



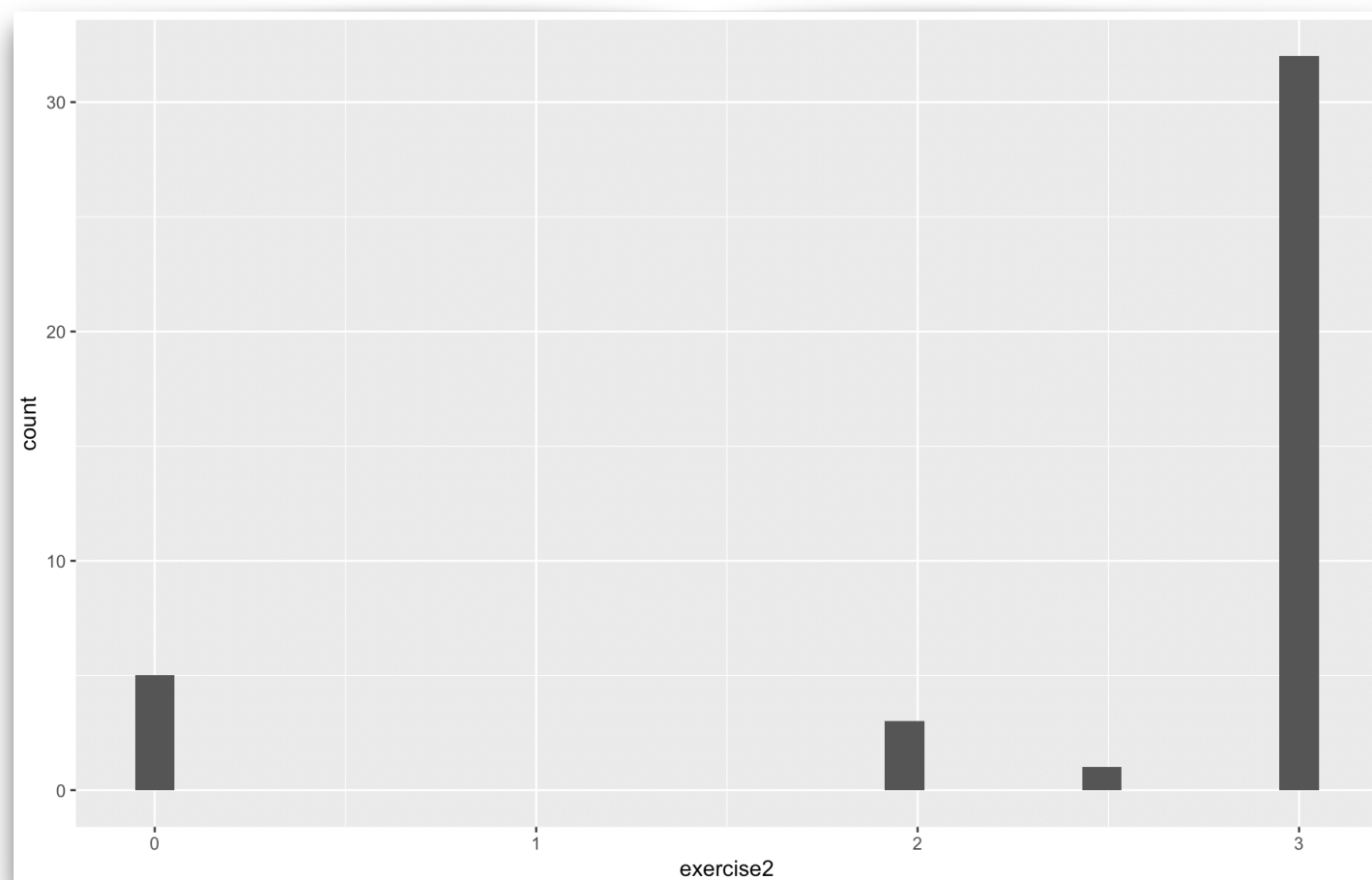
Week 4 notes:

- Exercises
- Journal Club



Exercises

- Week 2





Exercises

- Week 3 exercise due later today
- So far: 20 pull requests, lots of activity in the 'brainstorm-...' repos
- Reminder: I need to see "activity" from all group members



Journal club

Papers to be picked by 18.00
on 15th October; discuss it
with Hubert and I.

