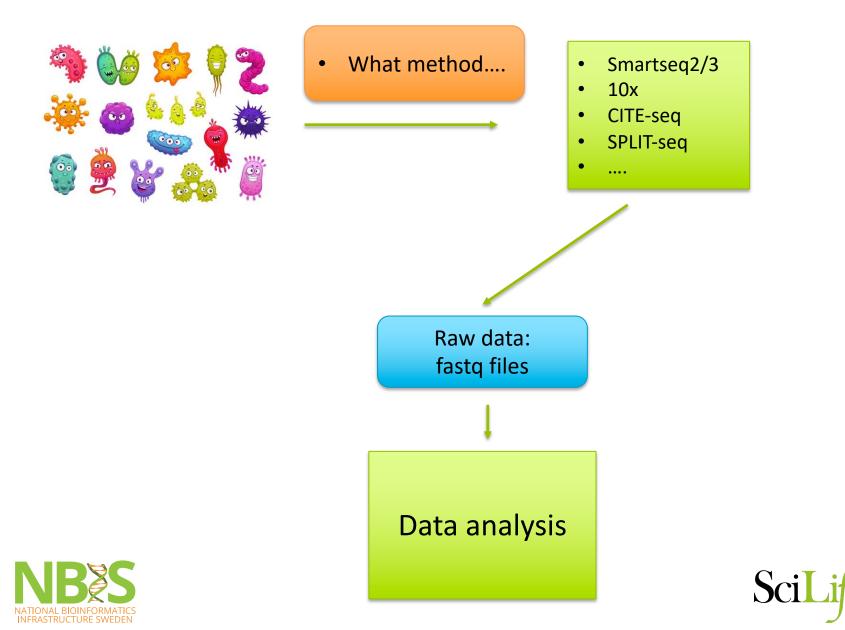
Practical information

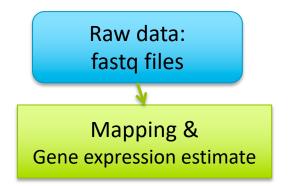
- All code and links to lectures etc. via our github page: <u>https://github.com/NBISweden/workshop-scRNAseq</u>
- Lunches: In Café Delta we have reserved tables.
 Just queue up and say that you are from the course.
- Course Dinner we will send around the menu and a form to fill out what dish you want.





