MULTI-OMICS INTEGRATION & PATTERN DISCOVERY IN PATIENT DATA USING SPATIALLY SEMANTIC TOPOGRAPHIC MAPS

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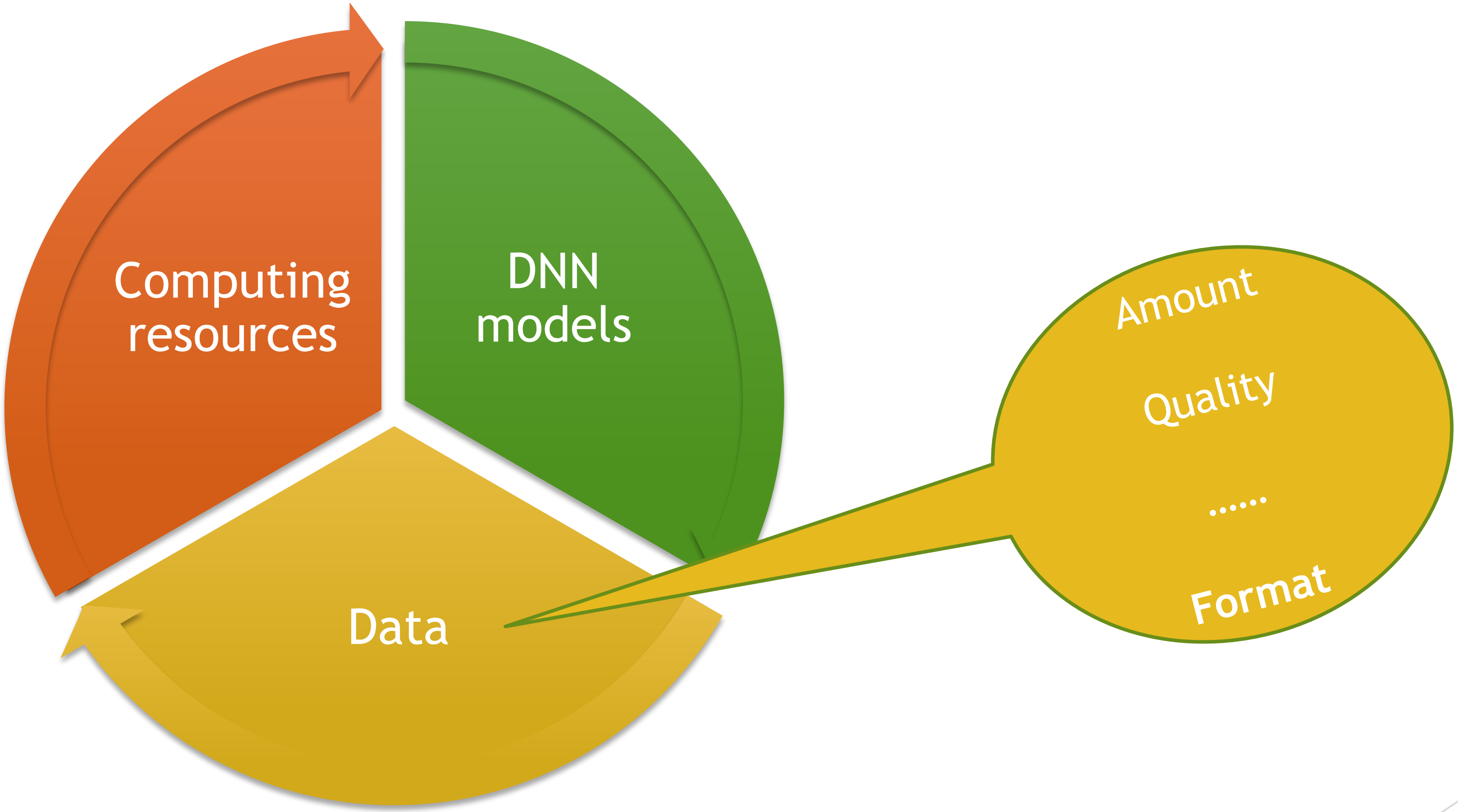
Departments of Radiation Oncology
Department of Electrical Engineering (by courtesy) & Molecular Imaging Program (MIPS)
Stanford University, Stanford, California

AI FOR PRECISION MEDICINE



FOUNDATION MODELS

nature medicine

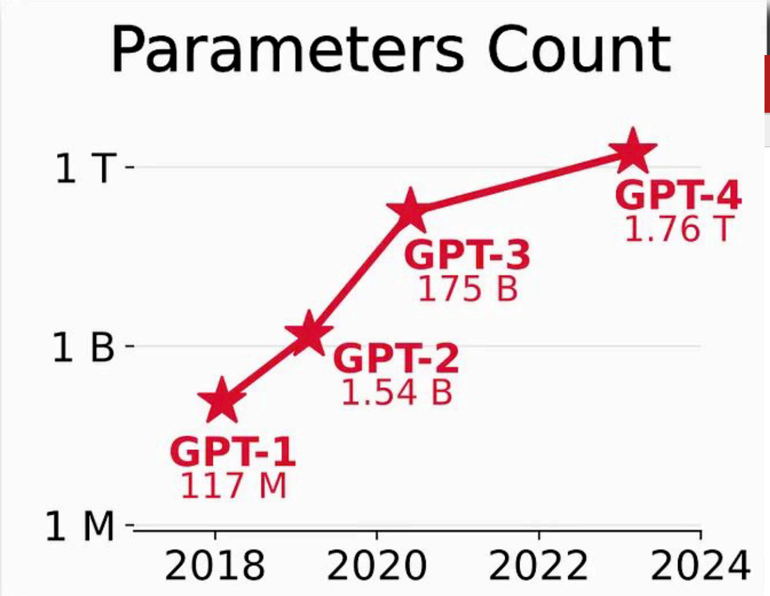
Article

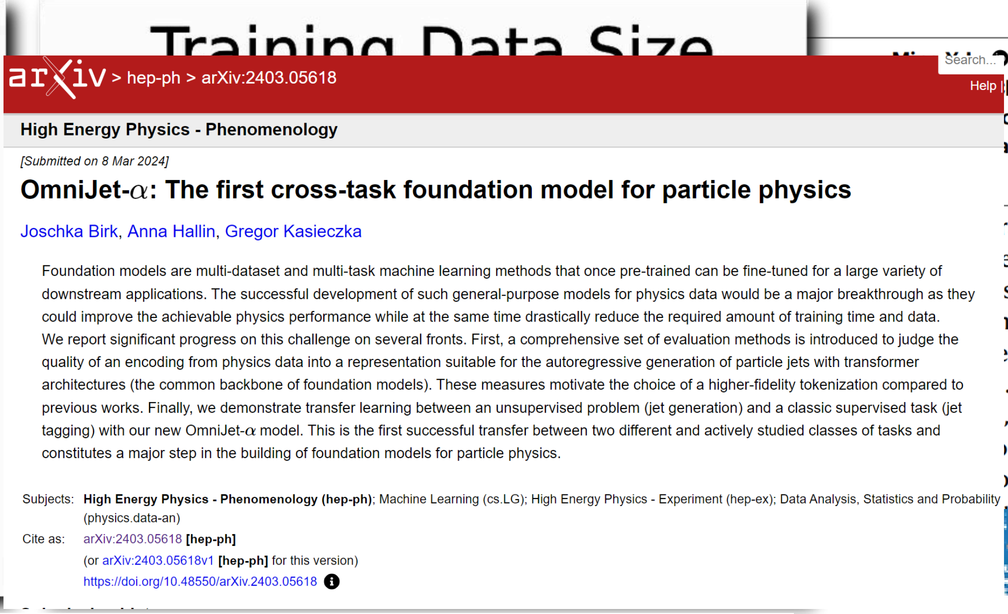
https://doi.org/10.1038/s41591-024-02856-4

A visual-language foundation model for computational pathology

[1,2,3,4,5,11], Bowen Chen[1,2,11], Drew F. K. Williamson[1,2,3,11],
hen[1,2,3,4,6], Ivy Liang[1,7], Tong Ding[1,7], Guillaume Jaume[1,2,3,4],
ov[1], Long Phi Le[2], Georg Gerber[1], Anil V. Parwani[8],
ang[1,2,3,4,9] & Faisal Mahmood[1,2,3,4,10]

rated adoption of digital pathology and advances in deep learning
ed the development of robust models for various pathology
s a diverse array of diseases and patient cohorts. However,
ing is often difficult due to label scarcity in the medical domain,
l's usage is limited by the specific task and disease for which
. Additionally, most models in histopathology leverage only
, a stark contrast to how humans teach each other and reason
pathologic entities. We introduce CONtrastive learning from
r Histopathology (CONCH), a visual-language foundation model





High Energy Physics - Phenomenology

[Submitted on 8 Mar 2024]

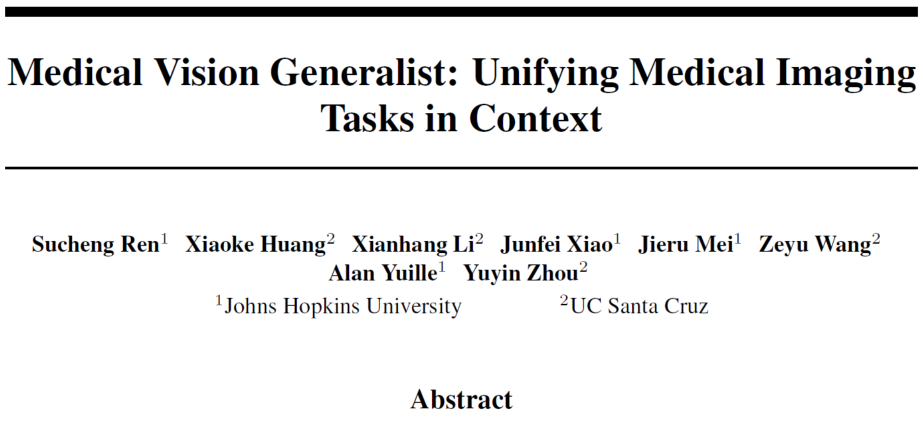
OmniJet-α: The first cross-task foundation model for particle physics

Joschka Birk, Anna Hallin, Gregor Kasieczka

Foundation models are multi-dataset and multi-task machine learning methods that once pre-trained can be fine-tuned for a large variety of downstream applications. The successful development of such general-purpose models for physics data would be a major breakthrough as they could improve the achievable physics performance while at the same time drastically reduce the required amount of training time and data. We report significant progress on this challenge on several fronts. First, a comprehensive set of evaluation methods is introduced to judge the quality of an encoding from physics data into a representation suitable for the autoregressive generation of particle jets with transformer architectures (the common backbone of foundation models). These measures motivate the choice of a higher-fidelity tokenization compared to previous works. Finally, we demonstrate transfer learning between an unsupervised problem (jet generation) and a classic supervised task (jet tagging) with our new OmniJet-α model. This is the first successful transfer between two different and actively studied classes of tasks and constitutes a major step in the building of foundation models for particle physics.

Subjects: **High Energy Physics - Phenomenology (hep-ph)**; Machine Learning (cs.LG); High Energy Physics - Experiment (hep-ex); Data Analysis, Statistics and Probability (physics.data-an)

Cite as: arXiv:2403.05618 **[hep-ph]**
(or arXiv:2403.05618v1 **[hep-ph]** for this version)
https://doi.org/10.48550/arXiv.2403.05618



Medical Vision Generalist: Unifying Medical Imaging Tasks in Context

Sucheng Ren[1] Xiaoke Huang[2] Xianhang Li[2] Junfei Xiao[1] Jieru Mei[1] Zeyu Wang[2]
Alan Yuille[1] Yuyin Zhou[2]
[1]Johns Hopkins University [2]UC Santa Cruz

Abstract

GENEFORMER & RSC-GPT

Home / News

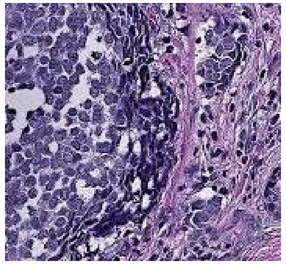
A New AI Tool Predicts Gene Expression in a Single Cell

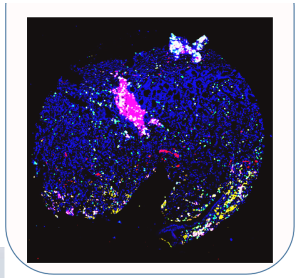
An artificial intelligence tool, scGPT, can identify cell types, predict the effects of disrupting genes, and pinpoint which genes interact with each other.

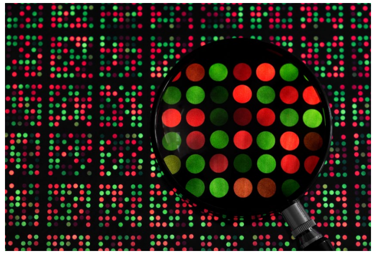
Carissa Wong, PhD
Aug 21, 2023 | 4 min read

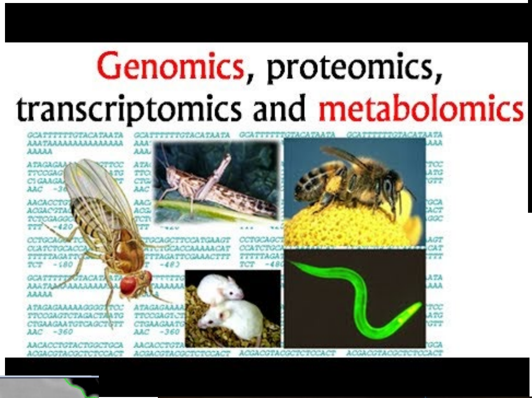
WHY IS HEALTHCARE AI CHALLENGING?

