



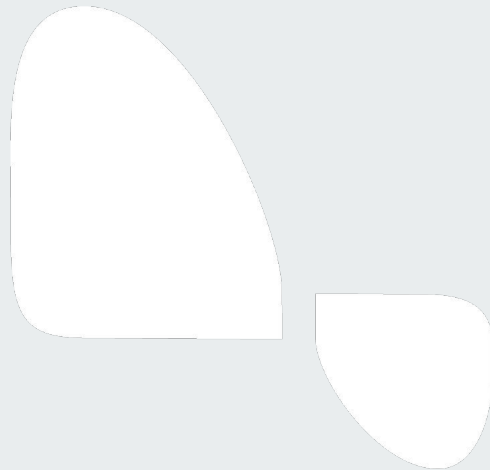
# Generative AI In Life(&)Science

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Postdoctoral Researcher

Department of Computer Science

IntroToML



# Generative AI in everyday life

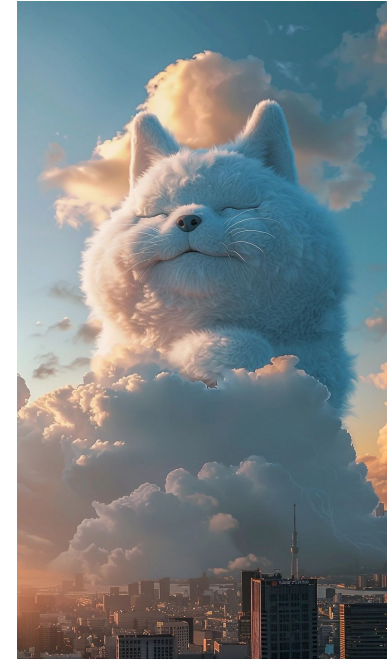
- content creation:
  - **Text** (GPT, Gemini, Llama, Claude, ...)
  - Image (Midjourney, DALL-E, ...)
  - Video (Sora, ...)
- Speech recognition (Whisper)
- Vector graphics (Adobe)
- **Developer tools** (GitHub Copilot)
- **Literature review** (scite)

chatGPT



<https://en.wikipedia.org/wiki/ChatGPT>

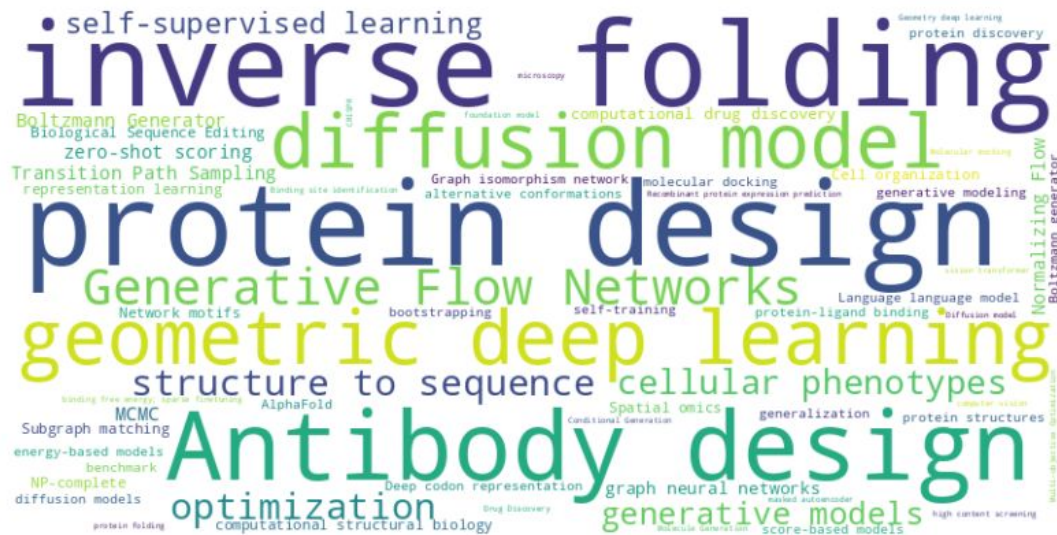
Midjourney



<https://www.midjourney.com/jobs/7437a988-5ed3-4de1-a916-61c85f49af6c?index=0>

# Why are generative models interesting for us?

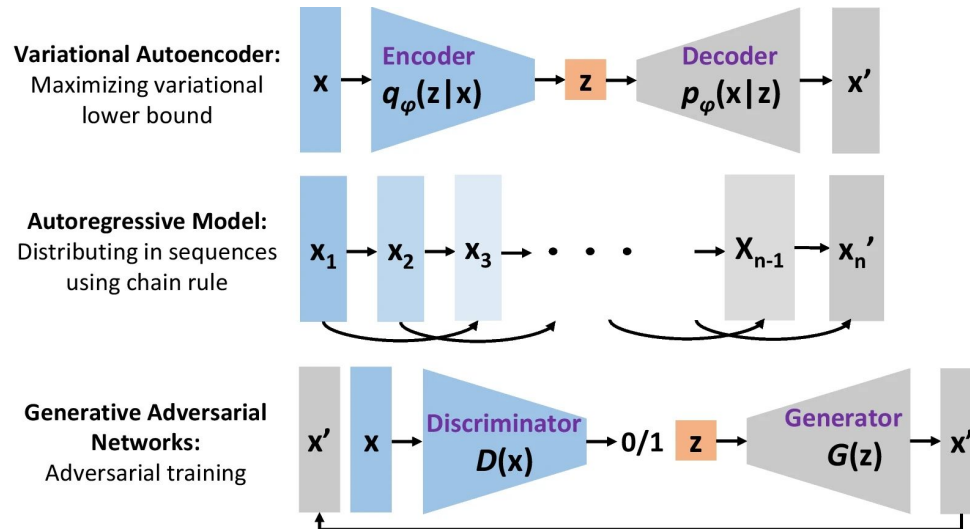
- **Synthetic data**
- **Drug discovery**
- **Molecular design**  
(protein, RNA, ...)
- **Perturbation/mutation**  
effect modeling
- ...



