
3000788 Intro to Comp Molec Biol

Lecture 25: Foundational and frontiers AI models in biology

Fall 2025



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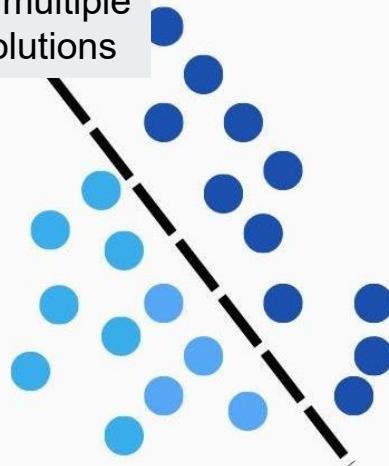
- Research Affairs
- Center of Excellence in Computational Molecular Biology (CMB)
- Center for Artificial Intelligence in Medicine (CU-AIM)

Today's agenda

- The rise of generative AI
- Generative model designs and assumptions
- Foundational model

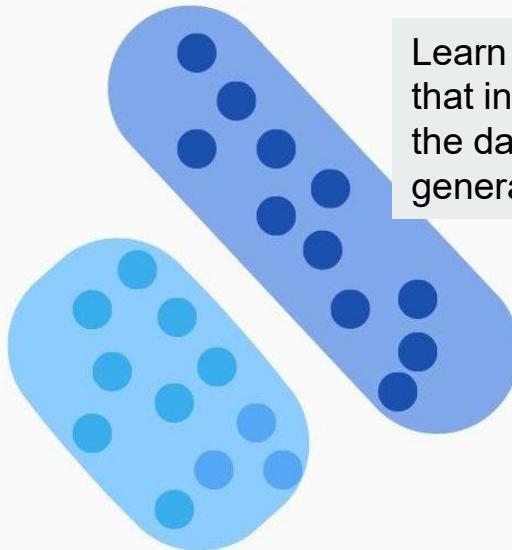
Importance of generative approach

Simple, multiple equal solutions



Discriminative

Learn factors
that influence
the data during
generation



Generative

10



vs

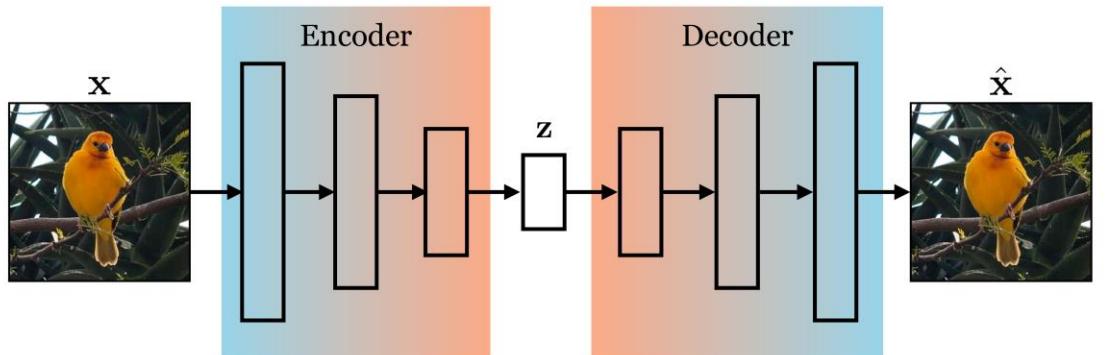


<https://www.turing.com/kb/generative-models-vs-discriminative-models-for-deep-learning>

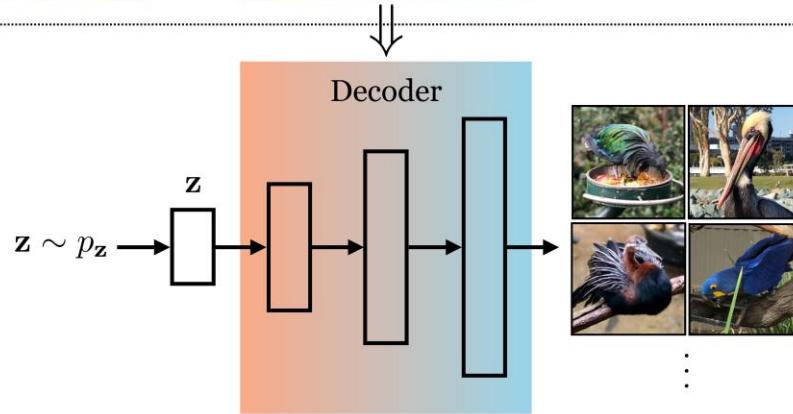
- It takes much more understanding to generate **realistic** data

Autoencoder is a primitive generative model

Autoencoder

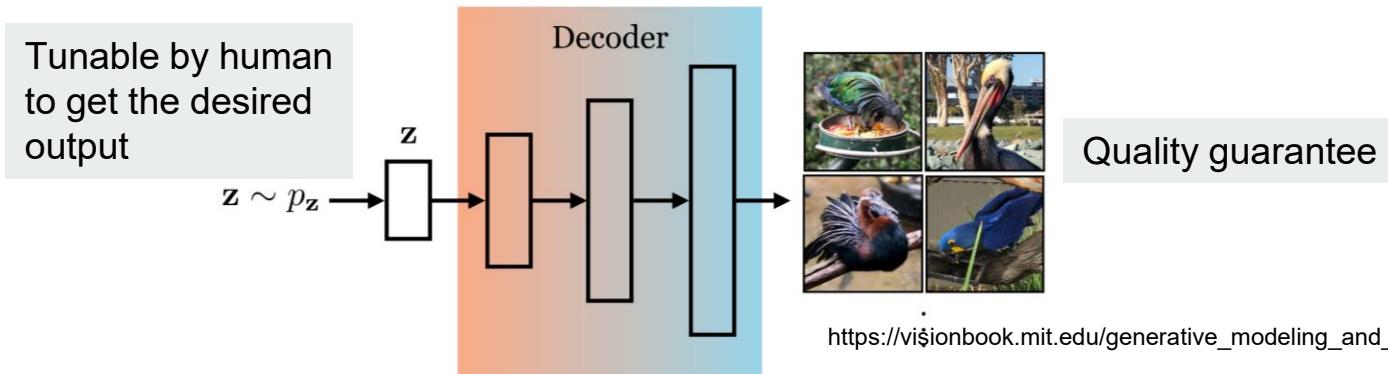


Generative model



- Decoder is a generator
 - Not well-trained
- No guarantee on how z determines output
- No guarantee that the output will be realistic given randomly selected z

Properties of a good generative model



- **Realism:** On a reasonable range of z , the outputs should be realistic
- **Smoothness:** Small change in z should ensure small change in output
- **Interpretability:** Space of z should be mappable to human-understandable concepts ← concept of latent variables in statistics

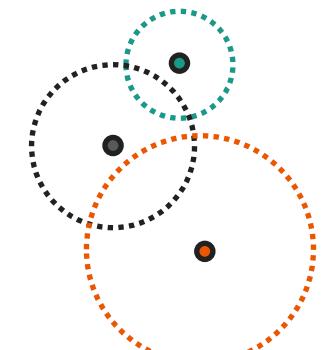
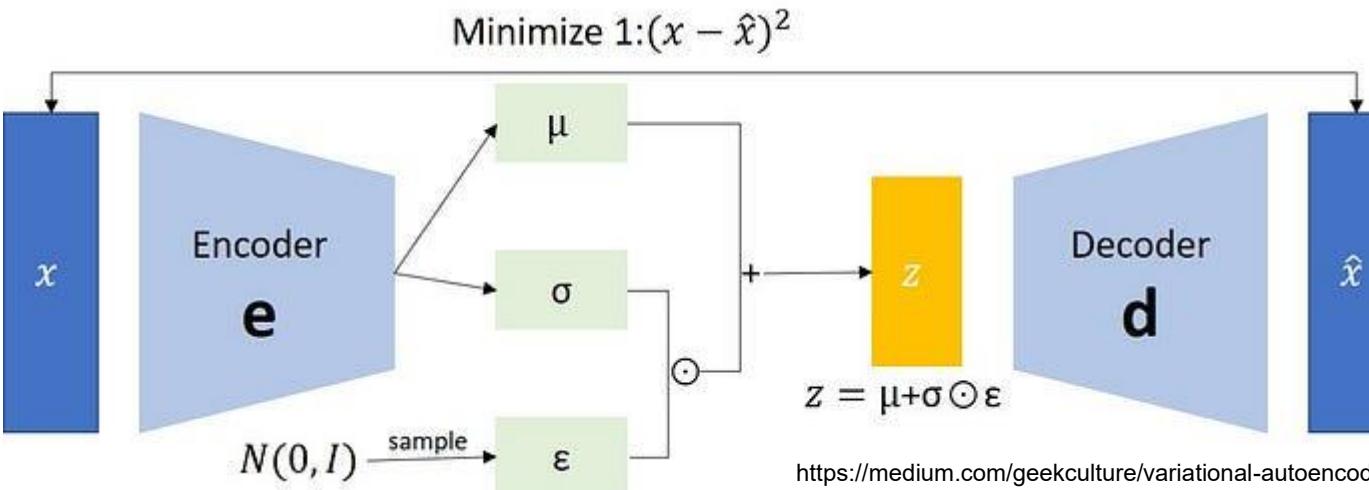


Generative model designs

Approaches for generative modeling

- Variational autoencoder (VAE)
- Generative adversarial network (GAN)
- Diffusion models
- Flow matching

