CHAIR FOR CLINICAL BIOINFORMATICS
SAARLAND UNIVERSITY

PRO-/SEMINAR: ROLE OF BIOINFORMATICS IN EPIGENETICS

WS 2020/21

M.Sc. Viktoria Wagner
s8vawagn@stud.uni-saarland.de

08/12/2020

Thanks for enrolling!

- **Why?**
  - Epigenetic modifications are crucial to development and differentiation
  - Can cause human diseases → important biomarkers
- **What?**
  - Methods to detect epigenetic modifications, mainly DNA-methylation and histone modifications
- **How?**
  - Papers selected for the seminar focus on bioinformatic methods in the epigenetics field
  - Experimental methods and examples of research applying these methods

CHAIR FOR
CLINICAL
BIOINFORMATICS
SAARLAND UNIVERSITY

- Proseminar (Bachelor's only, 5 CPs - graded):
    - At least in 3rd semester
    - Successful attendance of Bioinformatics I & Genetics lecture

- Seminar (Master's only, 7 CPs - graded):
    - No formal prerequisites
    - But proficient skills in **maths, programming, and bioinformatics** are assumed

- Good English skills as **all talks** will be held in English language!

CHAIR FOR
CLINICAL
BIOINFORMATICS
SAARLAND UNIVERSITY

1: Epigenetic prediction of complex traits and death

2: Quantitative comparison of DNA methylation assays for biomarker development and clinical applications

3: MethMotif: an integrative cell specific database of transcription factor binding motifs coupled with DNA methylation profiles

4: COCOA: coordinate covariation analysis of epigenetic heterogeneity

5: Assessment of computational methods for the analysis of single-cell ATAC-seq data

6: HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics

7: A comprehensive comparison of tools for differential ChIP-seq analysis

8: Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data

9: NOMeplot: analysis of DNA methylation and nucleosome occupancy at the single molecule

10: Dynamic changes in the epigenomic landscape regulate human organogenesis and link to developmental disorders

Name	Topic	Topic number
Sami Adbennour Laradji	Assessment of computational methods for the analysis of single-cell ATAC-seq data	1
Jennifer Czaja	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications	2
Anna Hartung	COCOA: coordinate covariation analysis of epigenetic heterogeneity	3
Guangyi Chen	Epigenetic prediction of complex traits and death	4
Omar Laham	Dynamic changes in the epigenomic landscape regulate human organogenesis and link to developmental disorders	5

Name	Topic	Topic number
Larissa Sue Fey	A comprehensive comparison of tools for differential ChIP-Seq analysis	6
Marie Detzler	HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics	7
Kalanika Elamaldeniya	MethMotif: an integrative cell specific database of transcription factor binding motifs coupled with DNA methylation profiles	8
Jens Petermann	NoMeplot: analysis of DNA methylation and nucleosome occupancy at the single molecule	9
Md. Adnan Karim	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data	10

Exchanging topics is possible until 15.12.2020 with notification of both students to the tutor

Event	Time	Comments
Registration	09.11.2020-20.11.2020	
Kick-off meeting [mandatory]	Today (08.12.2020)	Remote (Microsoft Teams)
Deadline to register in HISPOS OR de-register from seminar [mandatory]	04.01.2021	4 weeks after the kick-off meeting
Deadline for feedback [optional]	01.03.2021	2 weeks before the presentations
Presentations	15.03.2021	Remote (Microsoft Teams)
Summary submission deadline	22.03.2021	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
- Extensively proof-read your slides
- Speak freely and do not use cheat sheets

CHAIR FOR
CLINICAL
BIOINFORMATICS
SAARLAND UNIVERSITY

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 (before the presentation!):
  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/pro-seminar-role-of-bioinformatics-in-epigenetics/