NeurIPS GenBio 2023 spotlight paper keywords

# Common types of generative models

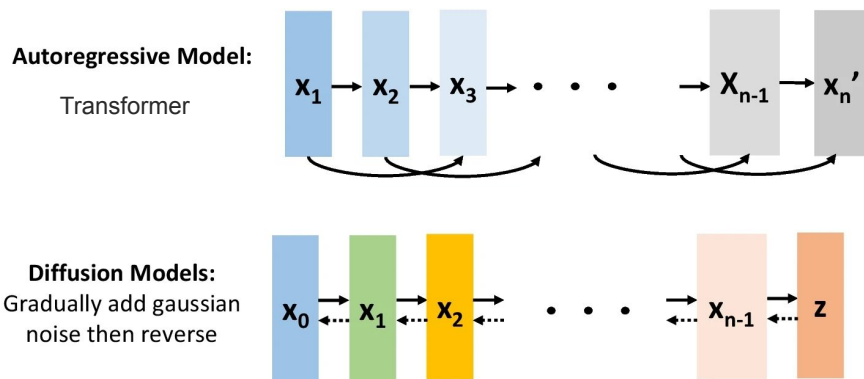
Once upon a time ...



<https://link.springer.com/article/10.1007/s43503-023-00017-z>

# Common types of generative models

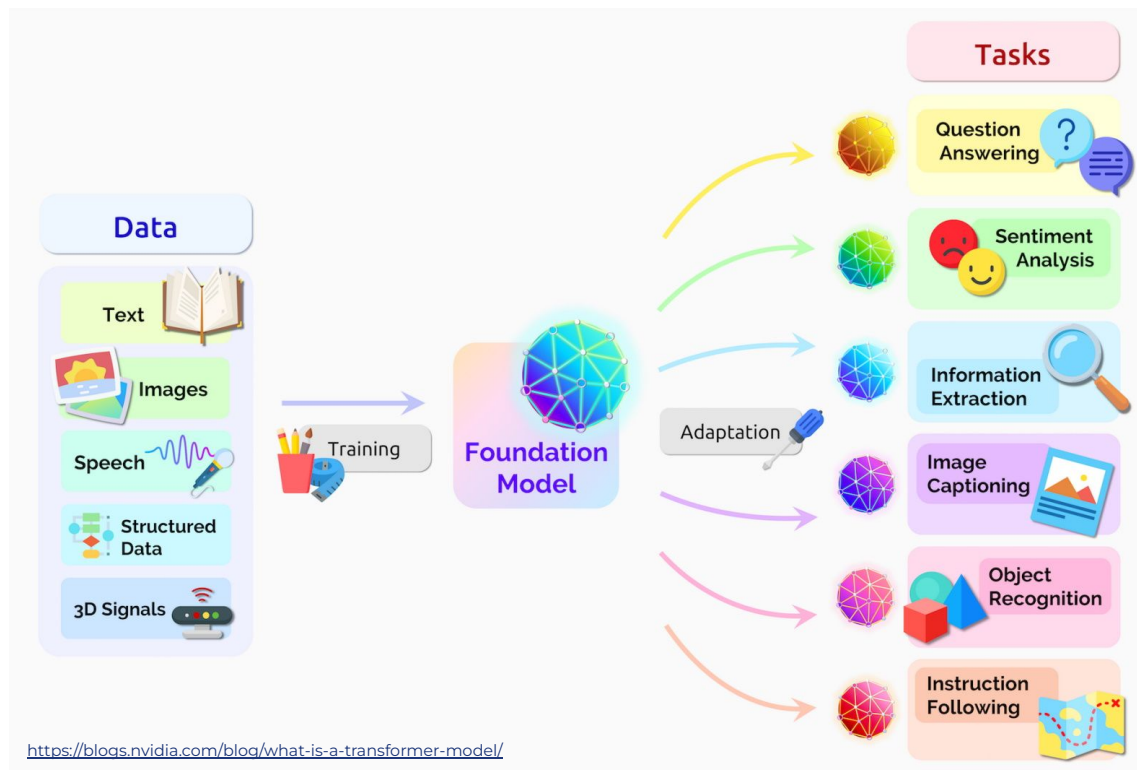
Transformers and Diffusion models are all the rage now and behind the impressive performance of many models.



<https://link.springer.com/article/10.1007/s43503-023-00017-z>

# Transformer

- Replaces many architectures for autoregressive and other tasks (CNNs and RNNs)
- Learns relationships between words in Sentences, AAs in proteins, ...





# Transformer

What makes this model architecture so special?

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## Attention Is All You Need

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**Ashish Vaswani\***  
Google Brain  
avaswani@google.com

**Noam Shazeer\***  
Google Brain  
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Google Research  
nikip@google.com

**Jakob Uszkoreit\***  
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usz@google.com

**Llion Jones\***  
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**Aidan N. Gomez\* †**  
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**Lukasz Kaiser\***  
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**Illia Polosukhin\* †**  
illia.polosukhin@gmail.com

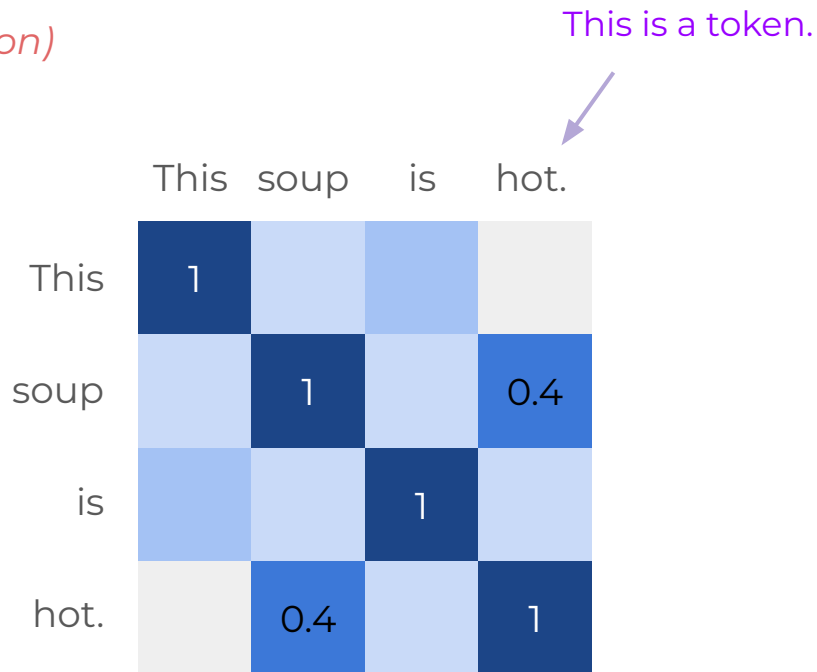
[2] Vaswani et al. (2017) Attention Is All You Need, *NeurIPS*.

