



# Foundation Models

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May 7, 2024



@BrookhavenLab

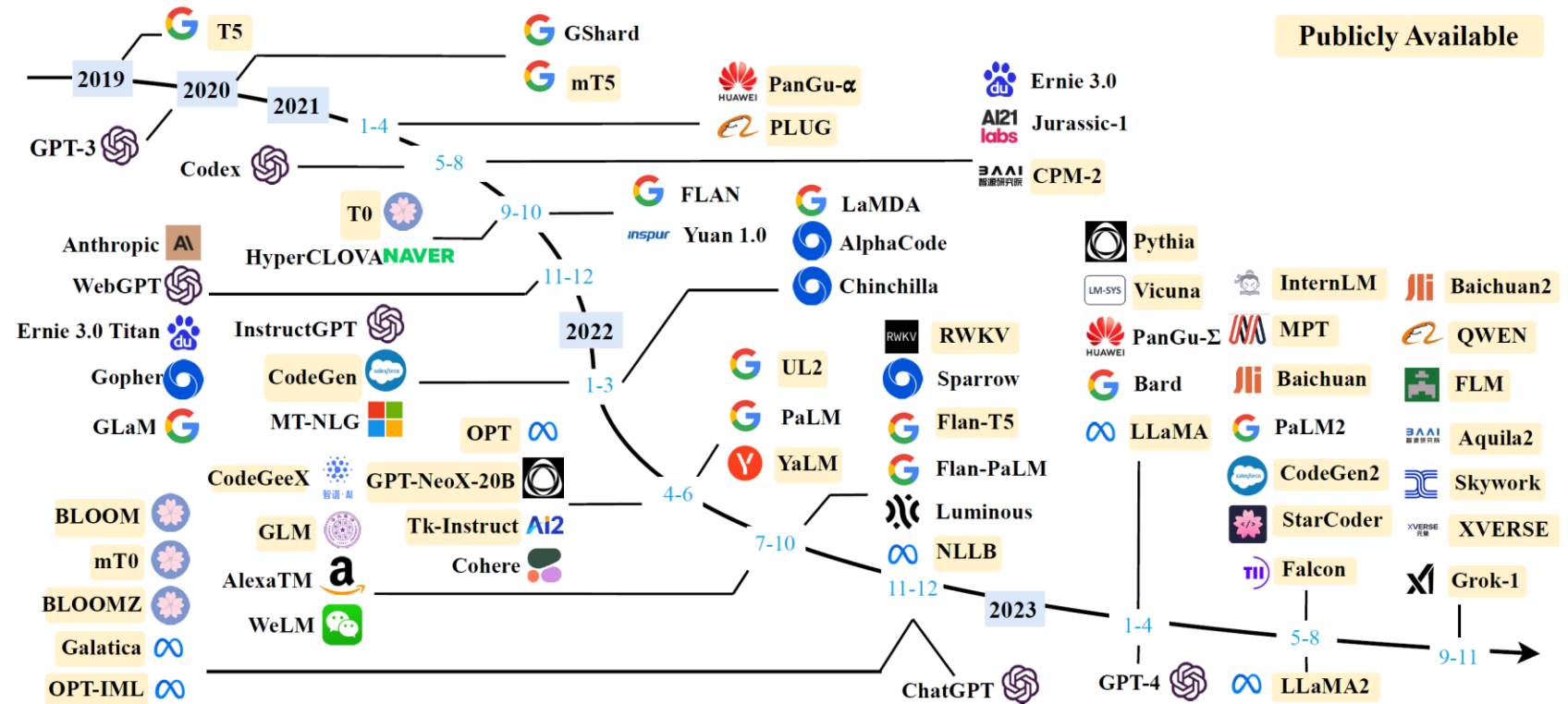
# Outline

- Introduction
- Foundation models in Scientific Domains:
  - Foundation Models for Cell Segmentation
  - Foundation Models for Structure Biology
  - Foundation Models for Fusion Energy
  - Generalizability of Foundation Models
  - Multimodal Foundation Models for Plant Disease Diagnose
  - Multiple LLM Agents for Scientific Discovery
- Future Works

# Introduction for Foundation Models

**Foundation models** are those trained on broad data (generally using self-supervision) and can be adapted to a wide range of downstream tasks.

A timeline of existing large foundation models (larger than 10B) in recent years.

