





#### 9PM

2AM in London (GMT), 11AM in Tokyo (GMT+9)

#### **Multiscale Models**

Moderator: Katy Börner, Indiana University

#### Presenters:

- Maria Brbic, Swiss Federal Institute of Technology Lausanne, Switzerland
- · Filipi N. Silva, Indiana University



#### AI Revolution

#### Generative AI paradigm and the era of foundation models



Model that has learnt features transferable to a wide range of downstream tasks

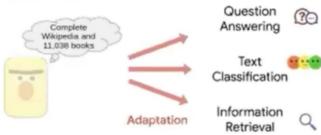


Tasks

Text corpus



#### Pretrained LM



How can we leverage these Al advances in single cell biology?

What are their current limitations for biomedical applications?

# Single-cell Data Is Challenging for Today's AI

1 Heterogenous experiments

2 Novel and unknown phenomena

3 Different modalities with different challenges

Marin (resk), EPFL

- 1 Heterogenous experiments
- 2 Novel and unknown phenomena
- 3 Different modalities

Today's talk: How to overcome some of these challenges

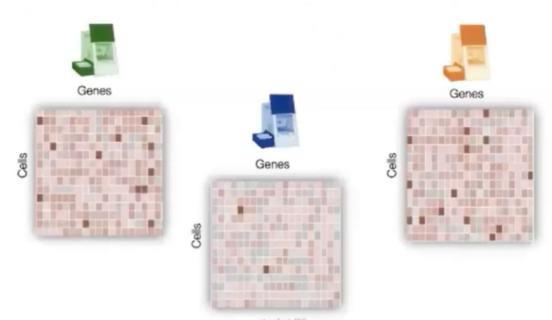
besi, (94),

## On Heterogeneity

Discovering Cell Types Across Tissues, Disease States & Species

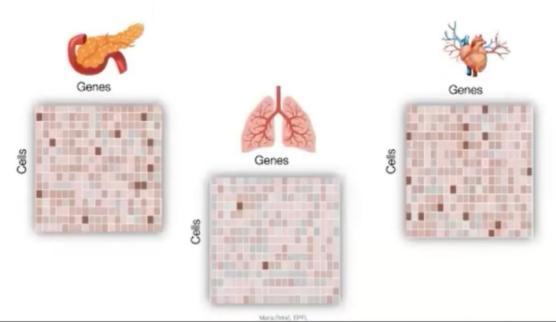
# Data with Large Heterogeneity

different labs...



# Data with Large Heterogeneity

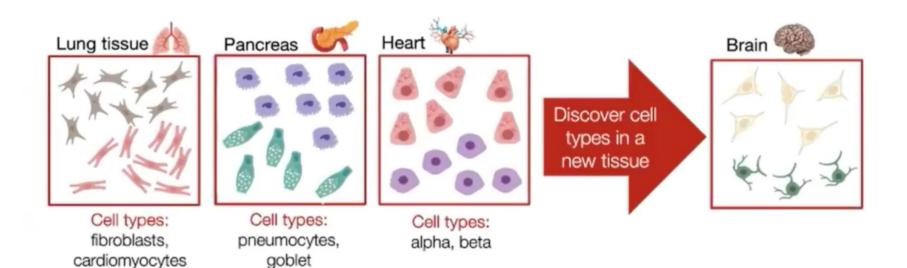
different tissues...



# How do we jointly analyze and gain new insights from these heterogenous datasets?

ris deski, EPFI.

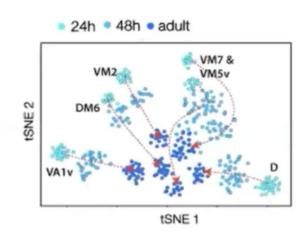
#### MARS: Learn Cell Embeddings to Discover Novel Cell Types



#### Cell Type Discovery across Experiments



Across tissues of the Mouse Cell Atlas



Xie\*, Brbic\* et al. eLife '21



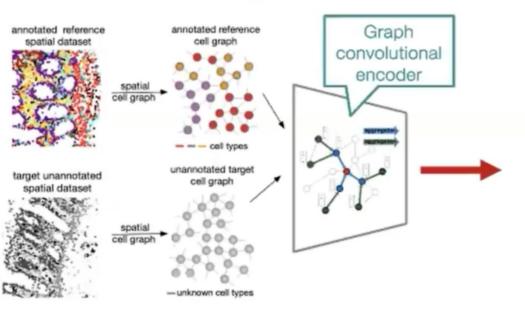
Fly Cell Atlas



Li\*, Janssens\* et al. Science '22



# \*\* STELLAR: Novel Cell Type Discovery Across Conditions



#### Known cell types



Novel / disease specific cell types



Brbic\*, Cao\*, Hickey\*, Tan, Snyder, Nolan, Leskovec Nature Methods' 22

16

#### Towards Universal Cell Embeddings

Can we create cell embeddings for any species, any set of genes?

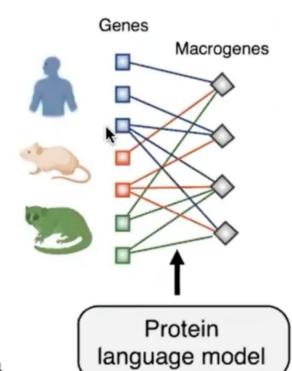


#### Our Approach: SATURN



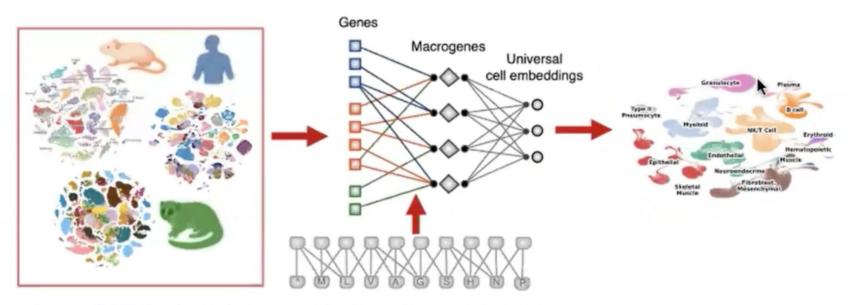
Key Idea: Map diverse sets of genes in the joint space of macrogenes

- Macrogenes: groups of functionally related genes
- Learn macrogene space using protein embeddings from language models



Rosen\*, Brbic\*, Roohani\*, Swanson, Li, Leskovec. Nature Methods '24

# SATURN: Integrating Datasets across Species



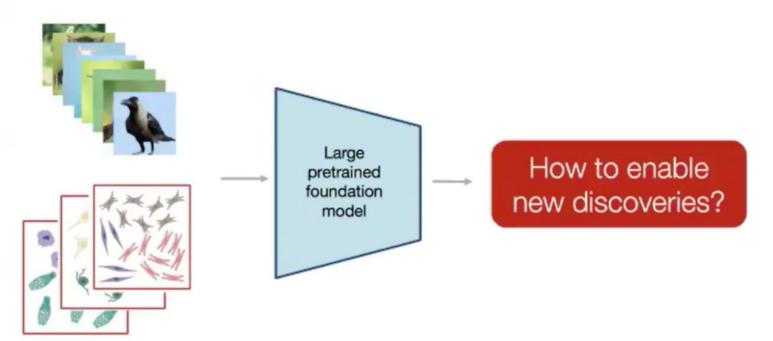
Rosen\*, Brbic\*, Roohani\*, Swanson\*, Li, Leskovec Nature Methods' 24

0to, 0%.

### On Discovery

Enabling Discovery from Foundations Models

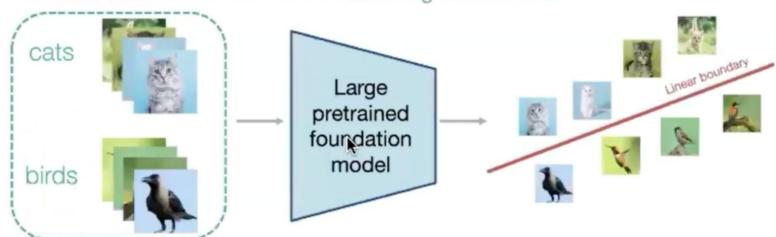
# How To to Enable New Discoveries from Foundation Models?



Maris Bed, 699.

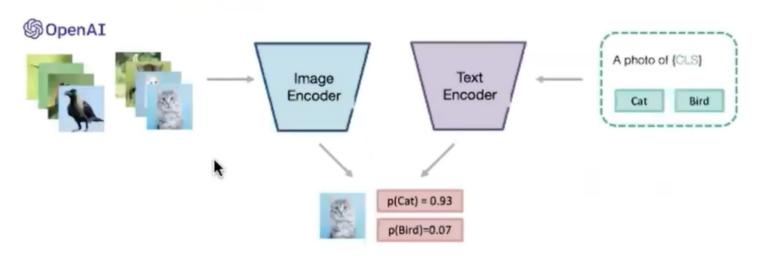
## Current Paradigms Still Require Supervision

- Current paradigms:
  - 1. Fine-tune on the task of interest using labeled data



## Current Paradigms Still Require Supervision

- Current paradigms:
  - 2. Zero-shot transfer on the task of interest using instructions

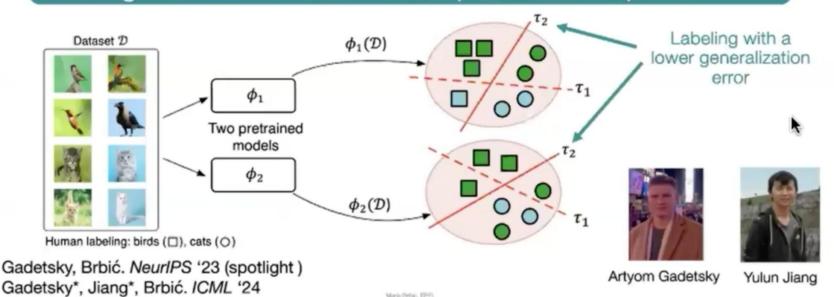


## How to Infer Labeling without

#### Any Supervision?



Key idea: Search for a labeling such that linear models will generalize well in different representation spaces

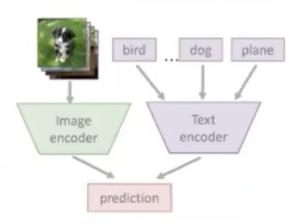


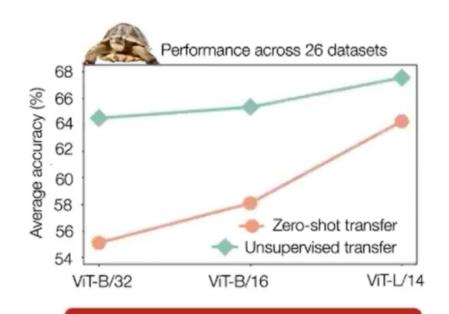
#### Unsupervised Transfer Outperforms Zero-Shot

#### SOTA unsupervised performance

26 datasets benchmark from CLIP

SopenAI Zero-Shot CLIP Model



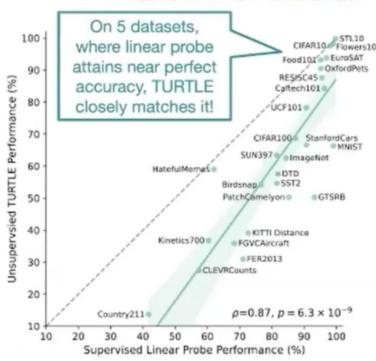


TURTLE is fully unsupervised!