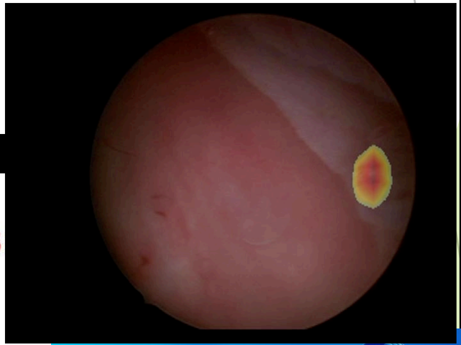
- Various data formats
- Noise, small sample size, missing data, bias, …

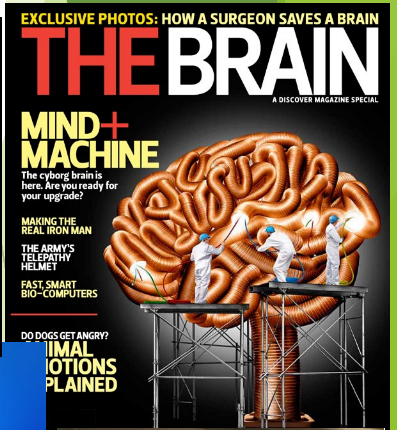







Genomics, proteomics, transcriptomics and metabolomics




EXCLUSIVE PHOTOS: HOW A SURGEON SAVES A BRAIN

THE BRAIN

A DISCOVER MAGAZINE SPECIAL

MIND+ MACHINE

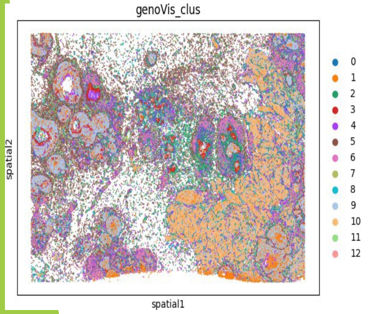
The cyborg brain is here. Are you ready for your upgrade?

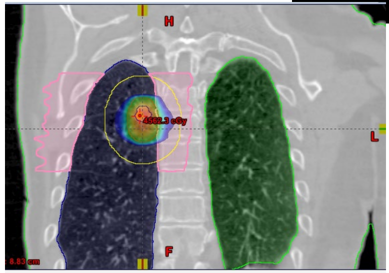
MAKING THE REAL IRON MAN

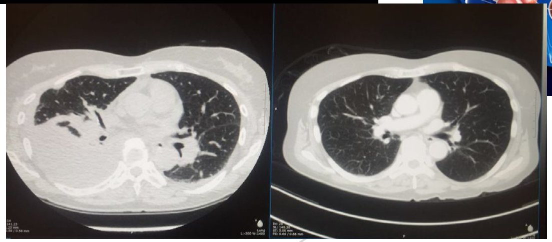
THE ARMY'S TELEPATHY HELMET

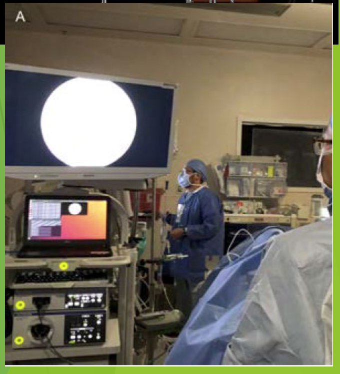
FAST, SMART BIO-COMPUTERS

DO DOGS GET ANGRY? …IMAL …IOTIONS …PLAINED









- Archimedes

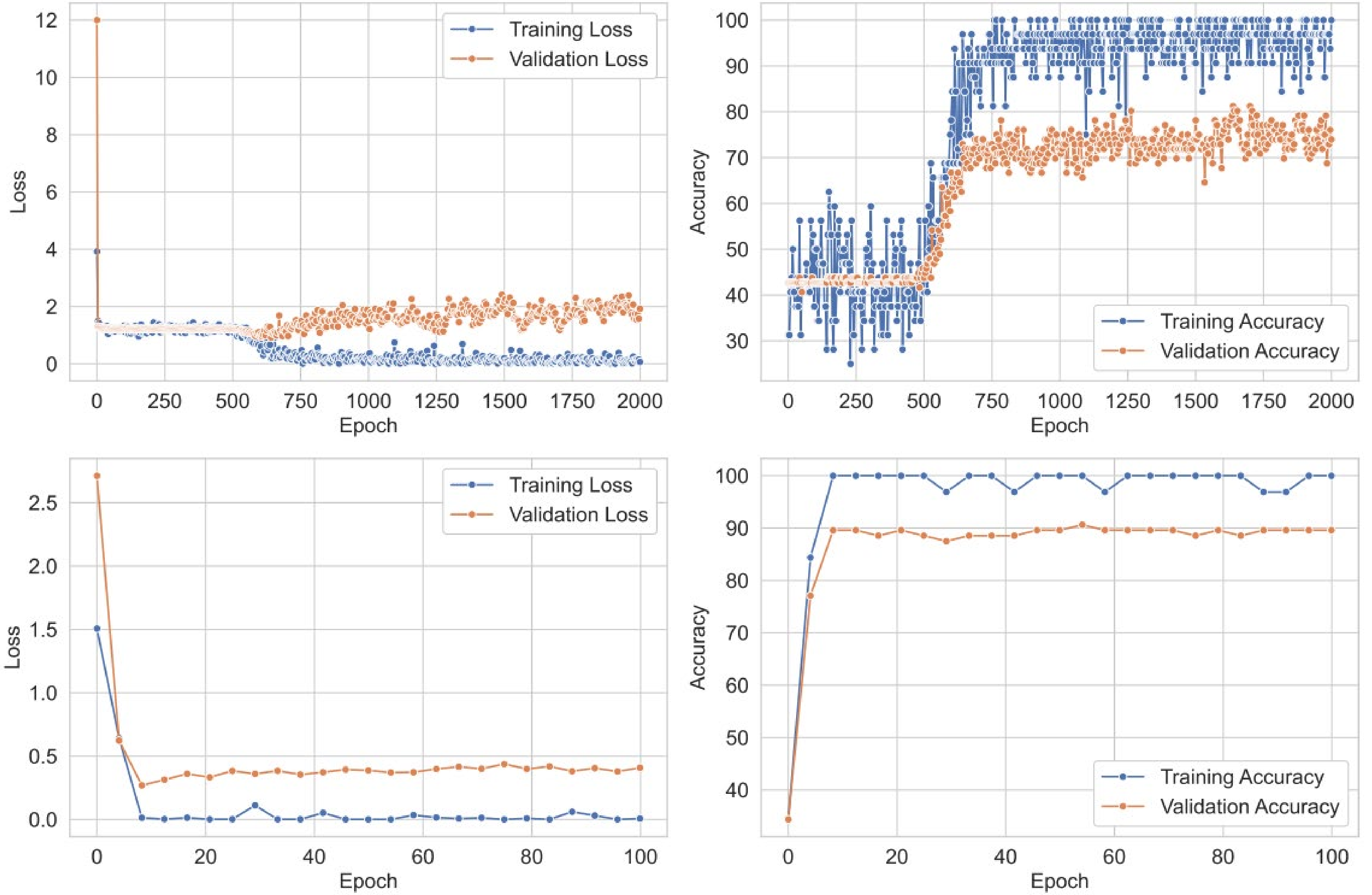
Give me a firm place to stand and a lever and I can move the Earth

- Archimedes

Give me sufficient CLEAN data, I can solve all inference problems

😊

Training and validation loss and accuracy of BERT and our new BERT - Amazon Factory report dataset (Nat. Biotech. Under review, 2025)



Data are presented in diverse formats

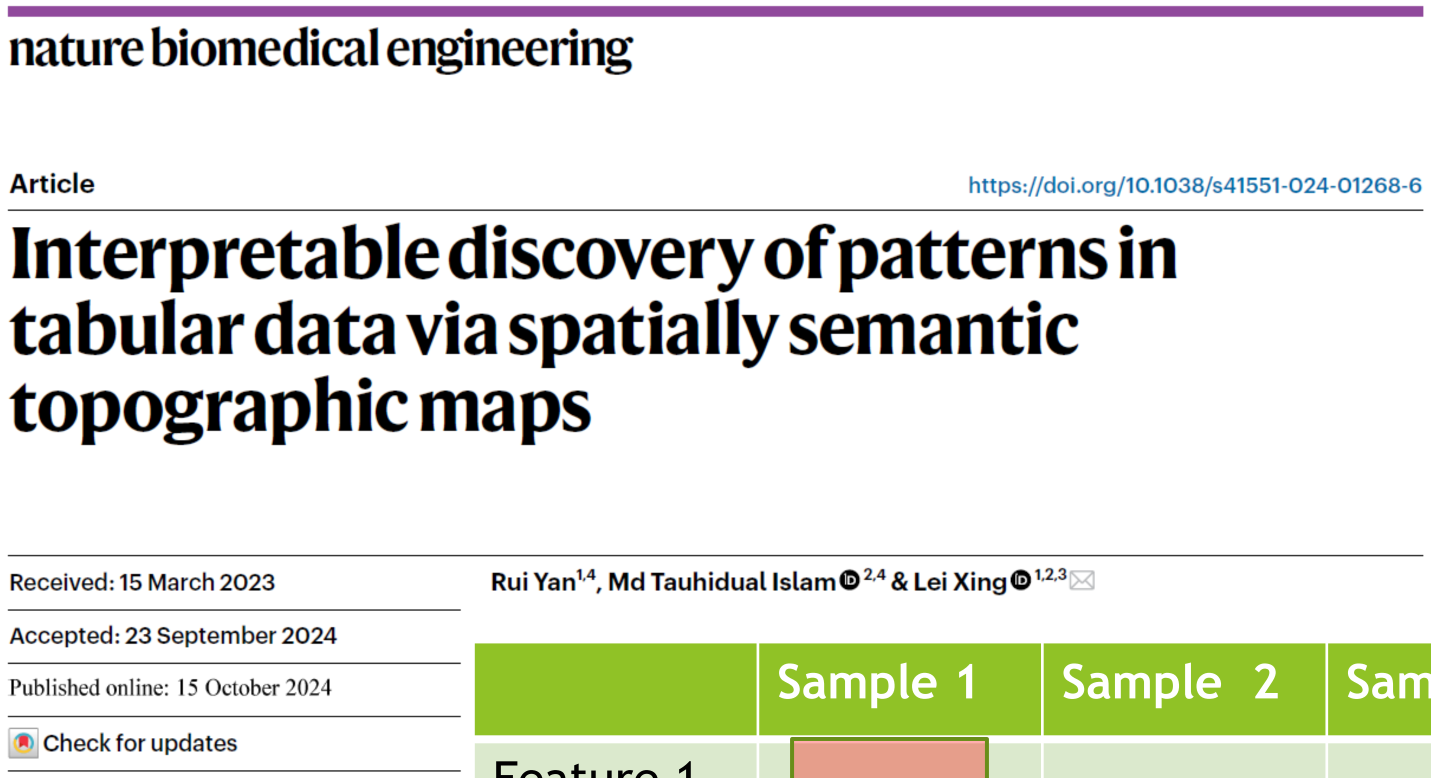
Image & video
- Different modalities

Table
- omics
- Multi-omics
- Sensory data
- Clinical trials

Language
- Different languages
- Specialties

Graph
- Bio-network
- Social network
- Pathology data
- Functional maps
- Spatial transcriptomics

R. Yan, T. Islam, L. Xing, Science Advances 10, 2024.


nature biomedical engineering

Article
https://doi.org/10.1038/s41551-024-01268-6

Interpretable discovery of patterns in tabular data via spatially semantic topographic maps

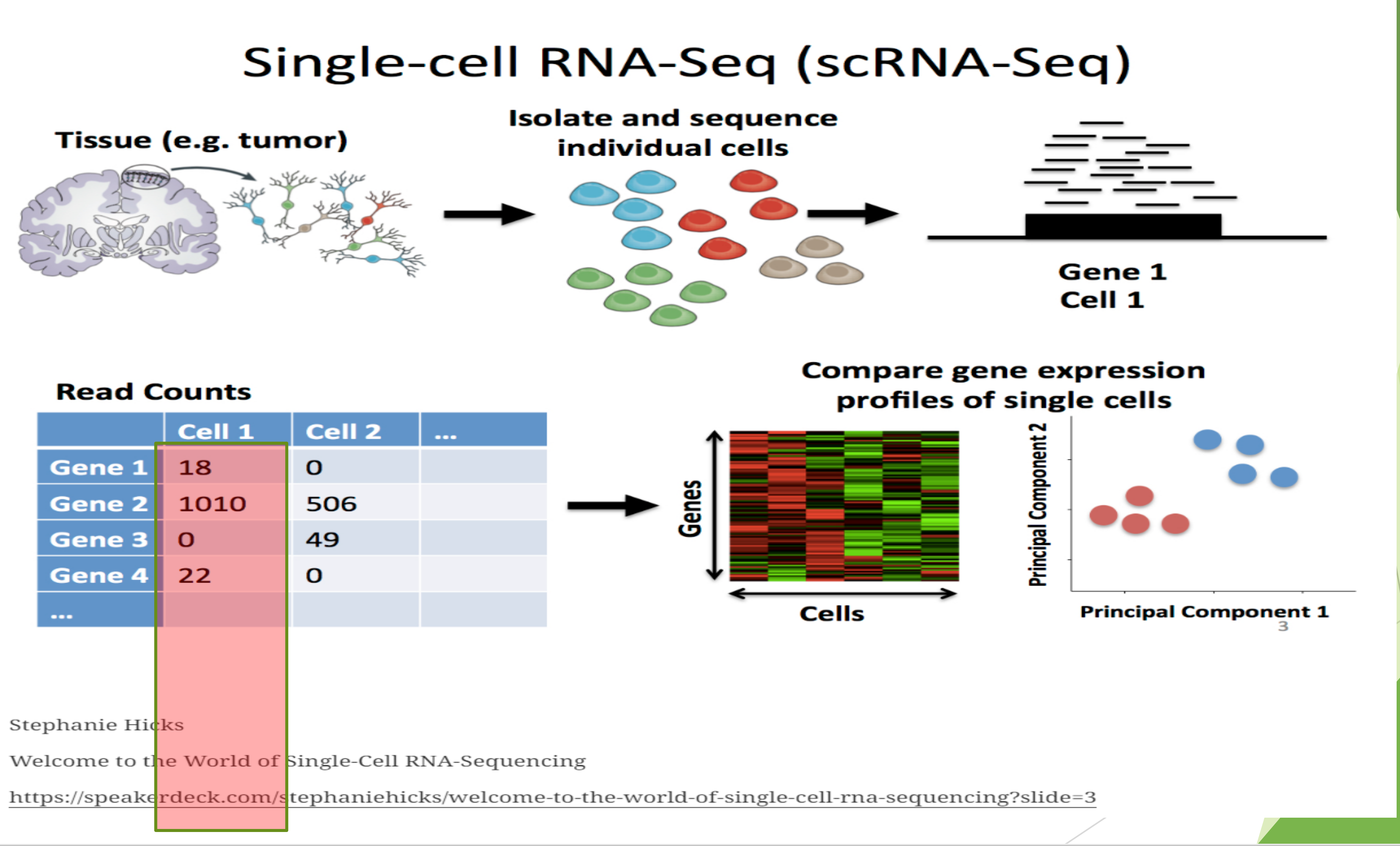
Received: 15 March 2023

Accepted: 23 September 2024

Rui Yan[1,4], Md Tauhidual Islam[2,4] & Lei Xing[1,2,3]