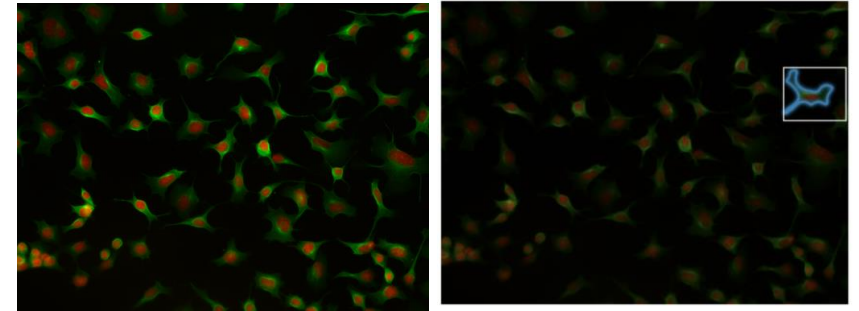


# Foundation Models for Cell Segmentation

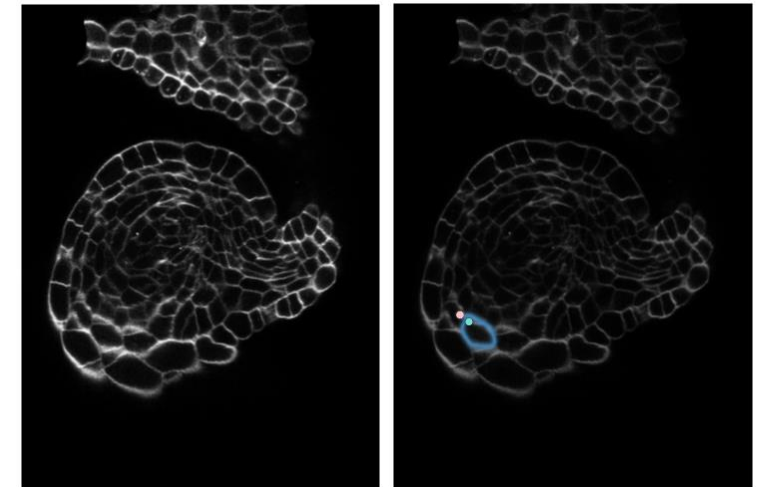
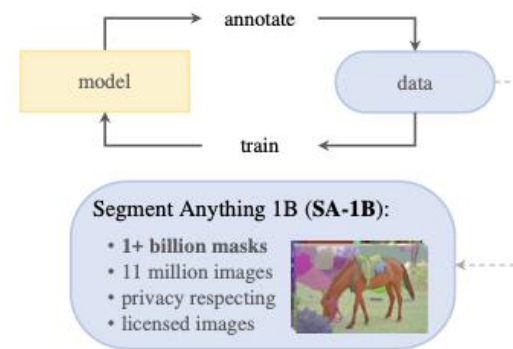
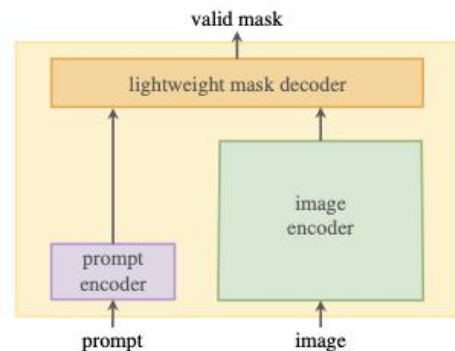
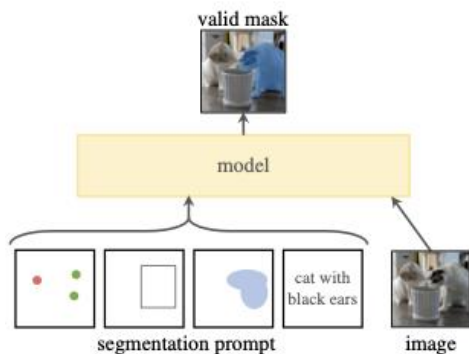
**Task:** 3D Cell segmentation

**Model:** Segment Anything Model (SAM)

- **400M** image-text pairs, **1B** masks from **11M** images
- Zero shot generalization ability
- Data engine: model-in-the-loop annotation

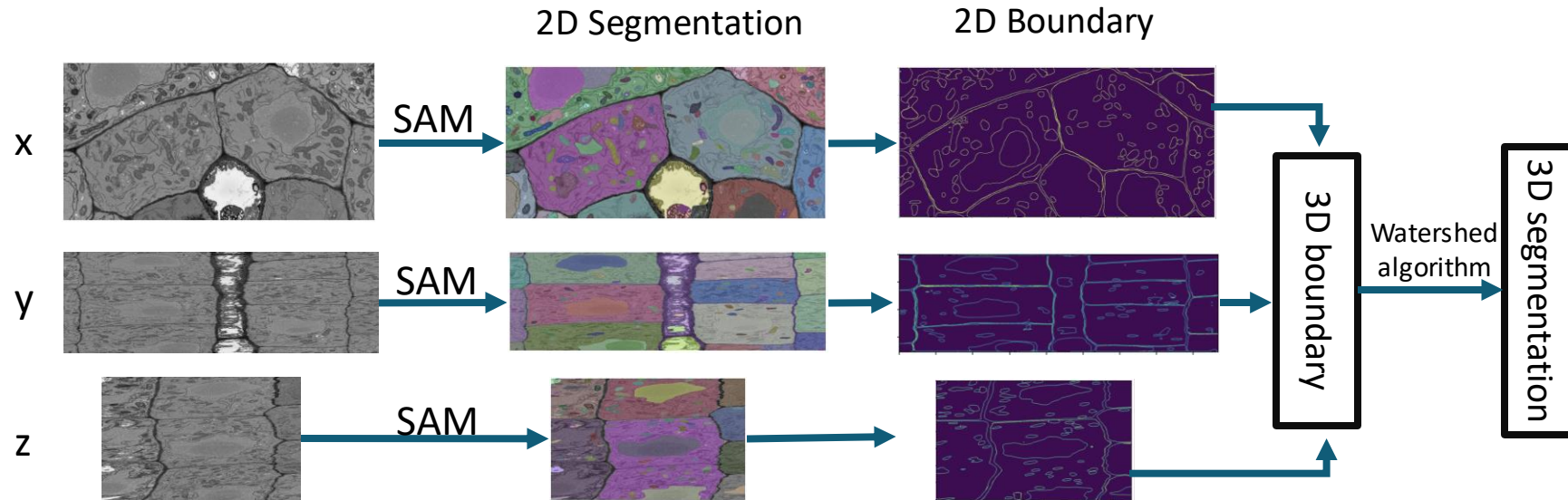


Box prompt



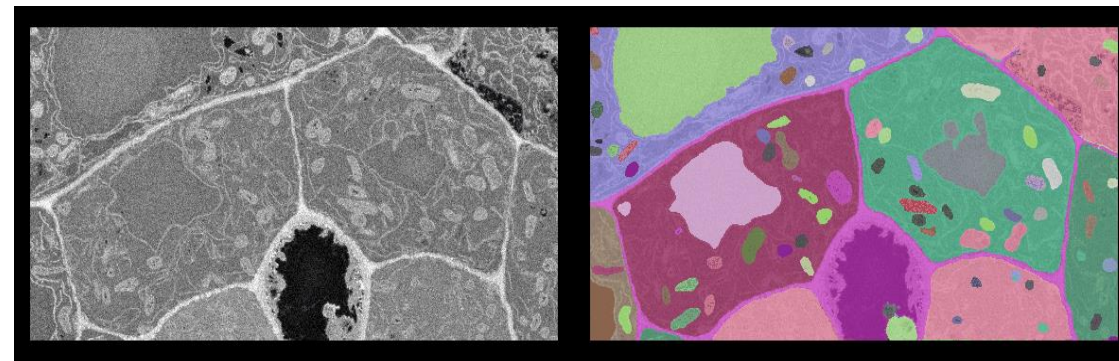
Point prompt  
(positive and negative)

# Foundation Models for Cell Segmentation



Advantages:

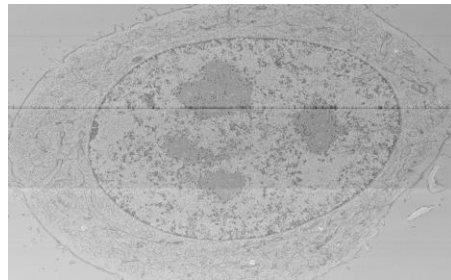
- No training needed
- No annotations needed