Gadetsky\*, Jiang\*, Brbić. ICML '24

26

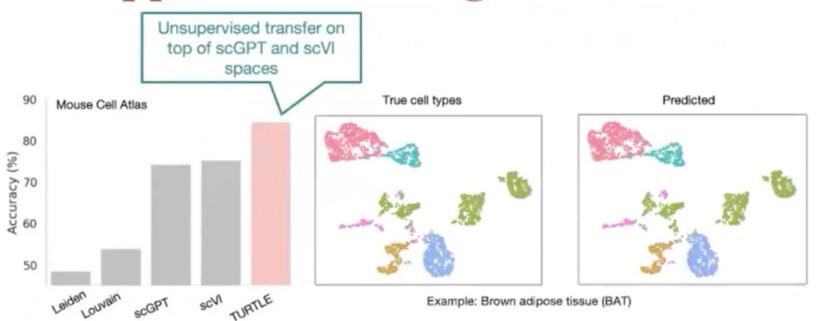
### TURTLE's Performance Is Correlated to Linear Probe





Maria Breac, DFR. 27

#### Application to Single-Cell Data



## On Multi-modality

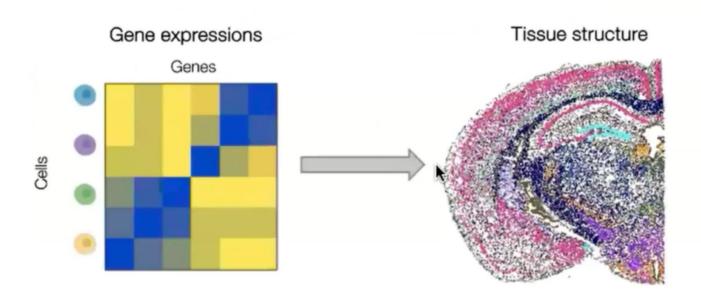
Generating Complex Tissue Structures from Gene Expressions

## AlphaFold For Cells

# Protein structure Protein sequence

Aris (Yes), EPP,

# AlphaFold For Cells



Arric (res), (DPI).



#### LUNA: From Cells to Locations

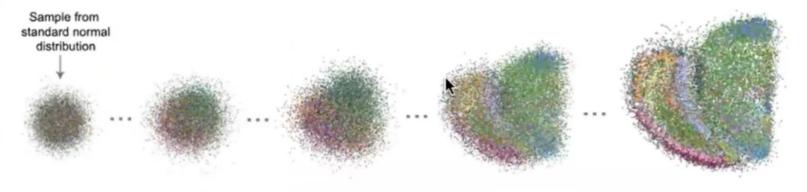
A generative model for mapping cells to their locations and generating tissue structures

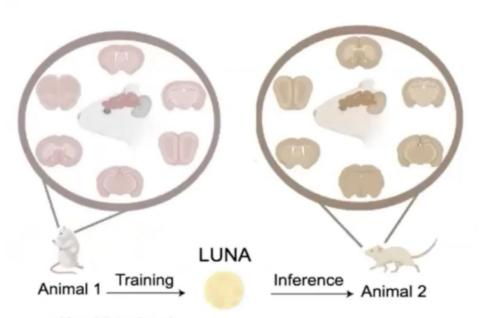




Yist Yu

u Chanakya Ekbote





#### Dataset:

 MERFISH Mouse Brain Atlas with over 4 million cells

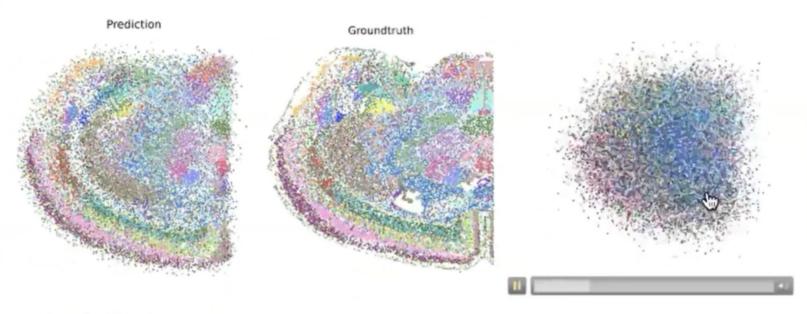
#### Training dataset:

2.85 million cells across
 147 slices from one mouse

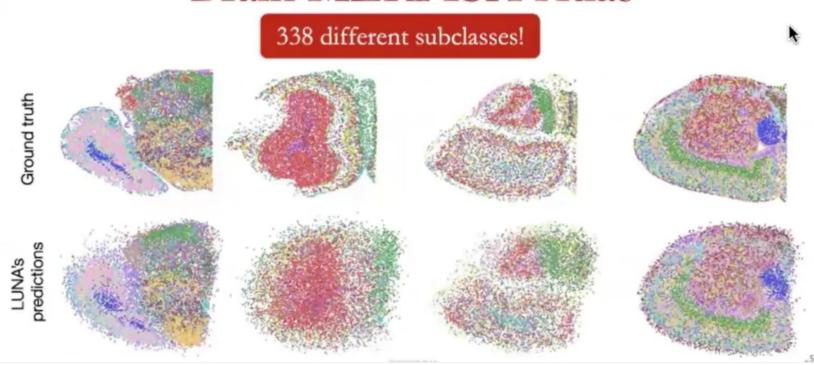
#### Target unlabeled dataset:

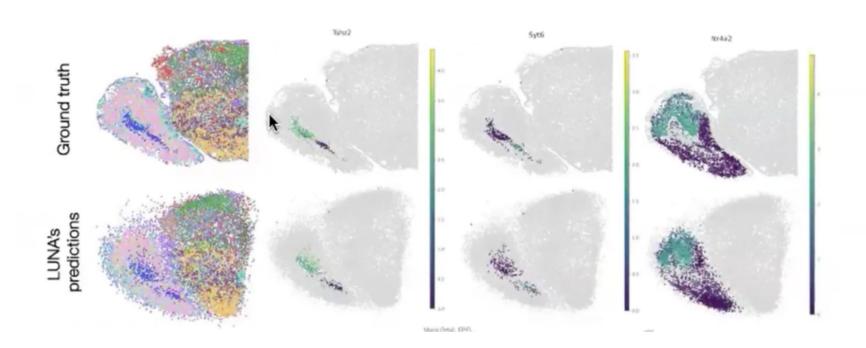
 1.23 million cells across 66 slices from another mouse

Unpublished work

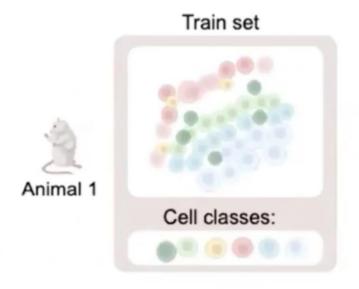


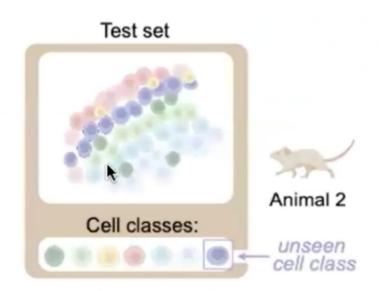
Unpublished work





### LUNA: Zero-Shot Setting

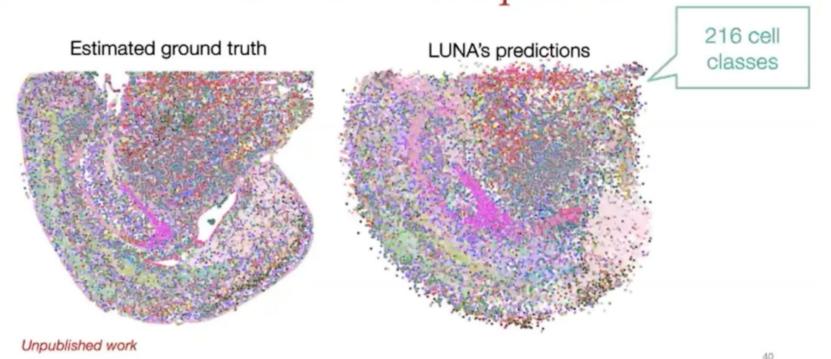




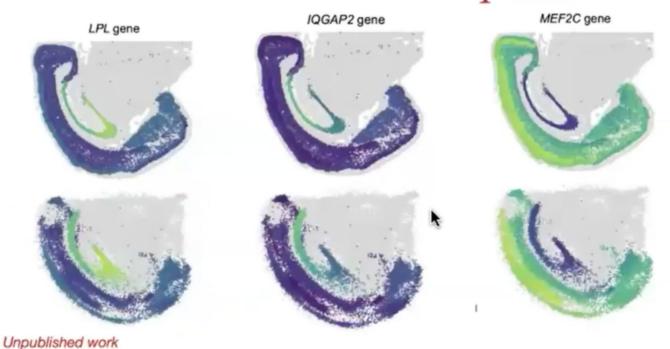
### Zero-Shot Generalization to Unseen Cell Types



# De Novo Reconstruction of CNS ScRNA-seq Atlas



# De Novo Reconstruction of CNS ScRNA-seq Atlas



# Acknowledgements

PhD students

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Ramon Vinās Tórne Myeongho Jeon

Research engineers Jeremy Goumaz

### Assistant:

Marie Künzle



### Collaborators:

Jure Leskovec, Stanford
Yanay Rosen, Stanford
Yusuf Roohani, Stanford
Kaidi Cao, Stanford
John Hickey, Duke
Hongjie Li, Baylor College of Medicine
Yuqi Tan, Stanford
Liqun Luo, Stanford
Michael Snyder, Stanford
Garry Nolan, Stanford
Pascal Frossard, EPFL
Chanakya Ekbote, MIT







# Generative AI for Decoding Single-Cell Complexity

Maria

Maria Brbić

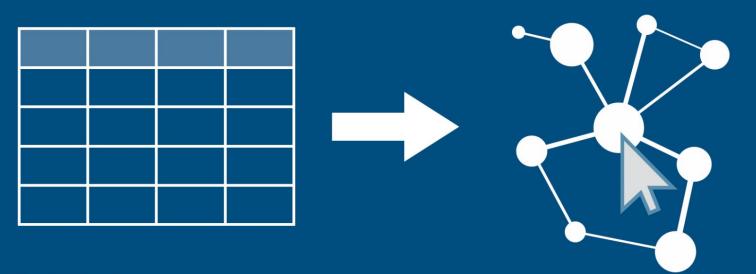






# Charting Complexity: Interactive real-time visualizations of large-scale networks and embeddings with Helios-Web

https://www.icloud.com/keynote/018HYK4JjBOCRA8N5NGjU7dVg#Embeddings Visualization reduced

