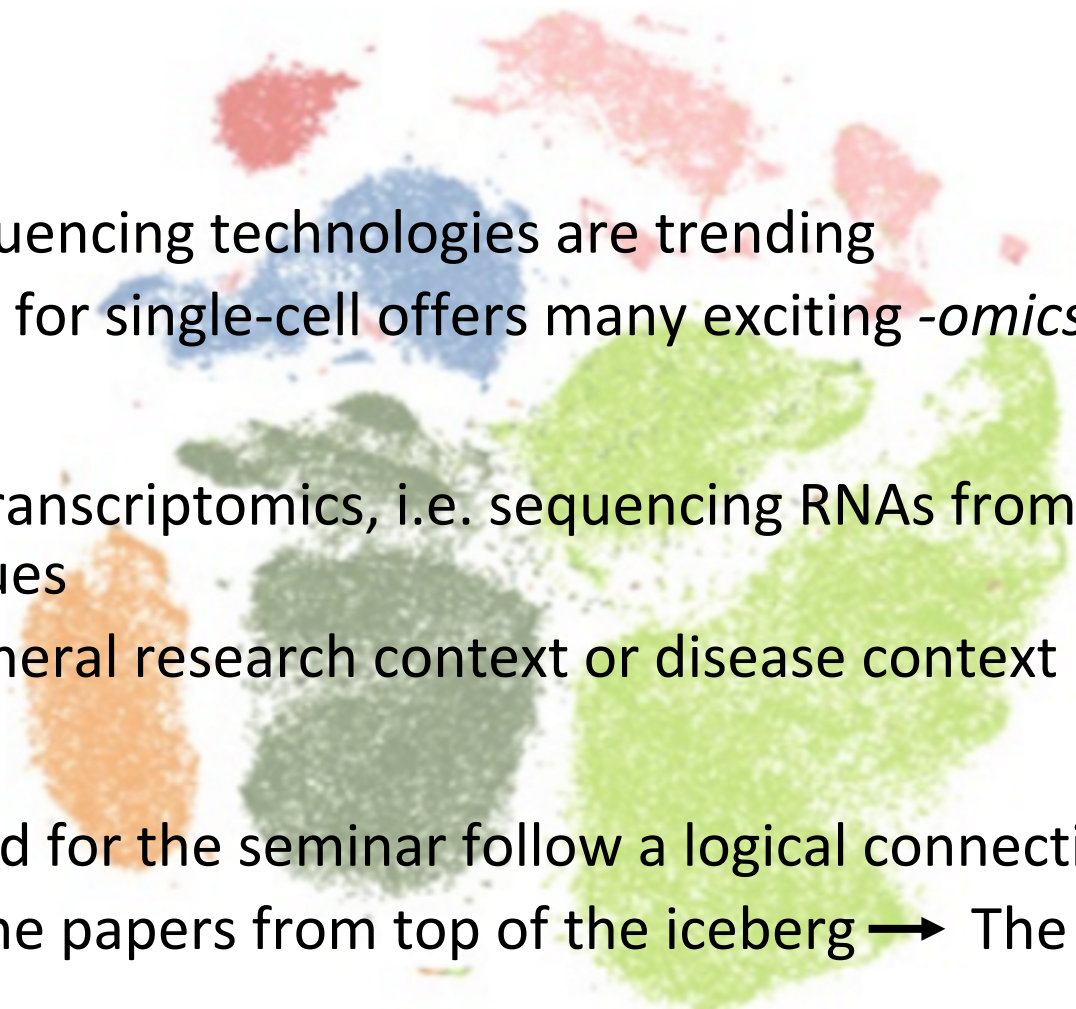


SEMINAR RNA-SEQ METHODS AND APPLICATIONS— KICK-OFF MEETING

Tutor:  
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**Thanks for enrolling!**

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- **Why?**
    - Single-cell sequencing technologies are trending
    - Bioinformatics for single-cell offers many exciting *-omics* applications
  - **What?**
    - We focus on transcriptomics, i.e. sequencing RNAs from populations of cell types and tissues
    - Can be in a general research context or disease context
  - **How?**
    - Papers selected for the seminar follow a logical connection & ordering
    - We selected the papers from top of the iceberg → The field is moving fast!