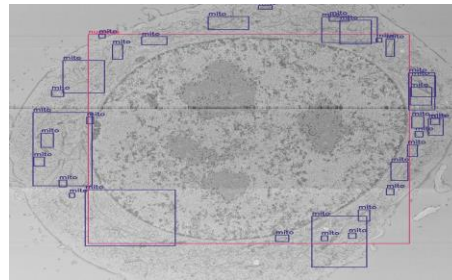
3D image segmentation result

# Foundation Models for Cell Segmentation

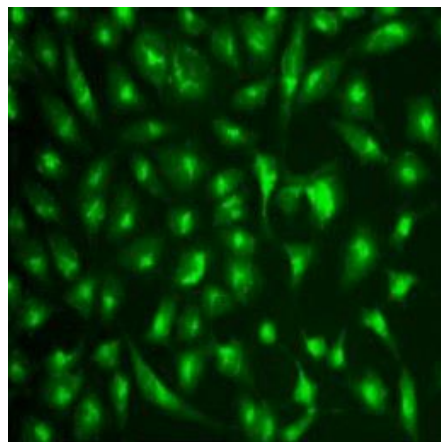
- Train an object detection model to provide the bounding boxes.
- Use the bounding boxes as prompt for SAM.



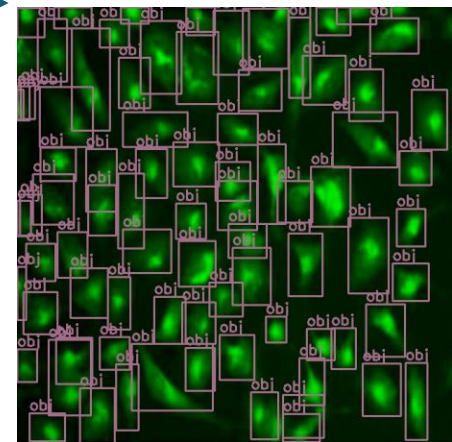
Object  
detection



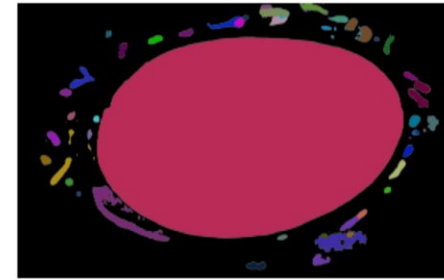
SAM



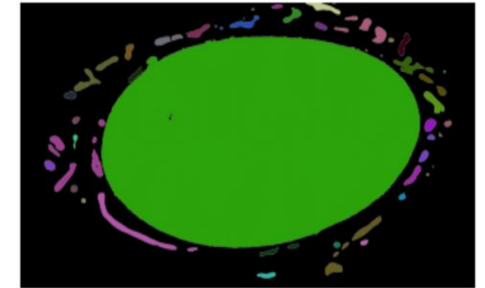
Original image



Bounding box prediction



Prediction



Ground truth

# Foundation Models for Structure Biology

- **Self-supervised learning** models trained on **vast amounts** of biological data
  - Protein sequence database (~1 billion of unlabeled sequences)
  - Protein structure database ( ~200k experimental structures)
- **Representation learning**: capture fundamental properties and patterns
  - Encode complex relationships between sequence, structure, and function
- **Efficient and scalable** prediction of biological properties and facilitate protein engineering
  - Guide rational protein design and optimization
  - Accelerate the discovery of novel proteins with desired characteristics

# Foundation Models in Structure Biology

## **ESM (Evolutionary Scale Modeling): Protein Foundation Models**

- Large protein language model with up to 15B parameters
- Trained on over 617 million diverse protein sequences
- Enhances the efficiency and accuracy of protein structure prediction
- Serves as a powerful tool for various downstream applications

## **ESM-IF (Inverse Folding): Predict protein sequence based on backbone structure**

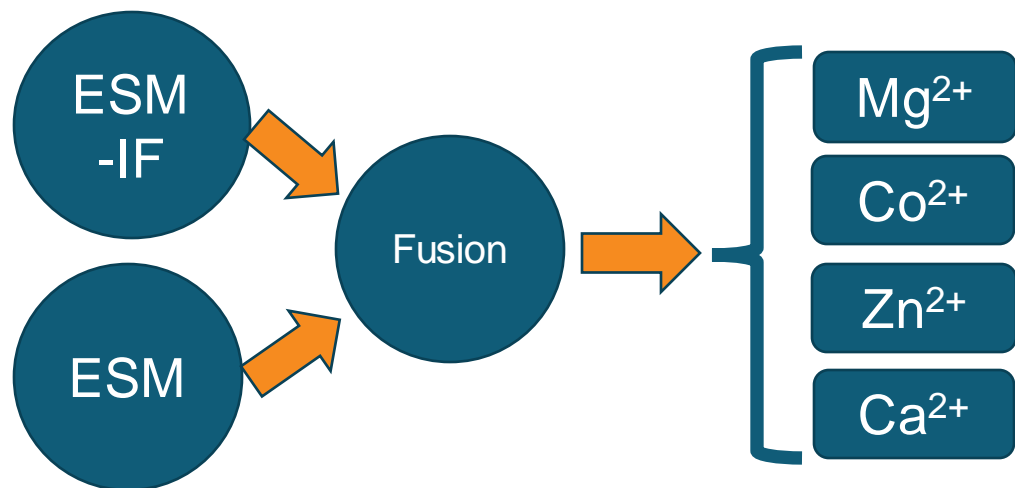
- Enables protein design and optimization:
- Training data: 16K experimental structures and 12M predicted structures from AlphaFold2



