



# Update

- Exercise 3 due at 18.00 tomorrow
- Exercises 1-2 have been marked, you should have received a Slack message like:

```
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github username: 
slack username: 
Name: 
Email: 
Matrikelnummer: 

exercise 1 url: 
exercise 1 issue: 
exercise 1 rmd:      yes
exercise 1 (total / 3): 3

exercise 2a repo: 
exercise 2a commits: 4
exercise 2b PR: 
exercise 2 (total / 3): 3
```



## Journal club

**Papers to be selected by 18.00 on 13th October;** discuss it with Hubert and I.

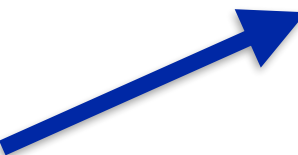
Start: Oct 12 or Oct 19

Journal Club schedule to be finalized by 19th October

Given the number of students, groups of 3 are recommended.

Use the #journal-clubs channel (e.g., to find a group member). I will put some suggestions there.

**Sign up by pull request (give a link to the paper, give initials of group members)**



Date	Lecturer	Topic	Exercise	JC1
14.09.2020	Mark + Hubert	admin; mol. bio. basics	R markdown; git(hub)	
21.09.2020	Mark	interactive technology/statistics session	group exercise: technology pull request	
28.09.2020	Hubert	NGS intro; exploratory data analysis	EDA in R	
05.10.2020	Hubert	mapping	Rsubread	
12.10.2020	Mark	limma + friends	linear model simulation + design matrices	
19.10.2020	Hubert	RNA-seq quantification	RSEM	
26.10.2020	Mark	edgeR+friends 1	basic edgeR/voom	
02.11.2020	Mark	edgeR+friends 2	GLM/DEXSeq	
09.11.2020	Kathi	hands-on session #1: RNA-seq	FASTQC/Salmon/etc.	<a href="#">Statistical significance for gen (RA, HH)</a>
16.11.2020	Hubert	single-cell 1: preprocessing, dim. reduction, clustering		<a href="#">Testing hypotheses about the the linear decomposition mode</a>
23.11.2020	Helena	hands-on session #2: cytometry	cytof null comparison	(Richard Affolter, Philip Hartou paper: tbd)
30.11.2020	Mark	single-cell 2: cell type definition, differential state	scRNA exercise 2	<a href="#">A Bayesian mixture model for t allelic expression in single cell:</a> Sundar, SmaragdaDimitrakopou

## limma (= linear models for microarray data) paper

### Linear models and empirical bayes methods for assessing differential expression in microarray experiments

[GK Smyth](#) - Statistical applications in genetics and molecular ..., 2004 - [degruyter.com](#)  

... This section describes how **gene-wise linear models** arise from experimental designs and states the distributional assumptions about the ... There may be more or fewer contrasts than coefficients for the **linear model**, although if more than the contrasts will be **linearly** dependent ...

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### Limma: linear models for microarray data

[GK Smyth](#) - ... and computational biology solutions using R and ..., 2005 - [Springer](#) 

... **limma** uses **linear models** to analyze designed microarray experiments (Yang and Speed, 2003; Smyth, 2004) ... reference microarray data, **linear modeling** is much the same as ordinary ANOVA or multiple **regression** except that a **model** is fitted for ... **Linear Models** Case Study 401 ...

☆  Cited by 4799 Related articles All 18 versions Import into BibTeX

### limma powers differential expression analyses for RNA-sequencing and microarray studies

[ME Ritchie](#), [B Phipson](#), [D Wu](#), [Y Hu](#)... - Nucleic acids ..., 2015 - [academic.oup.com](#) 

... **limma** powers **differential expression** analyses for RNA-sequencing and microarray studies. Matthew E. Ritchie. 1. Molecular Medicine Division, The Walter and Eliza Hall Institute of Medical Research, 1G Royal Parade, Parkville, Victoria 3052, Australia ...

☆  Cited by 3437 Related articles All 14 versions Import into BibTeX

## Linear Models and Empirical Bayes Methods for Assessing Differential Expression in Microarray Experiments\*

Gordon K. Smyth

Walter and Eliza Hall Institute of Medical Research  
Melbourne, Vic 3050, Australia

January 2004<sup>†</sup>

- seminal paper (cited >11,000 times)
- provides the foundation for a lot of (statistical) research in genomics
- we will digest this into a single lecture (**12 Oct**)