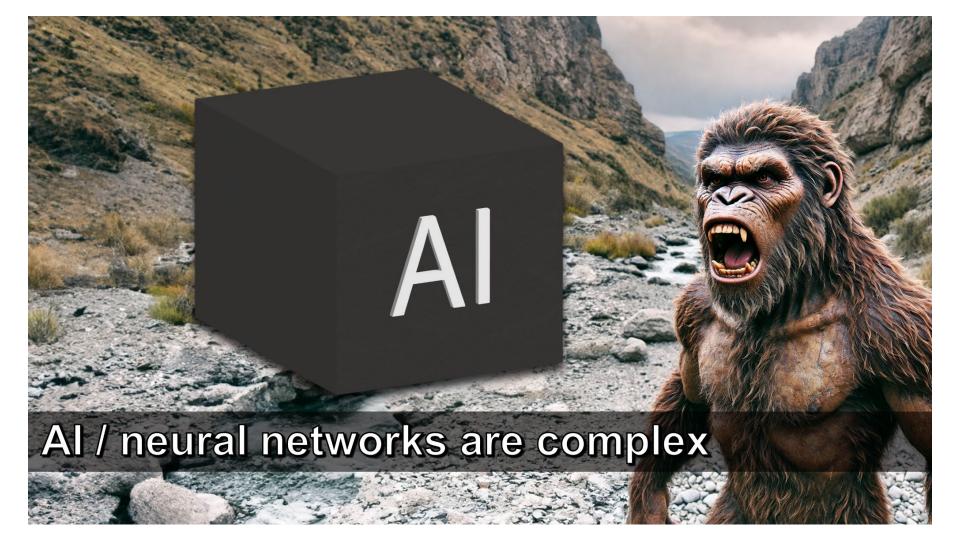


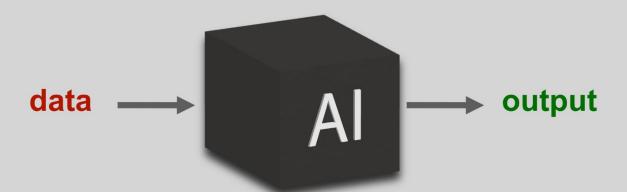


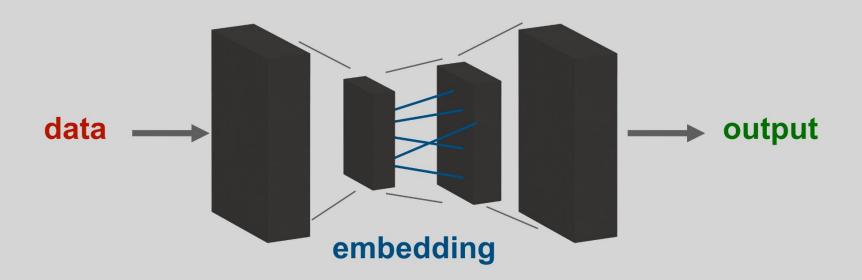
# Filipi N. Silva

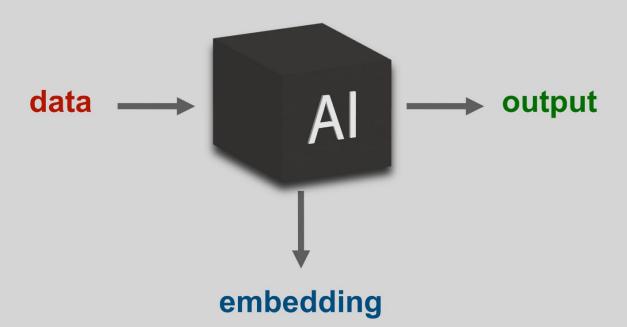
research scientist - Indiana University filipinascimento.github.io • filsilva@iu.edu

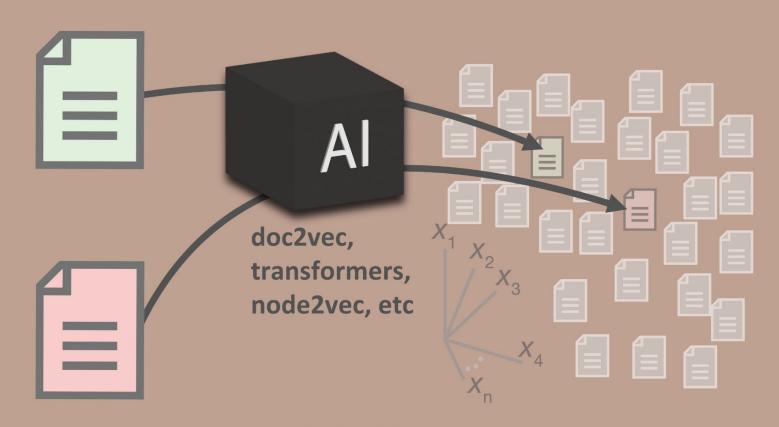




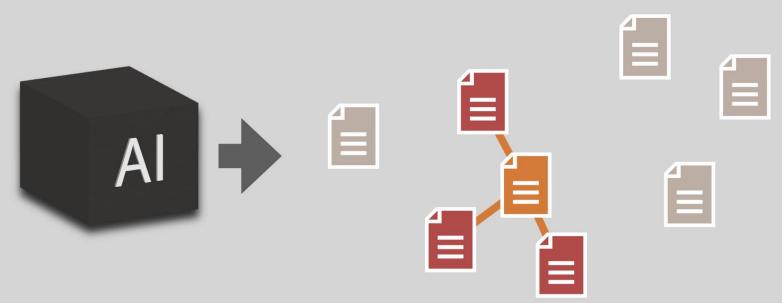






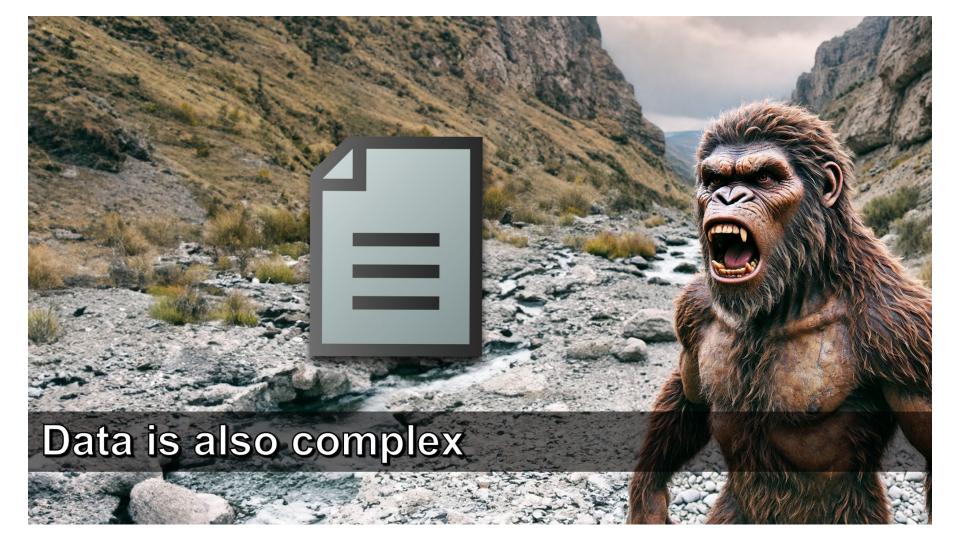


**Embeddings** 

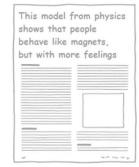


Recommendation systems

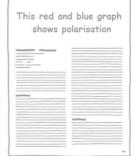
Databases/Search engine
Retrieval-Augmented Generation (RAG)
Anomaly Detection



### Types of Computational Social Science papers





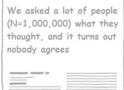








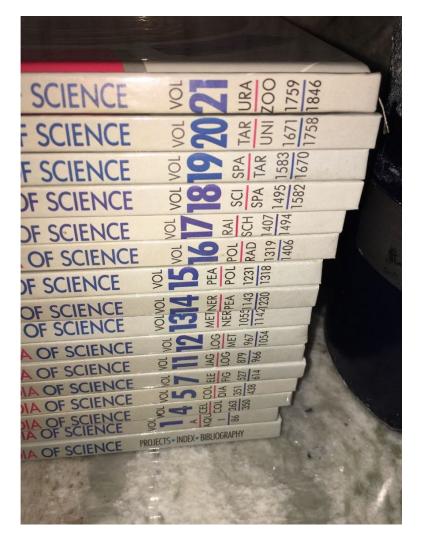
On the importance of
computational methods to
<insert discipline="" here=""></insert>
-



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by Chico Camargo (Twitter) https://twitter.com/evoluchico/status/1388137531552718860

Catchy Title:



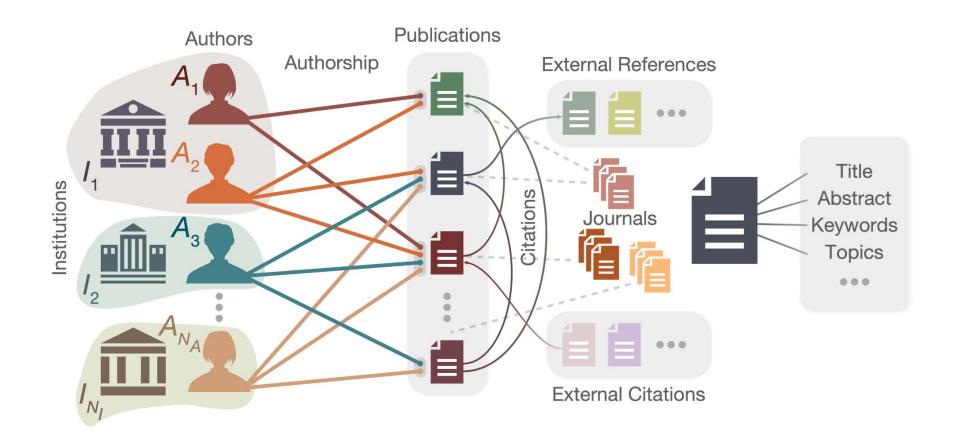
# **Science of Science**

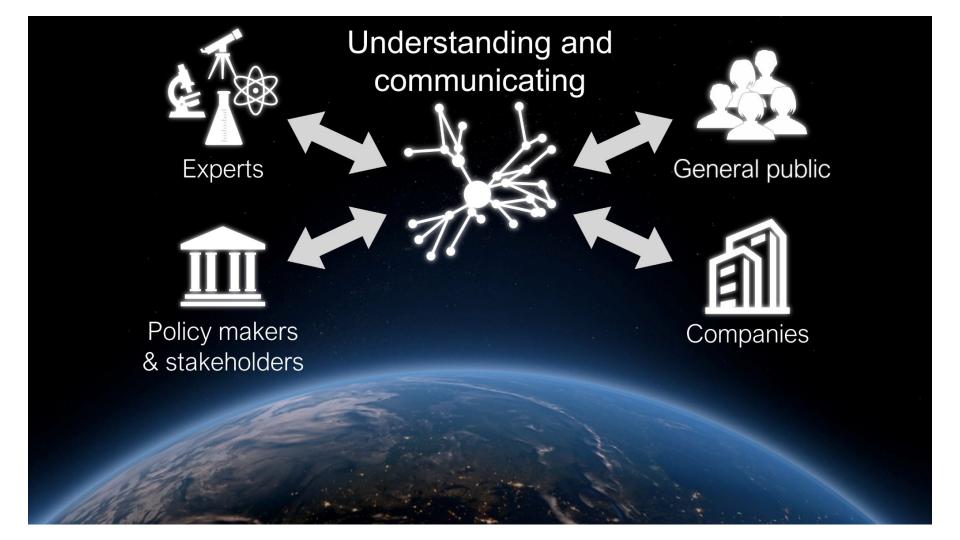
- How science is evolving?
- How researcher teams are formed?
- Is science becoming more interdisciplinary?
- Can we predict success in science?
- How to properly evaluate researchers? journals? papers?
- Can tools/approaches accelerate the scientific development?
- Can we predict the benefits of implementing a policy?
- •

