Update

- Reminders: exercises every week; top 9 (of 14) will be counted towards 30% of the grade; grade + feedback sent via Slack
- <u>Exercise 1 and Exercise 2 due at 18.00 tomorrow (30th Sep 2025)</u>; from now on, every exercise due the following Tuesday at 18.00

- 40 students registered, 42 GitHub users connected to org

- Exercise 1:
  - 31 R self-assessments received
  - 28 GitHub usernames received
  - 28 Issues received
- Exercise 2:
  - 11 groups/repos started (Exercise 2 Part a)
  - 10 pull requests received (Exercise 2 Part b)

Journal club

Papers to be selected by 18.00 on 14th October; please discuss it with Hubert and I before submitting <u>pull request</u>.
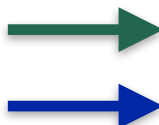
Start: Oct 20

Journal Club schedule to be finalized by 15th October

Groups of 2-3.

Use the #journal_clubs 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
15.09.2025	Mark+Hubert	admin; mol. bio. basics	quarto; git(hub)		
22.09.2025	Mark	interactive technology/statistics session	group exercise: technology PR		
29.09.2025	Hubert	NGS intro; exploratory data analysis	EDA in R		
06.10.2025	Hubert	mapping	Rsubread		
13.10.2025	Mark	limma + friends	linear model simulation + design matrices		
20.10.2025	Hubert	RNA-seq quantification	RSEM	X	X
27.10.2025	Mark	edgeR+friends 1	basic edgeR/voom	X	X
03.11.2025	Mark	edgeR+friends 2	advanced edgeR/voom	X	X
10.11.2025	Mark	hands-on session #1: RNA-seq	FASTQC/Salmon/etc.	X	X
17.11.2025	Hubert	single-cell 1: preprocessing, dim. red., clustering	clustering	X	X
24.11.2025	Mark	single-cell 2: clustering, marker gene DE	marker gene DE	X	X
01.12.2025	tba	hands-on session #2: single-cell RNA-seq	full scRNA-seq pipeline	X	X
08.12.2025	Mark	spatial omics 1	spatial statistics	X	X
15.12.2025	Mark	spatial omics 2	structures, DSP	X	X

University of Zurich[UZH]

Format your signup like this (in markdown):

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 |

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| 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 |
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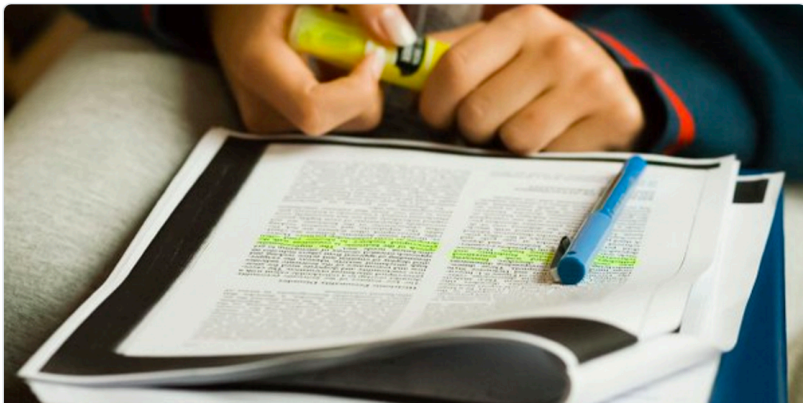# How to read a scientific paper

Lipi Thukral
@Sci_Lipi

Follow

Title->Abstract->Conclusion ->Hop to figures -> intro. -> results

How to (seriously) read a scientific paper

How to (seriously) read a scientific paper
Reading becomes easier with experience, but it is up to each scientist to identify the techniques that work best for them.
sciencemag.org

11:00 PM - 19 Mar 2017

https://github.com/jtleek/readingpapers

How much should you read?

Academic papers come out all the time. Thousands are published every year, including hundreds in any given specific area. Unless you devote yourself full time to reading academic papers you won't be able to keep up with them all. I believe in the idea that you should read papers that you find interesting. Science is awesome and you shouldn't waste your time on the boring parts if you can avoid it.

In general there are two main ways to find papers that I like. The way I used to do it was set up an aggregator with the RSS feeds from journals that I like, then I use the following (approximate) rates of reading parts of papers.

- 100% - read the title
- 20-50% - read the abstract
- 5-10% - look at the figures/captions
- 1-3% - read the whole paper

The new way that I do it is follow bioRxiv and a bunch of other people who have similar interests on Twitter. I use the above percentages for papers tweeted from aggregators and if I see a paper tweeted by 2-3 people I trust I usually end up reading that paper.

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

Journal Club procedure

– During/after journal clubs: give the presenters some constructive feedback

– Giving feedback (via Google form) is part of your JC grade! Feedback forms must be submitted within 1 week of presentation; comments will be sent to presenters (anonymously)

– JCs will be part of the recordings

Feedback form: 14.10. Redefining CpG islands using hidden Markov models

Presente

* Require

How would you rate the presenters' coverage of the topic? *

○ Poor

○ Fair

○ Good

○ Very Good

○ Excellent

How would you rate the presenters' knowledge of the topic? *

○ Poor

○ Fair

○ Good

○ Very Good

○ Excellent