# Transformer

What is attention? (*the ultra simplified version*)

## Corpus

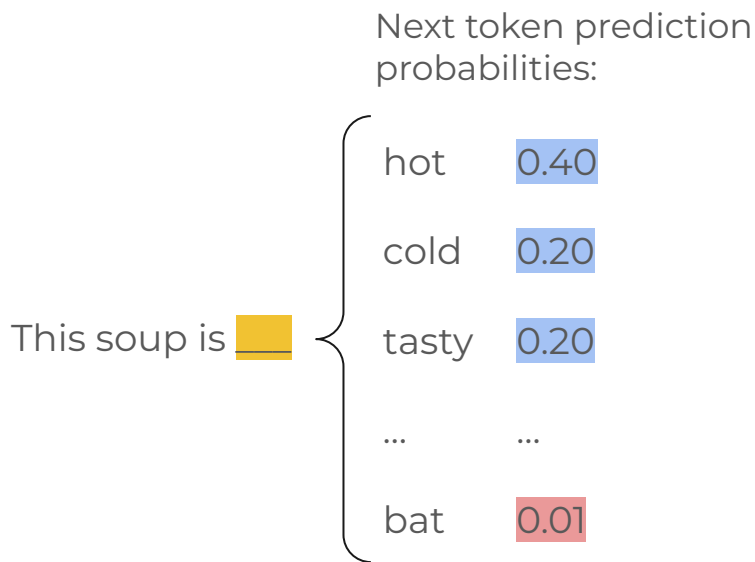
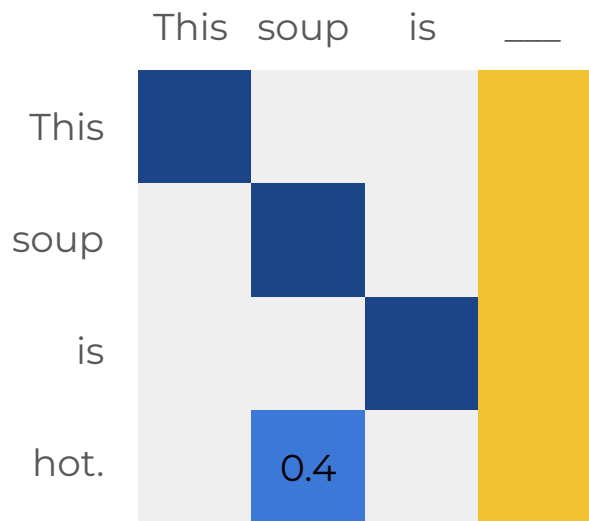
This soup is hot.  
This soup is tasty.  
This soup is hot.  
This soup is hot.  
This soup is cold.  
This soup is cold.  
This soup is hot.  
This soup is tasty.  
...  
This soup is bat.





# Transformer


How can we use attention? (*the ultra simplified version*)