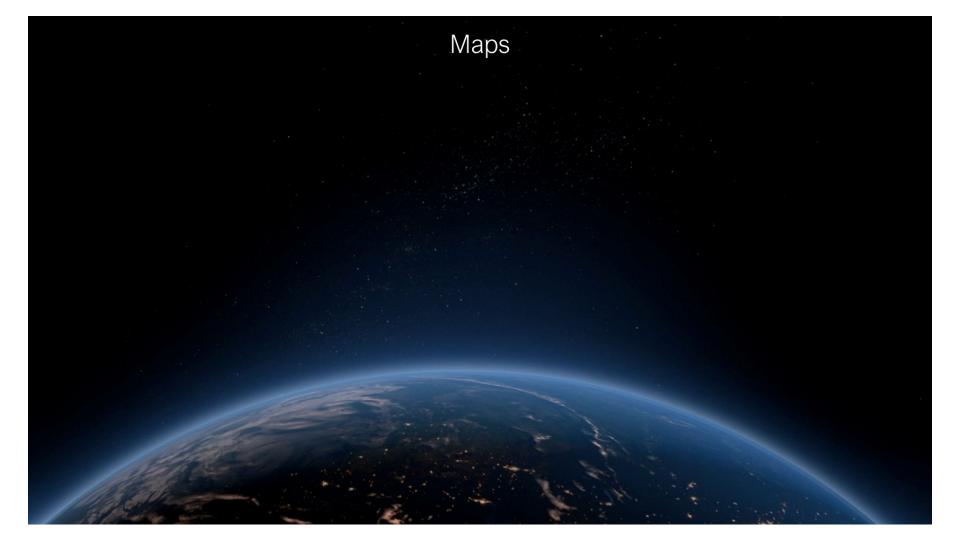


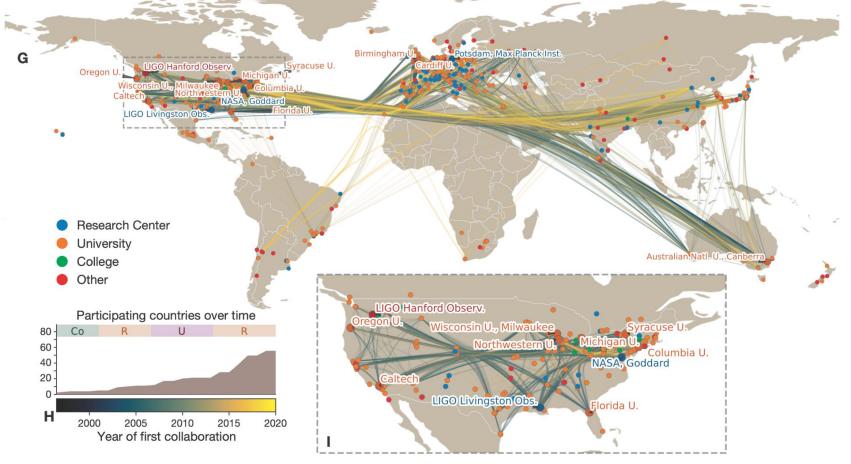
### **Publications**





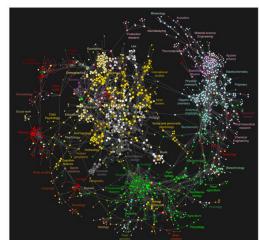




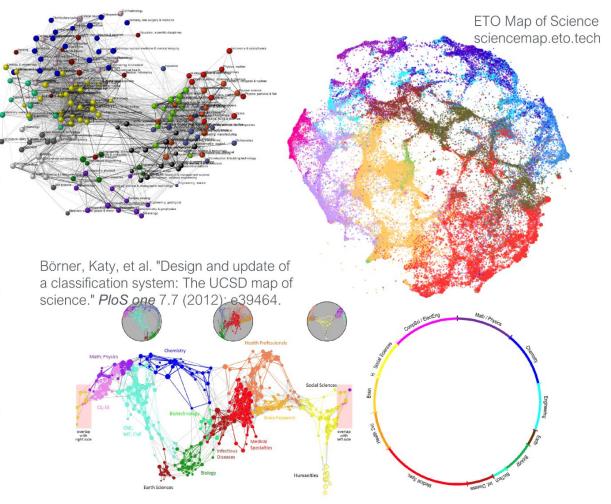


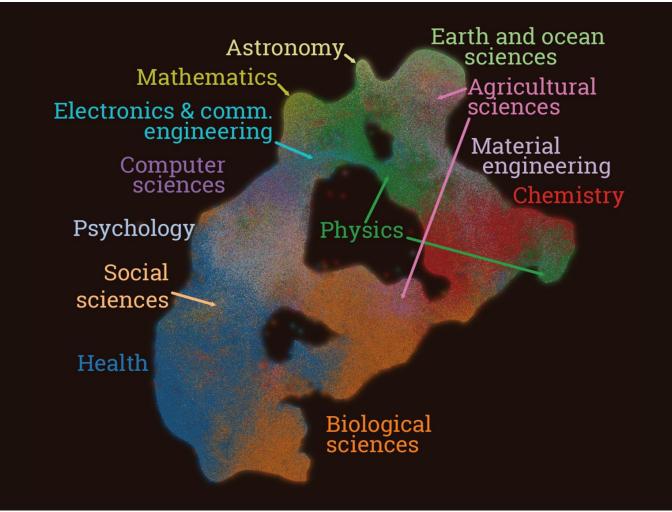
Börner, K., Silva, F. N., & Milojević, S. (2021). Visualizing big science projects. Nature Reviews Physics, 3(11), 753-761.

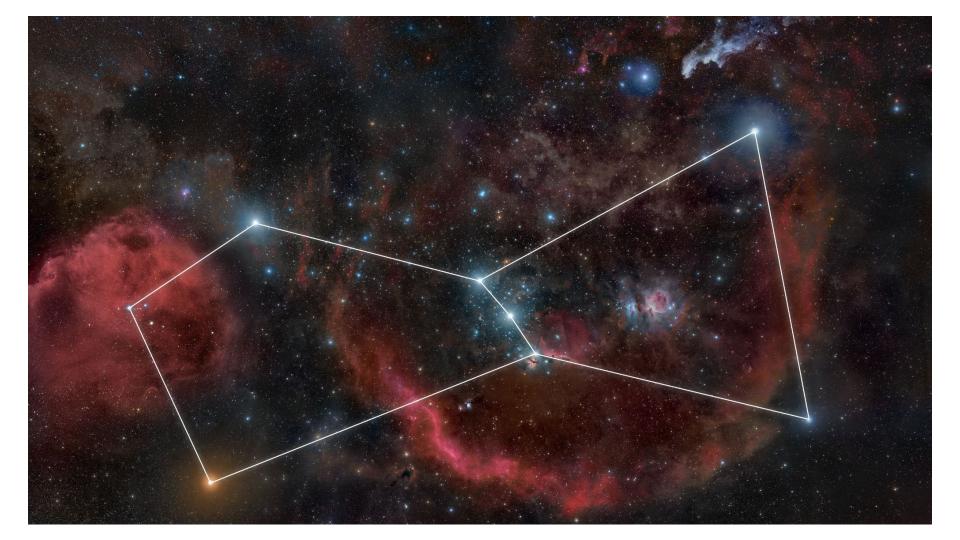
Leydesdorff, Loet, and Ismael Rafols. "A global map of science based on the ISI subject categories." Journal of the American Society for Information Science and Technology 60.2 (2009): 348-362.

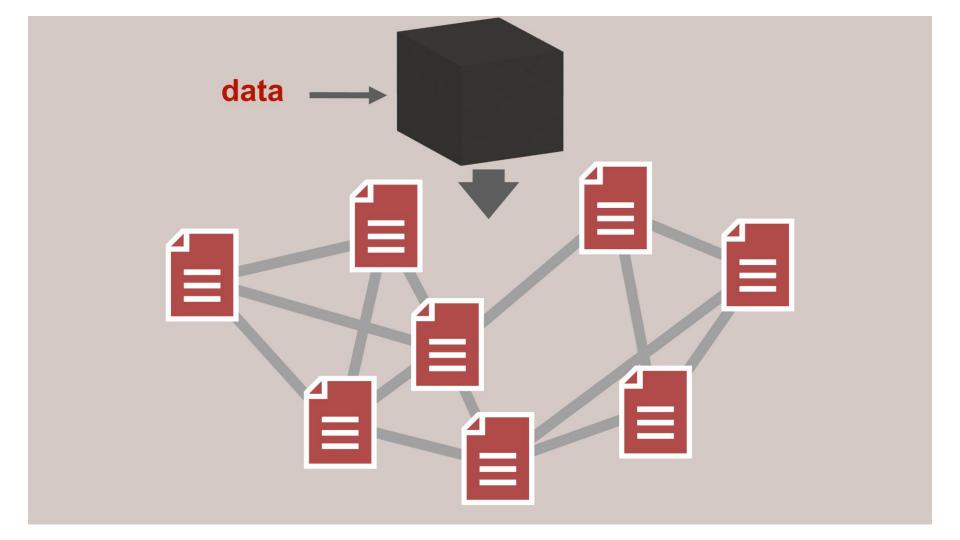


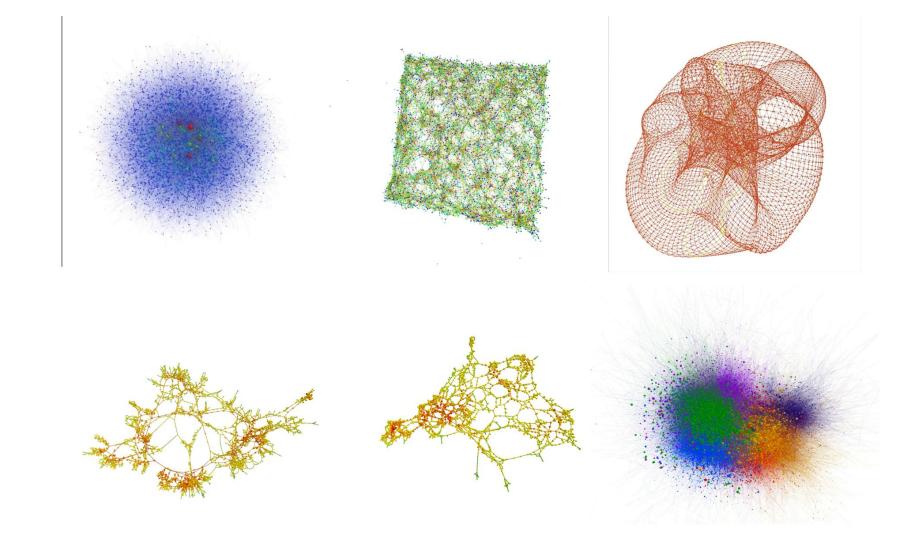
Bollen, Johan, et al. "Clickstream data yields high-resolution maps of science." PloS one 4.3 (2009): e4803.