	Sample 1	Sample 2	Sample 3	……	Sample N
Feature 1					
Feature 2					
Feature 3					
…					
…					
Feature M					

IMAGE REPRESENTATION OF OMICS DATA



Single-cell RNA-Seq (scRNA-Seq)

Tissue (e.g. tumor)

Isolate and sequence individual cells

Read Counts

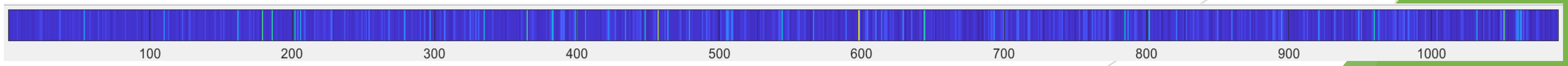
	Cell 1	Cell 2	…
Gene 1	18	0	
Gene 2	1010	506	
Gene 3	0	49	
Gene 4	22	0	
…			

Compare gene expression profiles of single cells

Stephanie Hicks

Welcome to the World of Single-Cell RNA-Sequencing

https://speakerdeck.com/stephaniehicks/welcome-to-the-world-of-single-cell-rna-sequencing?slide=3



Read Counts

	Cell 1	Cell 2	...
Gene 1	18	0	
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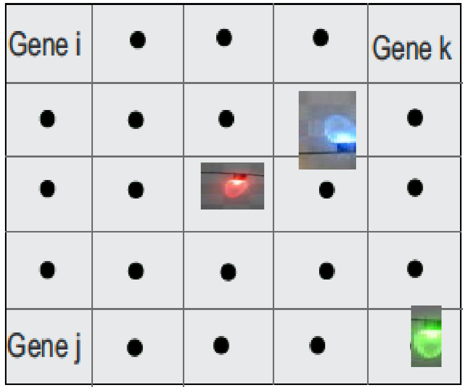
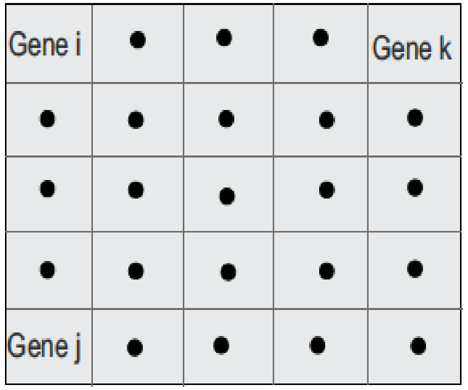
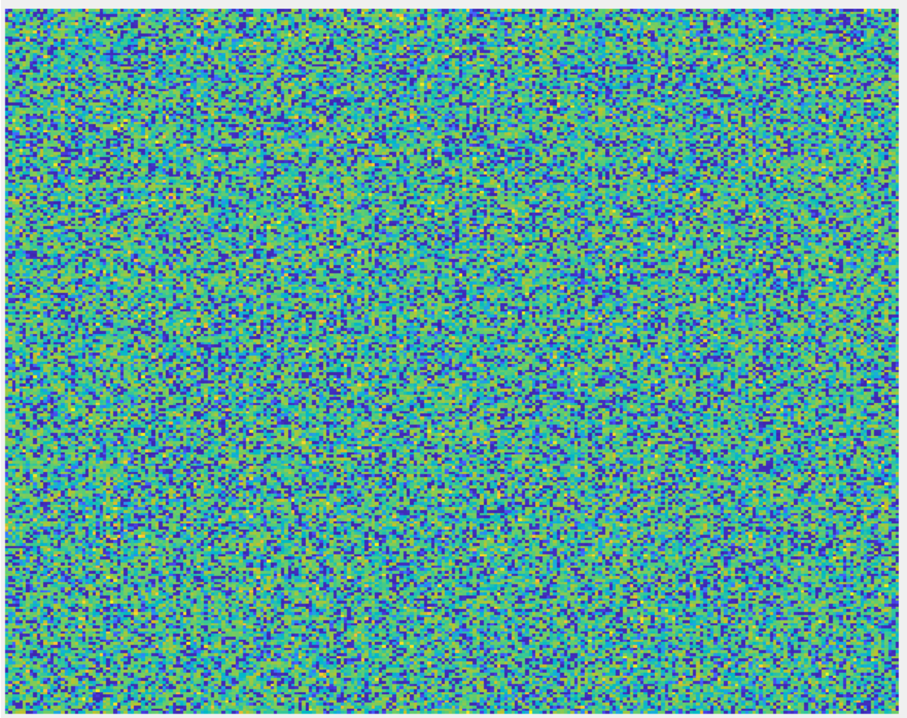
Gene 3	0	49	
Gene 4	22	0	
...			

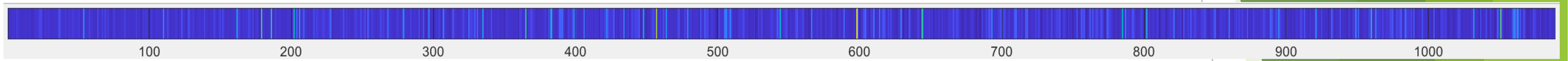




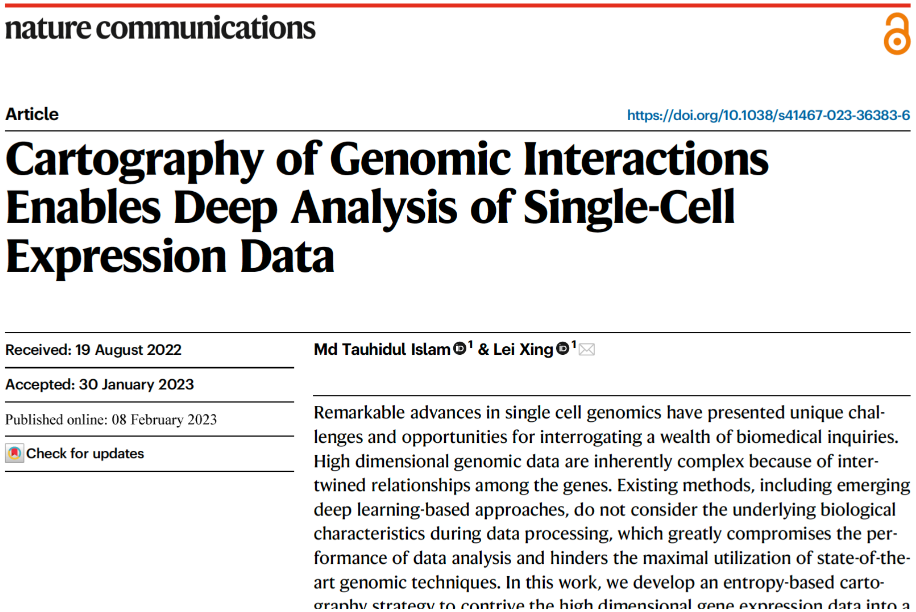


Expression vector of a Keratinocyte cell and it’s genomap

Vector



Data source: Nature 562, 367–372 (2018).


nature communications

Article

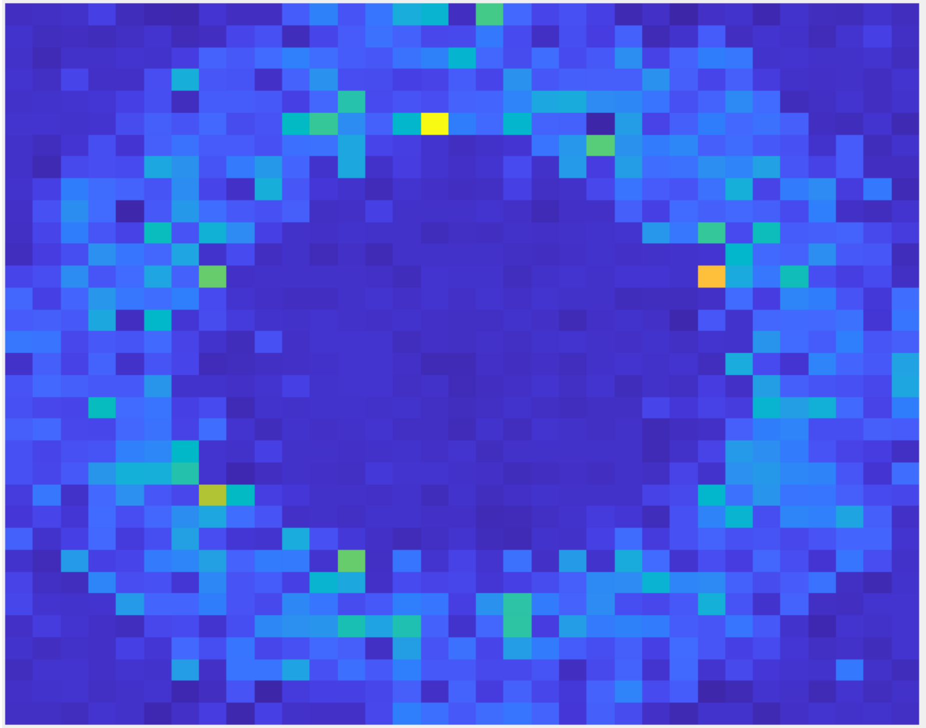
https://doi.org/10.1038/s41467-023-36383-6

Cartography of Genomic Interactions Enables Deep Analysis of Single-Cell Expression Data

Received: 19 August 2022
Accepted: 30 January 2023

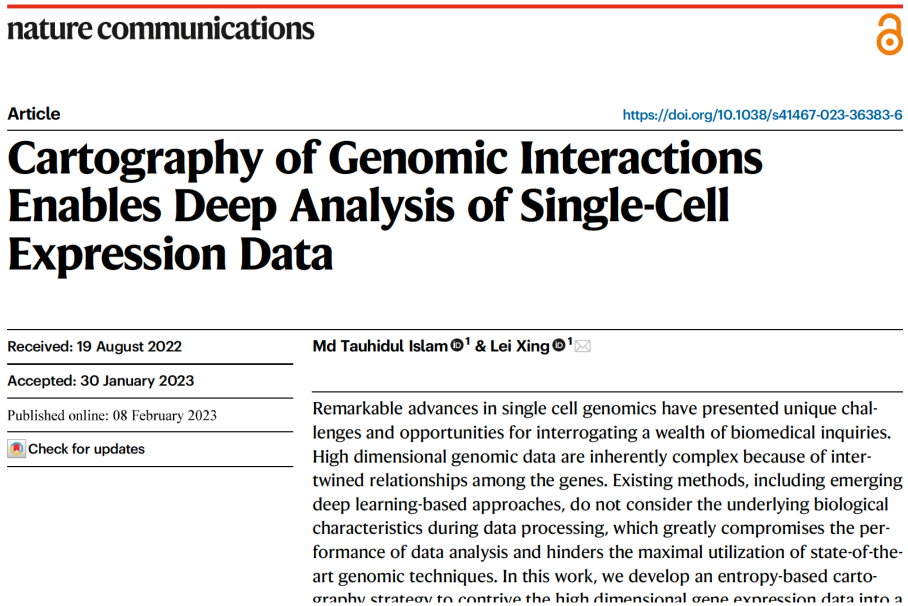
Md Tauhidul Islam[1] & Lei Xing[1]

Remarkable advances in single cell genomics have presented unique challenges and opportunities for interrogating a wealth of biomedical inquiries. High dimensional genomic data are inherently complex because of intertwined relationships among the genes. Existing methods, including emerging deep learning-based approaches, do not consider the underlying biological characteristics during data processing, which greatly compromises the performance of data analysis and hinders the maximal utilization of state-of-the-art genomic techniques. In this work, we develop an entropy-based cartography strategy to contrive the high dimensional gene expression data into a



Genomap

AI FOR OMICS DATA PROCESSING



nature communications

Article

https://doi.org/10.1038/s41467-023-36383-6

Cartography of Genomic Interactions Enables Deep Analysis of Single-Cell Expression Data

Received: 19 August 2022

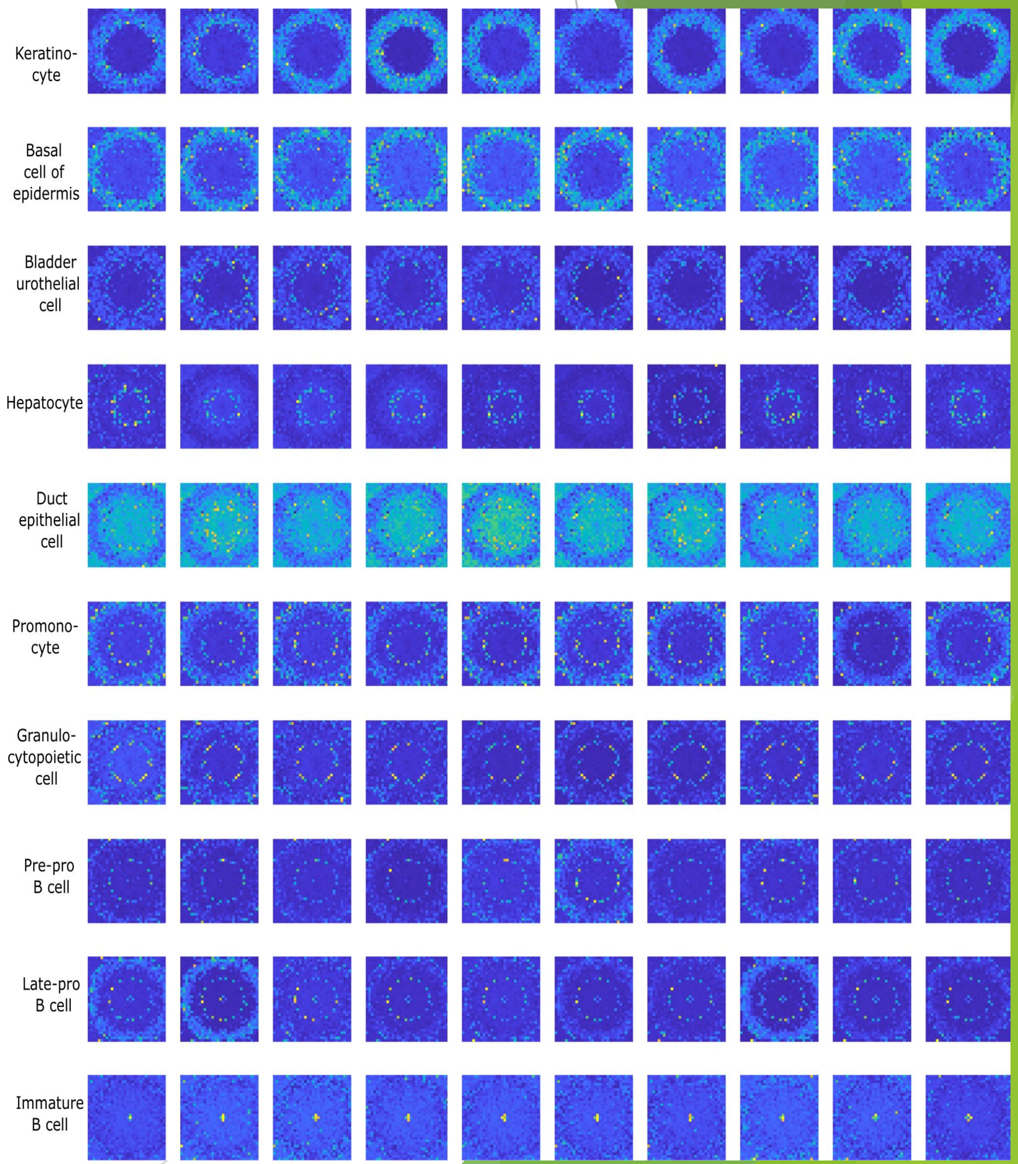
Accepted: 30 January 2023

Published online: 08 February 2023

Check for updates

Md Tauhidul Islam[1] & **Lei Xing**[1]