Variational autoencoder

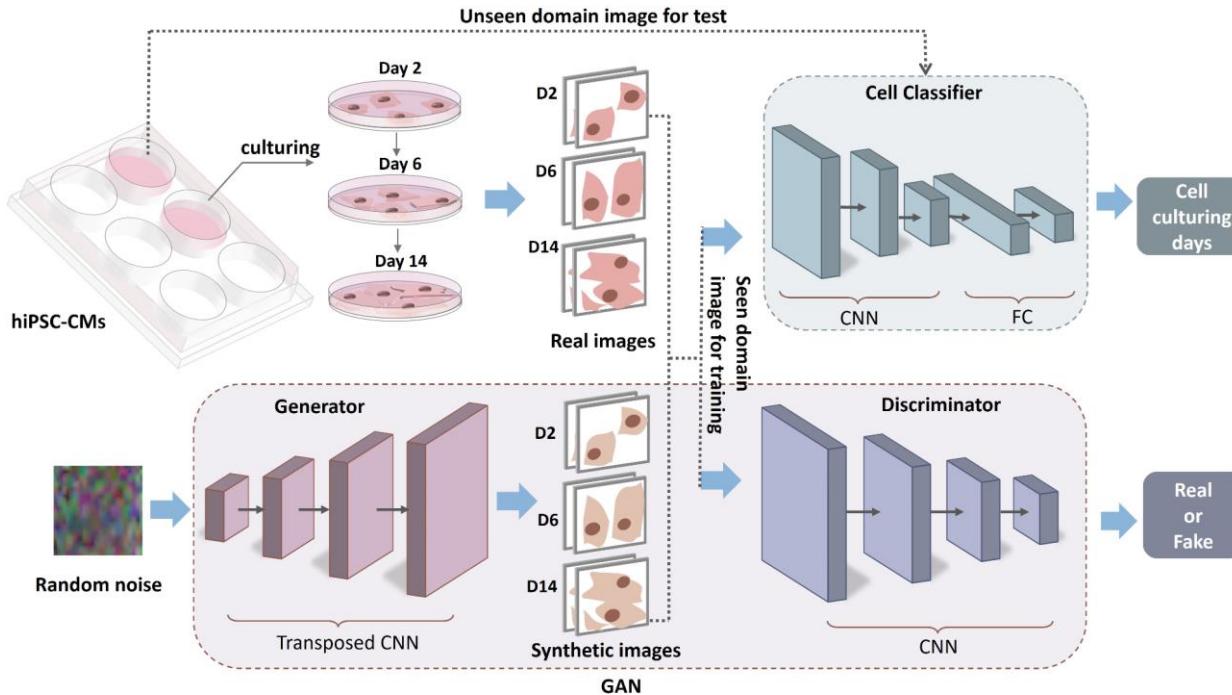


- Learn the Gaussian **mean** and **SD** of the representation for each input
 - Robust to noises / smoother representation space
- Sample from representation space before decoding

Key points of VAE

- **Collapse:** VAE can collapse to vanilla autoencoder with $\sigma = 0$
 - Force the representation space to resemble standard normal distribution with KL divergence: $D_{\text{KL}}(P \parallel Q) = \sum_{x \in \mathcal{X}} P(x) \log \frac{P(x)}{Q(x)}$.
- Representation space is both smooth and parametrized

Adversarial training

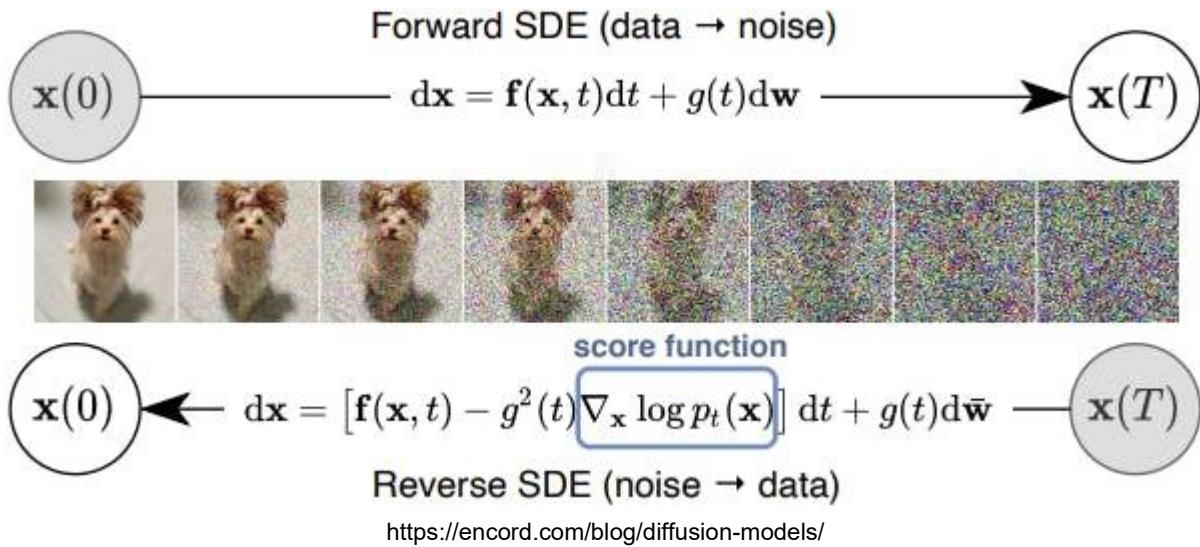


- **Generator** produce synthetic data
- **Discriminator** tries to tell if the data is real
- **Task-specific model** checks if the synthetic data match the desired characteristics

Key points of adversarial training

- Competitive learning process
 - Initially, **Generator** is poor, **Discriminator** easily learns to distinguish
 - As **Generator** learns, **Discriminator** has to follow
- Inefficiency
 - **Generator** does not learn from real data directly (input is pure noise)
 - Trained to match the generated data distribution with real data distribution (based on some statistics or representations of the data)
 - Small feedback from **Discriminator**'s output and performance
- Unstable

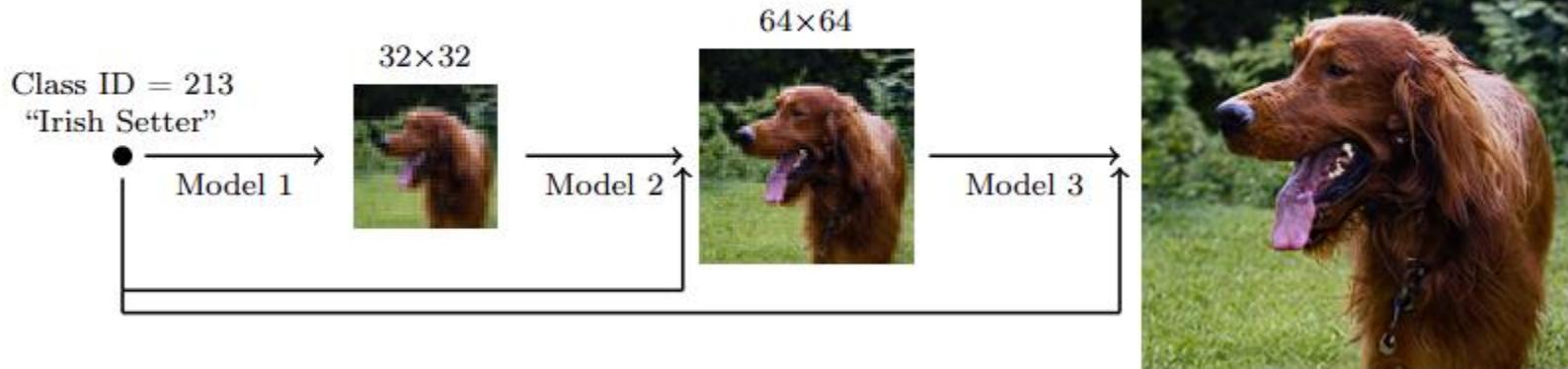
Stochastic diffusion



- Iteratively add small noises to the data for N steps
- Train a neural network that reverse the noise addition
 - Received noised data + time encoding as inputs

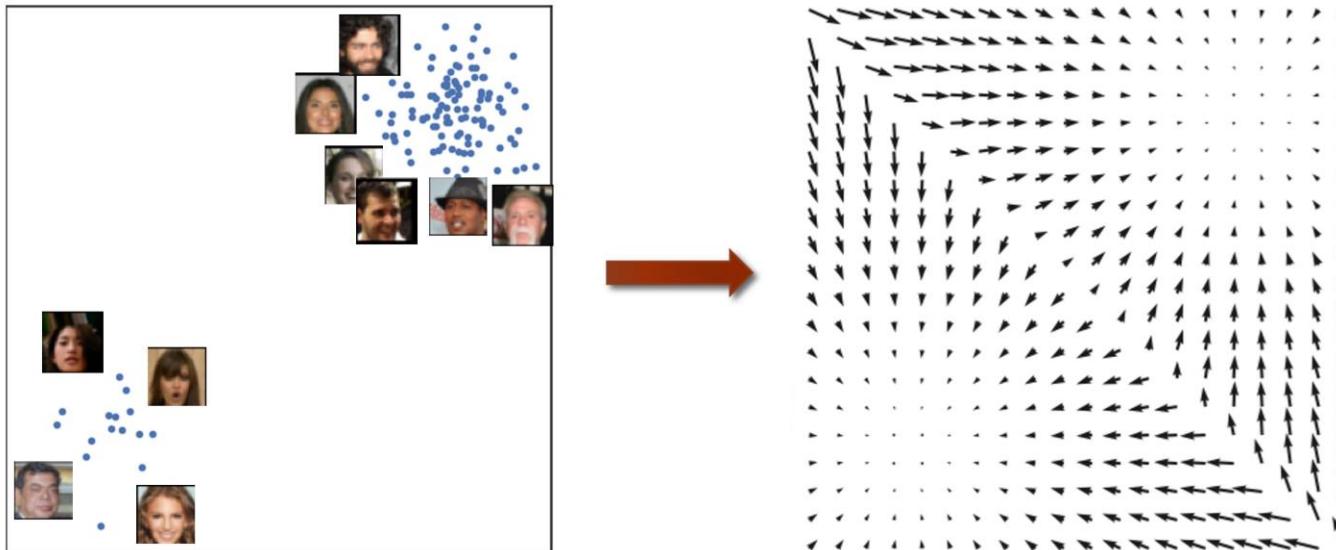
Cascade diffusion model

Ho, J. et al. <https://arxiv.org/pdf/2106.15282.pdf> (2021)



- Deal with large, high-resolution generation
- Multiple diffusion models applied sequentially
- Output from early model guides the generation of the next

