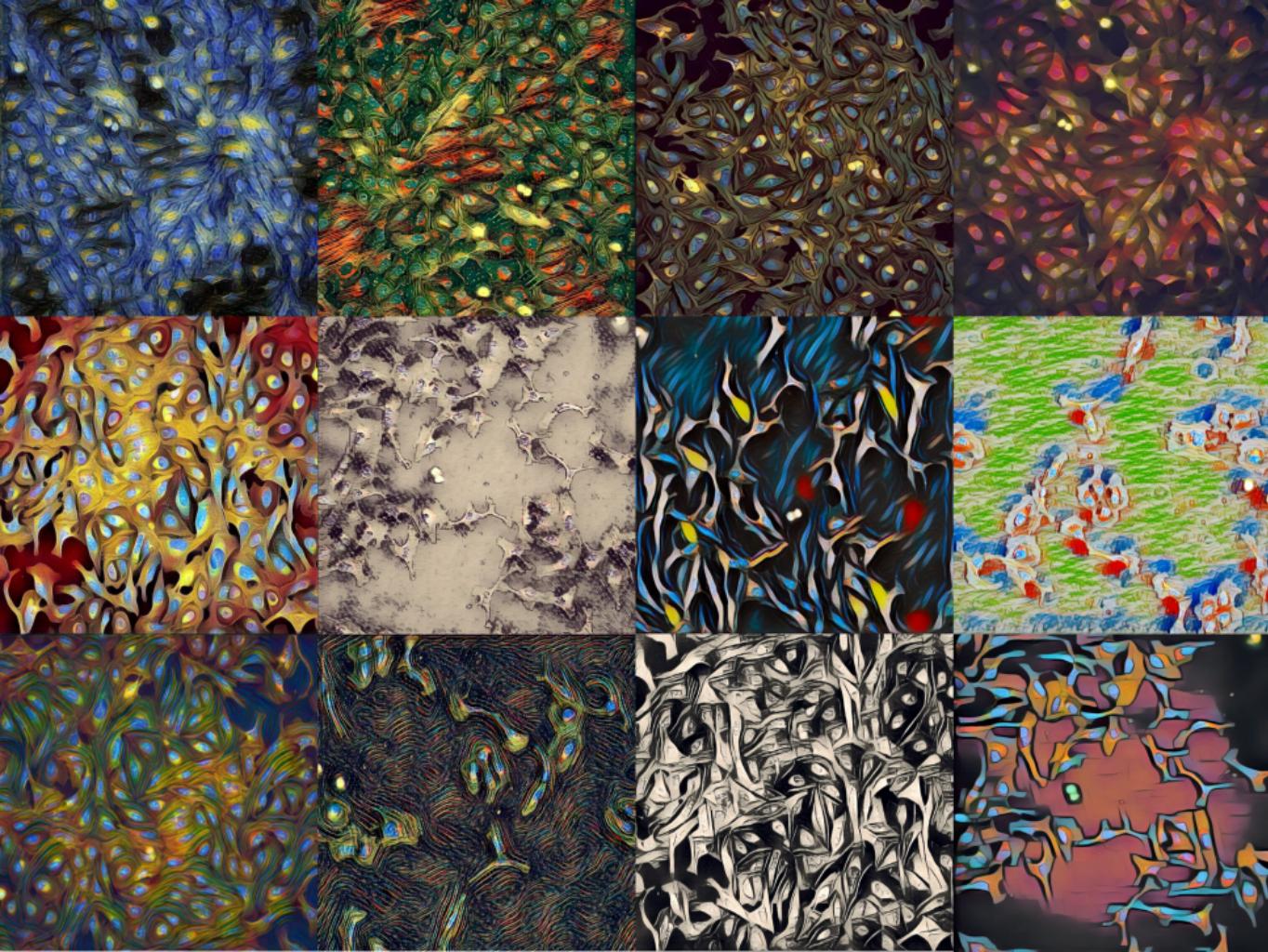


# 2024 Cytodata Hackathon

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September 17th, 2024



## Goals of the event

- Foster collaborations between biologists and computer scientists, to match problems and potential solutions
- Build a new tool to extract biological insights from JUMP, or discover something that can be followed-up with further experiments
- Showcase how to access the latest JUMP morphological profiles and explore new ways to process them

## Main items in the schedule

	Time
Start	9:30
Lunch	12:30-13:30
Break	15:20-15:40
Presentations and awards	17:20-18:20

## Notes

- The two tracks of the Hackathon are "best tool/method" and "best biological story"
- Teams will spread across the four conference rooms in this floor, including here
- All rooms will be connected on a Zoom call
- Mentors with biological and/or computational expertise will float around to help teams
- If you need to go outside just let us know when you are back to have someone pick you up
- Presentations at the end of the day will be five minutes per team

## Evaluation criteria

- Problem definition: Is the biological/technical problem well-defined?
- Creativity: How well does the team leverage existing tools to solve their problem? Are there any out-of-the-box ideas or methods?
- Potential: How much potential does the idea have to become a product (i.e., article, software)
- Execution: The quality of the implementation and presentation.

## Examples of project ideas

- How do we connect JUMP information to many other databases?
- Can we consistently identify plate layout effects?
  - Upon corrections of layout effects, how do we evaluate an improvement?
- Which chemical compounds that result in extreme phenotypes are found in JUMP?
- Specific biological stories (link on *Resources* slide)

# Mentors

Mentor	Focuses on
Anne	Biological Interpretation, Imaging
Paula	Biological Interpretation, Imaging
Niranj	Data analysis, Overall JUMP expert
Jess	Data analysis, Biological Interpretation
Tim	Tool-development, Spatial Bio
Hugo	JUMP bespoke tools, Chemoinformatics
John	Batch correction, External annotations
Alex	Statistics, mAP method

## Conference rooms

You can check your team and the associated room on the participants' spreadsheet

- Joshua Tree
- Badlands
- Crater Lake
- Acadia (this room)
- Huddle office (11017)

# Acknowledgements

Organizers and sponsors:



Artificial Intelligence & Bioinformatics  
for Precision Medicine



CytoData



# Resources

- [broad.io/jump](https://broad.io/jump): JUMP Hub, including tutorials, definitions and tips on how to access and wrangle morphological profiles.
- [broad.io/jump-explore](https://broad.io/jump-explore): Web-browser databases for no-code exploration
- [github.com/cytomining/copairs](https://github.com/cytomining/copairs): Library used to find pairs of perturbations and compute metrics between them
- [broad.io/monorepo](https://broad.io/monorepo): Additional libraries used by the Imaging Platform (advanced)
- [Examples](#) of existing biological stories based on JUMP data

# Questions?