scRNA-seq overview



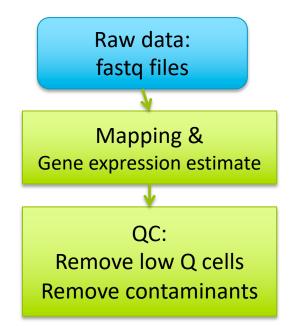


scRNA-seq analysis overview

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





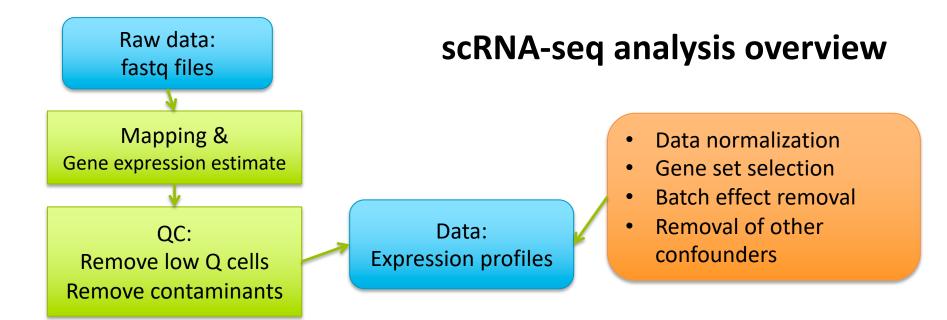


scRNA-seq analysis overview

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

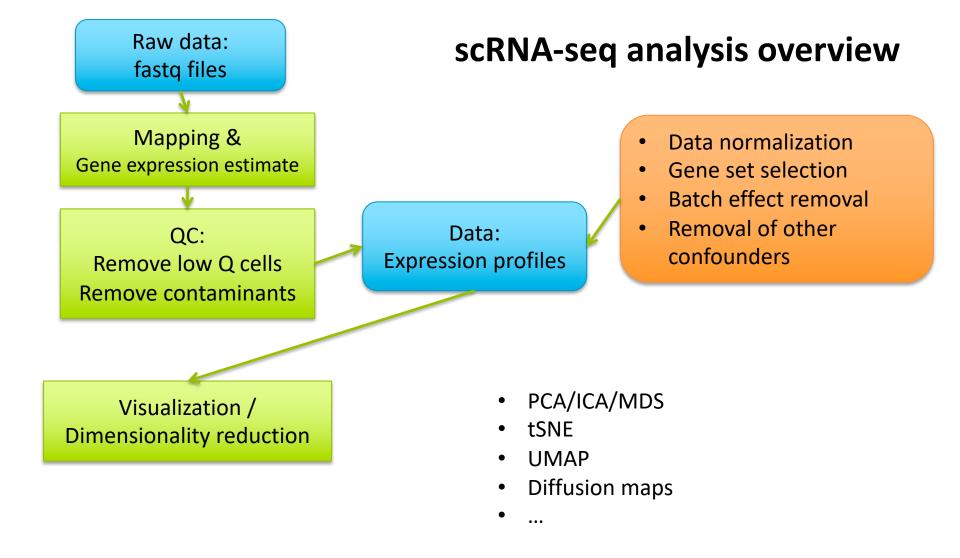






