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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 @loc@, 10, 2020. https://doi.org/10.1021/acssynbio.9b00523

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Last update: 2022/04/12 10:46