# Foundation Models in Structure Biology

## ESMBind: Protein-metal ion binding prediction

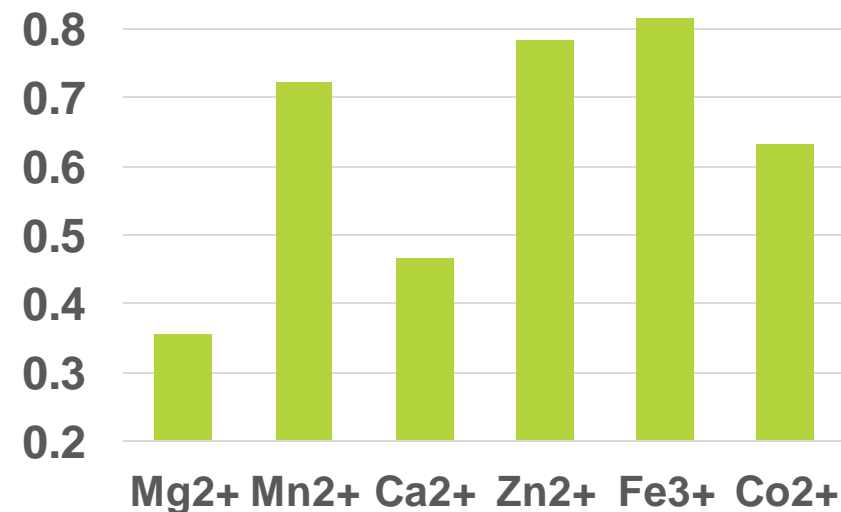
- ESM: Sequence embedding
- ESM-IF: Structure embedding
- Ion-specific models share the same upstream fused input



Fusion module:  
learns a **unified** feature  
from sequence and  
structure

ion-specific networks:  
binding prediction at  
**residue** level

## AUPRC



**SOTA** performance on common  
metal ions in protein

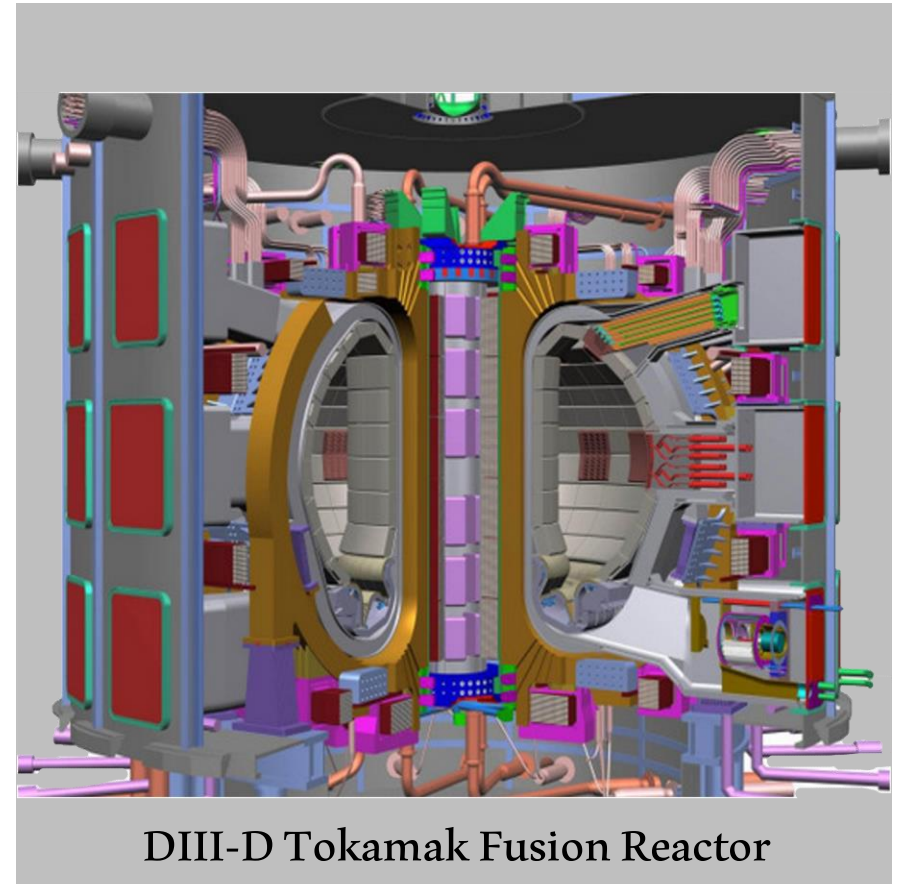
# Foundation Models for Fusion Energy

**Task:** Predict Disruptions in Fusion Device

**Challenge:** Disruptions have proven very difficult to predict with classic simulation tools, especially in real time.

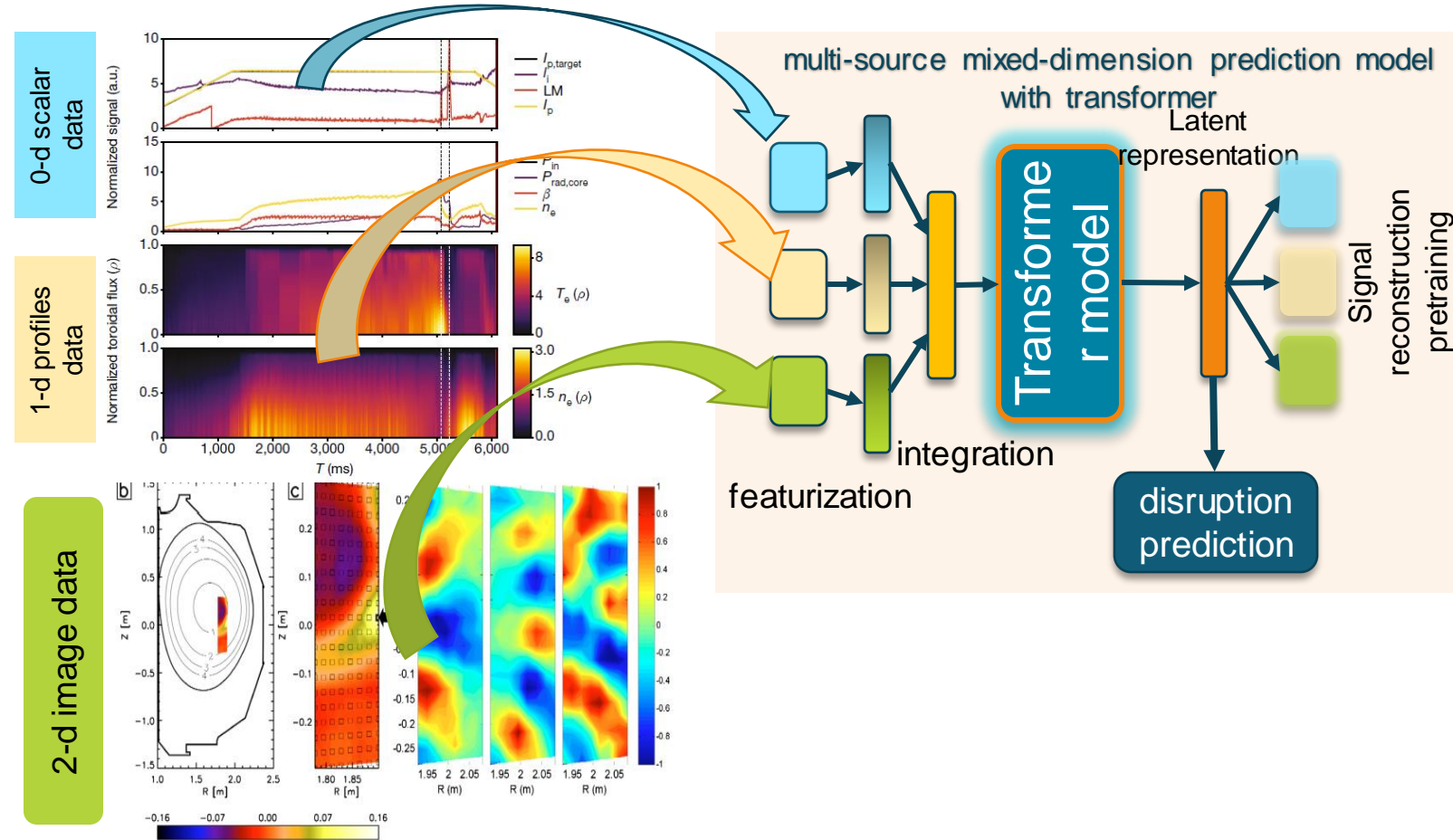
**Goal:** Develop foundation models on exascale computers to predict disruption events.