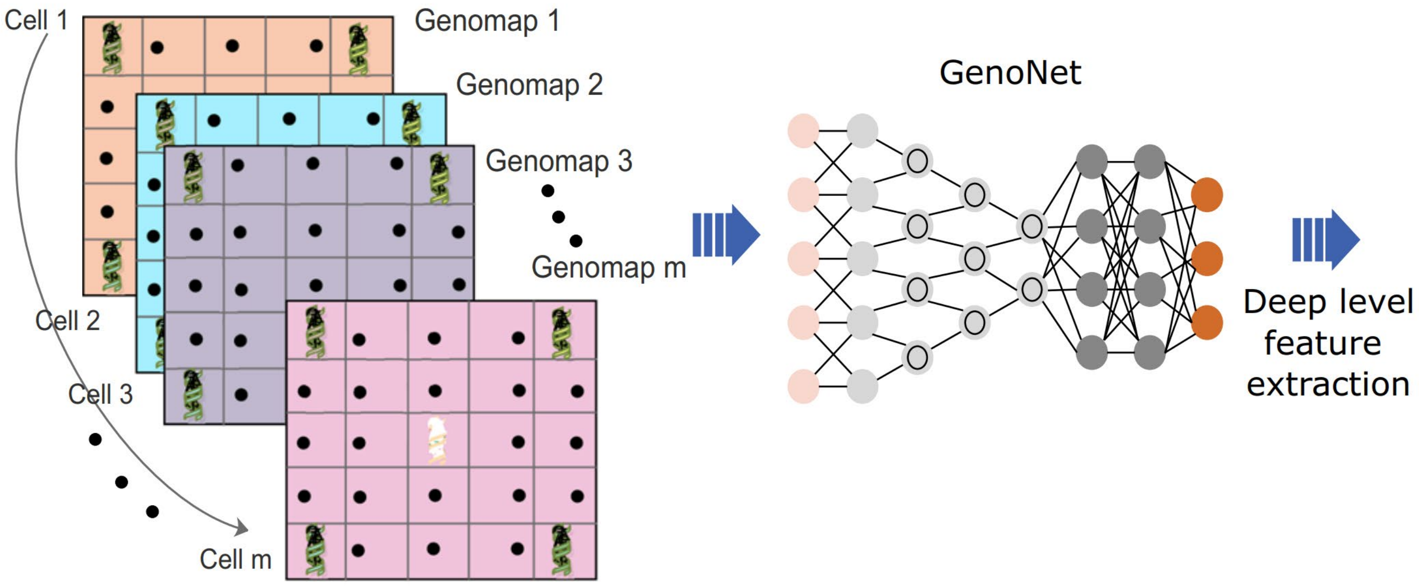
Remarkable advances in single cell genomics have presented unique challenges and opportunities for interrogating a wealth of biomedical inquiries. High dimensional genomic data are inherently complex because of intertwined relationships among the genes. Existing methods, including emerging deep learning-based approaches, do not consider the underlying biological characteristics during data processing, which greatly compromises the performance of data analysis and hinders the maximal utilization of state-of-the-art genomic techniques. In this work, we develop an entropy-based cartography strategy to contrive the high dimensional gene expression data into a

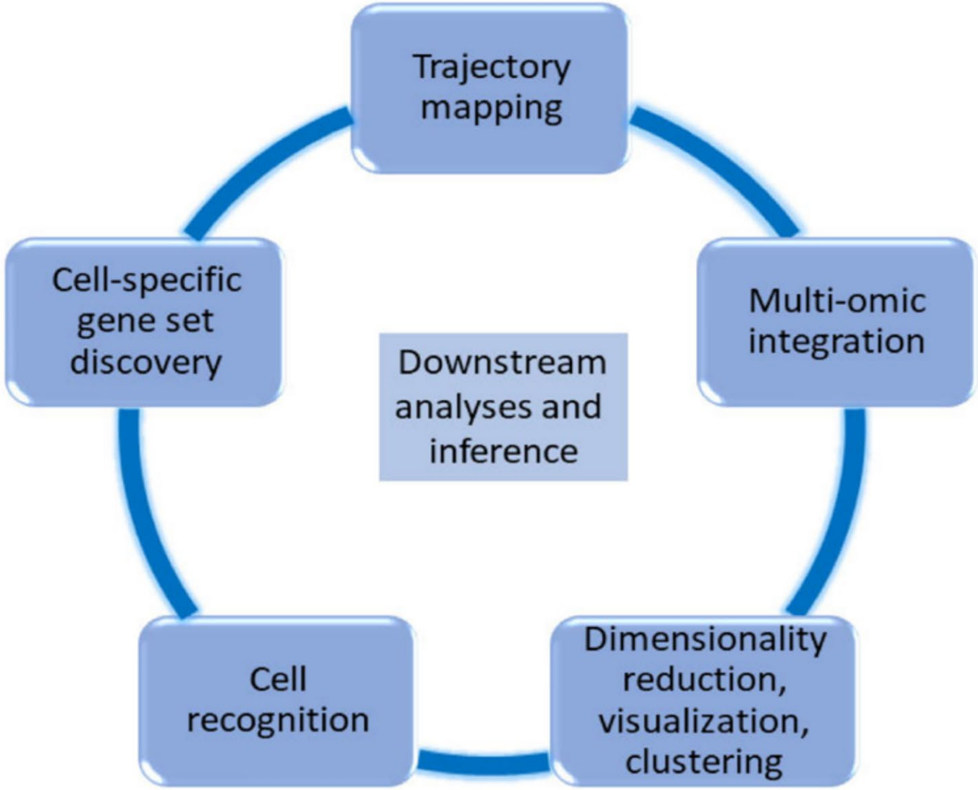


https://www.nature.com/articles/s41467-023-36383-6

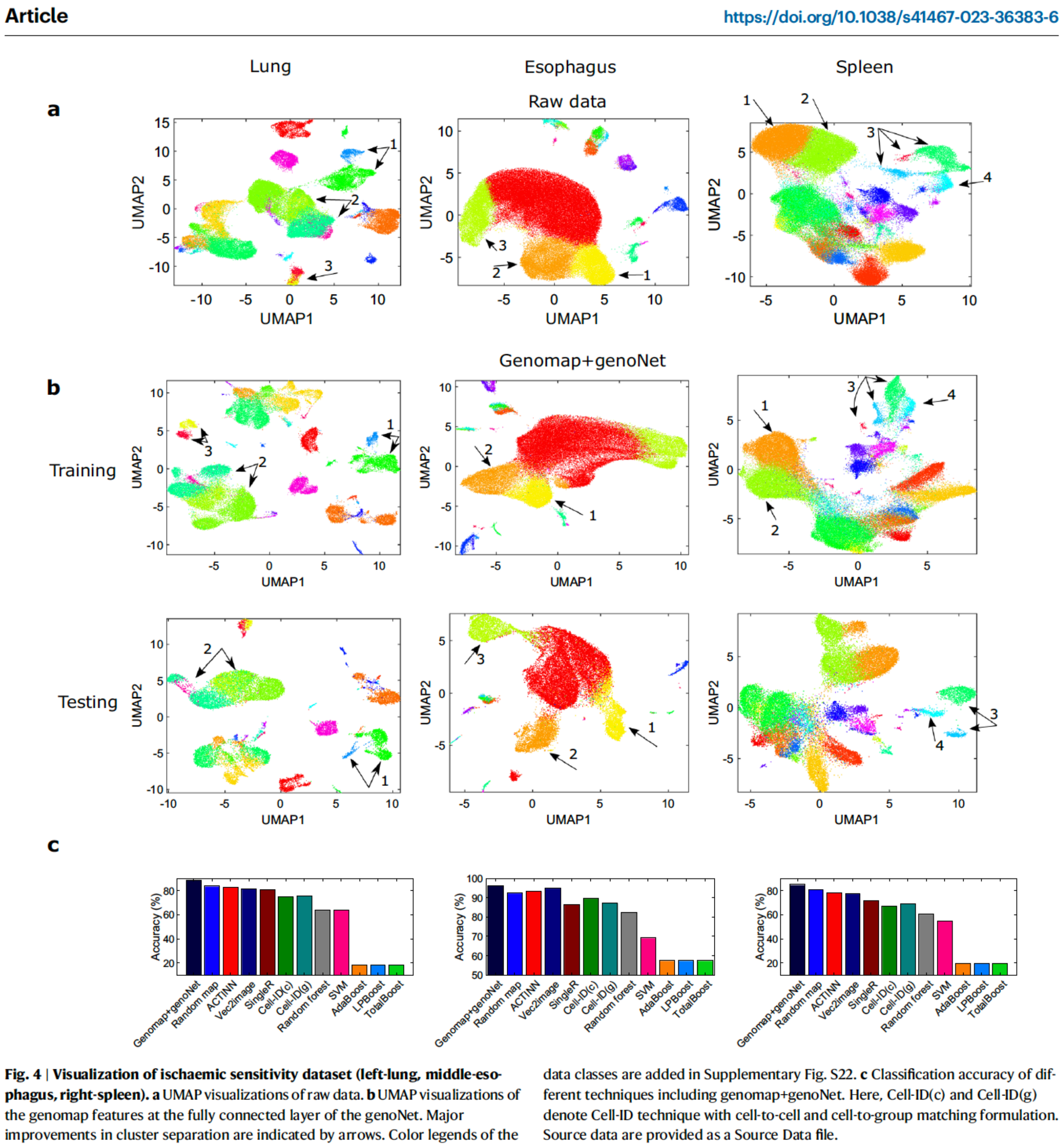
www.analyXus.com

Applications of omics-to-image conversion in single-cell biology





Islam, M.T. and Xing, L., 2023. Cartography of Genomic Interactions Enables Deep Analysis of Single-Cell Expression Data. Nature Communications, 14(1), p.679.

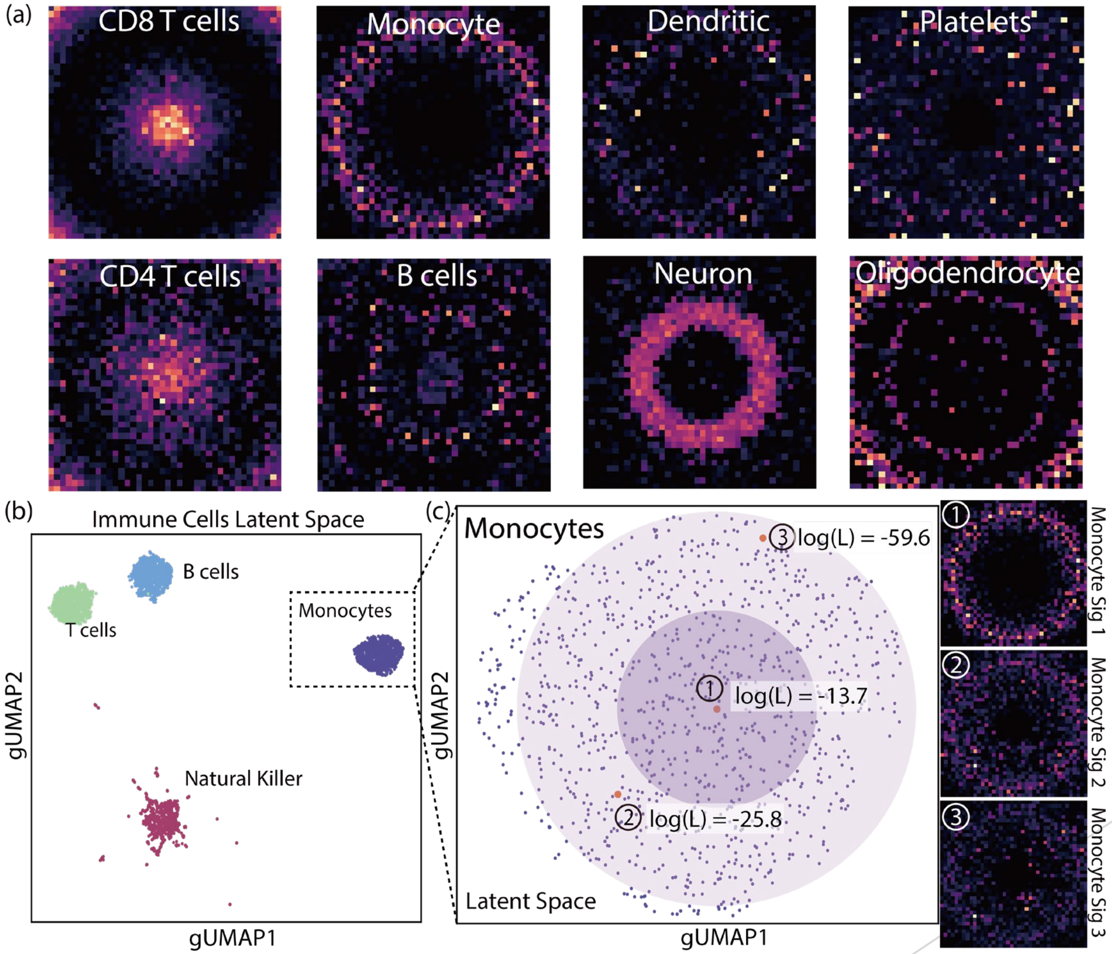


Article

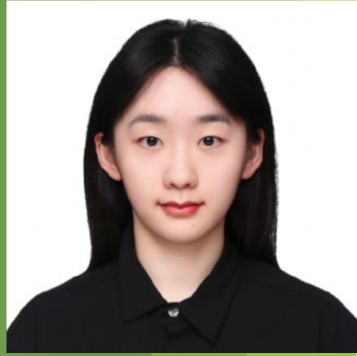
https://doi.org/10.1038/s41467-023-36383-6