Vector field induced by the diffusion process



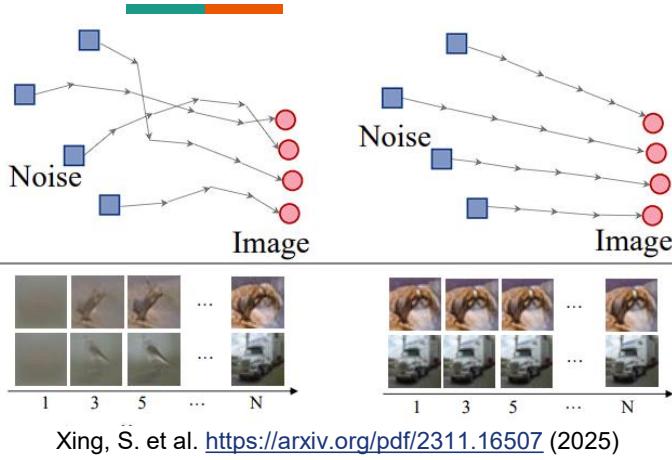
<https://yang-song.net/blog/2021/score/>

- Diffusion process create a vector field that point from data to noises
- Generation process reverses the vector field

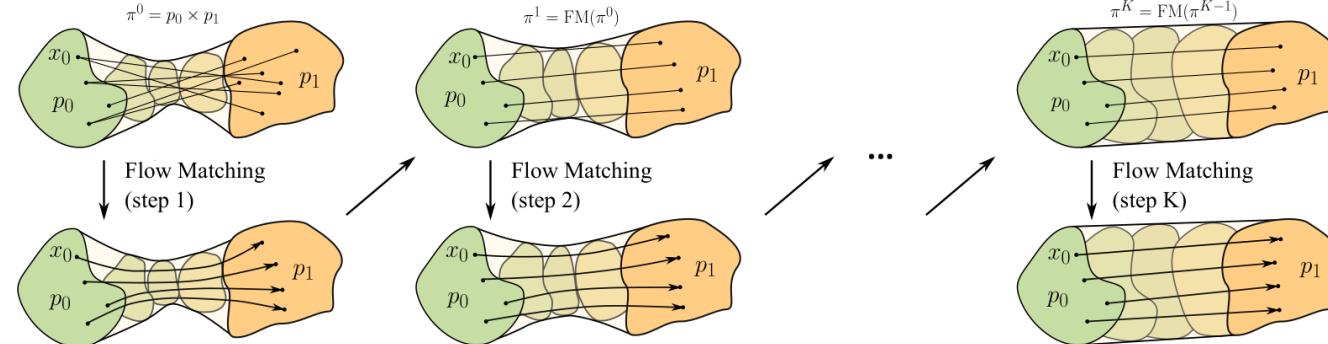
Key points of diffusion model

- Quality and computational cost scales with number of iterations
 - Can we speed-up?
- Stochastic noise addition is just one of many ways to map data points to a random distribution
 - Can we model other vector fields to map the data?
 - With more regular, straight paths ← easier to train and faster to generate
 - With easier control of the characteristics of the generated data

Flow matching



- Condition the model to learn straight paths
- Actual learned path will still be slightly curved (due to vector field's complexity)
- Improve over iterations

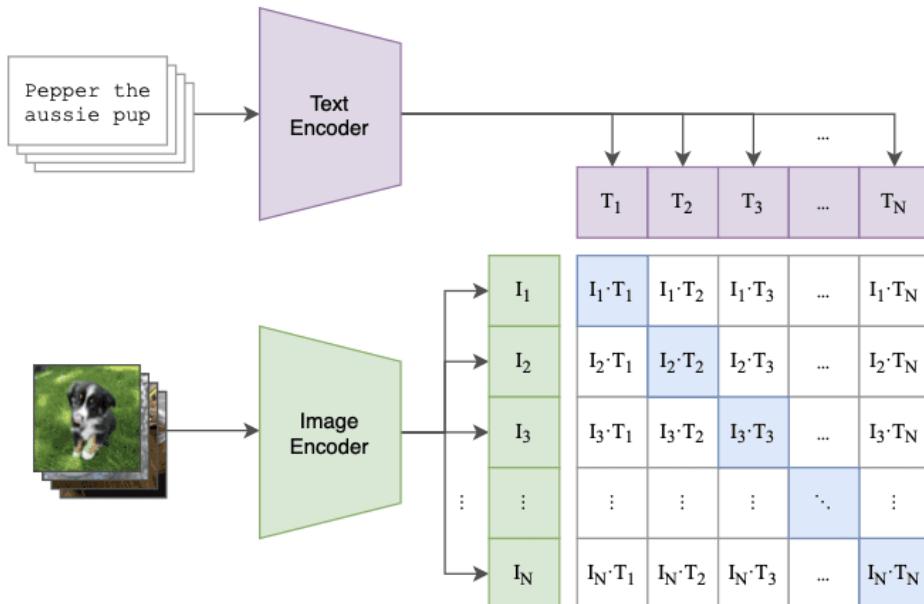


User define the time steps and initial (p_0 , p_1) mapping – randomly or guided by data



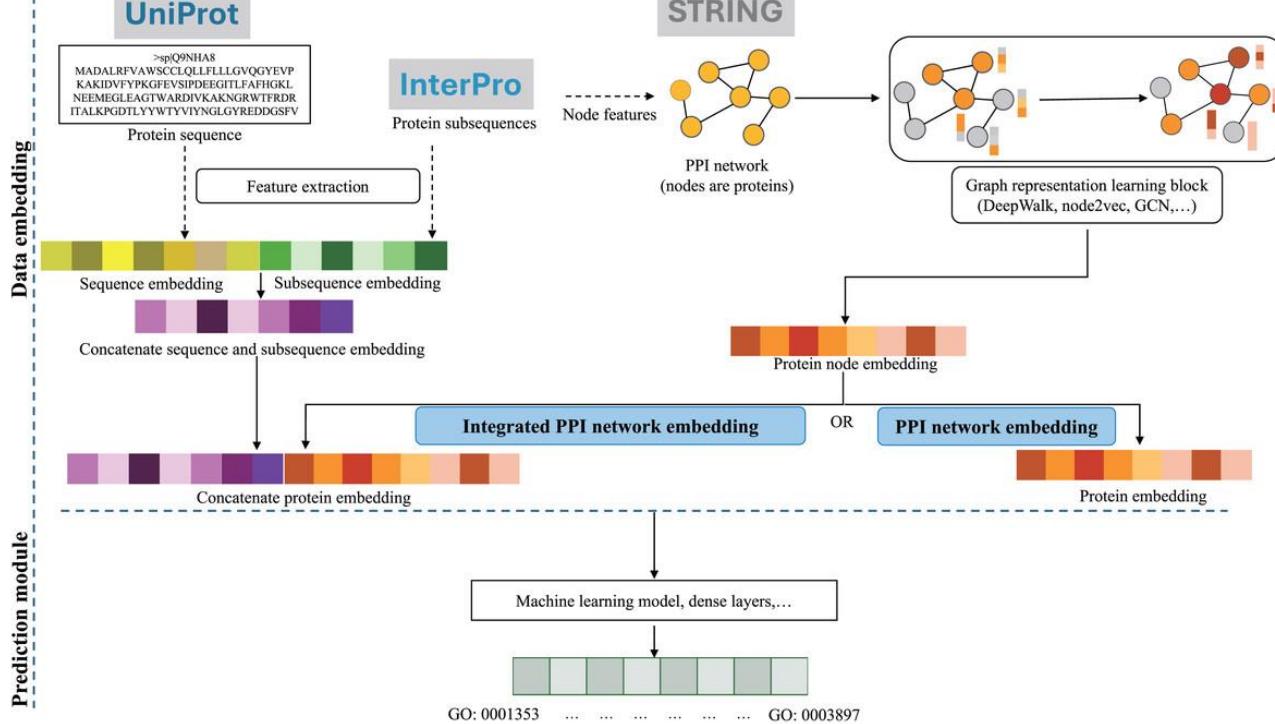
Cool things you can do to guide the learning of the AI

Contrastive training for multi-modal representations



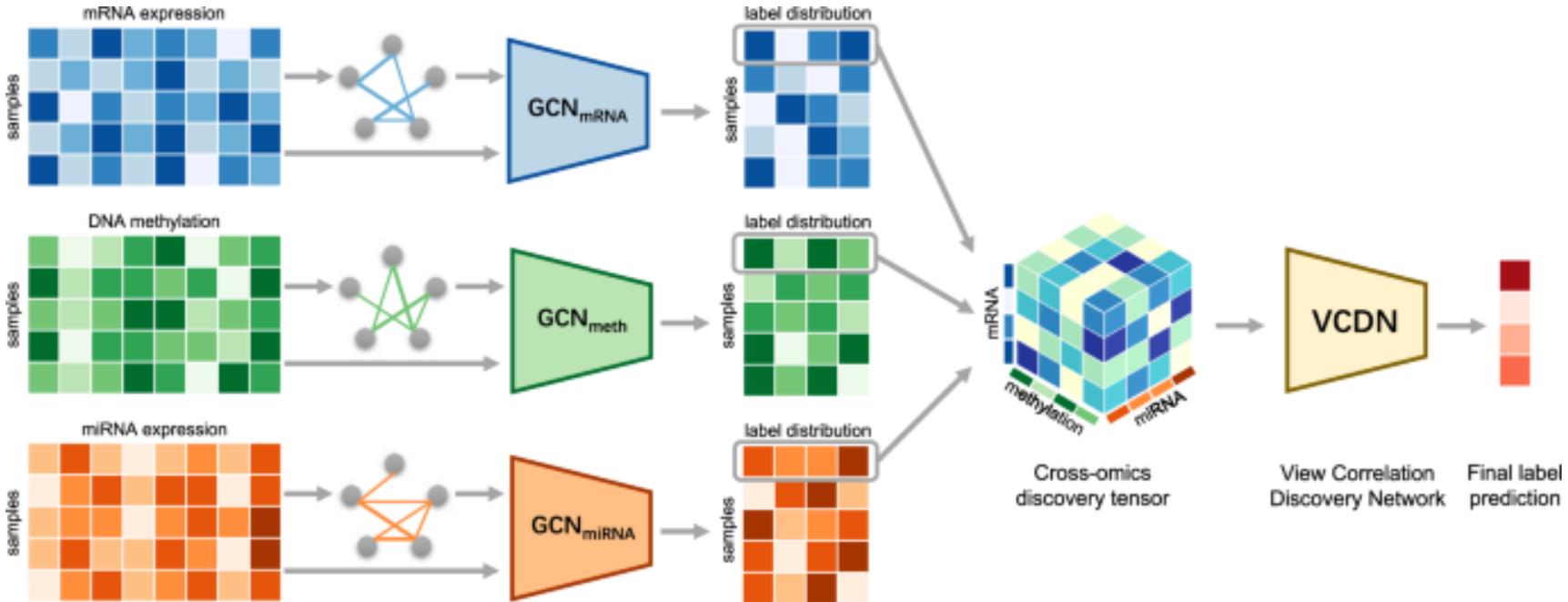
- Force representation for paired multi-modal data to be similar
- Can search one data type using prompt from another data type
- Basis behind image generation from text prompt