Journal Club schedule to be
finalized by 22nd October

Given the number of students,
groups of 2-3.

Use the #papers channel. I
have put several suggestions
there.

Signup by pull request.

Schedule

Date	Lecturer	Topic	Exercise	JC1	JC2
17.09.2018	Mark + Hubert	admin; mol. bio. basics	R markdown; git(hub)		
24.09.2018	Hubert	NGS intro; exploratory data analysis	EDA in R		
01.10.2018	Mark + Hubert	interactive technology/statistics session	group exercise: technology pull request		
08.10.2018	Hubert	mapping	Rsubread		
15.10.2018	Mark	limma + friends	linear model simulation + design matrices		
22.10.2018	Hubert	RNA-seq quantification	RSEM		
29.10.2018	Charlotte	hands-on session #1: RNA-seq	FASTQC/Salmon/etc.		X
05.11.2018	Mark	edgeR+friends 1	basic edgeR/voom		
12.11.2018	Mark	edgeR+friends 2	GLM/DEXSeq		
19.11.2018	Mark	single-cell dim. reduction + clustering; FDR	conquer		
26.11.2018	Lukas	hands-on session #2: cytometry	cytof null comparison		X
03.12.2018	Hubert	classification	MLInterfaces		
10.12.2018	Mark	loose ends: HMM, EM, robustness	segmentation, peak finding		
17.12.2018	Mark	hands-on session #3: single-cell RNA-seq	full scRNA-seq pipeline		X



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21 ## Schedule
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23 | Date | Lecturer | Topic | Exercise | JC1 | JC2 |
24 | --- | --- | --- | --- | --- | --- |
25 | 17.09.2018 | Mark + Hubert | admin; mol. bio. basics | R markdown; git(hub) | | |
26 | 24.09.2018 | Hubert | NGS intro; exploratory data analysis | EDA in R | | |
27 | 01.10.2018 | Mark + Hubert | interactive technology/statistics session | group exercise: technology pull request | | |
28 | 08.10.2018 | Hubert | mapping | Rsubread | | |
29 | 15.10.2018 | Mark | limma + friends | linear model simulation + design matrices | | |
30 | 22.10.2018 | Hubert | RNA-seq quantification | RSEM | | |
31 | 29.10.2018 | Charlotte | hands-on session #1: RNA-seq | FASTQC/Salmon/etc. | | X |
32 | 05.11.2018 | Mark | edgeR+friends 1 | basic edgeR/voom | | |
33 | 12.11.2018 | Mark | edgeR+friends 2 | GLM/DEXSeq | | |
34 | 19.11.2018 | Mark | single-cell dim. reduction + clustering; FDR | conquer | | |
35 | 26.11.2018 | Lukas | hands-on session #2: cytometry | cytof null comparison | | X |
36 | 03.12.2018 | Hubert | classification | MLInterfaces | | |
37 | 10.12.2018 | Mark | loose ends: HMM, EM, robustness | segmentation, peak finding | | |
38 | 17.12.2018 | Mark | hands-on session #3: single-cell RNA-seq | full scRNA-seq pipeline | | X |
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Enter:

- initials of all group members
- link (PubMed/Journal) to paper

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34 | 20.11.2017 | Mark | edgeR+friends 2 | [High Dimensional Classification with combined Adaptive Sparse PLS and Logistic Regression-
link](https://www.ncbi.nlm.nih.gov/pubmed/28968879) (TF, YY) | [BSmooth: from whole genome bisulfite sequencing reads to differentially
methylated regions](https://genomebiology.biomedcentral.com/articles/10.1186/gb-2012-13-10-r83) (SO) |

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