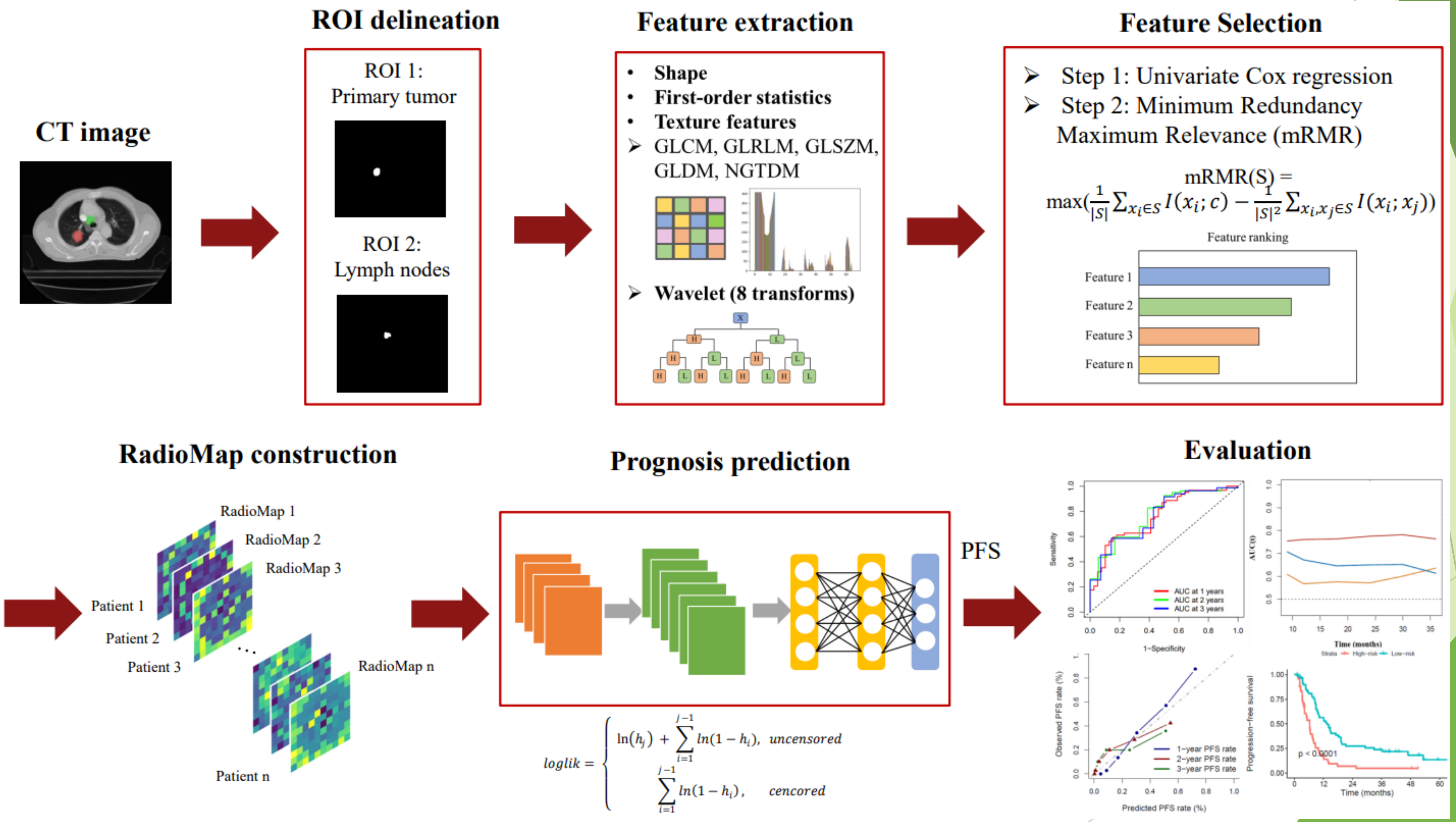
Fig. 4 | Visualization of ischaemic sensitivity dataset (left-lung, middle-esophagus, right-spleen). **a** UMAP visualizations of raw data. **b** UMAP visualizations of the genomap features at the fully connected layer of the genoNet. Major improvements in cluster separation are indicated by arrows. Color legends of the data classes are added in Supplementary Fig. S22. **c** Classification accuracy of different techniques including genomap+genoNet. Here, Cell-ID(c) and Cell-ID(g) denote Cell-ID technique with cell-to-cell and cell-to-group matching formulation. Source data are provided as a Source Data file.

Unveiling Tissue Heterogeneity through Genomic Interaction-Encoded Image Representation of RNA Sequencing Data



OMICSMAP-BASED DEEP RADIOMICS





CT image

ROI delineation

ROI 1:
Primary tumor

ROI 2:
Lymph nodes

Feature extraction

- **Shape**
- **First-order statistics**
- **Texture features**
  - GLCM, GLRLM, GLSZM, GLDM, NGTDM
  - **Wavelet (8 transforms)**

Feature Selection

- Step 1: Univariate Cox regression
- Step 2: Minimum Redundancy Maximum Relevance (mRMR)

$$\mathrm{mRMR(S)} = \max\left(\frac{1}{|S|}\sum_{x_i \in S} I(x_i; c) - \frac{1}{|S|^2}\sum_{x_i, x_j \in S} I(x_i; x_j)\right)$$

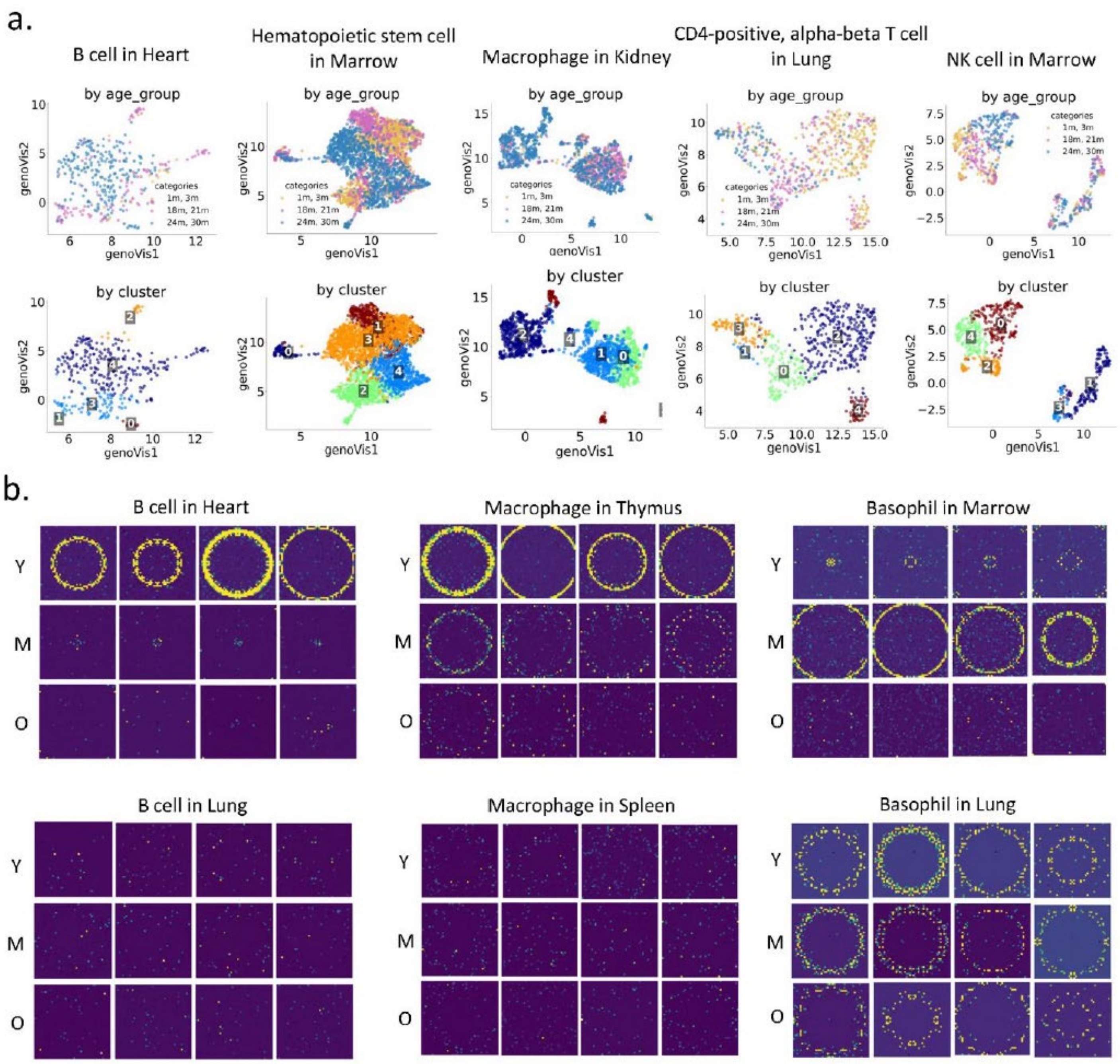
RadioMap construction

Prognosis prediction

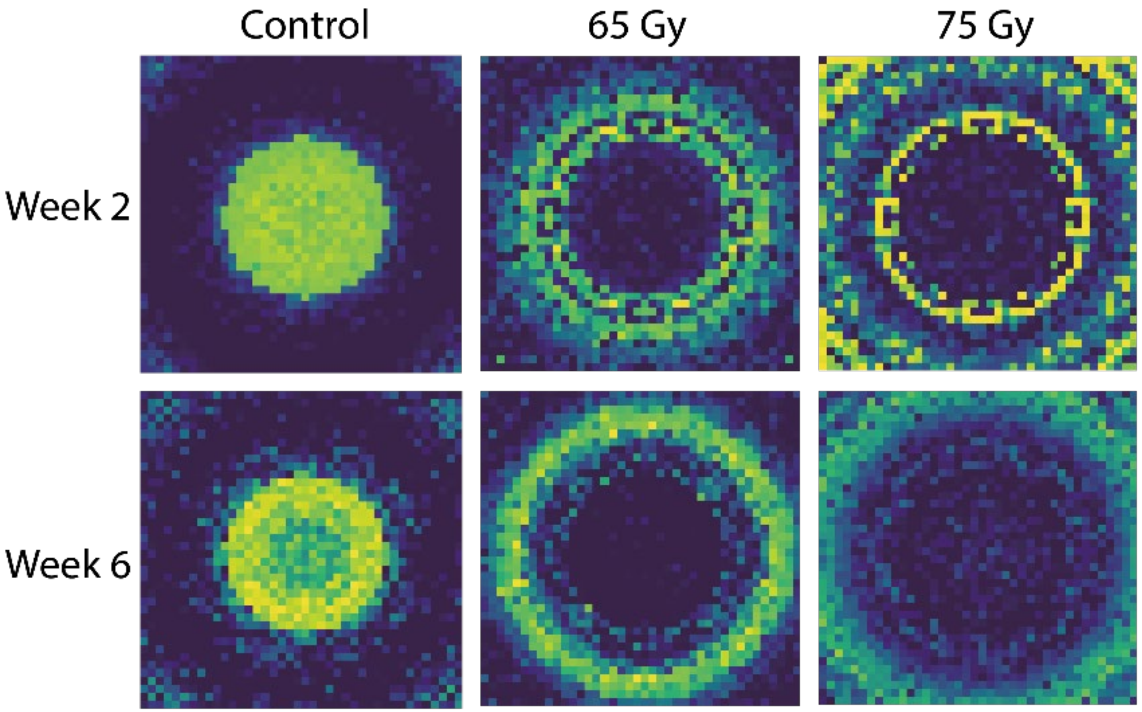
PFS

$$loglik = \begin{cases} \ln(h_j) + \sum_{i=1}^{j-1} ln(1-h_i), & uncensored \\ \sum_{i=1}^{j-1} ln(1-h_i), & cencored \end{cases}$$

Evaluation

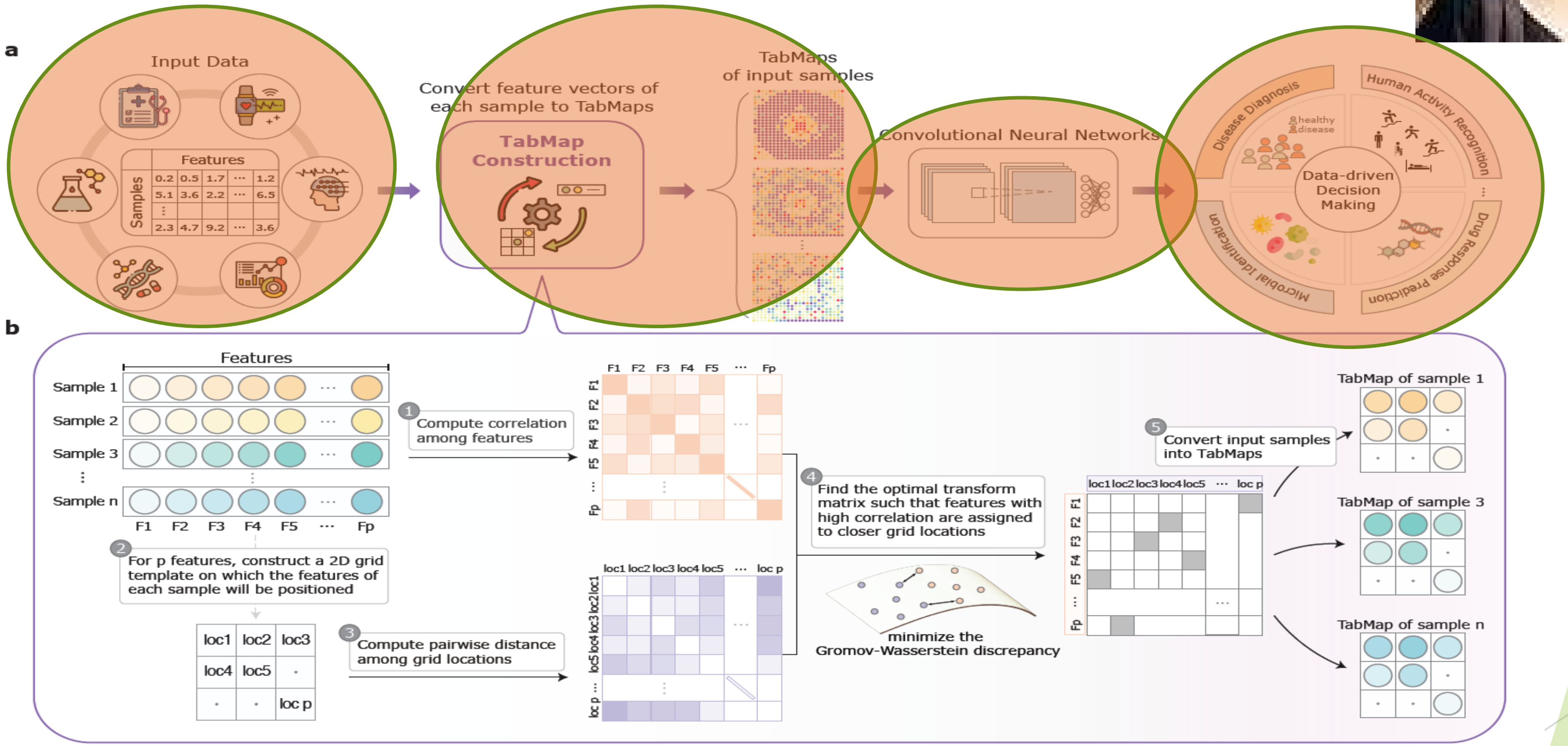

a.
B cell in Heart
Hematopoietic stem cell in Marrow
Macrophage in Kidney
CD4-positive, alpha-beta T cell in Lung
NK cell in Marrow
by age_group
by cluster
categories
1m, 3m
18m, 21m
24m, 30m
genoVis1
genoVis2
b.
B cell in Heart
Macrophage in Thymus
Basophil in Marrow
B cell in Lung
Macrophage in Spleen
Basophil in Lung
Y
M
O