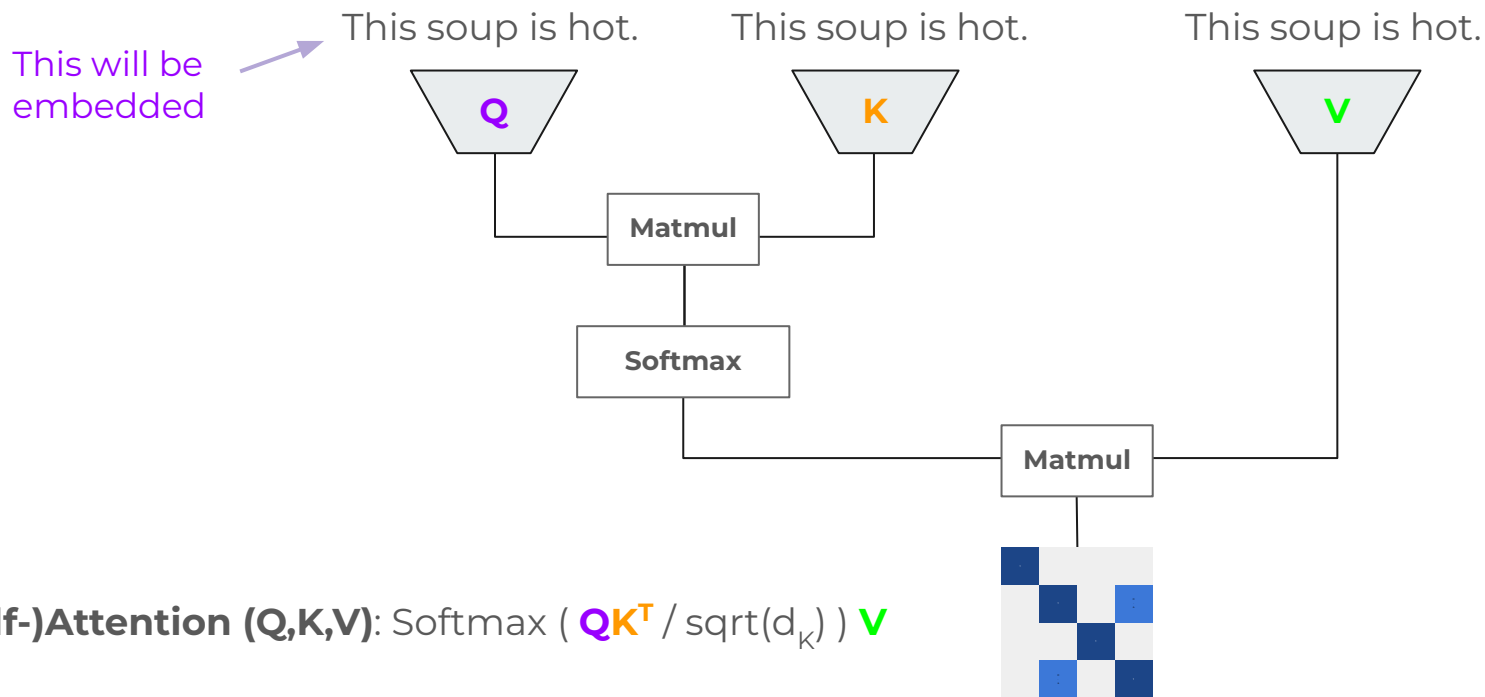
# Transformer

How can we use attention? (*the ultra simplified version*)

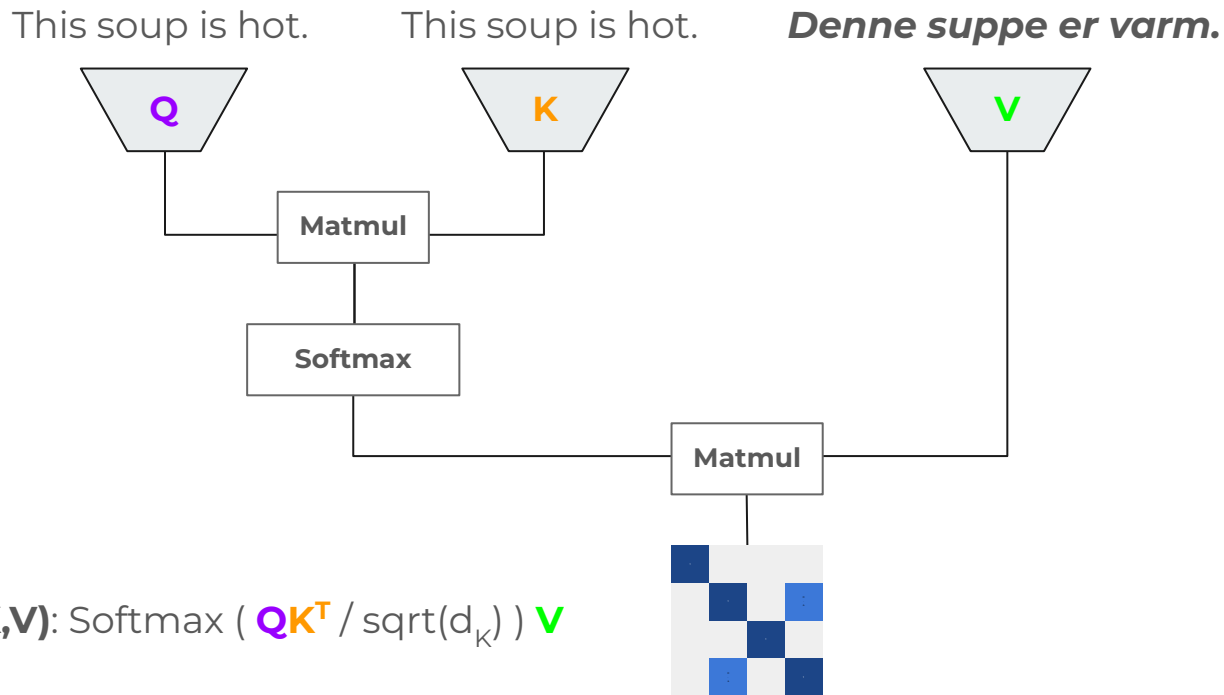
These probabilities can change with context:

It is <u>winter</u> . I <u>like</u> that this soup is 	hot	0.70
	cold	0.09
	tasty	0.20
	bat	0.01

