Update

- Reminders: exercises every week; top 9 (of 14) will be counted towards 30% of the grade; grade + feedback sent via Slack
- Exercise 1:
  - 27 students registered
  - 23 R self-assessments received
  - 23 GitHub usernames received
  - 23 Issues received
- Exercise 2:
  - 9 groups/repos started (Exercise 2 Part a)
  - 9 pull requests received (Exercise 2 Part b)

Journal club

Papers to be selected by 18.00 on 15th October; please discuss it with Hubert and I before submitting <u>pull request</u>.

Start: Oct 21

Journal Club schedule to be finalized by 15th October

Groups of 2.

Use the #journal-club channel (e.g., to find a group member, discuss papers). Hubert and I will put some suggestions there.

Sign up by pull request to the 'material' repo, README.md. "First come first served"

Date	Lecturer	Topic	Exercise	JC1	JC2
16.09.2024	Mark	admin; mol. bio. basics	quarto; git(hub)		
23.09.2024	Mark	interactive technology/statistics session	group exercise: technology pull request		
30.09.2024	Mark	limma + friends	linear model simulation + design matrices		
07.10.2024	Hubert	NGS intro; exploratory data analysis	EDA in R		
14.10.2024	Hubert	mapping	Rsubread		
21.10.2024	Hubert	RNA-seq quantification	RSEM	X	X
28.10.2024	Mark	edgeR+friends 1	basic edgeR/voom	X	X
04.11.2024	Mark	edgeR+friends 2	advanced edgeR/voom	X	X
11.11.2024	Mark	hands-on session #1: RNA-seq	FASTQC/Salmon/etc.	X	X
18.11.2024	Hubert	single-cell 1: preprocessing, dim. reduction, clustering	clustering	X	X
25.11.2024	tba	hands-on session #2: cytometry	cytof null comparison	X	X
02.12.2024	Mark	single-cell 2: clustering, marker gene DE	marker gene DE	X	X
09.12.2024	tba	hands-on session #3: single-cell RNA-seq (cell type definition, differential state)	full scRNA-seq pipeline	X	X
16.12.2024	Mark	spatial omics	spatial statistics	X	X

Format your signup like this (in markdown, of course):

README.md: paper title as link to website, initials of group members

| 01.11.2021 | Mark | edgeR+friends 1 | basic edgeR/voom | OUTRIDER: A Statistical Method for Detecting Aberrantly Expressed Genes in RNA Sequencing Data (BT, KN) | Powerful and robust non-parametric association testing for microbiome data via a zero-inflated quantile approach (ZINQ) (RM, DS) |
| 08.11.2021 | Mark | edgeR+friends 2 | advanced edgeR/voom | ZeitZeiger: supervised learning for high-dimensional data from an oscillatory system (TB, OF) | X |

```
| 01.11.2021  | Mark | edgeR+friends 1 | basic edgeR/voom | [OUTRIDER: A Statistical
Method for Detecting Aberrantly Expressed Genes in RNA Sequencing Data](https://
www.cell.com/ajhg/fulltext/S0002-9297(18)30401-4) (BT, KN)  | [Powerful and robust non-
parametric association testing for microbiome data via a zero-inflated quantile approach
(ZINQ)](https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-021-01129-3)
(RM, DS) |
| 08.11.2021  | Mark | edgeR+friends 2 | advanced edgeR/voom| [ZeitZeiger: supervised
learning for high-dimensional data from an oscillatory system](https://dx.doi.org/
10.1093%2Fnar%2Fgkw030) (TB, OF) | X |
```

Expectations: **journal club** presentation

- 20-25 minutes (+5 minutes discussion)
- MUST:
  ➡ be a paper about a **statistical** method in genomics
  ➡ be approved by Mark/Hubert
- Should:
  ➡ describe the biological context and/or data collected
  ➡ describe the (new) model used
  ➡ describe comparisons to existing methods
- Should not:
  ➡ be one of the papers discussed in detail in lectures: limma, edgeR, DEXSeq, etc.
- (since 2017) feedback forms from fellow students