Radiation Lung fibrosis



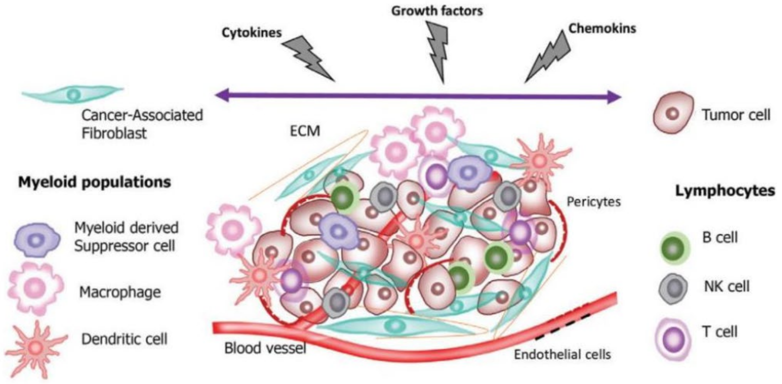
Visualization of bulk RNA sequencing of mouse lungs post radiation treatment. We convert 17 mouse lungs bulk RNA sequencing samples into genoMaps. Mouse lungs are treated with 0 Gy (control), 65 Gy or 75 Gy. RNA sequencing are performed either two or six weeks after the radiation.

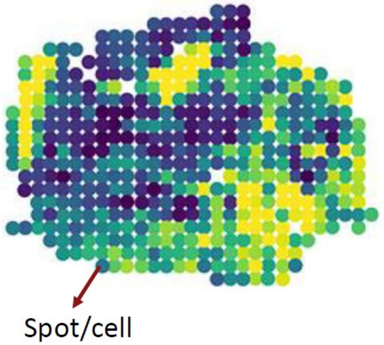
Tabular data



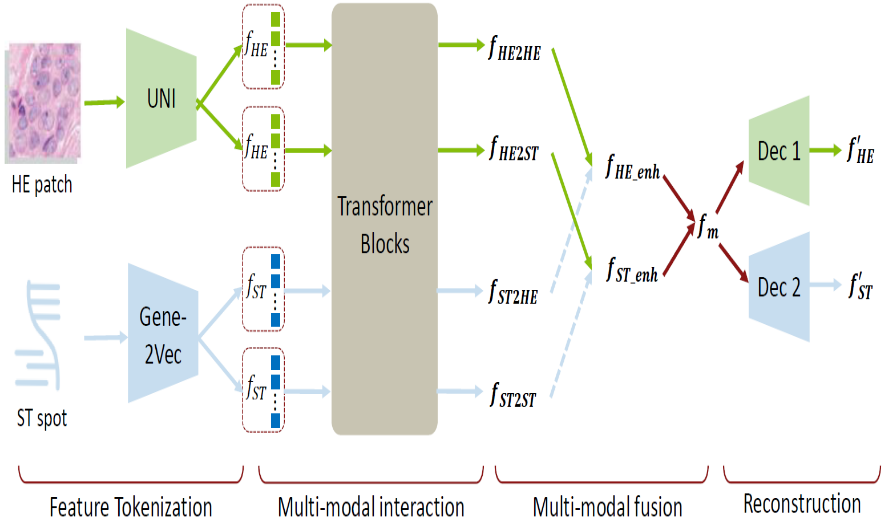
Yan R, Islam, M.T., and Xing, L., 2024. **Interpretable discovery of patterns in tabular data via spatially semantic topographic maps**, Nature Biomedical Engineering 8, 1-12, 2024.

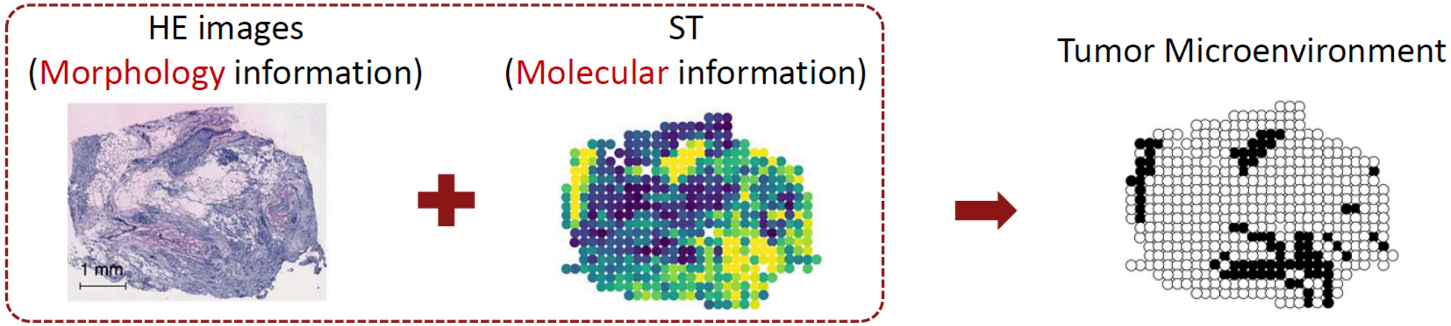
Spatial transcriptomics





HE + ST integration





Spot-level Tasks (Biology):

- ➢ Spatial domain detection.
- ➢ ST super-resolution.
- ➢ Cell type decomposition/deconvolution.
- ➢ ……

Patient-level Tasks (Clinical):

- ➢ Cancer subtyping.
- ➢ Gene mutation prediction.
- ➢ Response to immunotherapy.
- ➢ ……

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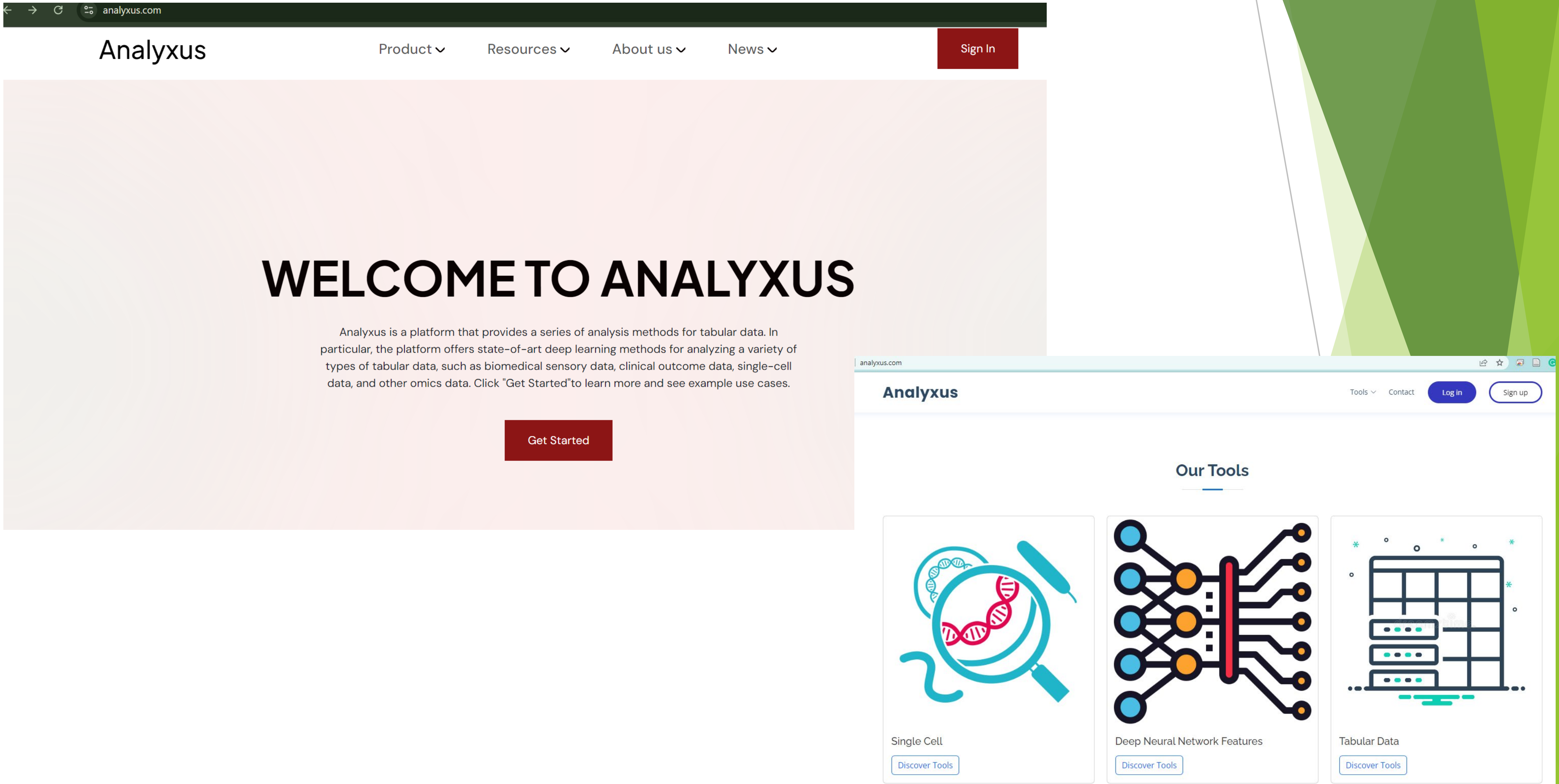


WELCOME TO ANALYXUS

Analyxus is a platform that provides a series of analysis methods for tabular data. In particular, the platform offers state-of-art deep learning methods for analyzing a variety of types of tabular data, such as biomedical sensory data, clinical outcome data, single-cell data, and other omics data. Click "Get Started"to learn more and see example use cases.

AI FOUNDATION MODELS

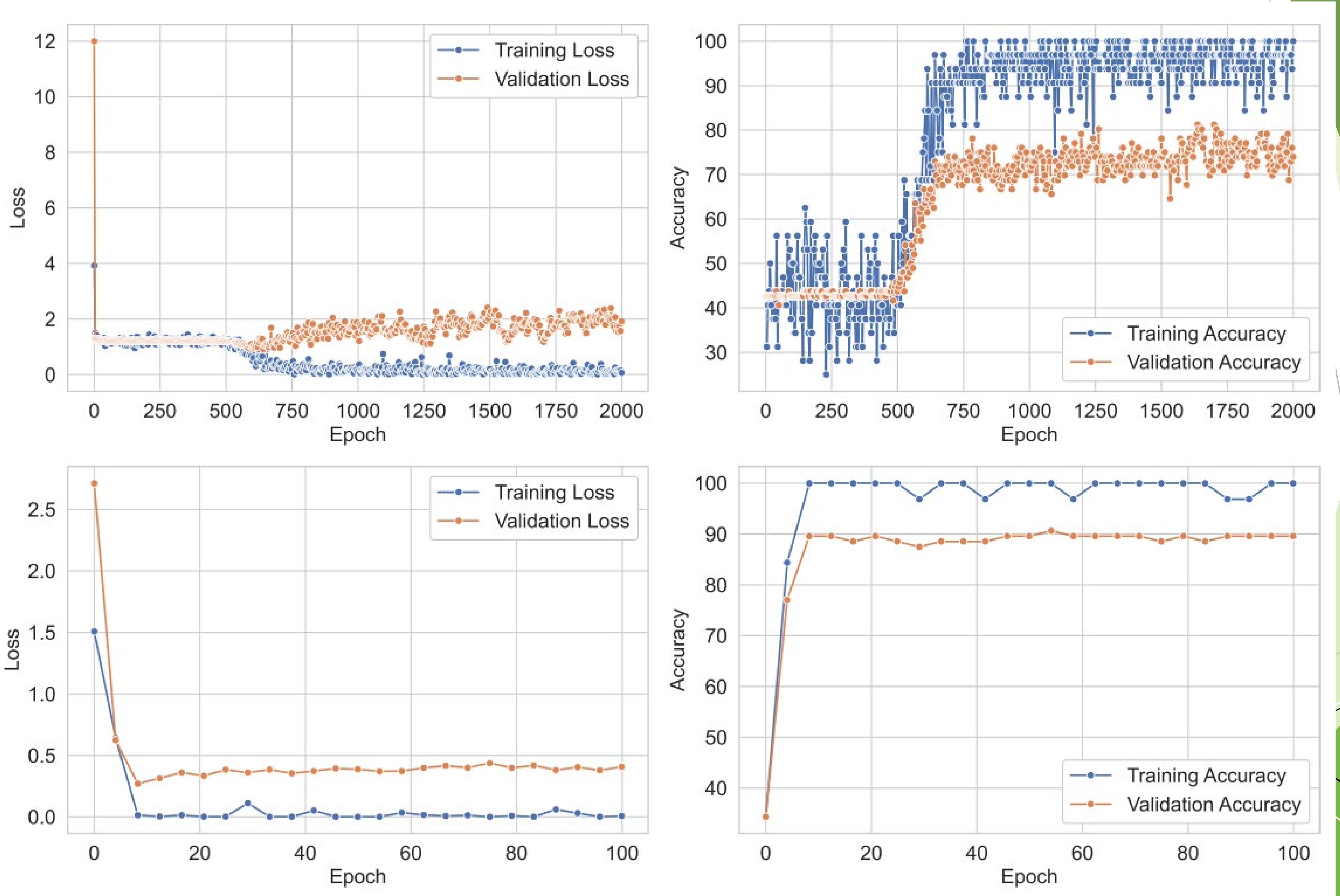
•**Definition**:
Foundation models are large-scale machine learning models trained on vast amounts of data. They are designed to be adaptable to a wide range of tasks.