# Transformer



# Transformer

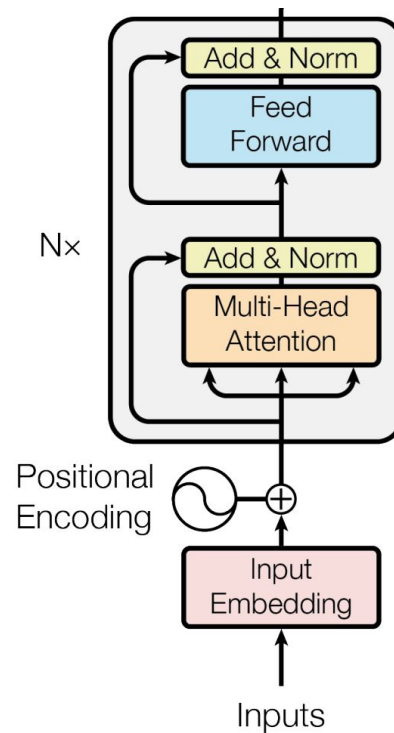


**Cross-Attention (Q,K,V):**  $\text{Softmax} ( \text{QK}^T / \text{sqrt}(d_k) ) \text{ V}$

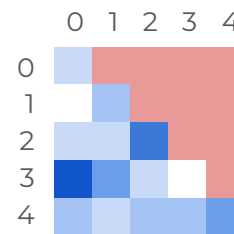
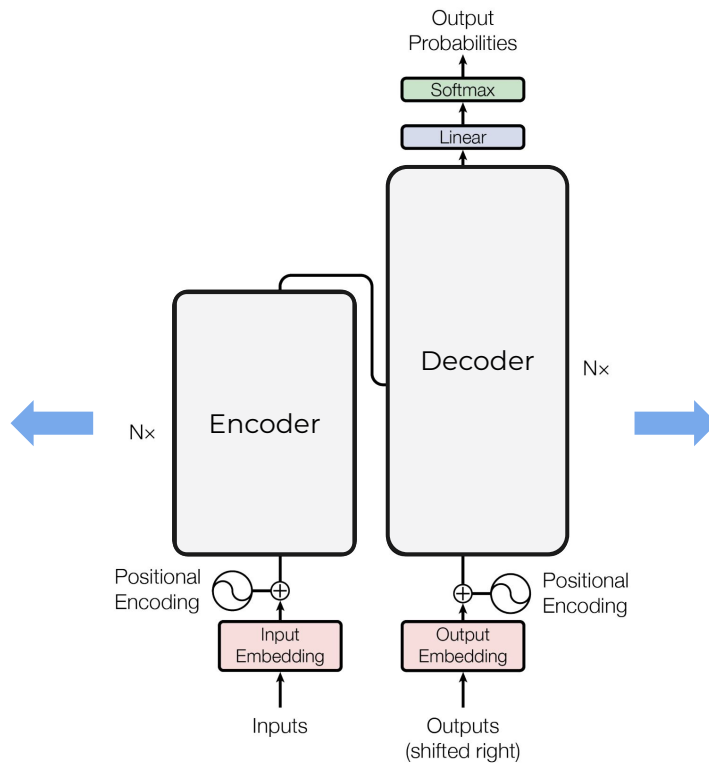
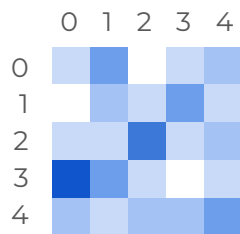
# Transformer

Apart from attention, the transformer architecture is pretty straightforward:

1. Attention
2. Normalization
3. Feed Forward NN
4. Normalization



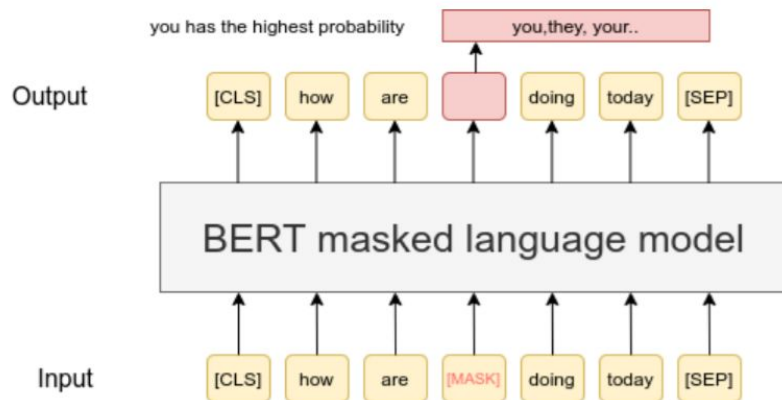
# Transformer



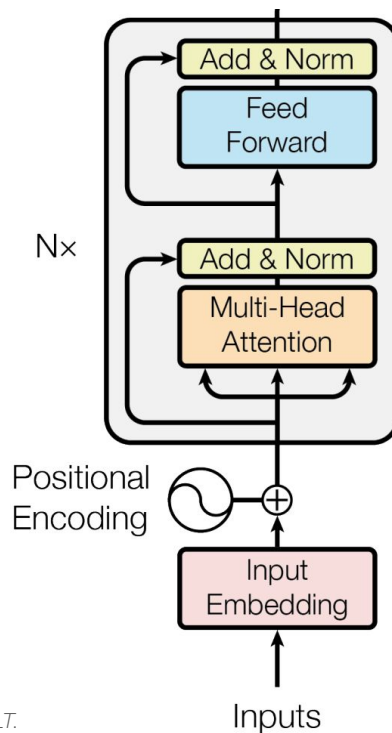
[2] Vaswani et al. (2017) Attention Is All You Need, *NeurIPS*.

# Transformer

BERT: Bidirectional Encoder Representations from Transformers



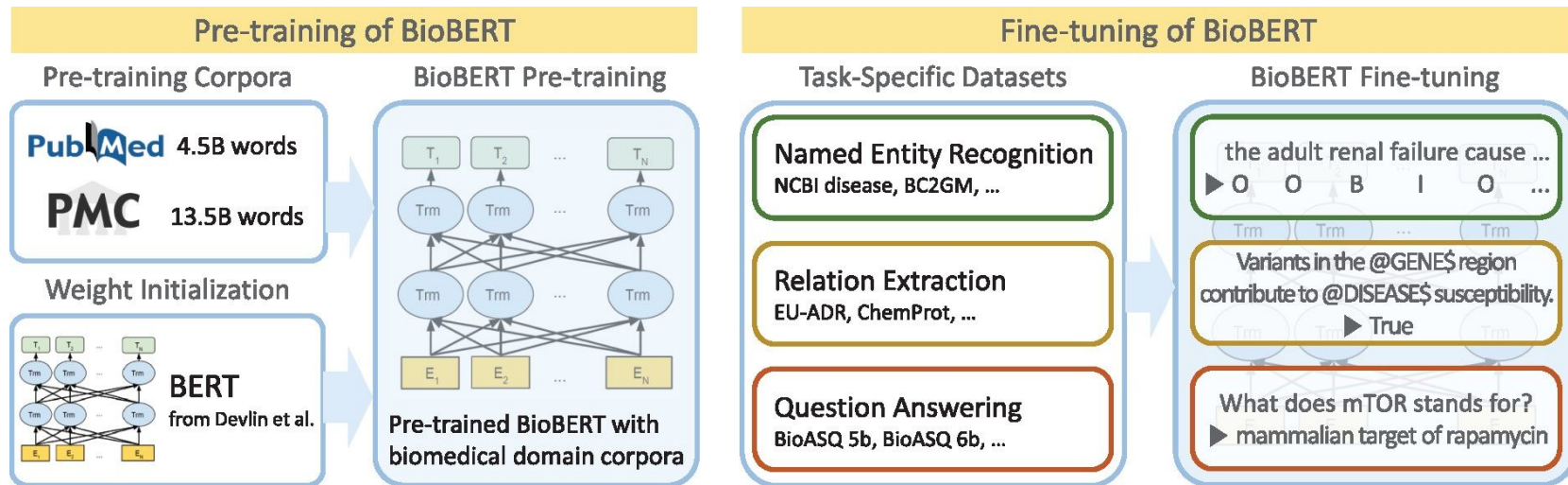
[https://www.sbert.net/examples/unsupervised\\_learning/MLM/README.html](https://www.sbert.net/examples/unsupervised_learning/MLM/README.html)



[3] Devlin et al. (2019) BERT: Pre-training of Deep Bidirectional Transformers for Language Understanding, *NAACL-HLT*.