Real-time models are being developed and trained to predict the disruption and take appropriate action.



# Foundation Models for Fusion Energy

- Train a 1.5B parameter GPT-like foundation model using ~10 TB training data collected from the DIII-D tokamak Fusion Reactor.
- Data fusion of 2D ECEi data along with 0-d scalar and 1-d profile diagnostic data

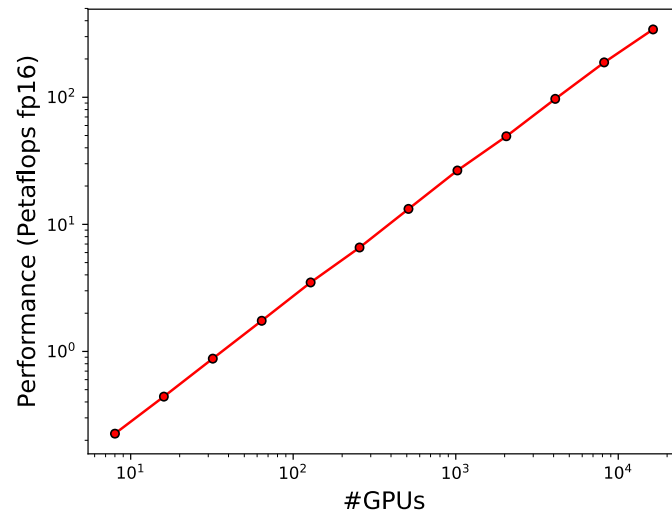


Electron Cyclotron Emission Imaging (ECEI)

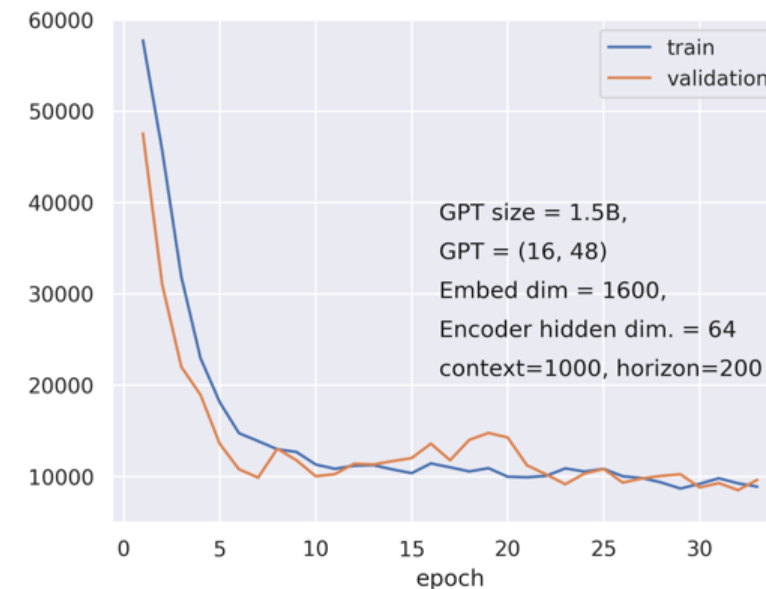
# Foundation Models for Fusion Energy

## Science Accomplishment and Impact

- Run the foundation model on Frontier cluster at ORNL with good scalability
- Improve predictive accuracy for disruption forecasting over previous ML tools

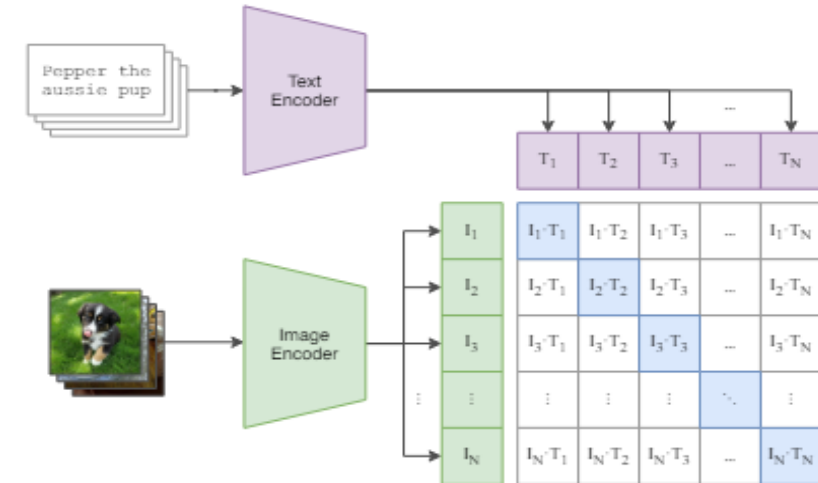
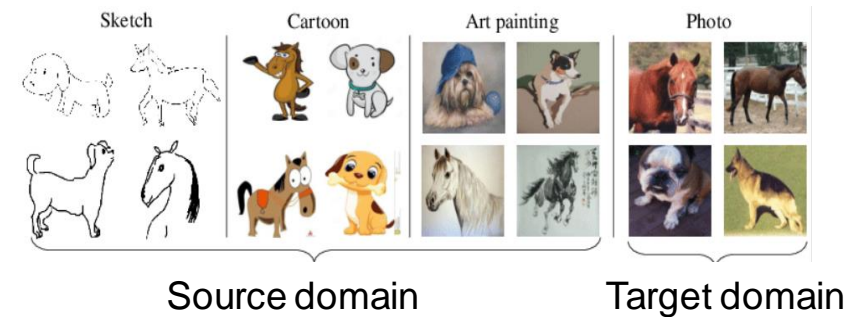


Scaling of model training on Frontier cluster at ORNL with 16,384 GPUs. Achieved 0.4 fp16 ExaFlops.