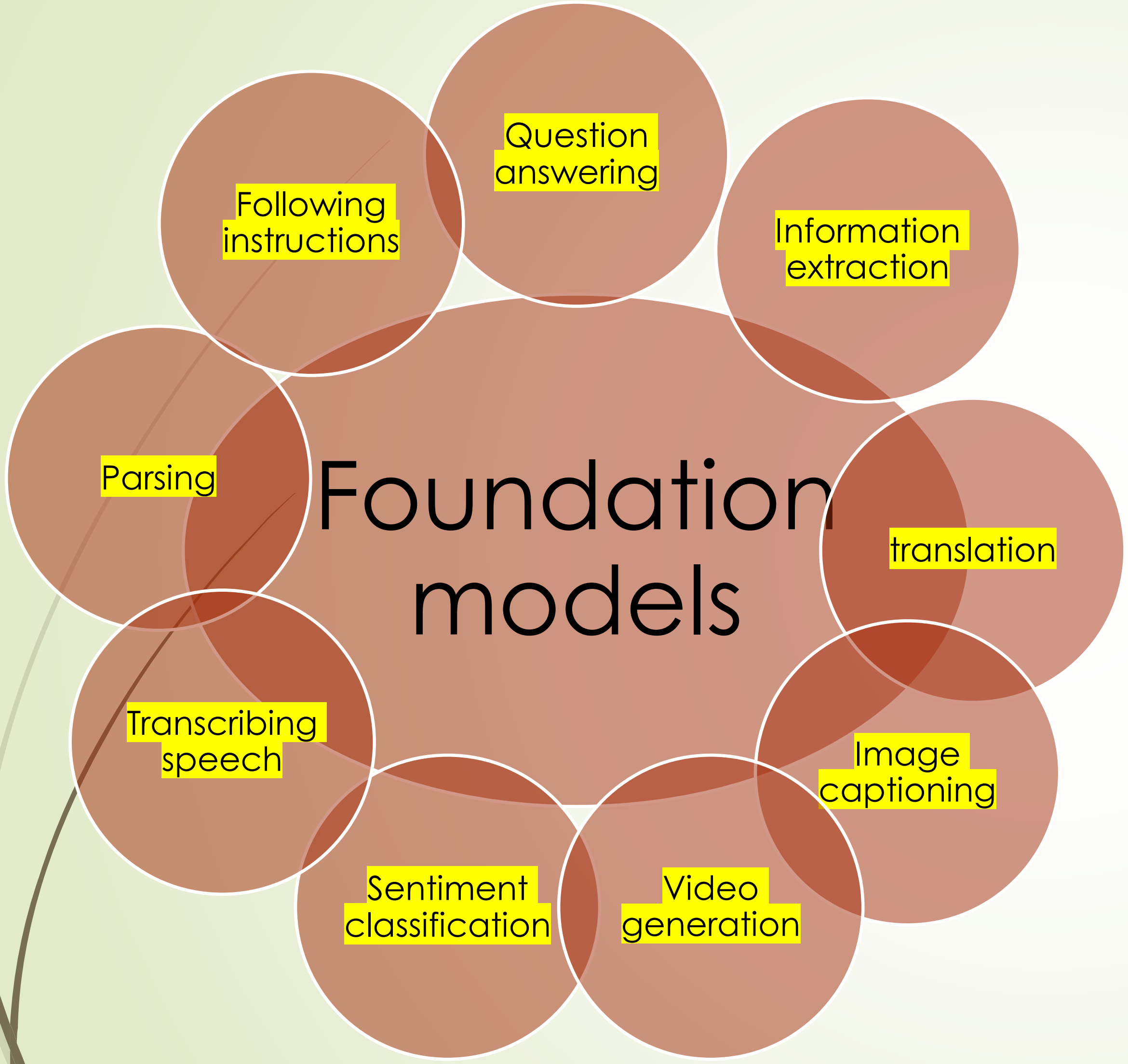
Characteristics:

- **Large scale:** large number of parameters & datasets
- **Generalization:** capable of performing various task-specific training
- **Adaptability:** can be fine-tuned for specific applications
- **Self-supervised**

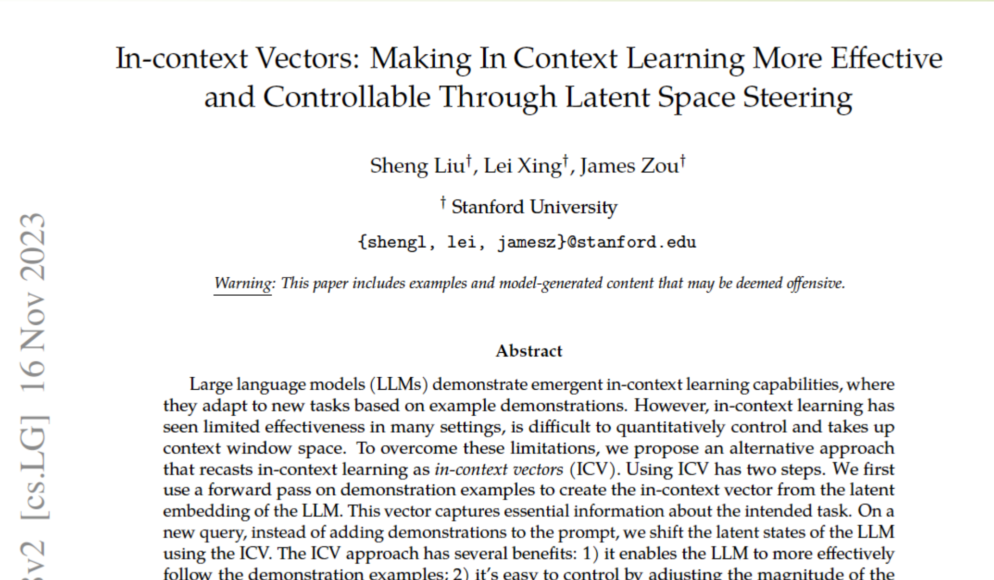
LLMs

Training and validation loss and accuracy of BERT and our new BERT - Amazon Factory report dataset (Nat. Biotech. Under review, 2025)





- Fine-tuning
- prompting
- In-context learning



v2 [cs.LG] 16 Nov 2023

In-context Vectors: Making In Context Learning More Effective and Controllable Through Latent Space Steering

Sheng Liu[†], Lei Xing[†], James Zou[†]
[†] Stanford University
{shengl, lei, jamesz}@stanford.edu

Warning: This paper includes examples and model-generated content that may be deemed offensive.

Abstract

Large language models (LLMs) demonstrate emergent in-context learning capabilities, where they adapt to new tasks based on example demonstrations. However, in-context learning has seen limited effectiveness in many settings, is difficult to quantitatively control and takes up context window space. To overcome these limitations, we propose an alternative approach that recasts in-context learning as *in-context vectors* (ICV). Using ICV has two steps. We first use a forward pass on demonstration examples to create the in-context vector from the latent embedding of the LLM. This vector captures essential information about the intended task. On a new query, instead of adding demonstrations to the prompt, we shift the latent states of the LLM using the ICV. The ICV approach has several benefits: 1) it enables the LLM to more effectively follow the demonstration examples; 2) it's easy to control by adjusting the magnitude of the

Automated radiotherapy treatment planning guided by GPT-4Vision

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Weixing Liang[3], Mark Buyyounouski[1], Erqi Pollom[1], Quynh-Thu Le[1],
Michael Gensheimer[1], Peng Dong[1], Yong Yang[1], James Zou[2,3]†, and Lei Xing[1]†
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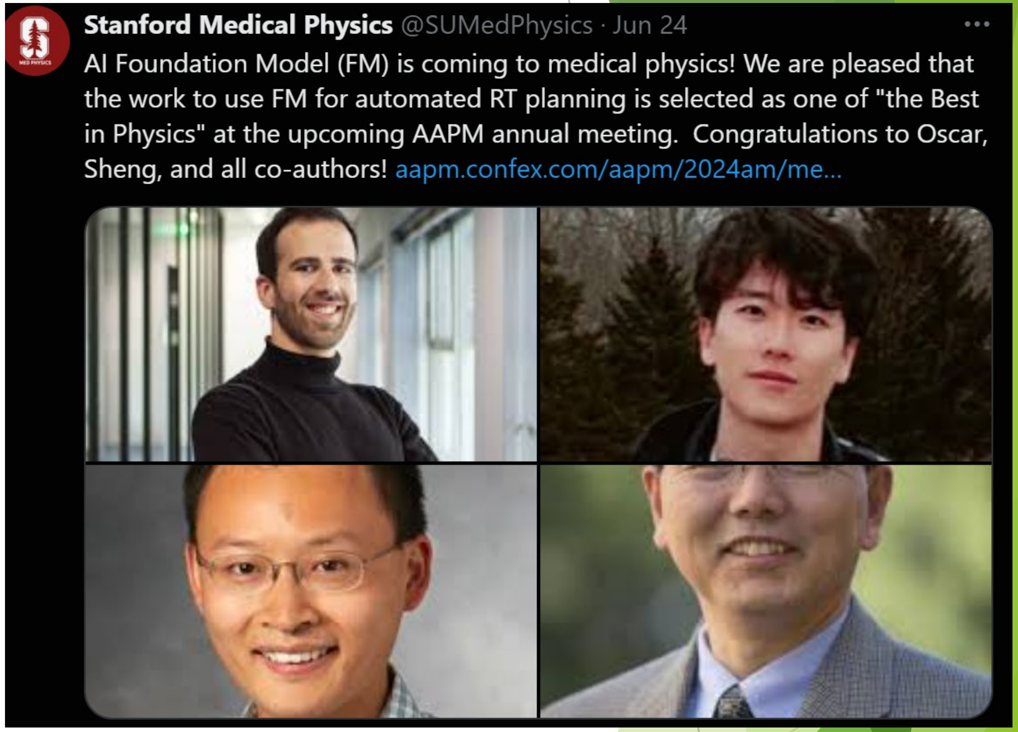
Abstract

Radiotherapy treatment planning is a time-consuming and potentially subjective process that requires the iterative adjustment of model parameters to balance multiple conflicting objectives. Recent advancements in frontier AI models offer promising avenues for addressing the challenges in planning and clinical decision-making. This study introduces GPT-RadPlan, an automated treatment planning framework that integrates radiation oncology knowledge with the reasoning capabilities of large multi-modal models, such as GPT-4Vision (GPT-4V) from OpenAI. Via in-context learning, we incorporate clinical protocols for various disease sites to enable GPT-4V to acquire treatment planning domain knowledge. The resulting GPT-RadPlan agent is integrated into our in-house inverse treatment planning system through an API. For a given patient, GPT-RadPlan acts as both plan evaluator and planner, first assessing dose distributions and dose-volume histograms (DVHs), and then providing "textual feedback" on how to improve the plan. In this manner, the agent iteratively refines the plan by adjusting planning parameters, such as weights and objective doses, based on its suggestions. The efficacy of the automated planning system is showcased across multiple prostate and head & neck cancer cases, where we compared GPT-RadPlan results to clinical plans produced by human experts. In all cases, GPT-RadPlan either outperformed or matched the clinical plans, demonstrating superior target coverage and organ-at-risk sparing. Consistently satisfying the dosimetric objectives in the clinical protocol, GPT-RadPlan represents the first multimodal large language model agent that mimics the behaviors of human planners in radiation oncology clinics, achieving promising results in automating the treatment planning process without the need for additional training.



Stanford Medical Physics @SUMedPhysics · Jun 24

AI Foundation Model (FM) is coming to medical physics! We are pleased that the work to use FM for automated RT planning is selected as one of "the Best in Physics" at the upcoming AAPM annual meeting. Congratulations to Oscar, Sheng, and all co-authors! aapm.confex.com/aapm/2024am/me...

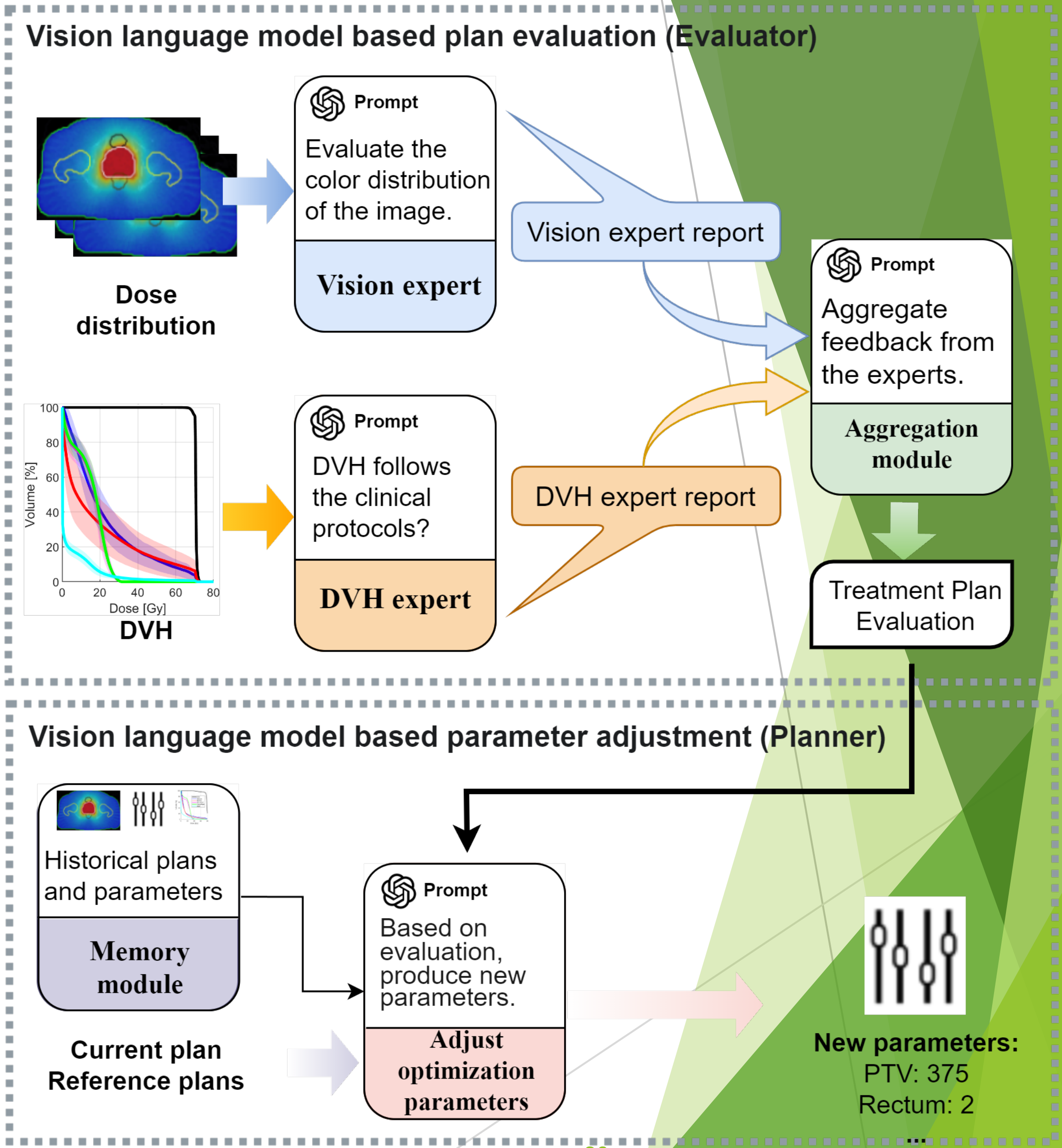
Liu S, Pastor-Serrano O, ….., arXiv preprint arXiv:2406.15609, 2024