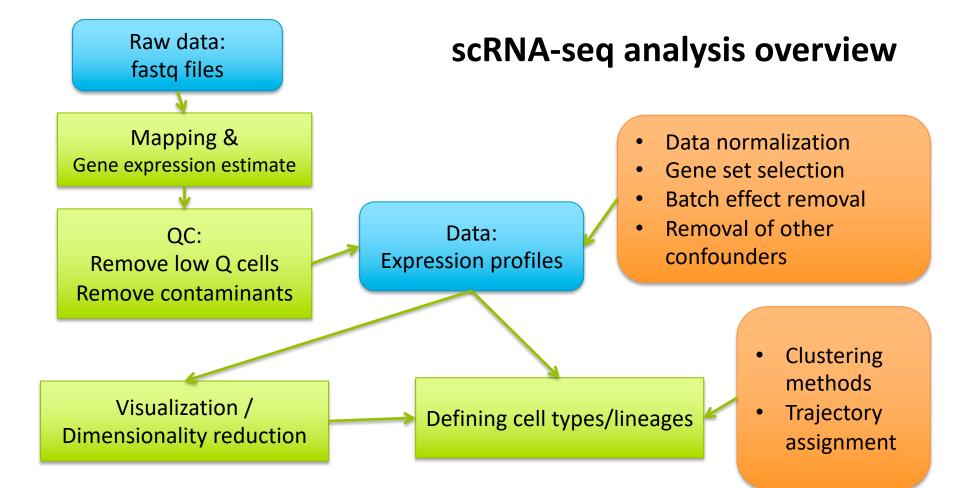






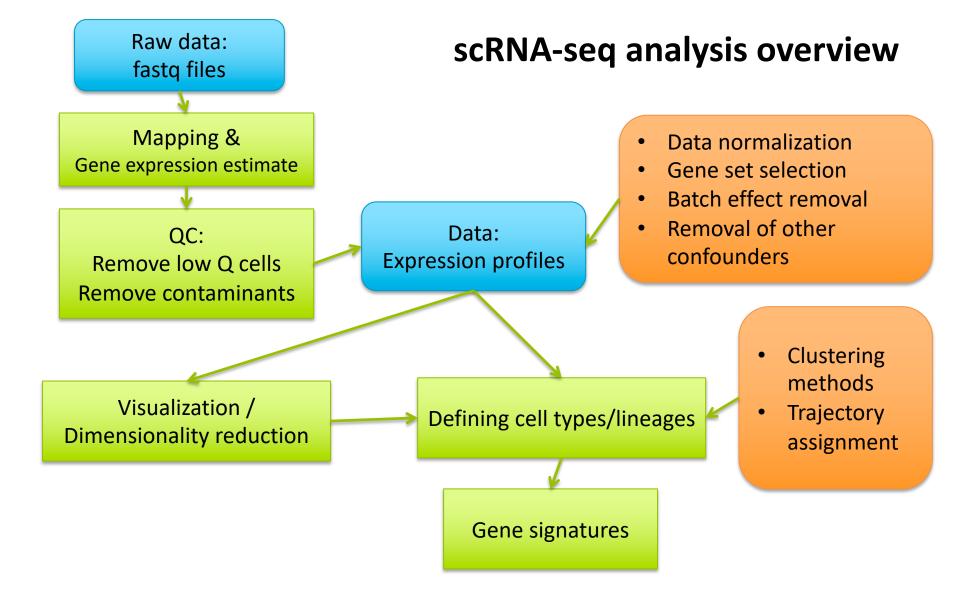






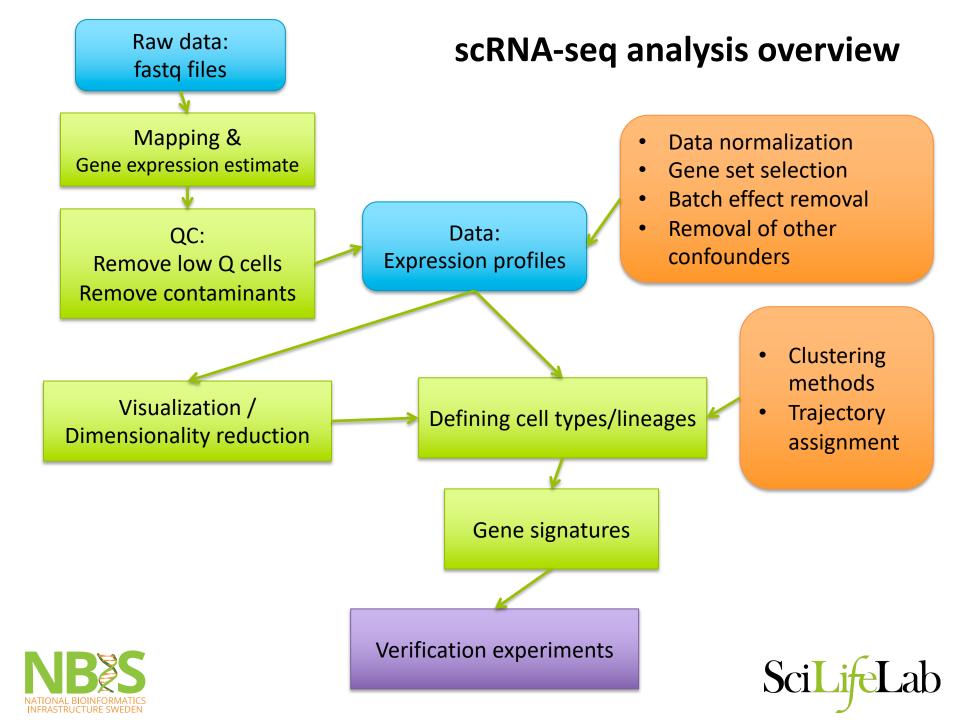




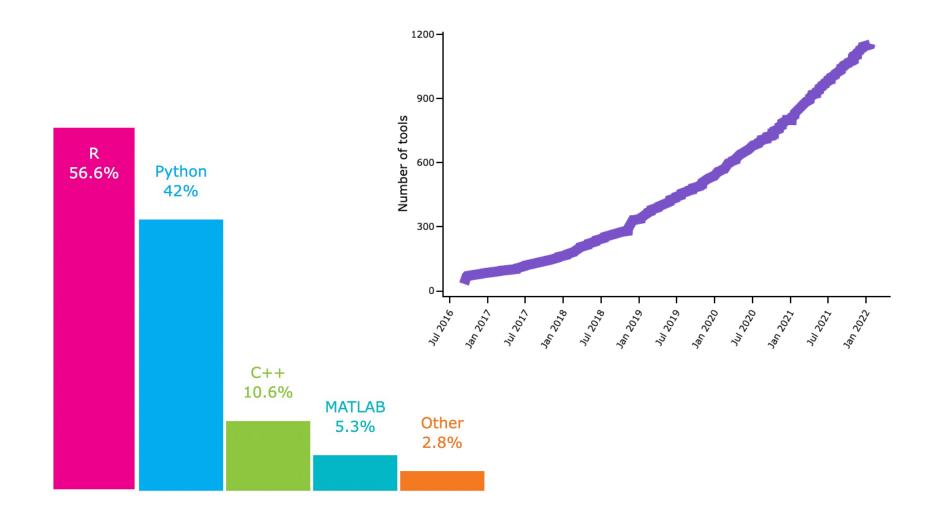








Many available tools for analysis





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.





PLEASE ASK QUESTIONS!

💤 slack