# Transformers in Biology

Many transformers out there for biological data: - **Medical data**



[4] Lee et al. (2019) BioBERT: a pre-trained biomedical language representation model for biomedical text mining, *Bioinformatics*.



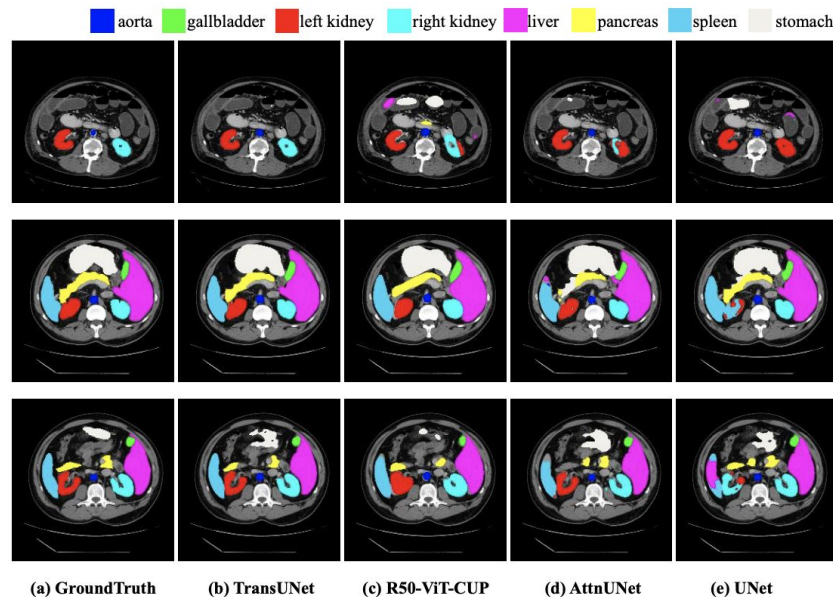
# Transformers in Biology

Many transformers out there for biological data:

- **Medical data**
- RNA: CodonBert
- Proteins: AlphaFold, ESM

They can be used for many downstream tasks:

- **Medical image analysis**
- Mutational effect prediction
- Protein, antibody, vaccine, ... design
- Gene therapy



[5] Chen et al. (2022) TransUNet: Transformers Make Strong Encoders for Medical Image Segmentation, *CoRR*.

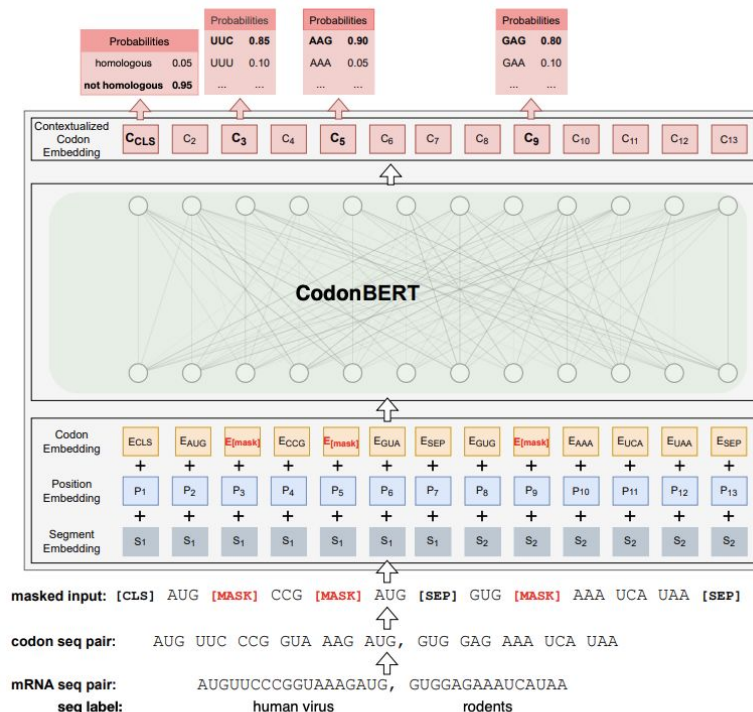
# Transformers in Biology

Many transformers out there for biological data:

- Medical data
- **RNA: CodonBert**
- Proteins: AlphaFold, ESM (open source!)

They can be used for many downstream tasks:

- Medical image analysis
- **Mutational effect prediction**
- Protein, antibody, **vaccine**, ... **design**
- **Gene therapy**



[6] Li et al. (2023) CodonBERT: Large Language Models for mRNA design and optimization, *NeurIPS*.

# Transformers in Biology

Many transformers out there for biological data:

- Medical data
- RNA: CodonBert
- **Proteins**: AlphaFold, **ESM**

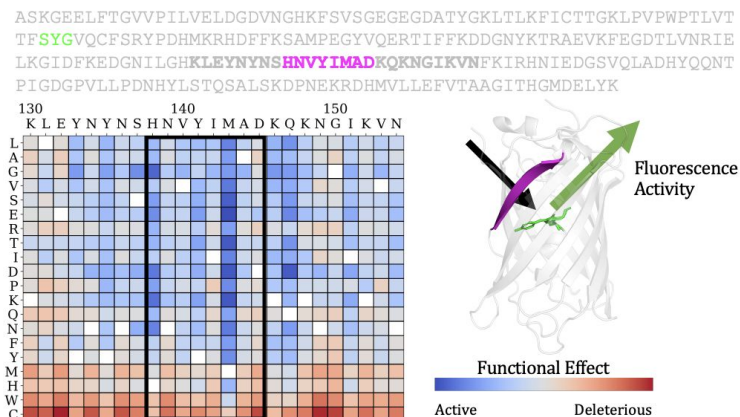
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[7] Meier et al. (2021) Language models enable zero-shot prediction of the effects of mutations on protein function, *NeurIPS*.