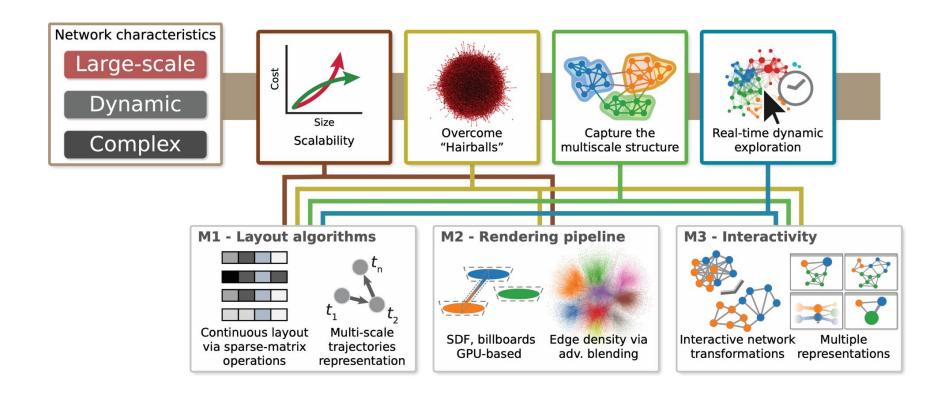


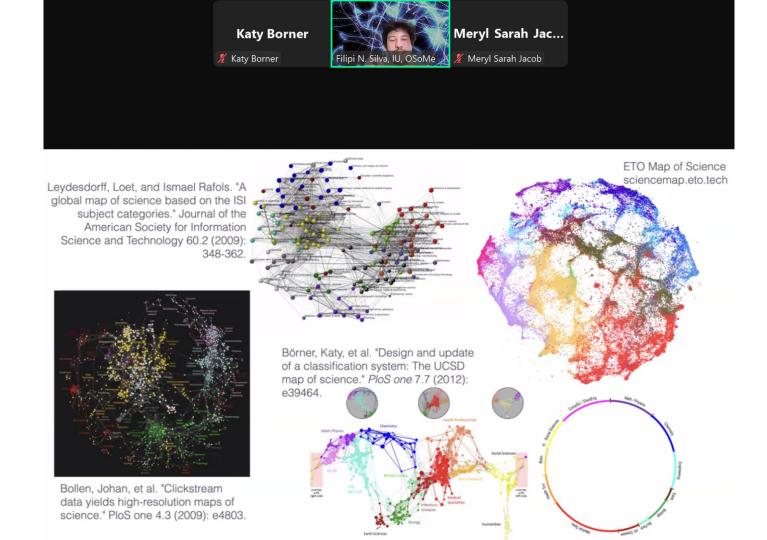


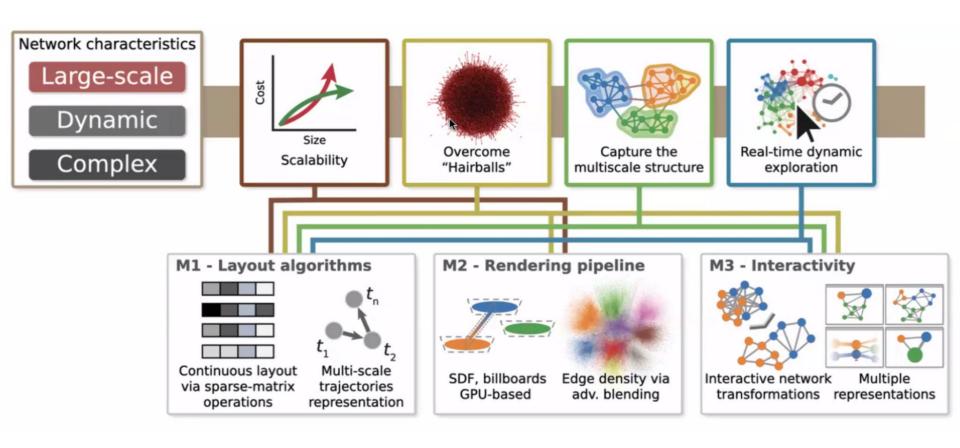














An open-source visualization library for the web

heliosweb.io



## Open-source web framework

can be integrated in websites, portals, dashboards ...

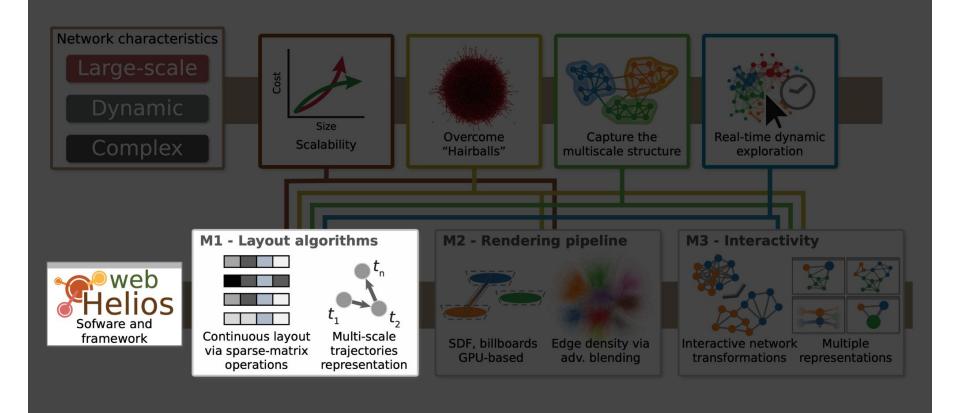
# **Optimized rendering and layouts**

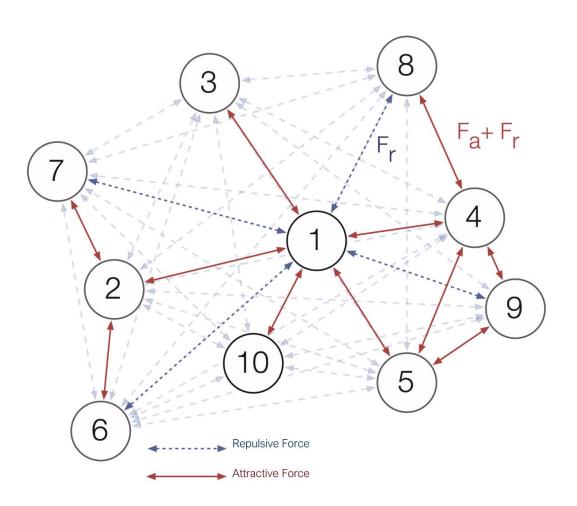
can visualize large networks, high-quality rendering ...

# Interactivity\*

allows picking, filtering, navigation, multi-representations ...

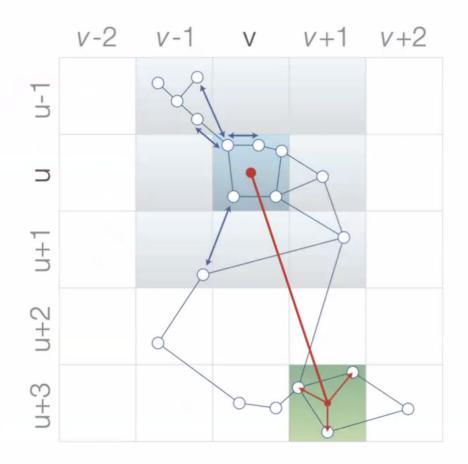
\*in development





# Layout optimizations

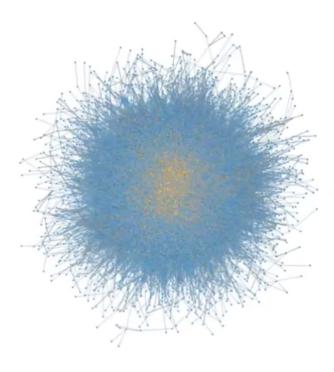
- Molecular dynamics simulation is O(N²).
- We can use multipole expansion (FM3):
- Segment the space
- Real-time continuous layout



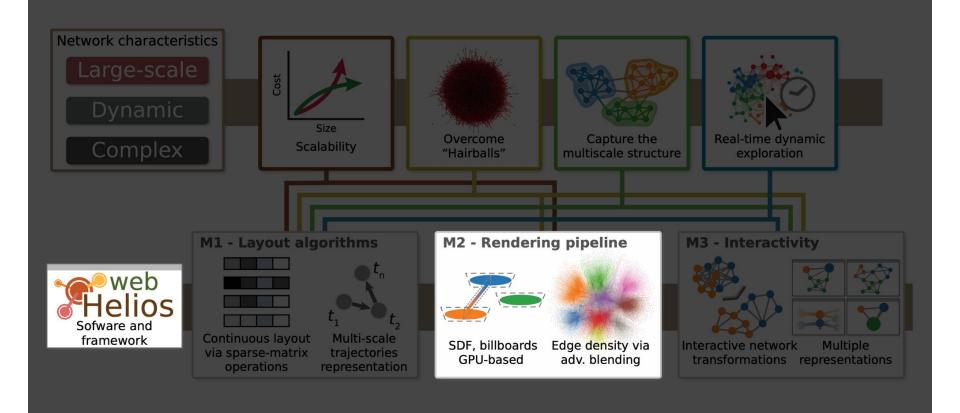
\* S. Hachuland M. Jünger. Drawing large graphs with a potential-field-based multilevel algorithm. In International Symposium on Graph Drawing, pp. 285–295. Springer, 2004. doi: 10.1007/978-3-540-31843-9\_29

### **Wiki Medicine and Mathematics**

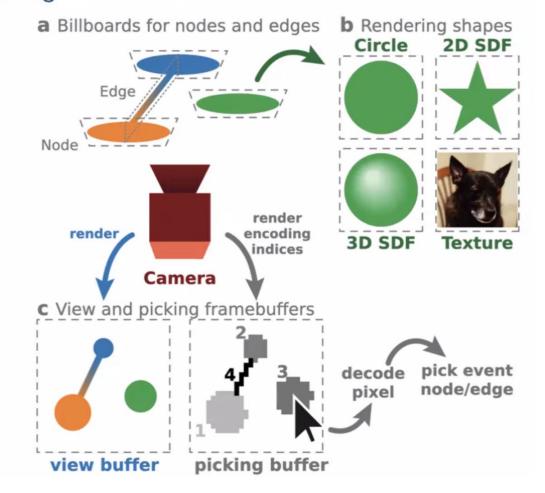


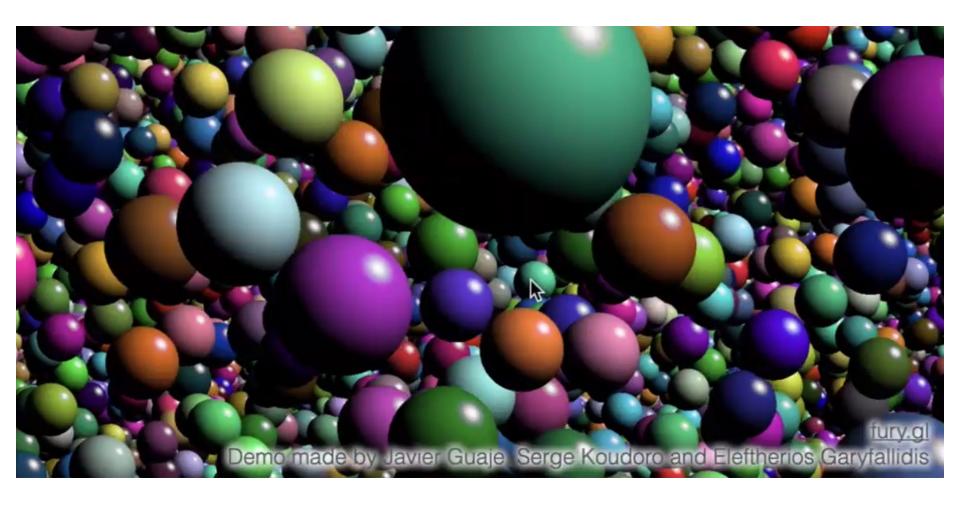


Visualizing Complex Networks (CDT-5) Silva, F. N. and Costa, L. da F. http://dx.doi.org/10.13140/RG.2.2.21310.74567/1