- RNA sequencing is one of the most widespread NGS-based methods (and third generation sequencing methods)
- Developed years ago but also an expanding field in terms of platform/technologies and analysis methods
- A very common approach to gene expression quantification (and beyond) in current Molecular Biology
- Papers proposed attempt to give an overview of current methods and some examples of actual applications in research



- Seminar (Master's only, 7 CPs - graded):
  - No formal prerequisites
  - But good skills in **maths, programming, and bioinformatics** are assumed
- Good english skills as **all talks** will be held in english language!

Event	Time	Comments
Registration	25.04.2022 - 15.05.2022	
Kick-off meeting [mandatory]	Today (31.05.2022)	
Deadline to register in HISPOS or de-register from seminar [mandatory]	21.06.2022	3 weeks after the kick-off meeting
Deadline for feedback [optional]	13.09.2022	2 weeks before the presentations
Presentations	27.09.2022	In person
Summary submission deadline	04.10.2022	1 week after the presentations

	Student	Topic
Proseminar	Aleen Aladani	4. Interpretation of differential gene expression results of RNA-seq data: review and integration
Seminar	Ritika Bansal	1. Simulation-based comprehensive benchmarking of RNA-seq aligners
	Sneha Thomas	2. CoCo: RNA-seq read assignment correction for nested genes and multimapped reads
	Maira Mirza	3. Accurate spliced alignment of long RNA sequencing reads
	Aram Papazian	6. RNA-Seq of Tumor-Educated Platelets Enables Blood-Based Pan-Cancer, Multiclass, and Molecular Pathway Cancer Diagnostics
	Vahid Atabaigielmi	7. The transcriptomic response of cells to a drug combination is more than the sum of the responses to the monotherapies
	Shing Cho Lin	8. A Nextflow pipeline for T-cell receptor repertoire reconstruction and analysis from RNA sequencing data
	Ayesha Amin	9. Accurate expression quantification from nanopore direct RNA sequencing with NanoCount

## Certificate requirements:

### 1. Successful presentation:

- Talk: **30 minutes** for a Proseminar and **40 minutes** for a Seminar
- Discussion: **5 minutes** during which you should be able to answer questions from the tutors/audience

### 2. Attendance to all presentations is **mandatory**

### 3. Submitting a summary report:

- Short description of the presented topic(s)
- Ca. 2 pages of text, excluding title (page), references, figures, tables etc..
- No figures, tables or formulas required
- Main structure: title page, main text (with or without subsections), references
- It is recommended to write the report using LaTeX to train scientific writing

## Final grade:

- Primarily based on the given presentation & follow-up discussion
- Might be influenced by the quality of the submitted summary report

Most importantly:

# Practice!

But also:

- Try to reduce the amount of text
  - prevent showing entire sentences
  - use figures or visualizations provided by the literature
- Rule of thumb:
  - you should be able to explain everything that's shown on your slides
- Proof-read your slides
- Speak freely and do not use cheat sheets



## We expect you to:

- Read our presentation guidelines:  
<https://www.ccb.uni-saarland.de/wp-content/uploads/2017/01/guidelines.pdf>
- Fill-out and send the presentation checklist along with your slides:  
[https://www.ccb.uni-saarland.de/wp-content/uploads/2014/09/presentation\\_guidelines.pdf](https://www.ccb.uni-saarland.de/wp-content/uploads/2014/09/presentation_guidelines.pdf)
- Ask for feedback or formulate questions whenever you are stuck
- Independently use the available literature to enhance your knowledge on the assigned topic
  - *See also our **recommended reading** literature on the course site!*

**Any questions?**