

Schedule : Spring 2022

This is the tentative schedule of Mélange group for the Fall 2021 semester.

Meeting time & Place : Tuesdays 9:30 AM - 10:30 AM (MST/MDT) in ISTeC Room (CSB 305), and via Webex.

WEEK	DATE	TOPIC	PRESENTER
1	1/18		
2	1/25	Paper critique	Everyone
3	2/1		
4	2/8	Paper critique	Everyone
5	2/15	?	?
6	2/22	Batch Binary Edwards	William Scarbro
7	3/1	Program Equivalence	Louis-Noël Pouchet
8	3/8	Linear scan register allocation	Louis-Noël Pouchet
9	3/22	The Mapping of Linear Recurrence Equations on Regular Arrays	Corentin Ferry
10	3/29	Scheduling Reductions	Nana Yin
11	4/5	Master's Thesis: Iterative optimization in the polyhedral model	Louis-Noël Pouchet
12	4/12	A Unified Dynamic Programming Framework for the Analysis of Interacting Nucleic Acid Strands: Enhanced Models, Scalability, and Speed	Chiranjeb Mondal
13	4/19		Vidit Save
14	4/26		William Scarbro
15	5/3		Shenmou Liu

Previous Semesters, including legacy reading lists

1. [Fall 2021](#)
2. [Spring 2021](#)
3. [Fall 2020](#)
4. [Fall 2019](#)
5. [Spring 2019](#)

Standard paper study questions

1. Write a short (max 5 sentences) summary of the paper.
2. What is the problem addressed in the paper?
3. Why is the problem important?
4. How do the authors address the problem?
5. How do they evaluate their approach?
6. What is the punch-line (key cool idea, or “what I got out of this paper”)? This is often different for different people and different from what the authors may have intended.
7. Make a list of deeper questions that you would like discussed in the meeting.

Current Reading Pool

- Charles E. Leiserson, Neil C. Thompson, Joel S. Emer, Bradley C. Kuszmaul, Butler W. Lampson, Daniel Sanchez, Tao B. Schardl. **There's plenty of room at the Top: What will drive computer performance after Moore's law?** In *Science*, 6495, 2020.
<https://www.microsoft.com/en-us/research/uploads/prod/2020/11/Leiserson-et-al-Theres-plenty-of-room-at-the-top.pdf>
- Mark E. Fornace, Nicholas J. Porubsky, Niles A. Pierce. **A Unified Dynamic Programming Framework for the Analysis of Interacting Nucleic Acid Strands: Enhanced Models, Scalability, and Speed.** In *@/oc@*, 10, 2020. <https://doi.org/10.1021/acssynbio.9b00523>

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