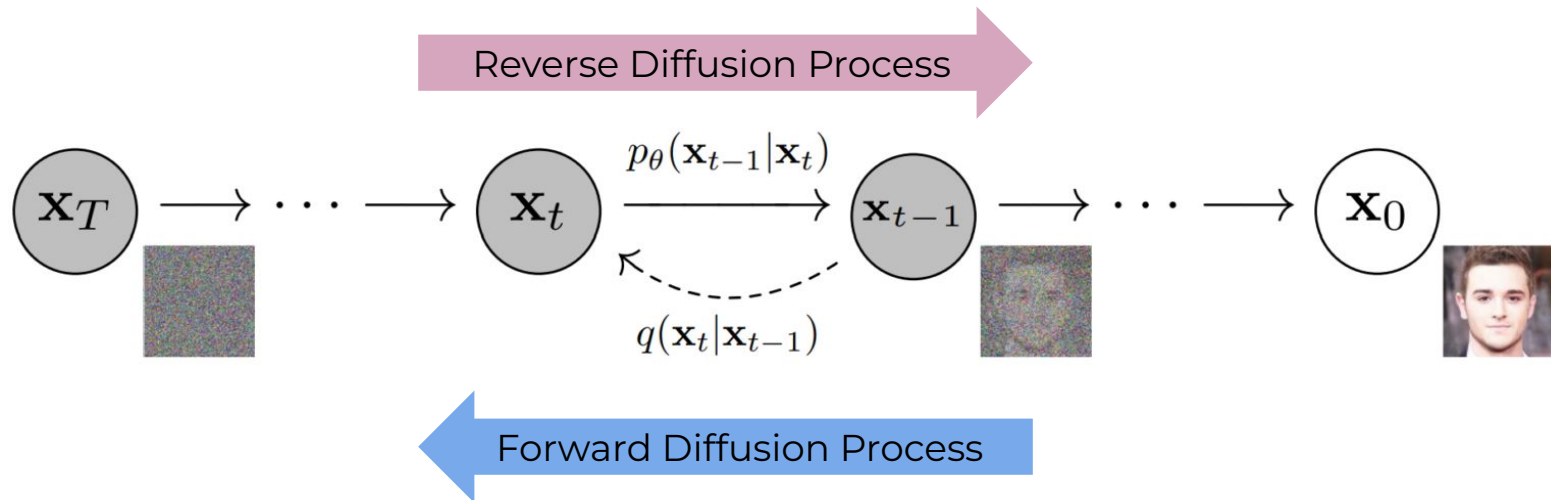
## Language models enable zero-shot prediction of the effects of mutations on protein function

Joshua Meier <sup>1,2</sup> Roshan Rao <sup>3</sup> Robert Verkuil <sup>1</sup> Jason Liu <sup>1</sup>  
Tom Sercu <sup>1</sup> Alexander Rives <sup>1,2</sup>



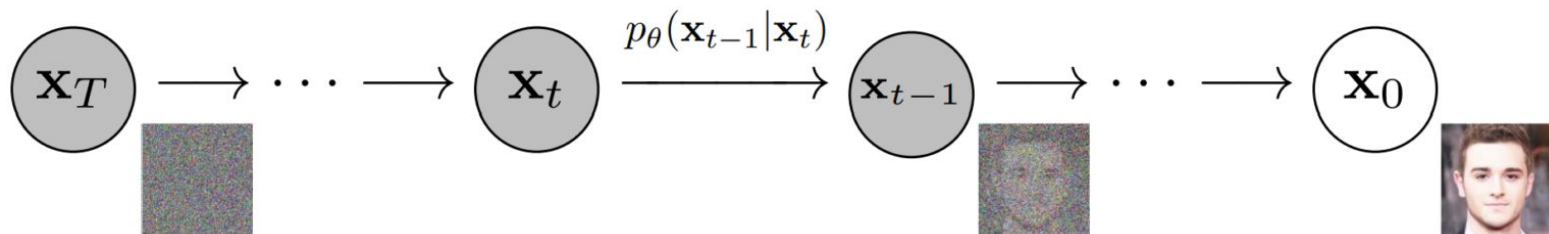
# Diffusion - DDPM

*Denoising Diffusion Probabilistic Models*



# Diffusion

How can we learn to remove noise?

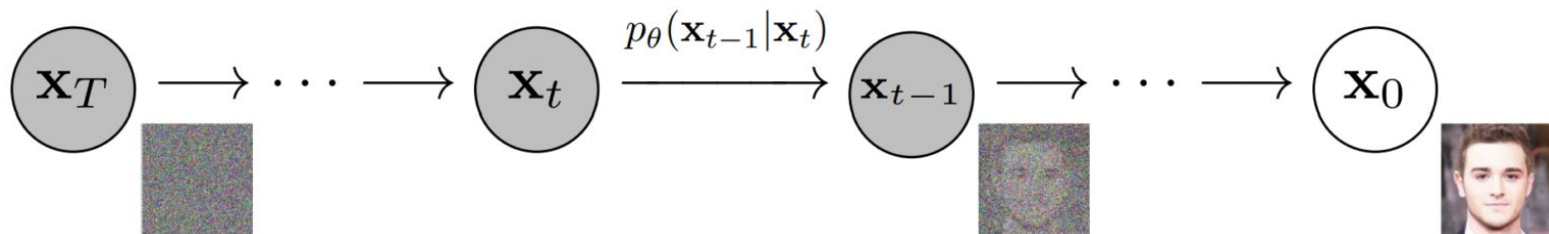


$$p_\theta(\mathbf{x}_{t-1}|\mathbf{x}_t) := \mathcal{N}(\mathbf{x}_{t-1}; \underbrace{\boldsymbol{\mu}_\theta(\mathbf{x}_t, t)}_{\text{mean}}, \boldsymbol{\Sigma}_\theta(\mathbf{x}_t, t))$$

$$\boldsymbol{\mu}_\theta(\mathbf{x}_t, t) = \frac{1}{\sqrt{\alpha_t}} \left( \mathbf{x}_t - \frac{\beta_t}{\sqrt{1 - \bar{\alpha}_t}} \boldsymbol{\epsilon}_\theta(\mathbf{x}_t, t) \right)$$

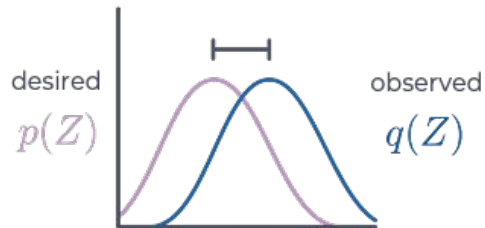
# Diffusion

How can we learn to remove noise?