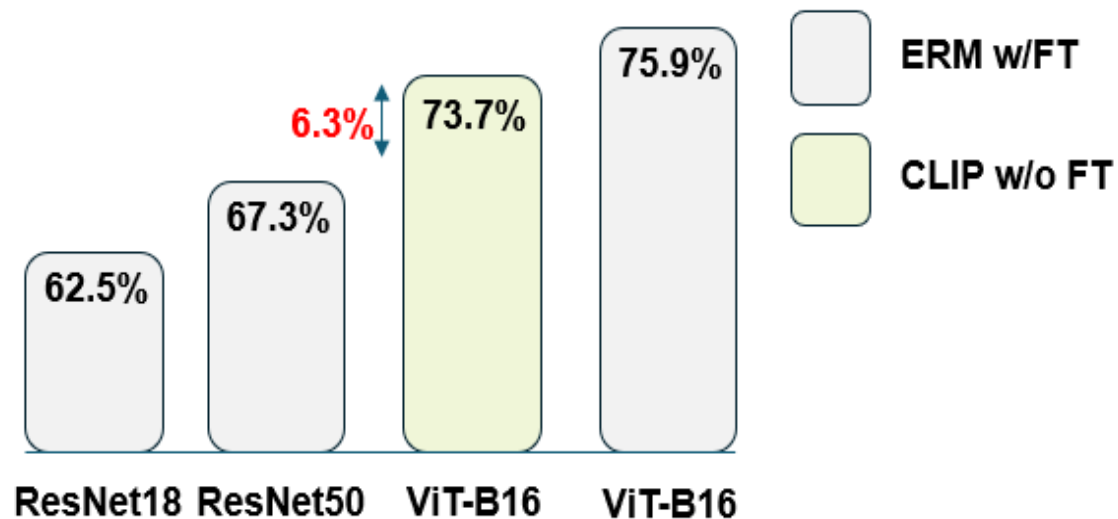
# Generalizability of Foundation Models

- **Domain Generalization (DG)** aims to learn a generalizable model trained on observed source domains, and directly applied on the target domain which is unseen during training.
- **Visual-language model (VLM)** are trained on massive datasets, like CLIP<sup>[1]</sup> model, trained on 400 million pairs of images and texts. The diverse data that help VLMs demonstrate impressive zero-shot ability.



# Generalizability of Foundation Models

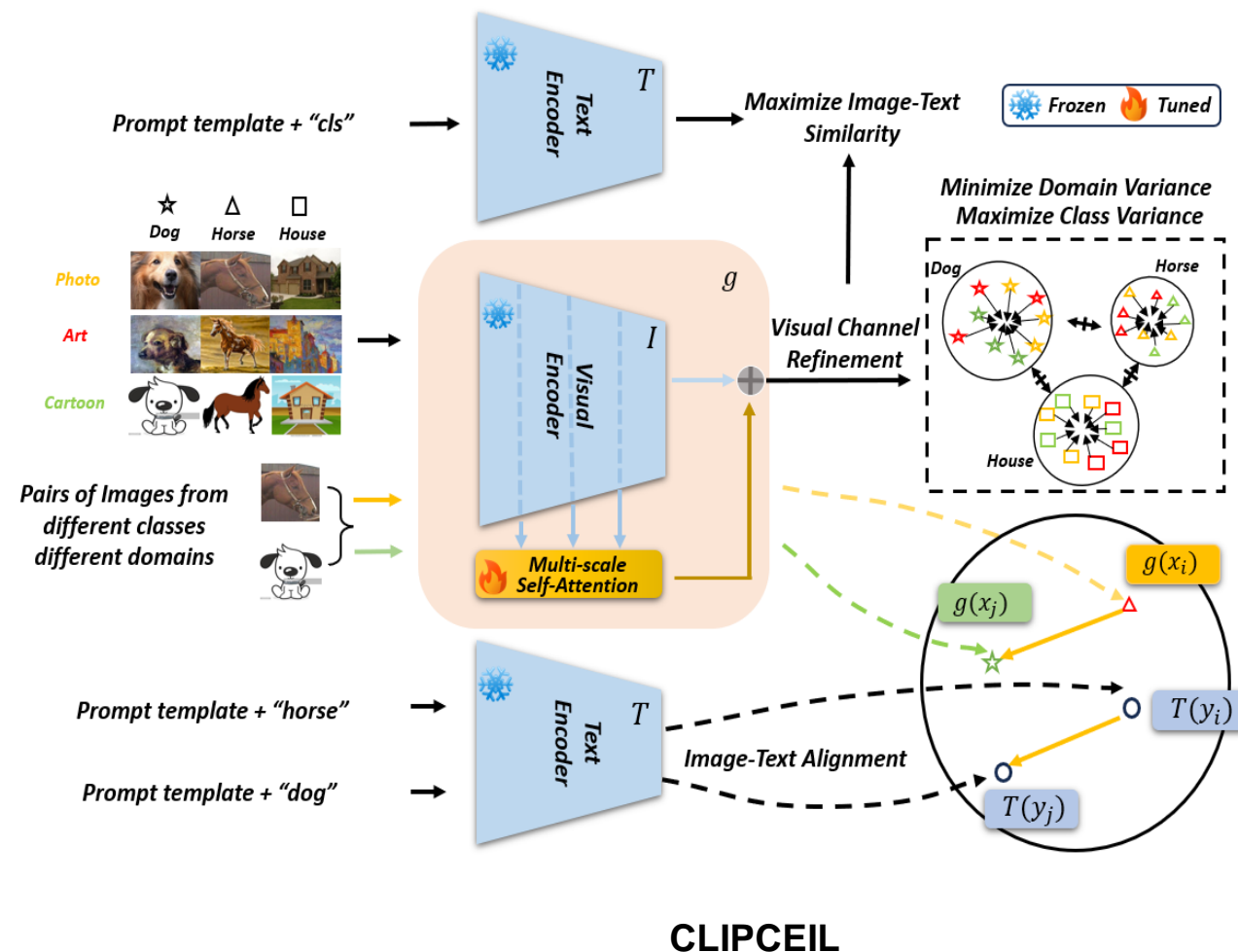
*Are the large visual language models good and good enough for generalizability?*