GPT-RadPlan

- Based on GPT4-Vision

- Evaluation module:
- DVH Expert – compares metrics with protocol/intent
- Image expert – evaluates dose distribution and presence of hot/cold spots
- Aggregation module – improvement suggestions

- Planner module: suggest new parameters based on
- Stored information from previous iterations
- The current plan
- 3 reference approved plans from the same disease site


Vision language model based plan evaluation (Evaluator)

Dose distribution

Prompt
Evaluate the color distribution of the image.
Vision expert

Vision expert report

Prompt
Aggregate feedback from the experts.
Aggregation module

DVH

Prompt
DVH follows the clinical protocols?
DVH expert

DVH expert report

Treatment Plan Evaluation

Vision language model based parameter adjustment (Planner)

Historical plans and parameters
Memory module

Current plan
Reference plans

Prompt
Based on evaluation, produce new parameters.
Adjust optimization parameters

New parameters:
PTV: 375
Rectum: 2
...

AI & FOUNDATION MODELS FOR FUTURE HEALTHCARE

Deep and Wide Learning: Sample Interrelationship-Informed Representation Learning for Enhanced Data-Driven Decision-Making

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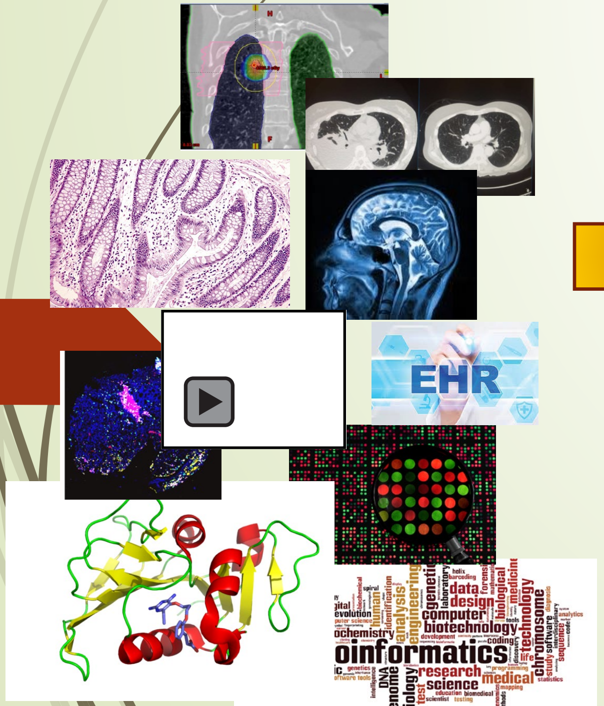
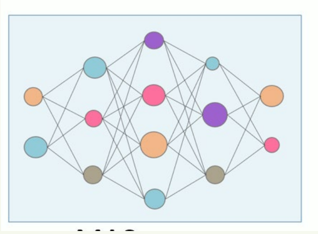
MULTIMODALITY & MULTISCALE FOUNDATION MODEL

DATA



Foundation Models

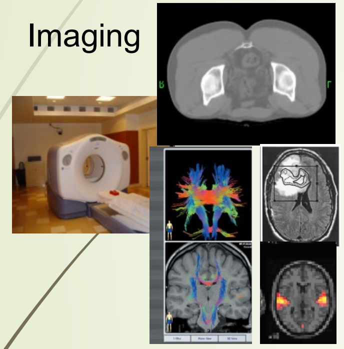


TASKS

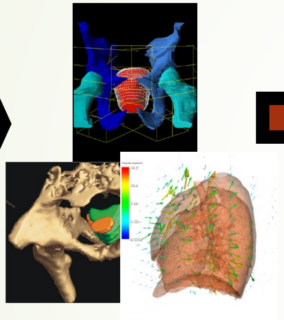
- Sentiment analysis
- Image processing
- Information extraction
- Instruction following
- Parsing
- Transcribing speech
- Biomarkers discovery

FM/AI IN CLINICAL WORKFLOW OF RADIATION THERAPY

Imaging



Modeling



Treatment planning

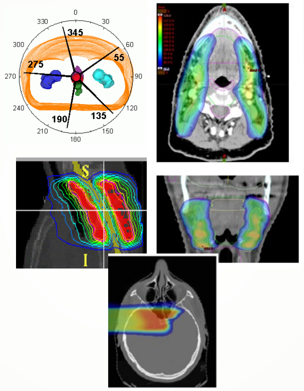


Image-guided patient setup & delivery

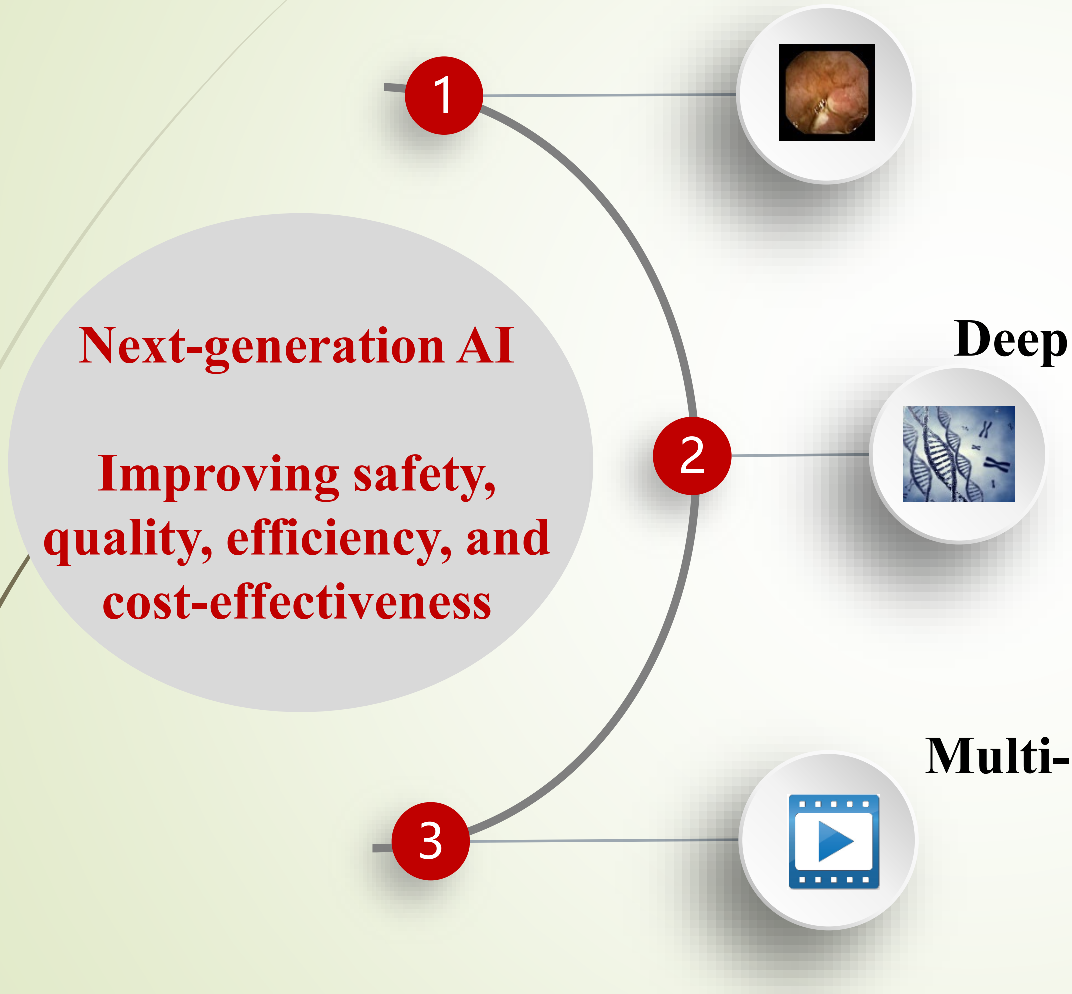
Follow up

Image reconstruction
Differen modalitie
OAR segmentation
supervise
Supervised planning
. . . .
Monoscopic imaging
. . .
Therapeutic response
. . . .

High dimensional imaging
Real-time
Tumor detection & segmentation
Detectio
Unsupervised
. . .
Stereoscopic imaging
. .
Survival
. . . . .

Sparsification compression
Sparse representat
Image registration
Intra- modalit
Reimforcement learning
. . .
Cone beam CT
. . . .
Toxity
. . . .

Summary



Next-generation AI

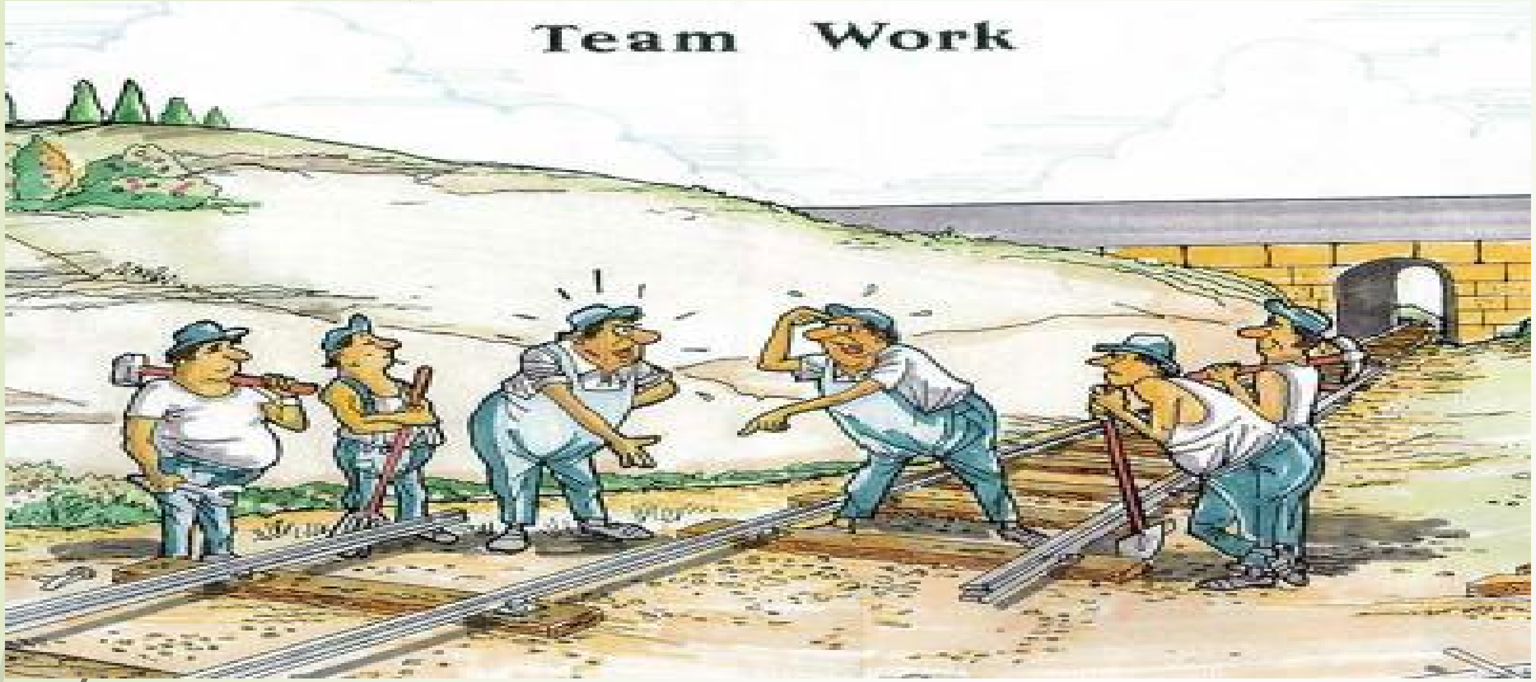
Improving safety, quality, efficiency, and cost-effectiveness

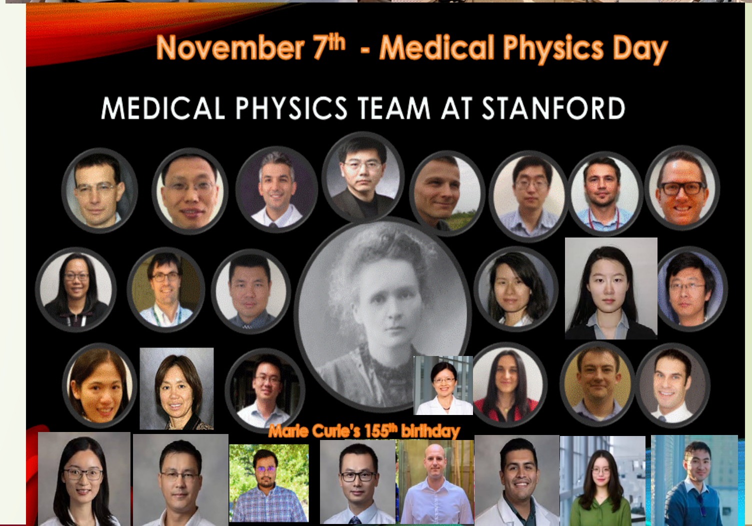
1 **Data pre-processing for deep learning**

2 **Deep omics data analysis**

3 **Multi-modality FMs**

Acknowledgements





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