Forcing a shared representation space



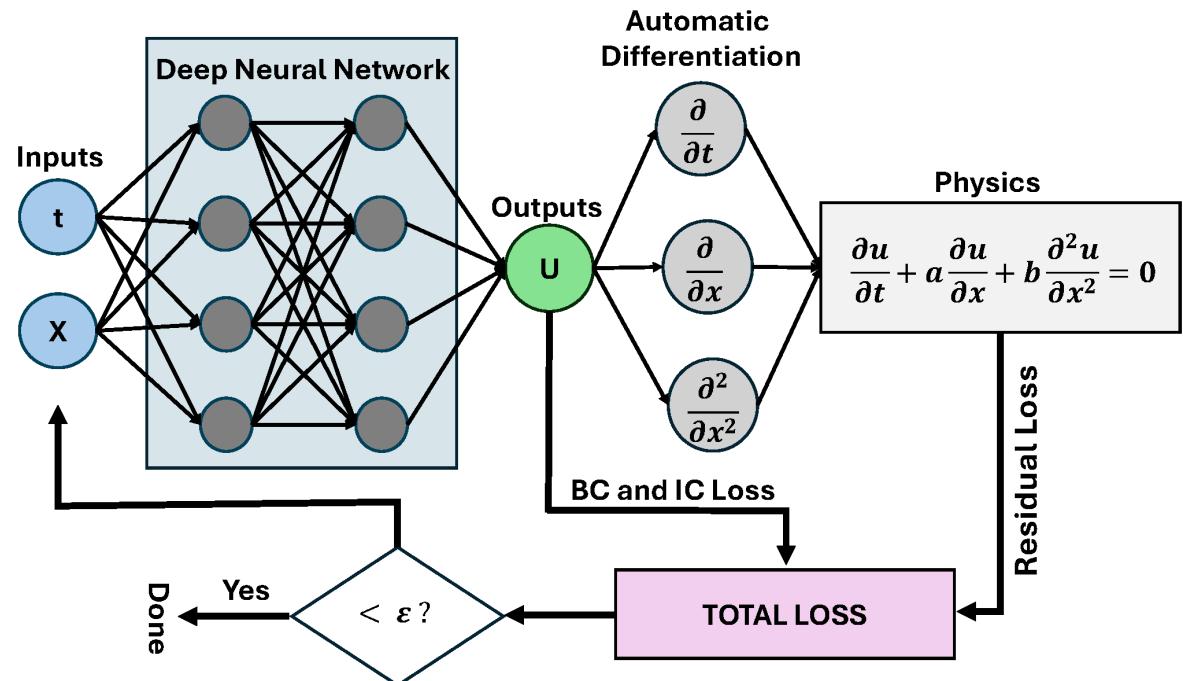
- Condition the learning to make representations from multiple raw data types computationally compatible
- Additive, concatenate, etc.

Multi-omics integration via shared representation



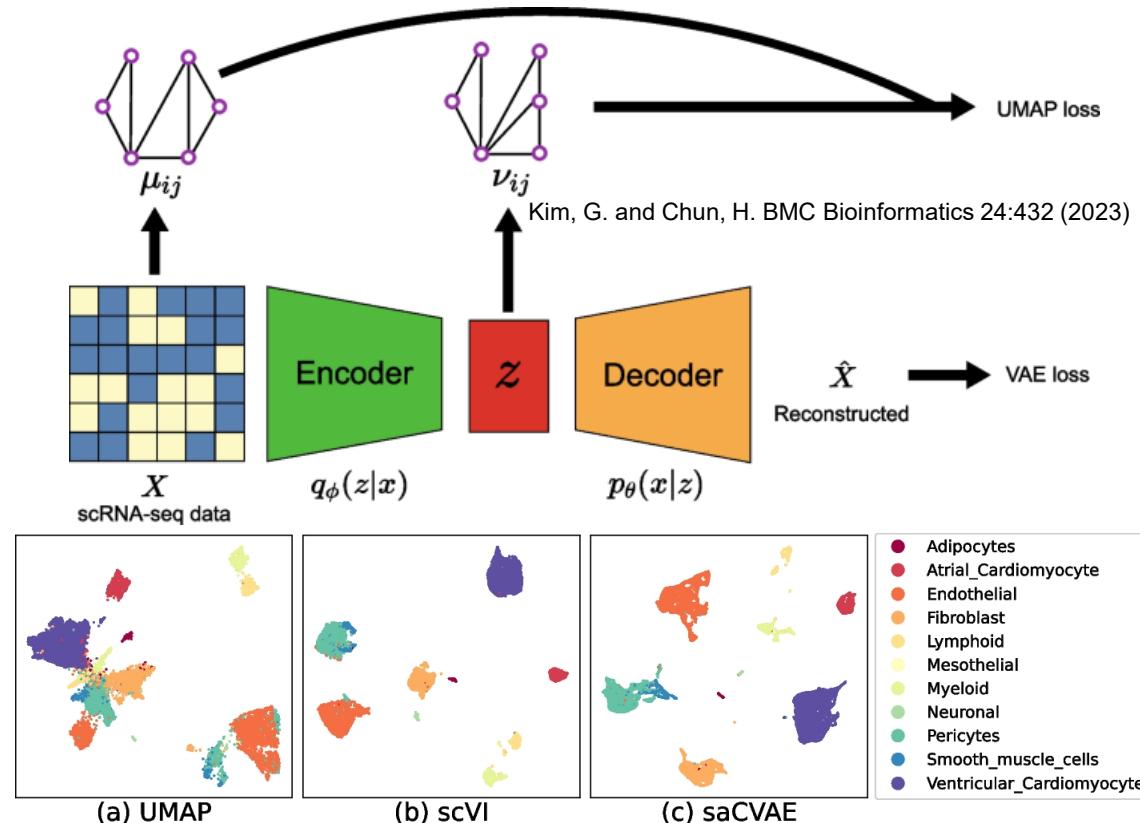
Forcing model to mimic natural mechanisms

- Physics-Informed Neural Network
- During training, add loss functions that compare the model's output behavior to laws of physics



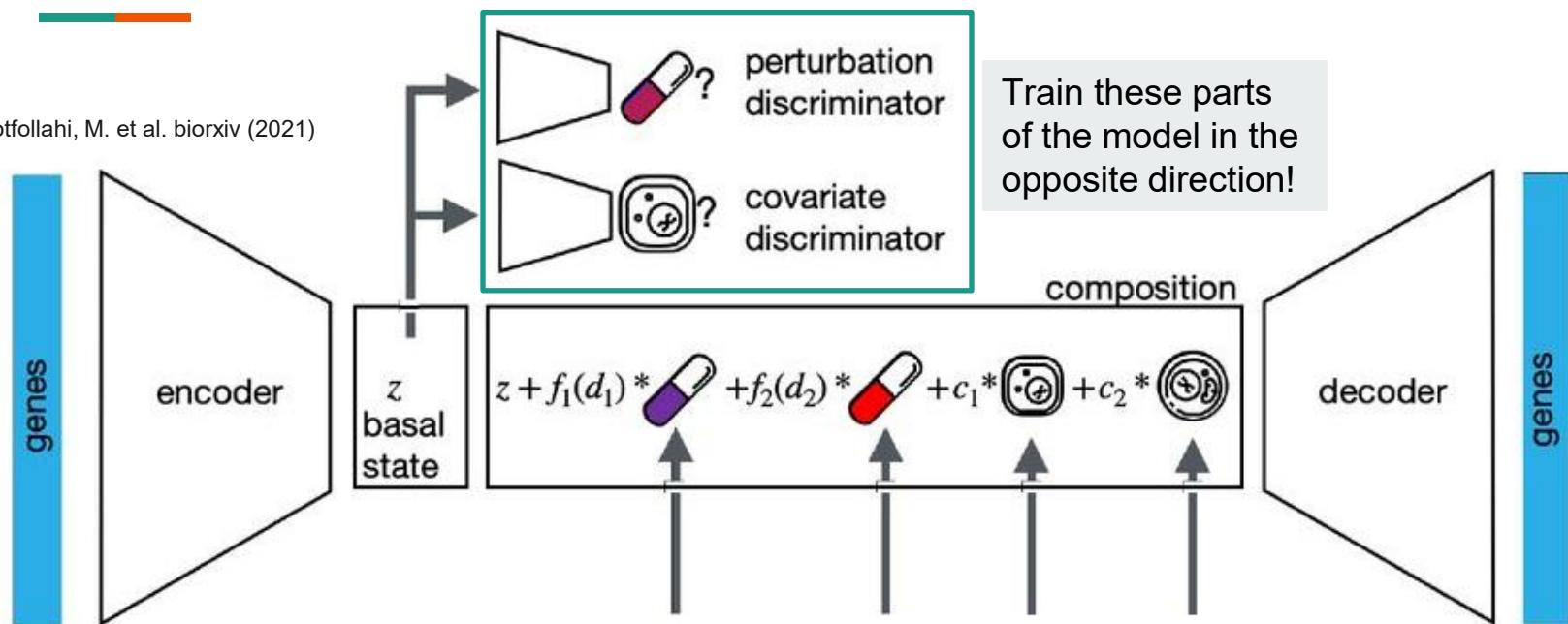
Guided representation with sample-similarity network

- Key: Discriminative ML does not utilize sample-sample similarity
- Guide representation by forcing it to mimic UMAP reconstruction of sample similarity network