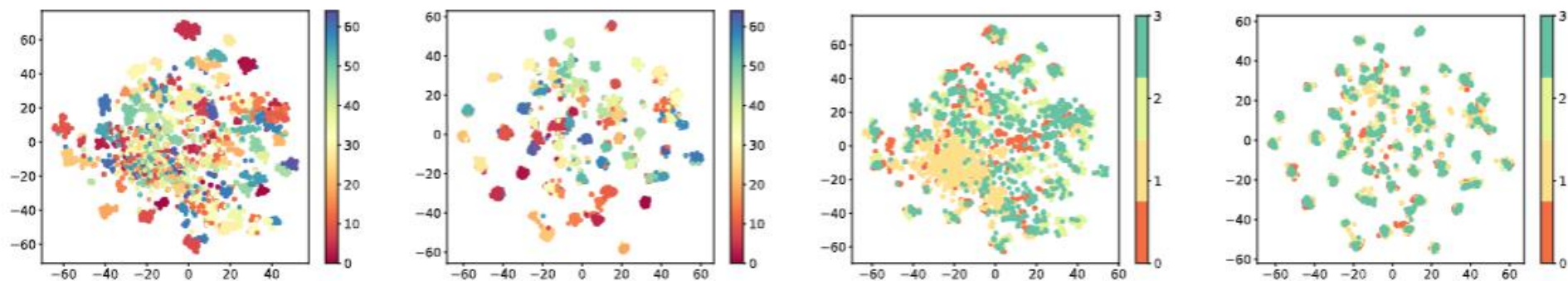
We evaluated the model's generalizability experiments. Even without fine-tuning, CLIP outperforms trained ResNet50 by 6.3%. *Although CLIP has shown impressive performance, there is still some scope for improvement.*

# Generalizability of Foundation Models

- CLIPCEIL (Boosting Domain Generalization with **CLIP** by **C**hannel **rE**finement and **I**mage-text **aL**ignment) introduces a lightweight module to fine-tune the CLIP and employ the multi-scale visual features.
- We proposed channel refinement module to ensure each channel contains domain-invariant (minimizing domain variance) and class-relevant (maximizing class variance) information.
- To align the image and text, we maximize the image-text similarity and calculate direction loss using text class descriptions based on data pairs from different classes and domains.



# Generalizability of Foundation Models



(a) Zero-shot across classes (b) CLIPCEIL across classes (c) Zero-shot across domains (d) CLIPCEIL across domains

Model	Venue	PACS	VLCS	OfficeHome	TerraInc	DomainNet	Avg
*SAGM [48]	CVPR'23	86.6	80.0	70.1	48.8	45.0	66.1
*DomainDrop [12]	ICCV'23	89.5	78.3	71.8	-	44.4	-
CLIP Zero-Shot	-	96.2	81.7	82.4	33.4	57.5	70.2
Lin.Probing	-	96.5	82.6	80.4	50.2	57.6	73.5
ERM [44]	-	93.7	82.7	78.5	52.3	53.8	72.2
MIRO [4]	ECCV'22	95.6	82.2	82.5	<b>54.3</b>	54.0	73.7
CoOp [61]	IJCV'22	96.0	81.1	83.5	47.0	59.8	73.5
CoCoOp [60]	CVPR'22	95.7	83.1	84.3	50.4	60.0	74.7
DPL [54]	Arxiv'22	<b>97.3</b>	84.3	84.2	52.6	56.7	75.0
CLIPCEIL	Ours	<b>97.3±0.1</b>	<b>84.7±0.2</b>	<b>85.6±0.1</b>	53.8±0.2	<b>61.2±0.1</b>	<b>76.5±0.1</b>



# Multimodal Foundation Models for Plant Disease Diagnose

## Goal:

- Develop a computational framework for plant disease detection, surveillance, and prediction.
- Develop the concept of Digital Twins to connect physical and digital representations of plant diseases, enabling timely decision-making and scalable exploration of disease management strategies.

## Challenges:

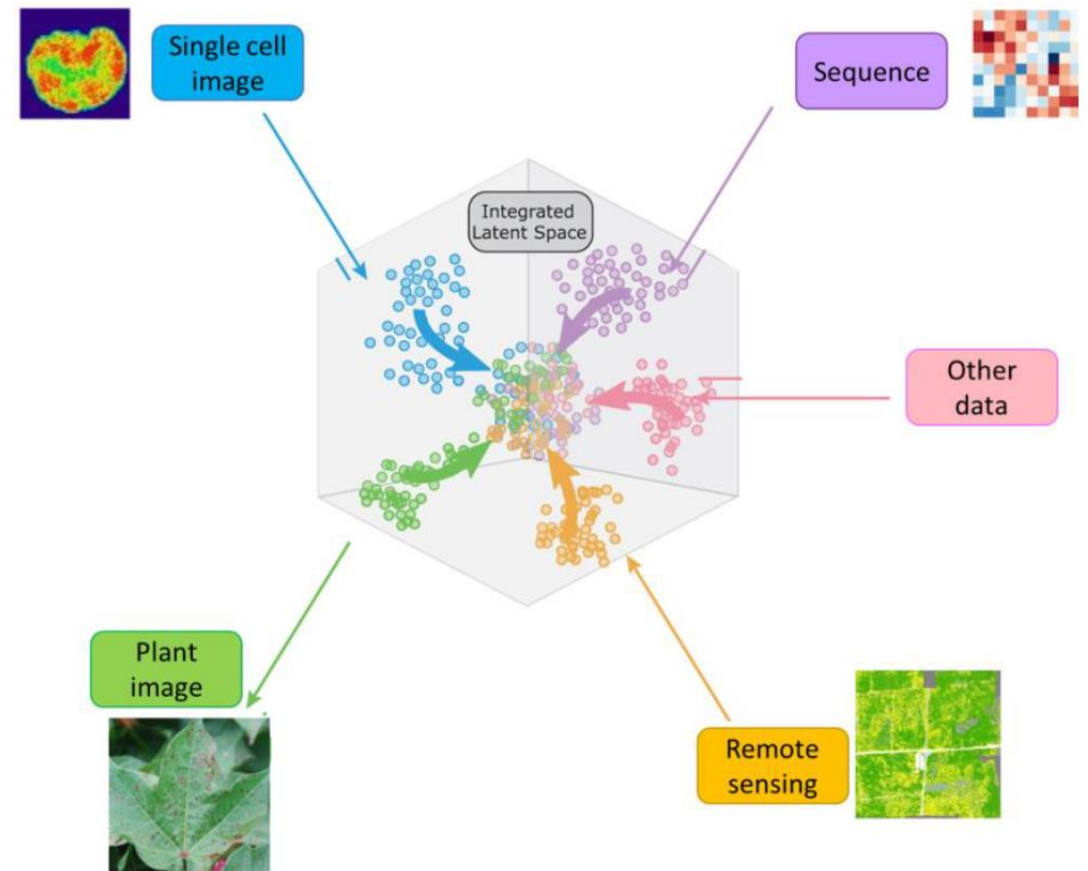
- Various modalities and scales to accurately detect and predict plant diseases.

