

SEMINAR SINGLE-CELL RNA SEQUENCING – KICK-OFF MEETING

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WELCOME

Thanks for enrolling!

- 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!



- 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!

1: Systematic comparison of single-cell and single-nucleus RNA-sequencing methods (Sili Vettiyara Sunil)

2: zUMIs – A fast and flexible pipeline to process RNA sequencing data with UMIs (Berit Andres)

3: Modular and efficient pre-processing of single-cell RNA-seq (Iyanuoluwani Owolabi)

4: Bias, robustness and scalability in single-cell differential expression analysis (DEBANGANA CHAKRABORTY)

5: Classification of low quality cells from single-cell RNA-seq data (Baris Kalem)

6: Supervised classification enables rapid annotation of cell atlases (Johanna Elena Schmitz)

7: The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells (Ipshita Kanungo)

8: RNA velocity of single cells (Muhammad Hamid)

9: Inference and analysis of cell-cell communication using CellChat (Shusruto Rishik)

10: Benchmarking algorithms for gene regulatory network inference from single-cell transcriptomic data (Hsin Yu Wu)

All papers should be freely accessible via the university VPN

Event	Time	Comments
Registration	26.04.2021 - 16.05.2021	
Kick-off meeting [mandatory]	Today (08.06.2021)	Remote
Deadline to register in HISPOS OR de-register from seminar [mandatory]	29.06.2021	3 weeks after the kick-off meeting
Deadline for feedback [optional]	06.09.2021	1 week before the presentations
Presentations	13.09 / 14.09.2021	Remote (Microsoft Teams)
Summary submission deadline	20.09.2021	1 week after the presentations

Meetings are performed remotely via **Microsoft Teams**



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
- 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?

<https://www.ccb.uni-saarland.de/teaching/seminar-single-cell-rna-sequencing-summer-term-2021/>

@ KIST Europe

Deep learning Project with ChEMBL database

Contact for further information or questions

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