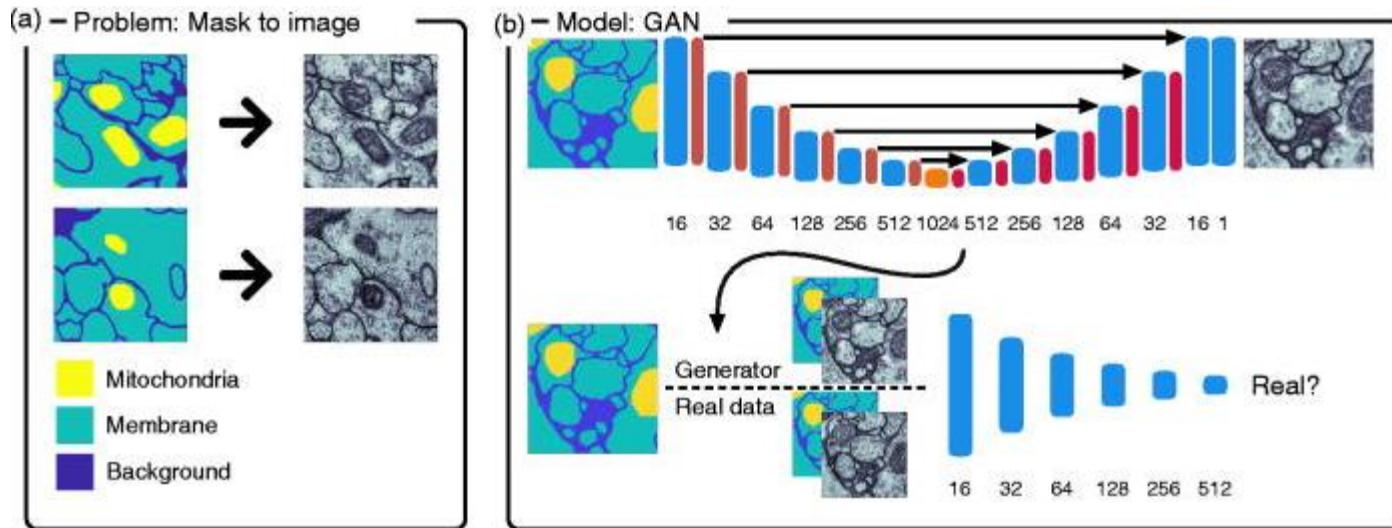
Debiasing

Lotfollahi, M. et al. biorxiv (2021)



- Sometimes, we want to remove batch effect/bias in the data
- Can we train the model to “ignore/lose” knowledge?

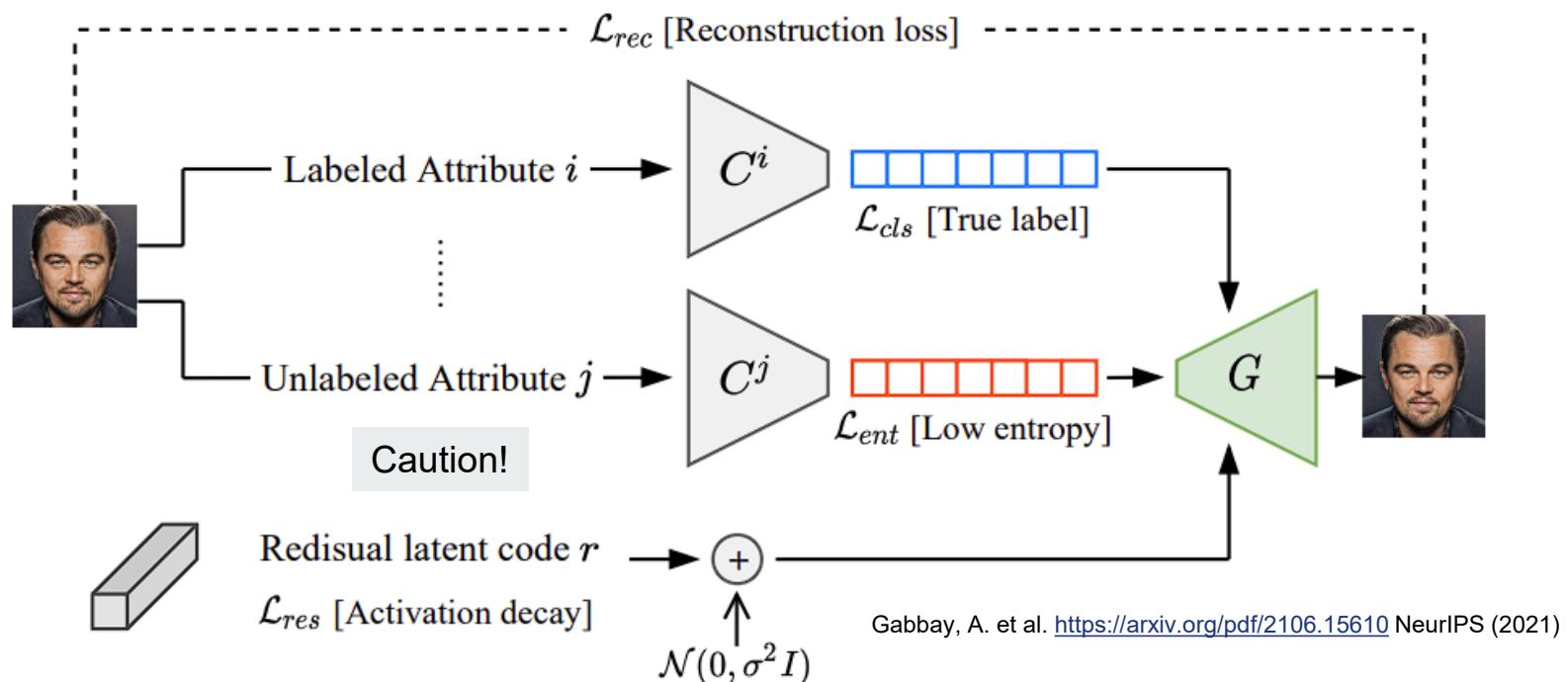
Conditional generative process



Midtvedt, B. et al. Applied Physics Review 8:011310 (2021)

- Add conditions as input to the **Generator** and the **Discriminator** to guide the generated data distribution and characteristics

Learning to disentangle



- Simultaneous learning of known and unknown factors and generation



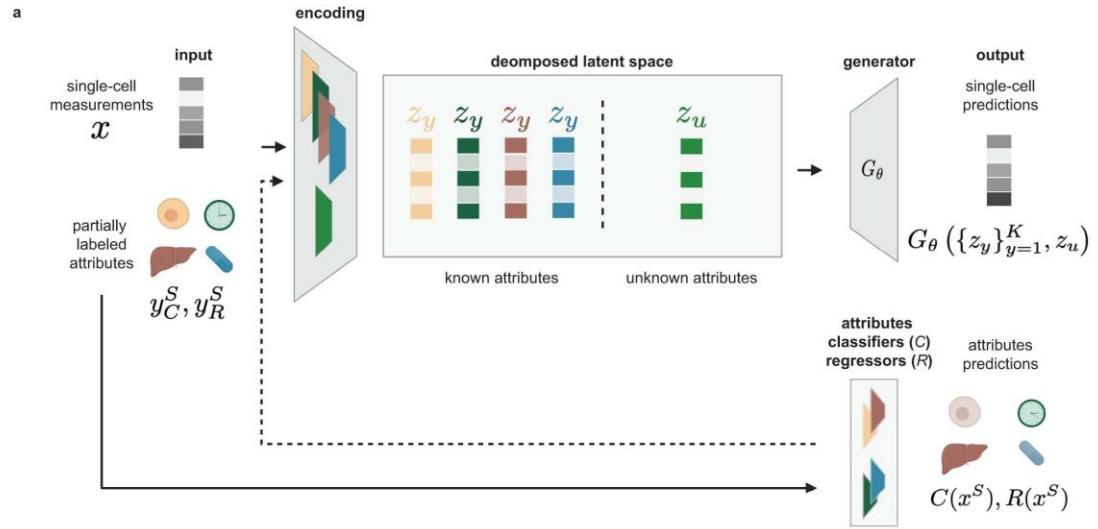
Applications in biology

Roles of generative models in biology

- Imputation with synthetic data
 - Generate data with desired treatment / disease effects
 - Analyze as if they are real observations
- Disentangle factors that affected the observation
 - Through conditional generative process
- Integrate multi-omics data
- Molecular design

Disentangle factors influencing gene expression

- Distribution of generated data compared to real data, stratified by factors
- Regularization of unknown factors
- Accuracy of known factor predictions



Piran, Z. et al. Nature Biotechnology 42:1678-1683 (2024)

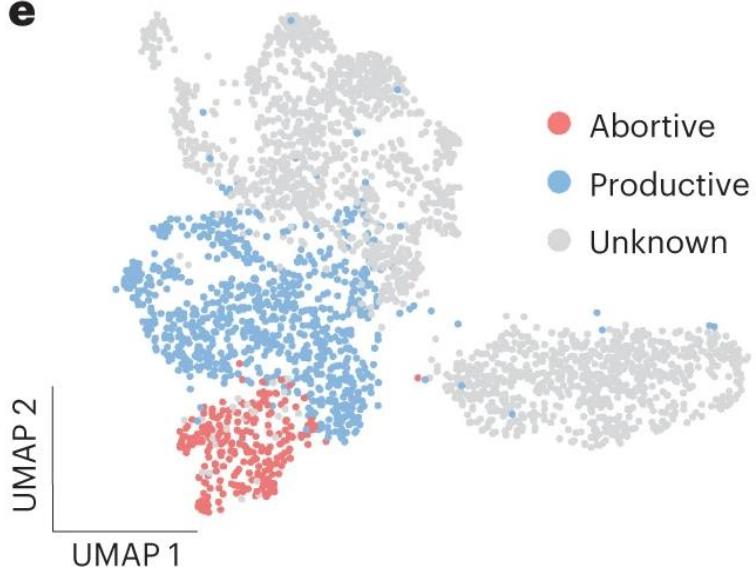
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$$\mathcal{L} = \underbrace{\|x - G_\theta(\{z_y\}_{y=1}^K, z_u)\|}_{\mathcal{L}_{cmp}} + \lambda \underbrace{\|z_u\|}_{\mathcal{L}_{min}} + \underbrace{\sum_{C \in \mathcal{C}} H(y_C^S, C(x^S)) + \sum_{R \in \mathcal{R}} \|y_R^S - R(x^S)\|}_{\mathcal{L}_{cls}}$$