# Multimodal Foundation Models for Plant Disease Diagnose

Heterogeneity of data:

- Remote sensing images (large scale)
- Plant pictures (medium scale)
- live-cell images from Optical microscopy (small scale)
- Electronic microscopy (micro-scale)
- Genomic sequence

**Multi-modal Foundation Models** are utilized to align and integrate data from various modalities into a common latent space.



# Multiple LLM Agents for Scientific Discovery

## LLM-based agent

An LLM-based agent is a comprehensive framework consisting of planning, tools, and memory. The LLM acts as a central controller that provides planning and calls external tools to solve complex tasks.

## Limitations for existing LLM-based

- Most existing tools uses a single LLM agent.
- Existing tools are not for scientific applications.
- Existing tools usually encounter reliability concerns.

# Multiple LLM Agents for Scientific Discovery

## LLM-based agents for scientific research

- *Involving the planning agent and evaluation agent.* The planning agent first makes the decisions. Then, the evaluation agent evaluates the results, provide feedback and guidance on how to refine the decisions.
- *Integrating advanced scientific tools and evaluation tools.* Enhancing the suitability of LLM-based agents by integrating advanced scientific tools and evaluation tools.
- *Incorporating human expertise into the loop.* we leverage the human verbal description into the prompt and make the agent align with human values and preferences. Human interaction can take place both during the planning and evaluation phases

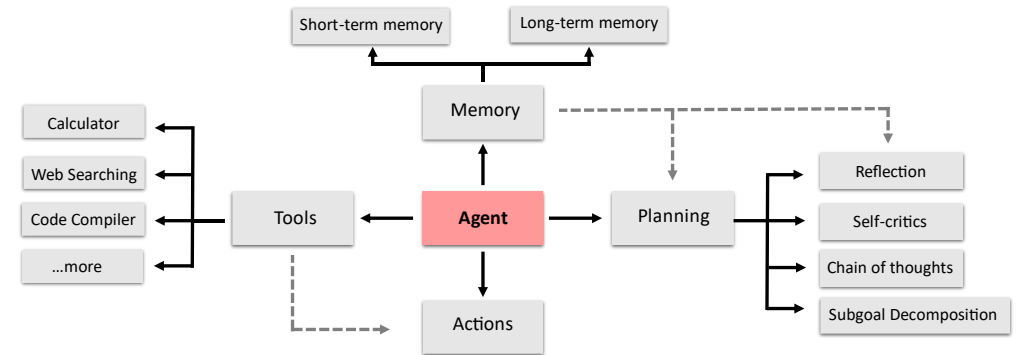


Figure 1 The overall structure of existing LLM-based agents.

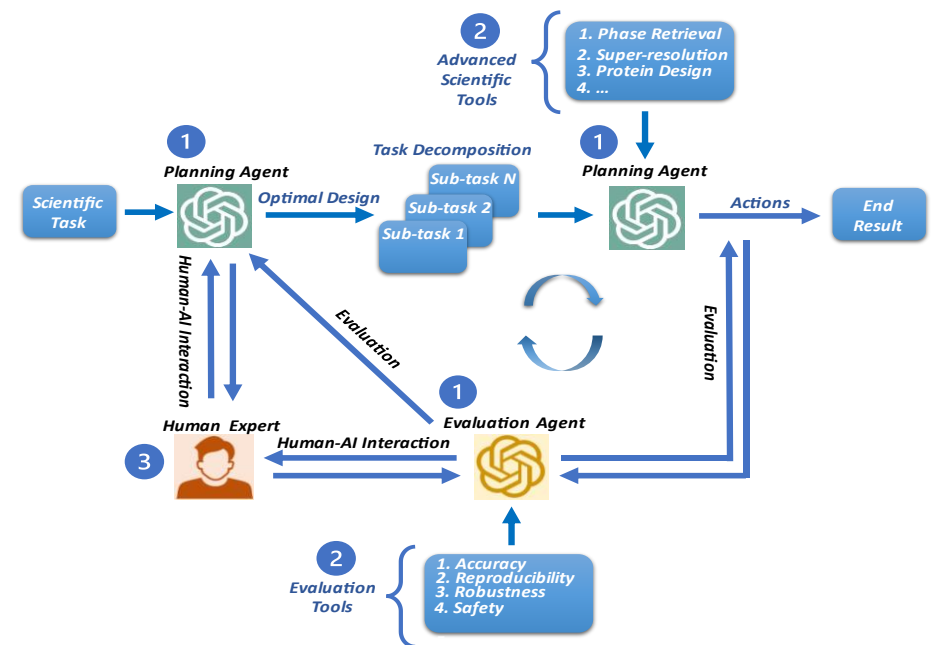


Figure 2. The overall architecture of the proposed scientific LLM-based agents

# Future Works

## **Other Architectures other than Transformer**

- Mamba -- Selective State Spaces

## **Model compression**

- Knowledge distillation
- Quantization

**Dataset condensation:** condensing large datasets into a compact set of synthetic samples

## **Other strategy**

- Mixture of Experts (MOE)

***Thank you!***