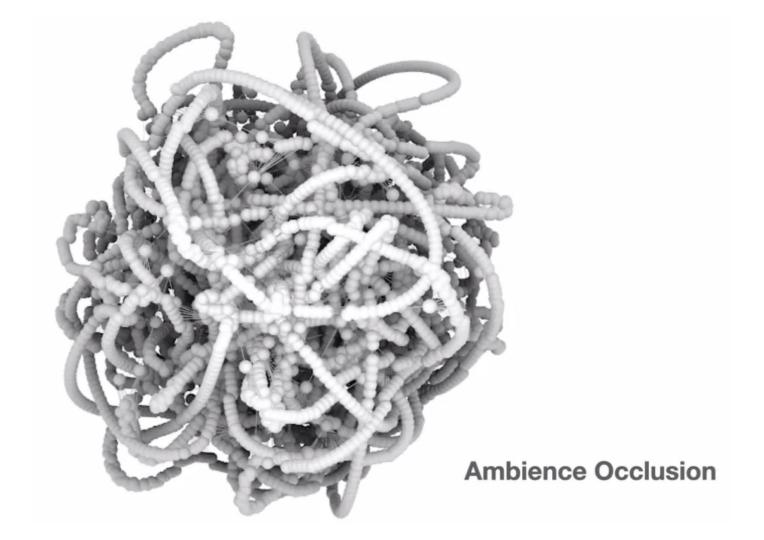
# Rendering in the GPU

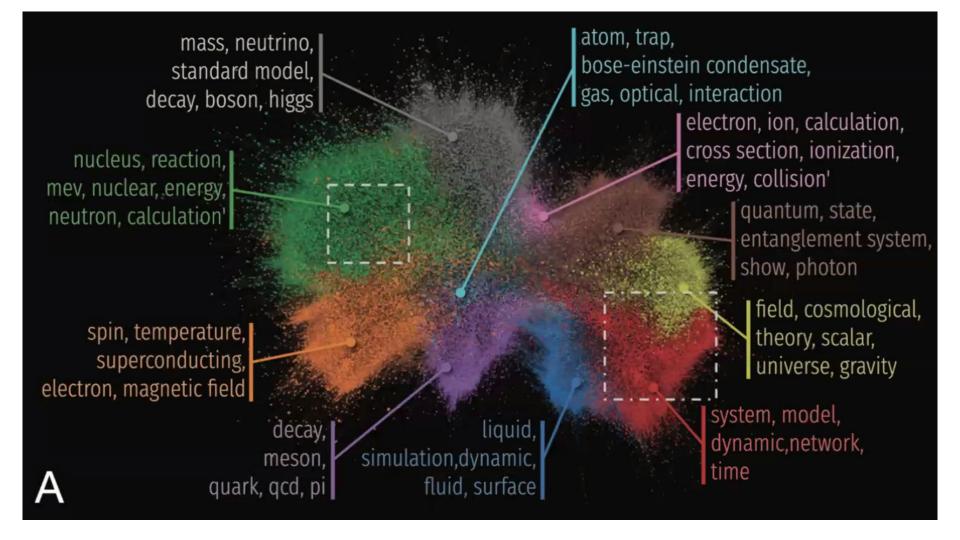


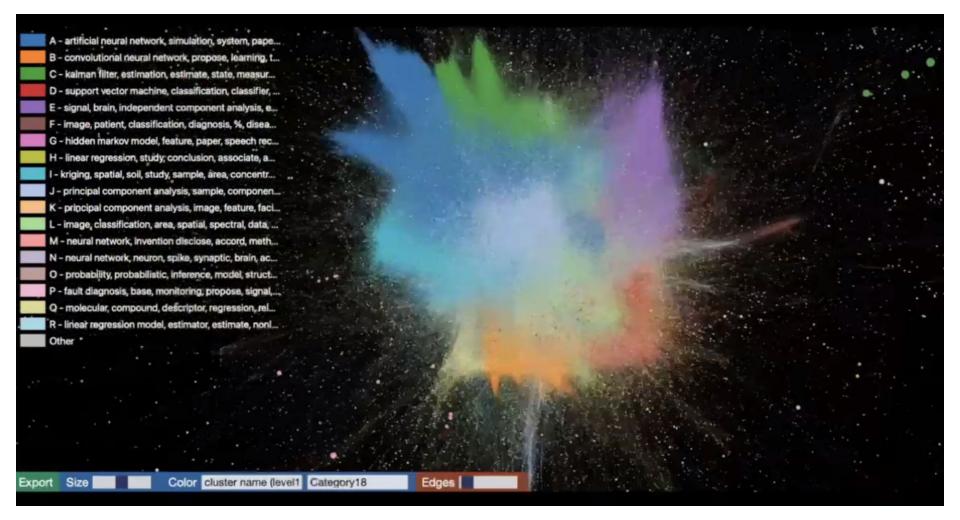


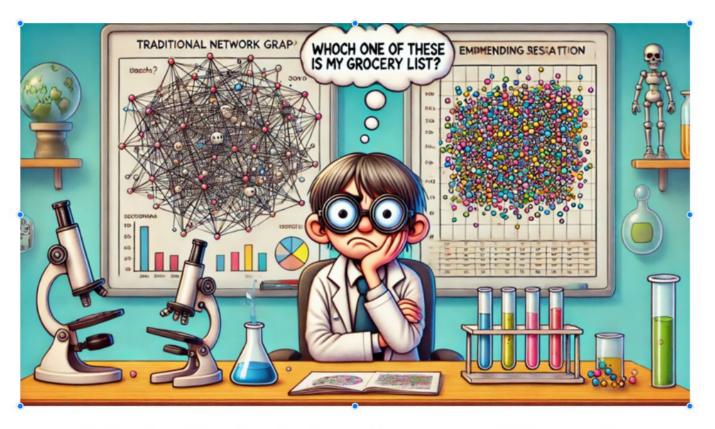
# Rendering

**Edge density** 

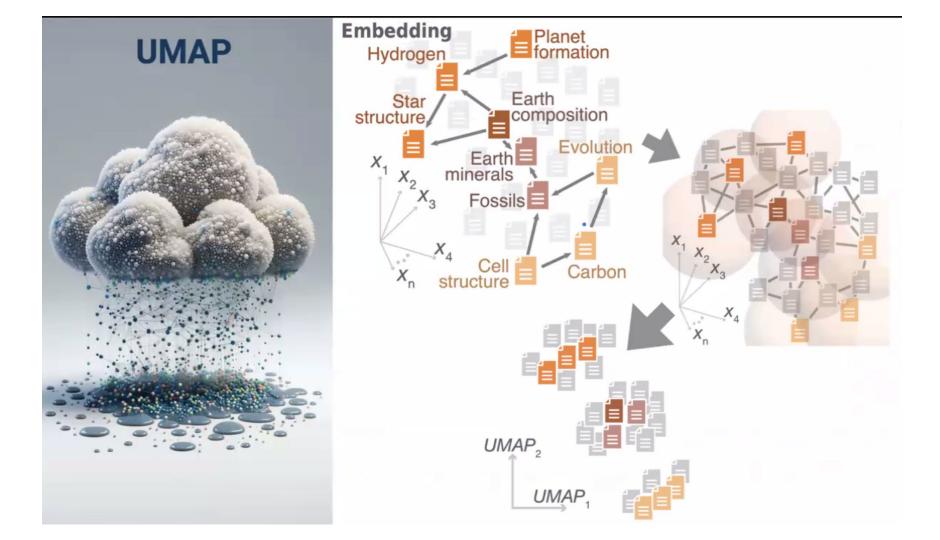


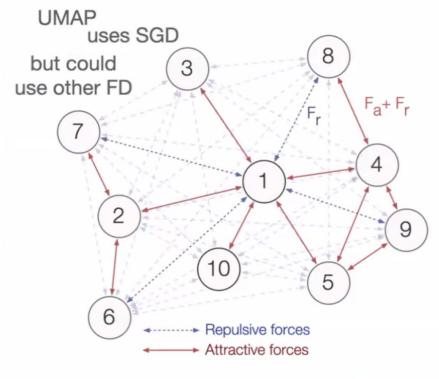






Ok, but what about embeddings?





For large embeddings: >10M points

**Negative samples rate:** Number of repulsive interactions to update for each positive.

increased to 10 (default = 5)

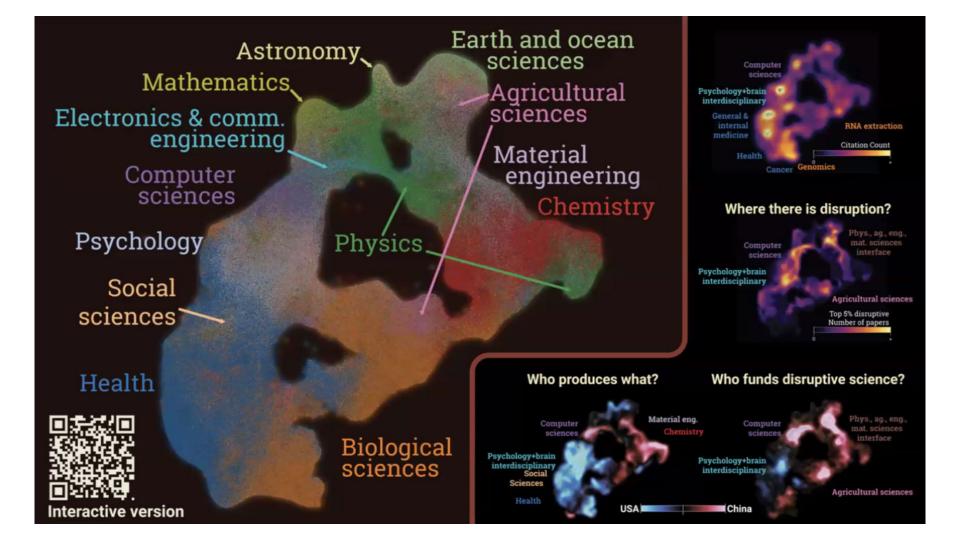
**Epochs:** Number of iterations increased to 200000 (default = 200) !!!