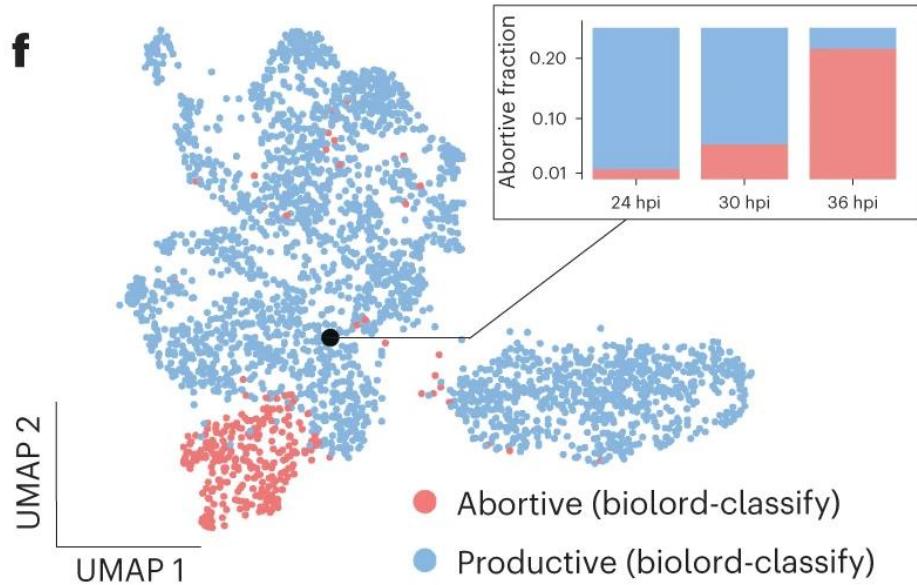
Label imputation



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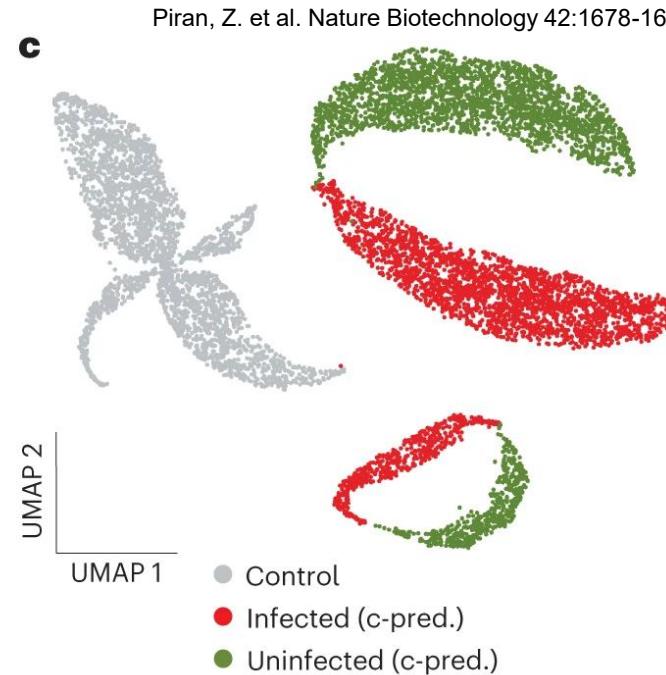
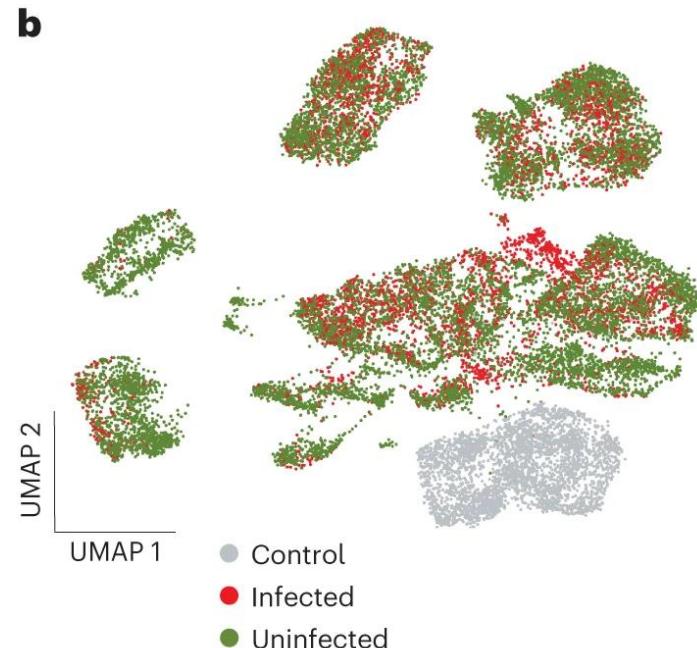
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Piran, Z. et al. Nature Biotechnology 42:1678-1683 (2024)

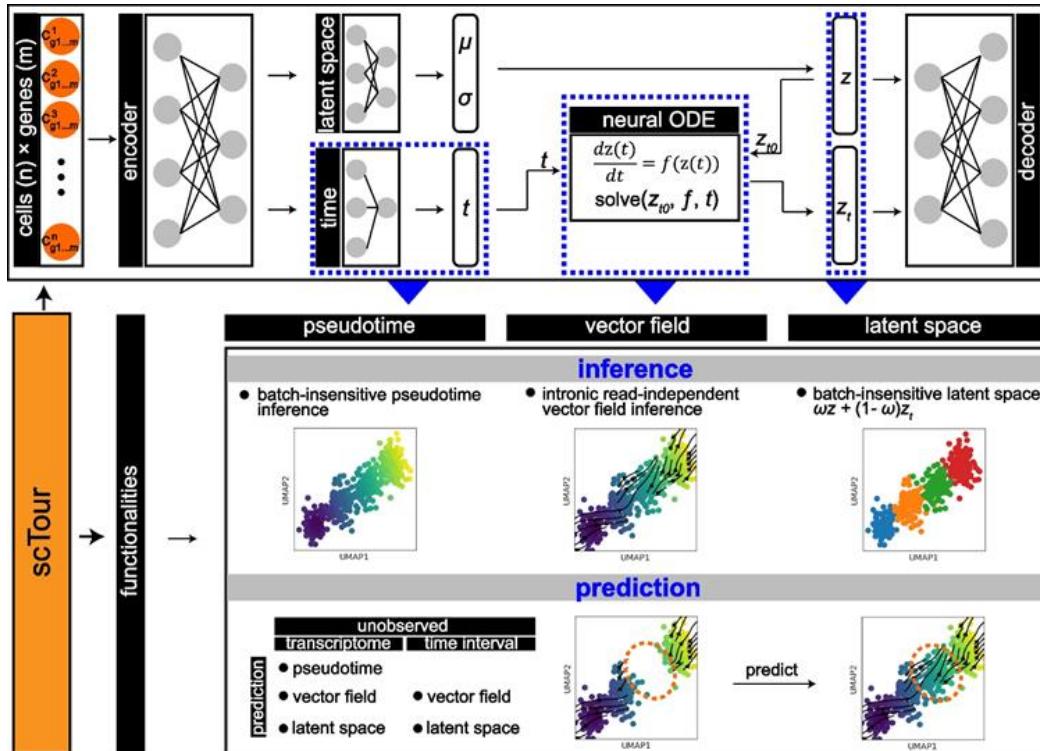
- Use the classifier part of the framework

Counterfactual inference



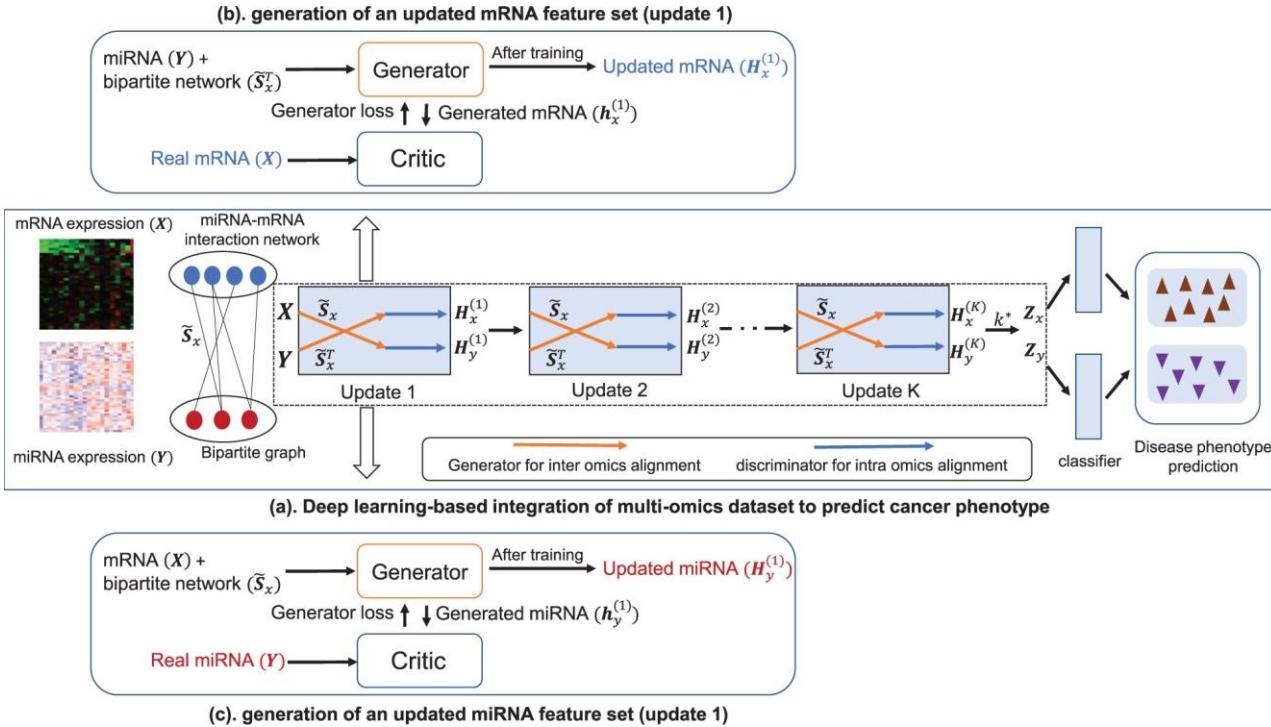
- Simulate infected and uninfected gene expressions from control cells

