

# Strategies for presenting journal club

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# Strategies for presenting journal club and reading papers

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# Reading a paper

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Time (effort)

High



Low

Understand it

Look at figures / skim text

Skim the figures

Read the abstract  
Read the title

Number of papers

Few



Many

A lot

## Why journal clubs

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JCs are widely used, especially in biology. Multiple reasons, including

- keeping up with the literature
- provide training in reading and evaluating papers
- (thereby) learning what makes a good paper (in your field)
- training in discussing science
- presentation skills

What **you** want/need to get out of JC depends on career stage and experience.

You should show up **prepared**, preferably most of the time.

Two axis of effort (preparation): for presenter and for participant

Do you present/read 1 or  $>1$  paper

- "Long time, big paper". Example: DGM weekly journal club (claiming to be "longest running JC in human genetics". One paper, 1 hour. Objective is to learn about important advances in a broad field.
- "Quick filtering". 2m per paper selected from a list of "interesting" papers. Only outcome is "worth a second look?". Objective: to rapidly filter a large set of papers.
- "Learn a field". Objective is to cover a medium amount of papers to find the important contributions, questions etc. **This is us right now.** We should probably cover  $>1$  paper in 30m.

# Why read papers

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- learn biology / statistics
- understand the biological questions / use cases in a research field
- understand how these questions are translated into computational questions
- understand the computational methods
- learn about / be inspired regarding open problems
- learn about new datasets

Several of these points can be rephrased into

“what can I use from this work in my own research”

# Questions

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What are the high-level (usually biological, sometimes statistical) question(s)

What does the method *promise* to deliver

(for a biological method: what data does it produce? What is inferred?)

How does the paper show that the this delivery “works”, and how convincing is it?

What products (data, methods, code) is available

We are interested in big picture questions, like

What are the biological questions we can answer with scEpigenomics?

What are examples of this in practice?

Why scEpigenomics and not scRNA?

How is data organized? Aggregation across loci or samples? Resolution?

Normalization / prediction / inference.