Number of neighbors: Number of neighbors in the NN graph increased to 30 (default = 15) !!! umap-learn.readthedocs.io

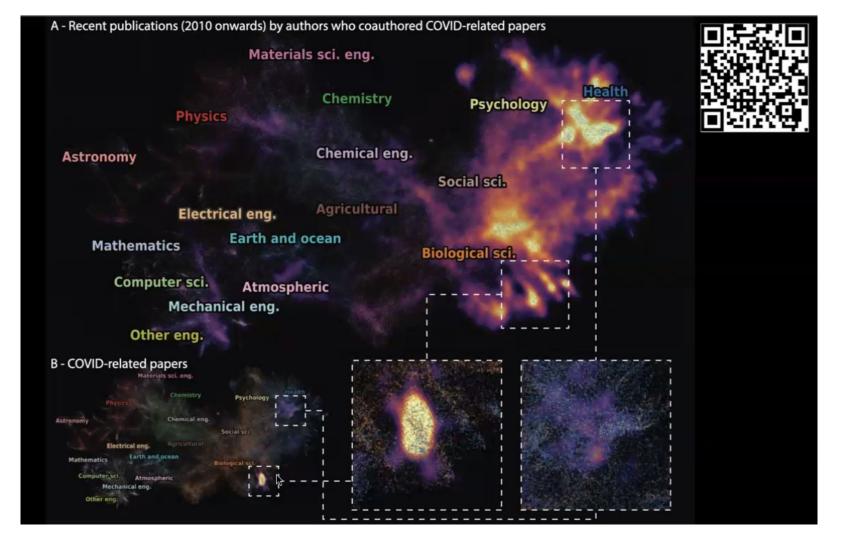
 $\frac{\text{attractive}}{\partial \mathbf{y}_i} \sim \sum_{j} v_{ij} w_{ij} (\mathbf{y}_i - \mathbf{y}_j) - \gamma \sum_{j} \frac{1}{d_{ij}^2 + \epsilon} w_{ij} (\mathbf{y}_i - \mathbf{y}_j).$ 

**GPU** version (much faster!)

beware: it has bugs that lead to bad projections https://docs.rapids.ai/api/cuml/stable/api/#umap

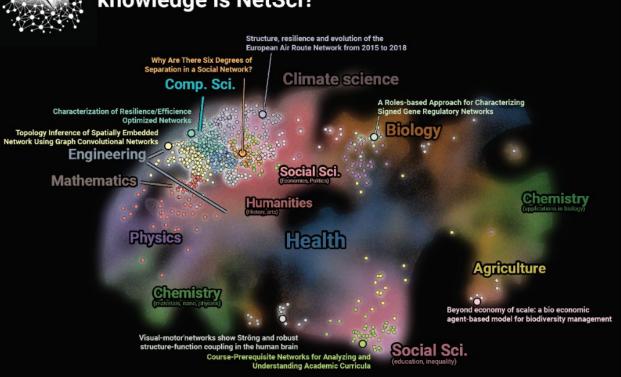


#### Who produces what? Who funds disruptive science? Material eng. Phys., ag., eng., Computer Computer mat. sciences Chemistry sciences sciences interface Psychology+brain Psychology+brain interdisciplinary interdisciplinary Social **Sciences** Agricultural sciences Health USA China

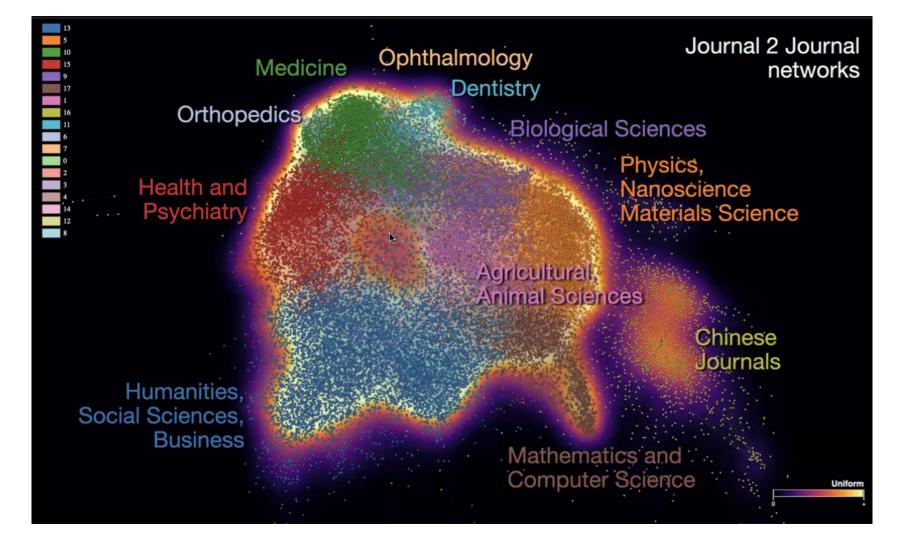


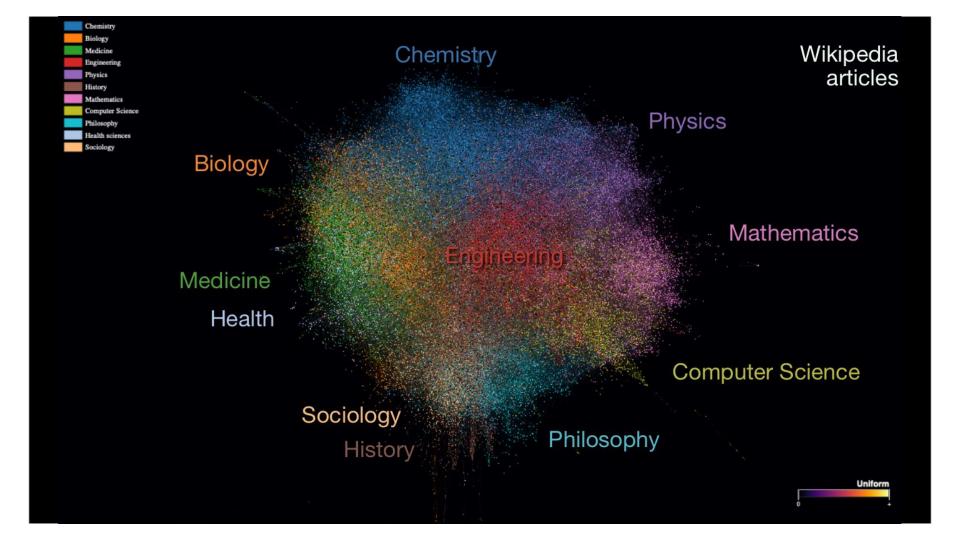


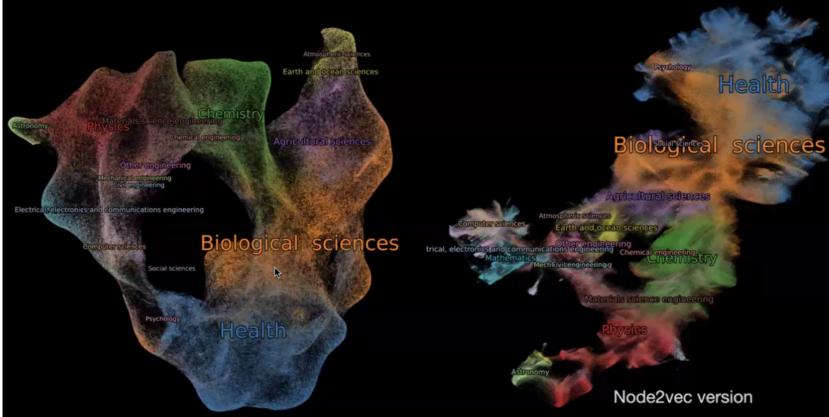
## Where in the world of knowledge is NetSci?



A science map constructed from the titles and abstracts of publications in the Web of Science. On top of that, we project NetSci contributions from 2023 and 2024.

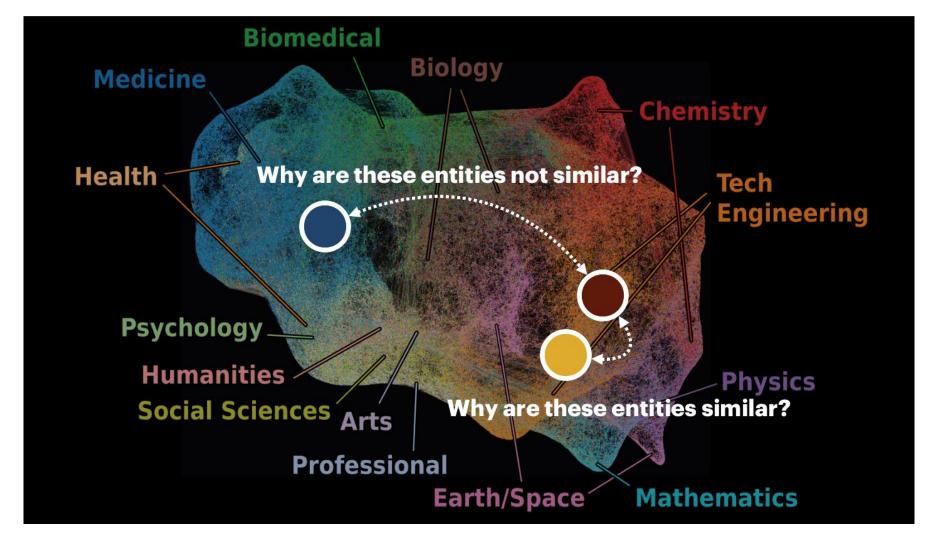


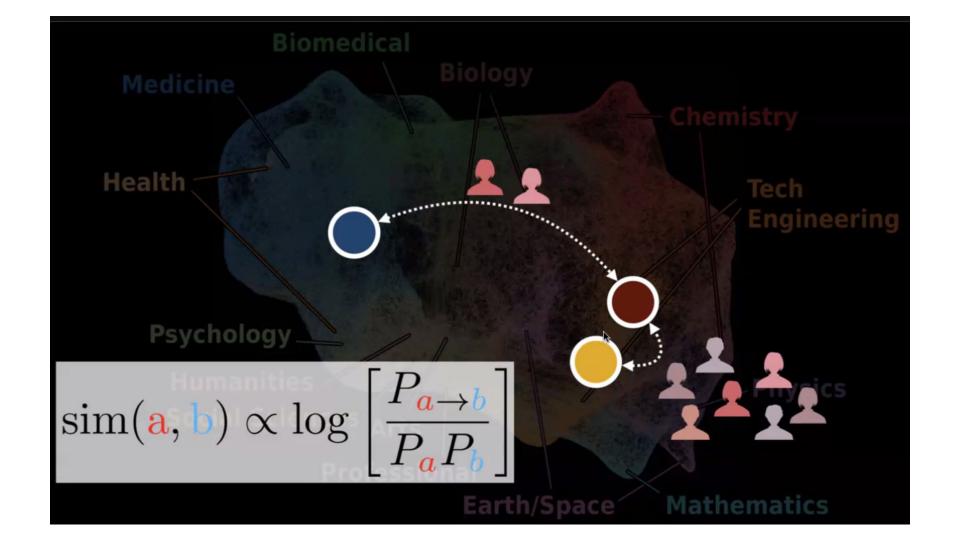


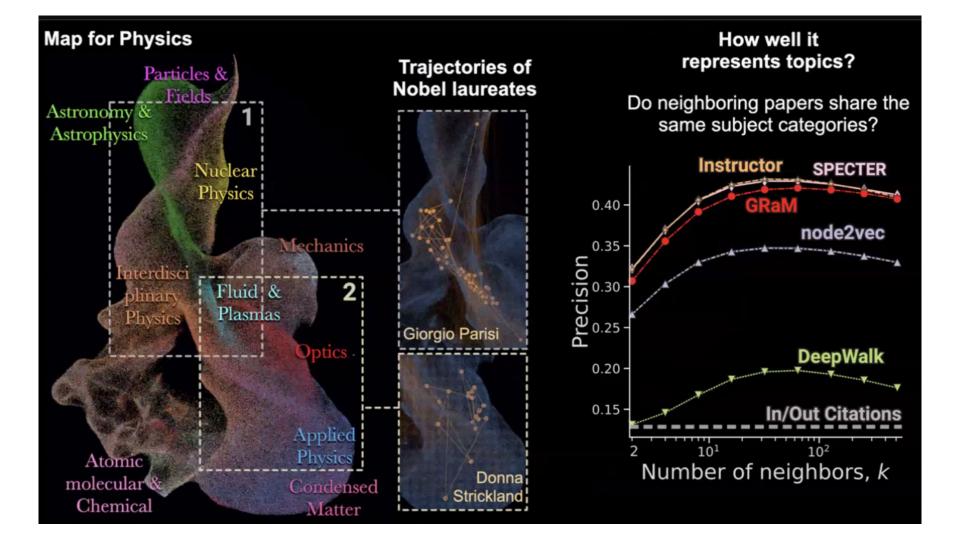


SPECTER (titles + fine tuning via citation network) embedding of the whole science
Microsoft Academic Graph (more than 200M works)