Neural ODE fitting to single-cell trajectory



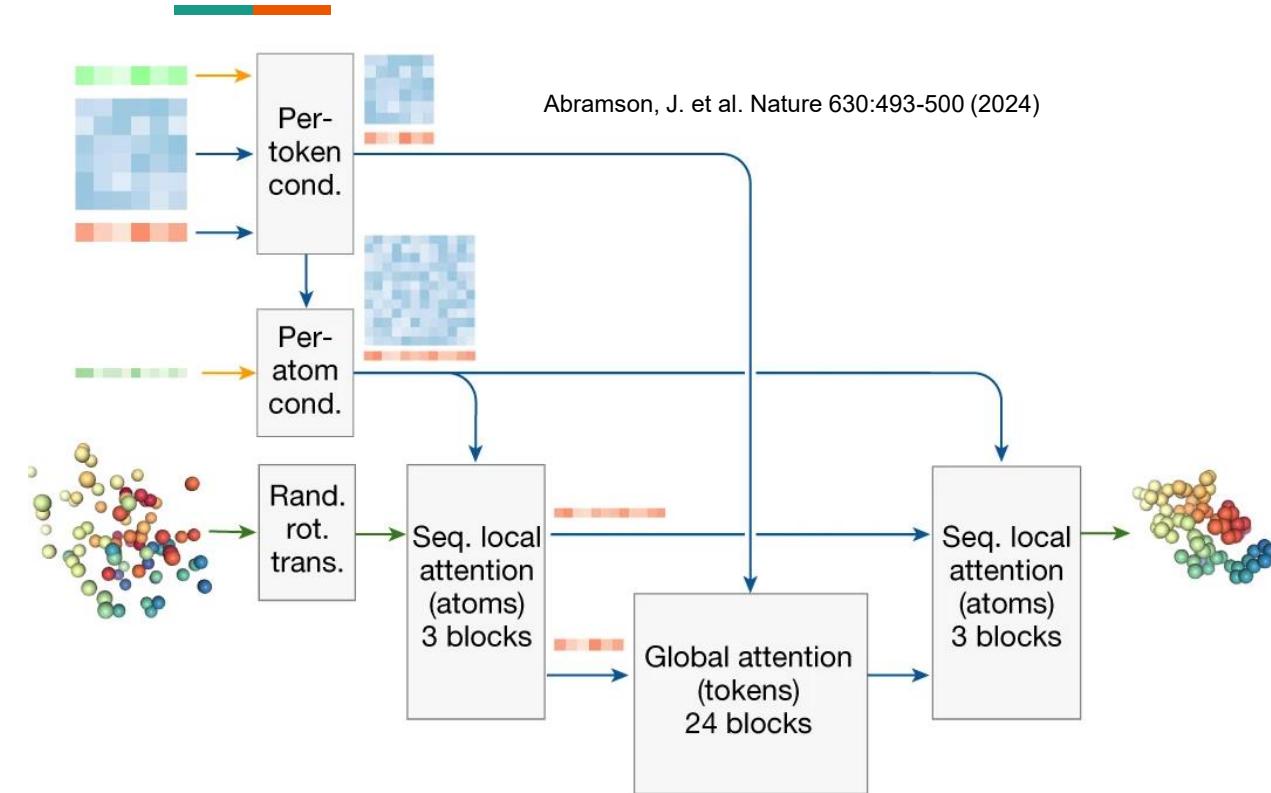
- Assumption: Changes in gene expression during cell development follow ordinary differential equation (ODE)
- Joint estimation of time, vector field, and cell states
- Use inferred time to reconstruct gene expression

Multi-modal generative process



- Use vertical, cross-omics relationships to guide the co-generative process
- Use different omics as feedback for the generation of the other omics

Diffusion module in AlphaFold v3

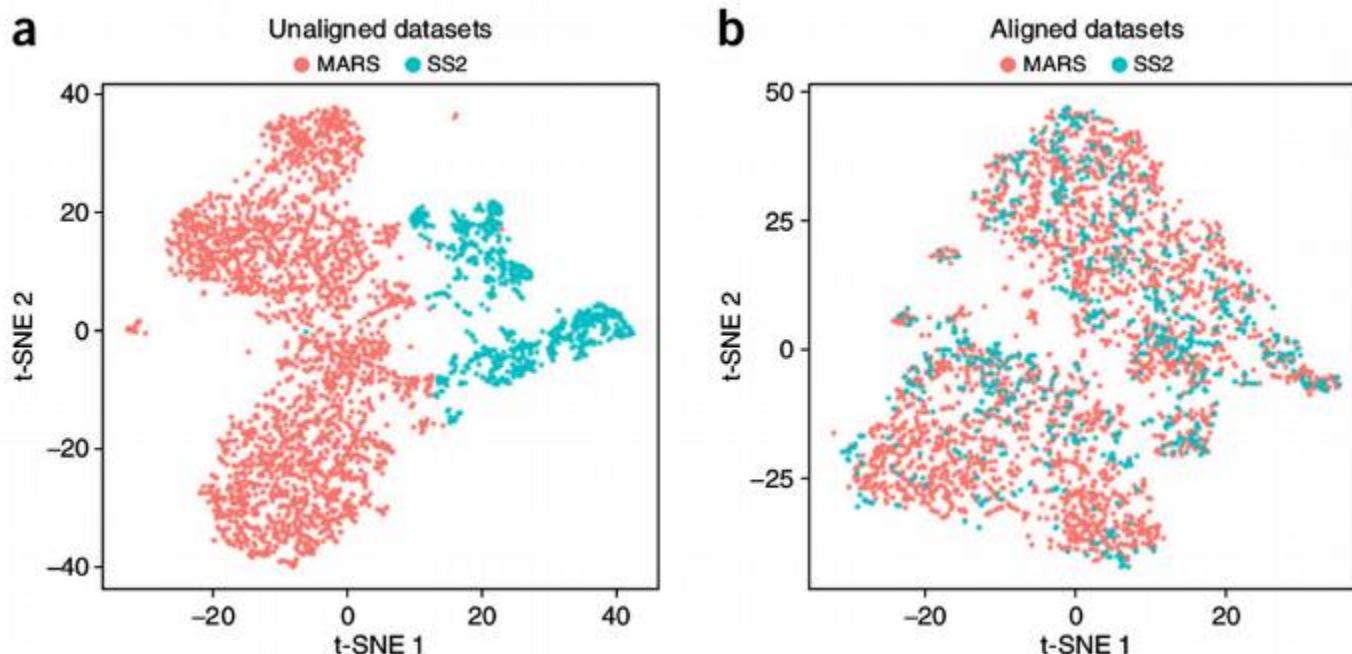


- Guided by representations of input sequences and pairwise distances
 - Fed into the denoising steps
- Combine denoising at high-resolution and low-resolution



The need for foundational approaches

High bias across biological datasets



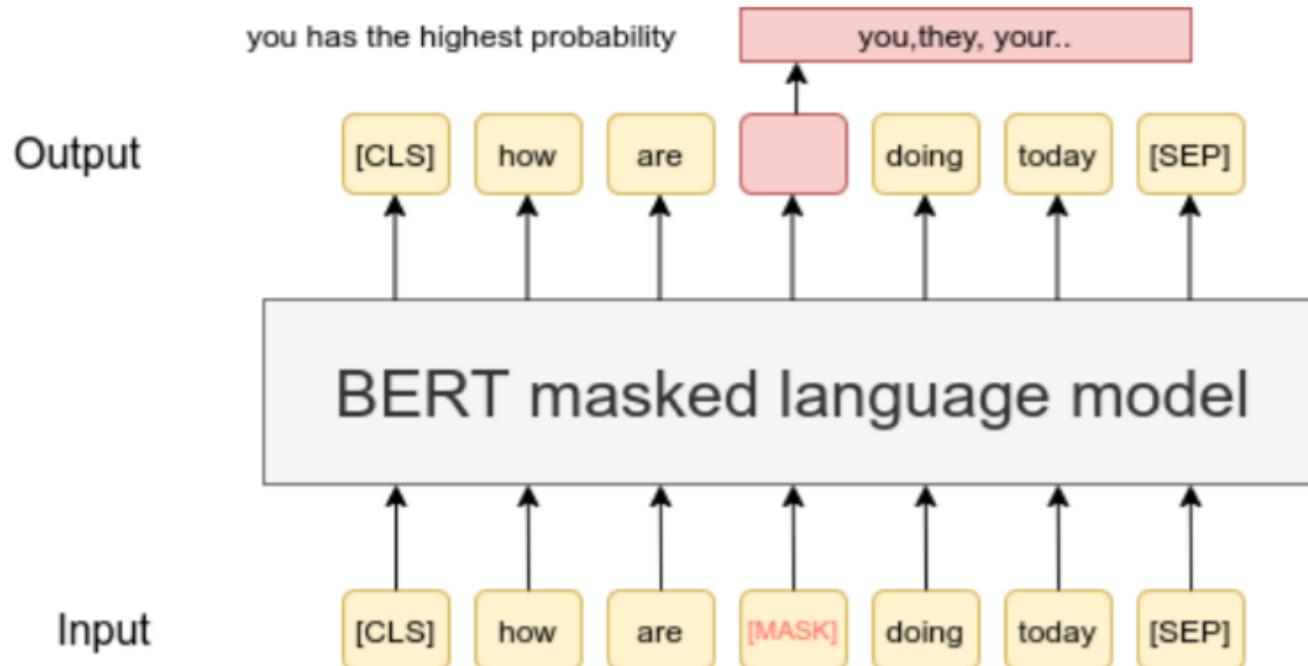
Model that understand data across batches

- Train model across multiple datasets, batches, and modalities
 - No common target output
 - Learn to impute / generates
- A **foundation model** is an AI model that was trained on diverse datasets and was able to capture the essences of the data that generalize across batches
 - Can be used off-the-shelf (zero-shot learning)
 - Can be fine-tuned on a target dataset (few-shot learning)
 - Can be adapted for diverse prediction tasks

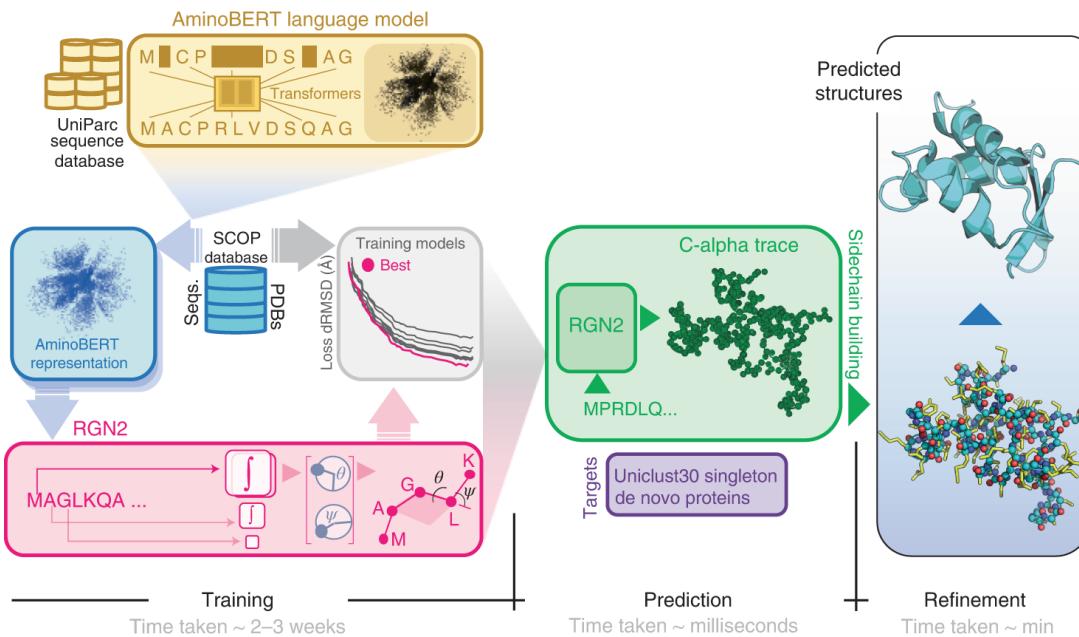
Masked training and next-token prediction

- Masked training
 - Intentionally withholding pieces of the data
 - Train the model to predict the missing values
 - Learn from partially observed context
 - Next-token prediction
 - For sequence data
 - Given early entries, predict the next entries
 - Dataset-agnostic training targets
-
- ACACTTT GAA
AC GATCAGAA
ACTGATTG TT
- ACACTTT G
AC G
ACTGA G

Masked language model (LM)

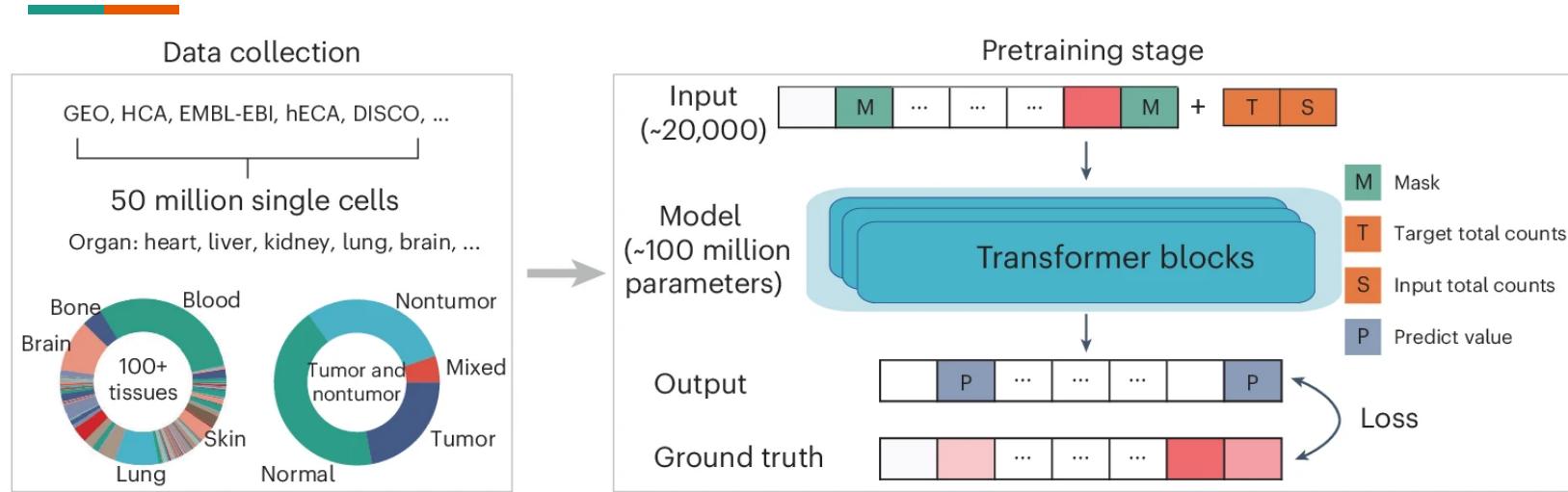


MSA-free protein LM for structural prediction



- More emphasis of masked LM training
 - Learn co-evolution
- Use LM embedding to replace MSA
- Good for orphan proteins (no relatives) and engineered proteins

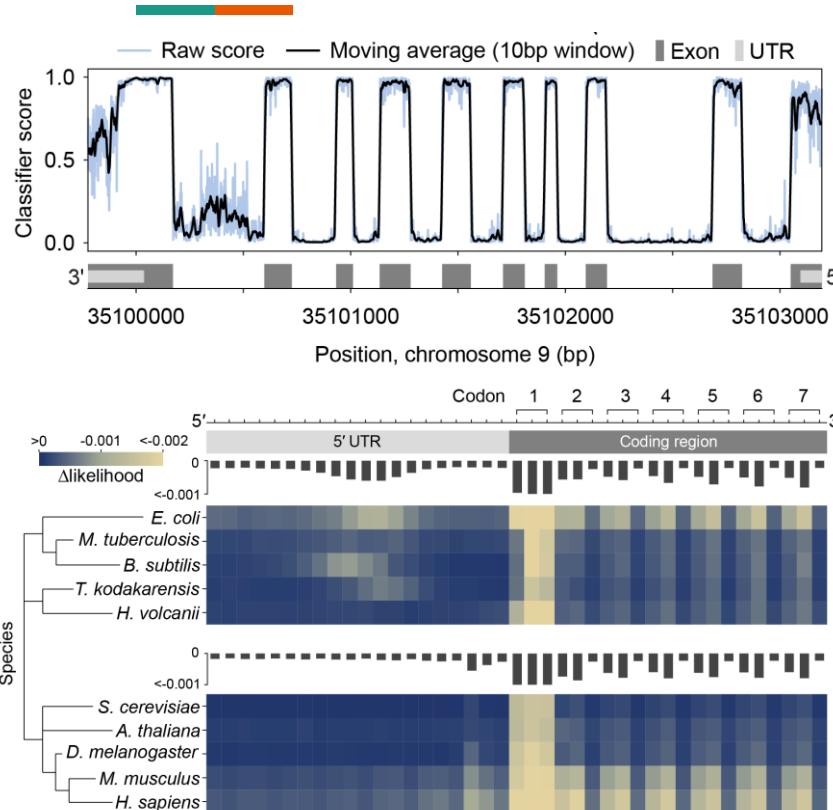
A foundation model for single-cell transcriptomics



Hao, M. et al. Nature Methods 21:1481-1491 (2024)

- Trained on >50 millions single-cells
- Masked training: gene expression levels
- Adapted to predict drug response, cell type annotation, etc.

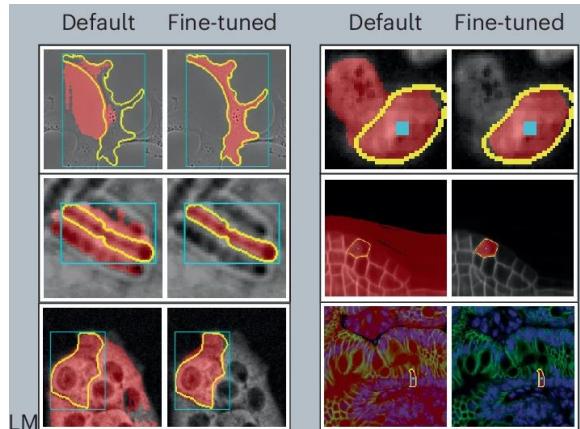
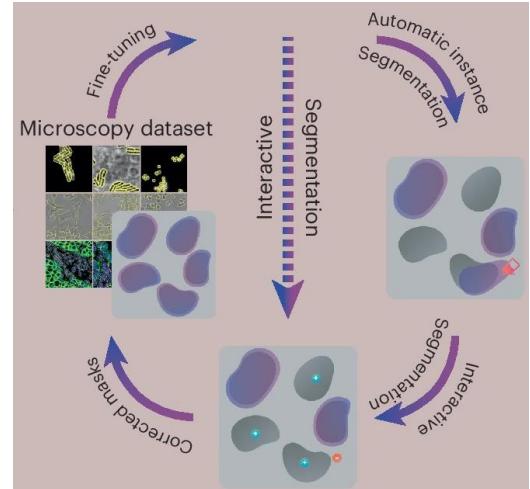
EVO2: A foundation model for genomics



- Trained on all reference genomes
- Next nucleotide sequence prediction
- Learned intron-exon boundaries and the codon structure of genes
 - Built into the representation
 - No explicit training

A foundation model for microscopy

- Segment Anything for Microscopy
- Default: Trained on 1 billion objects in non-biology photos
- Fine-tuned: Update model using images from specific microscopic modality
- Reduced data requirement for creating a new model on your own dataset



Summary

- Generative approach enhances AI's understanding of real-world data through learning to create realistic synthetic data
- **Assumption:** With enough data diversity, if the AI can generate, which is a very difficult task, it must have learned to mimic the actual mechanisms that produced the data
- In contrast to typical supervised AI which may understand the data only on some aspects necessary for making accurate predictions

Any question?

- See you next time