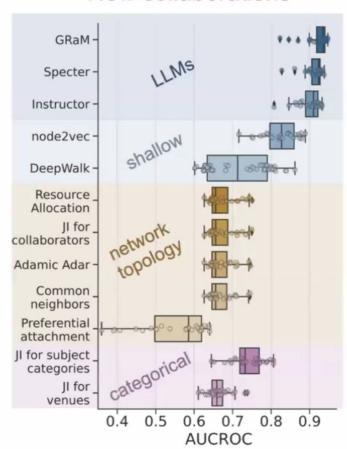
Ongoing project with YY Ahn, Sadamori Kojaku and others

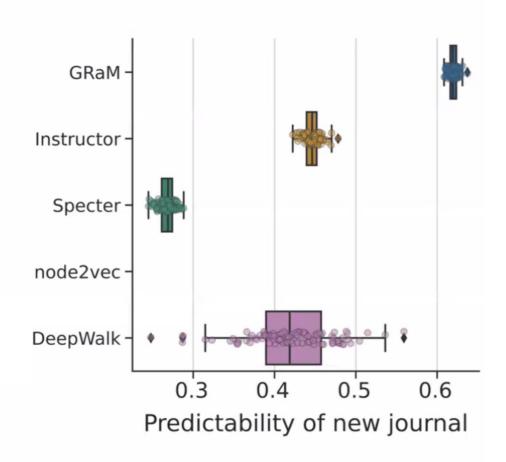


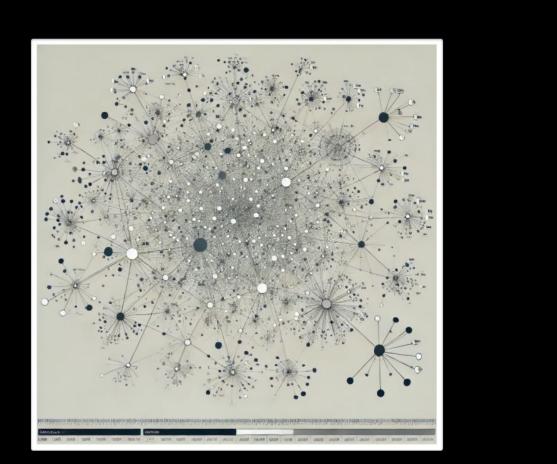


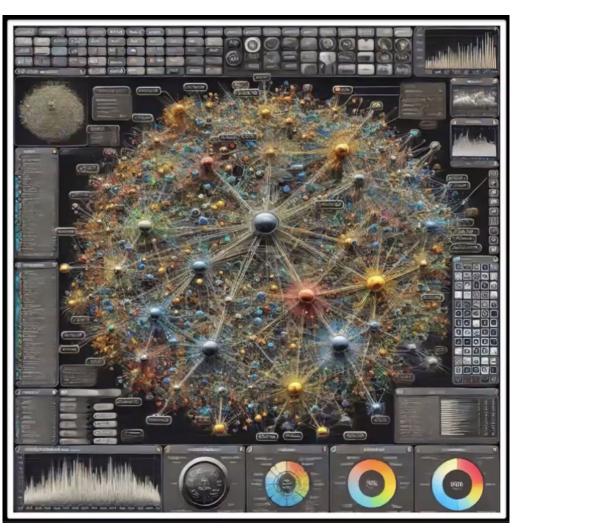


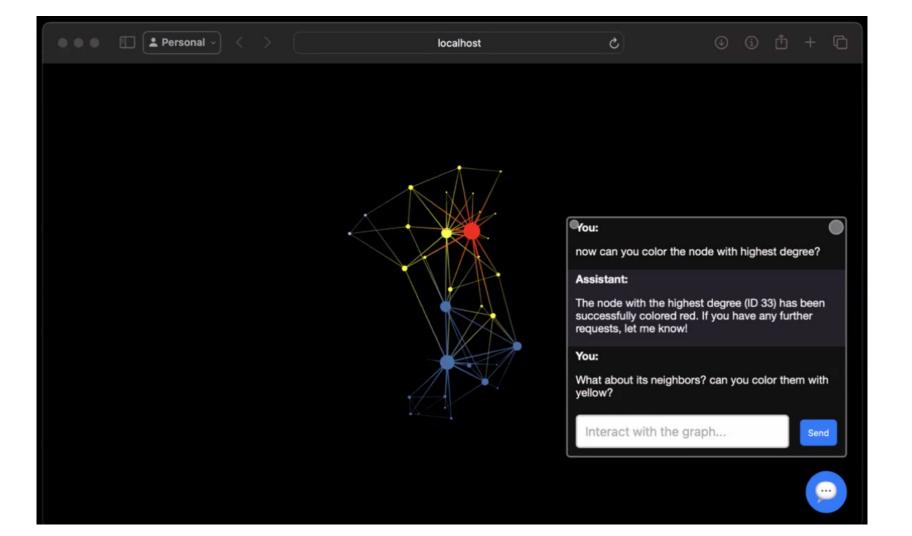
## Predictive power of the GRaM New collaborations

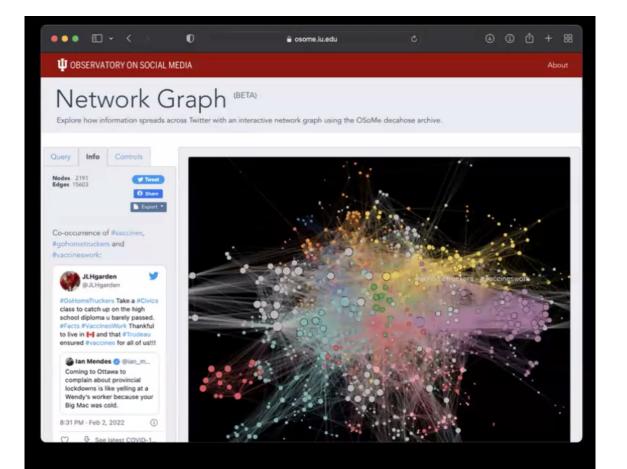




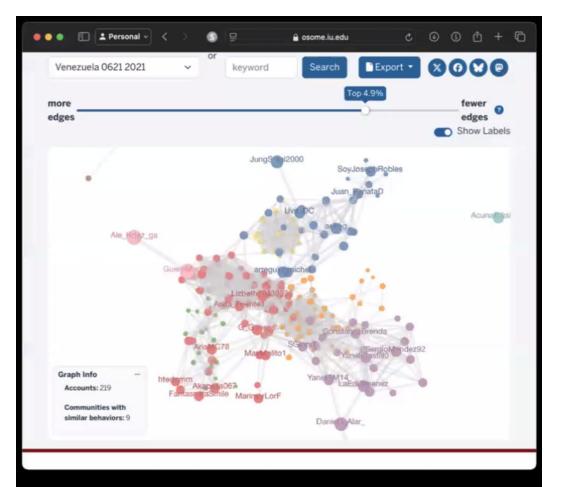






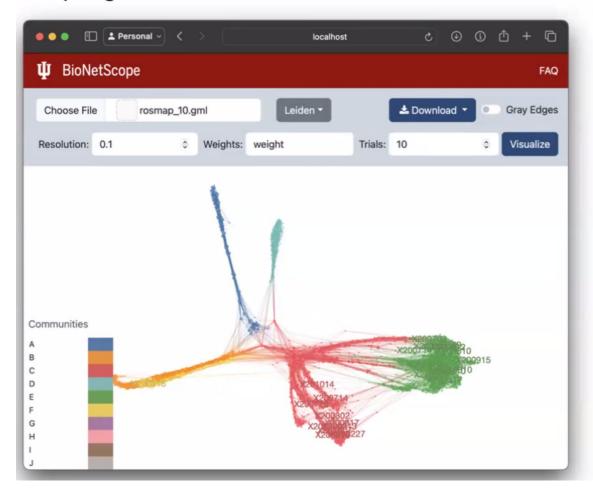


http://osome.iu.edu/tools/networks



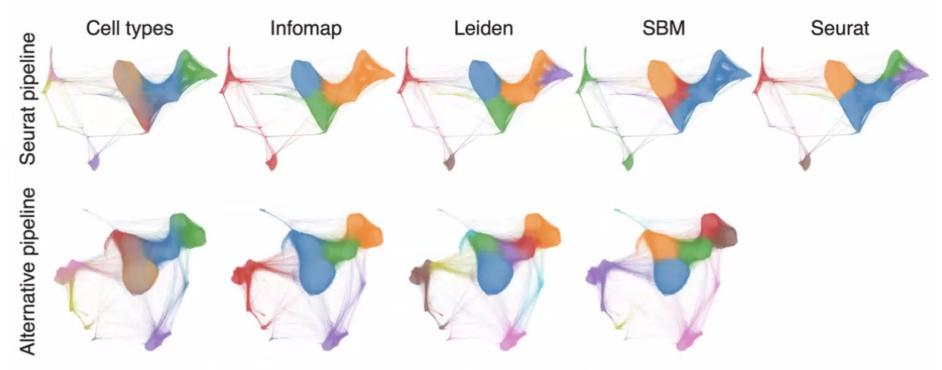
https://osome.iu.edu/tools/coordiscope

#### Adapting these models and tools for biomedical research



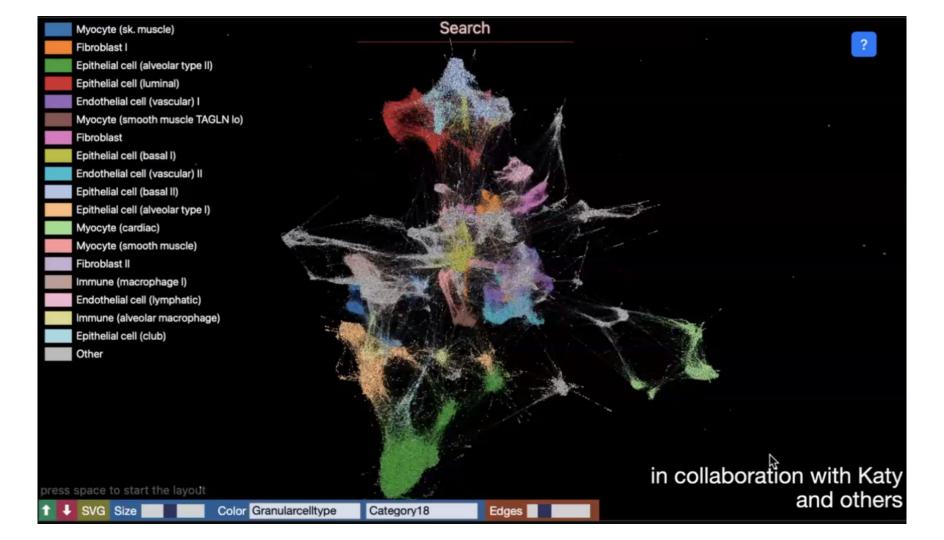
- Single cell RNA-seq data
- Microbiome associations with tissue gene expression
- Brain networks across age
- Metabolomics

#### Cell Type Differentiation Using Community Detection



68k human Peripheral Blood Mononuclear Cells (PBMCs) scRNA-seq dataset

Fatemi Nasrollahi, F. S., Silva, F. N., Liu, S., Chaudhuri, S., Yu, M., Wang, J., ... & Fortunato, S. (2024). Cell Type Differentiation Using Network Clustering Algorithms. bioRxiv, 2024-12.



# Thanks

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https://humanatlas.io/events/2024-24h

#### Questions

How do we define a Multiscale Human?

How do we map a Multiscale Human?

How do we model a Multiscale Human?

How can LLMs or RAGs be used to advance science and clinical practice?

## Thank you