**WE LEARN TO PREDICT THE SAMPLED NOISE!**

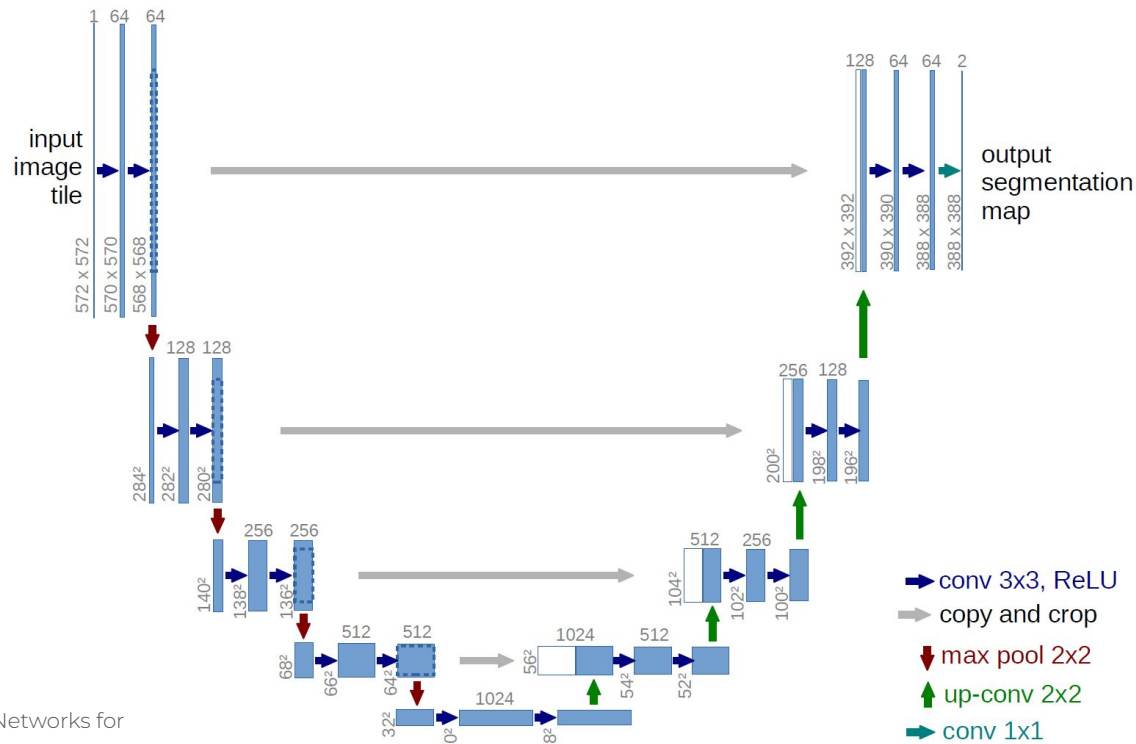
$$L_{\text{simple}}(\theta) := \mathbb{E}_{t, \mathbf{x}_0, \epsilon} \left[ \left\| \epsilon - \epsilon_\theta(\sqrt{\bar{\alpha}_t} \mathbf{x}_0 + \sqrt{1 - \bar{\alpha}_t} \epsilon, t) \right\|^2 \right]$$



# Diffusion

The typical architecture:

UNets

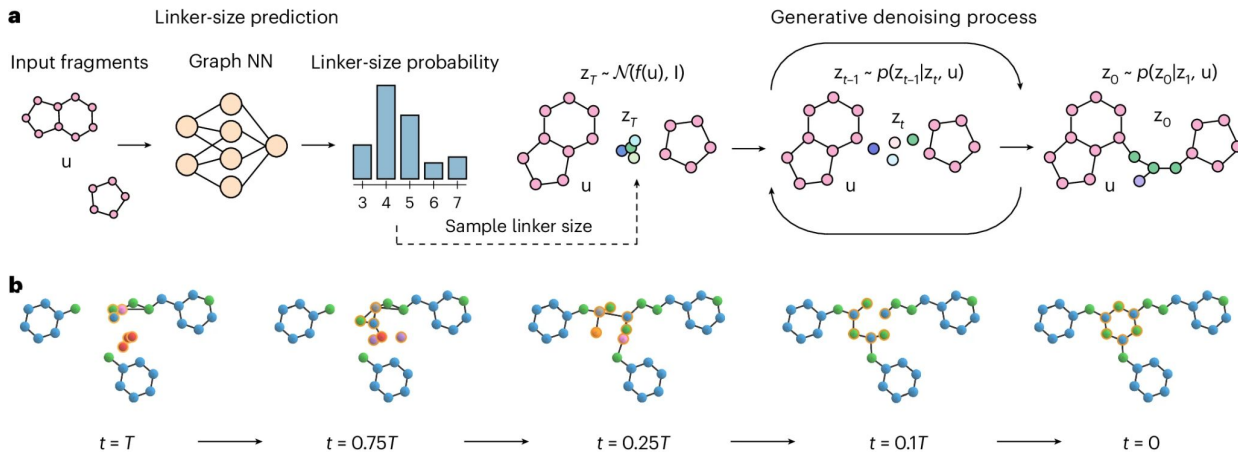


[9] Ronneberger et al. (2015) U-Net: Convolutional Networks for Biomedical Image Segmentation, *MICCAI*.

# Diffusion in Biology

Applications:

- Protein and **molecule design**: TopoDiff, **DiffLinker**, ...
- Protein-ligand interaction modeling: DiffDock, ...
- ...



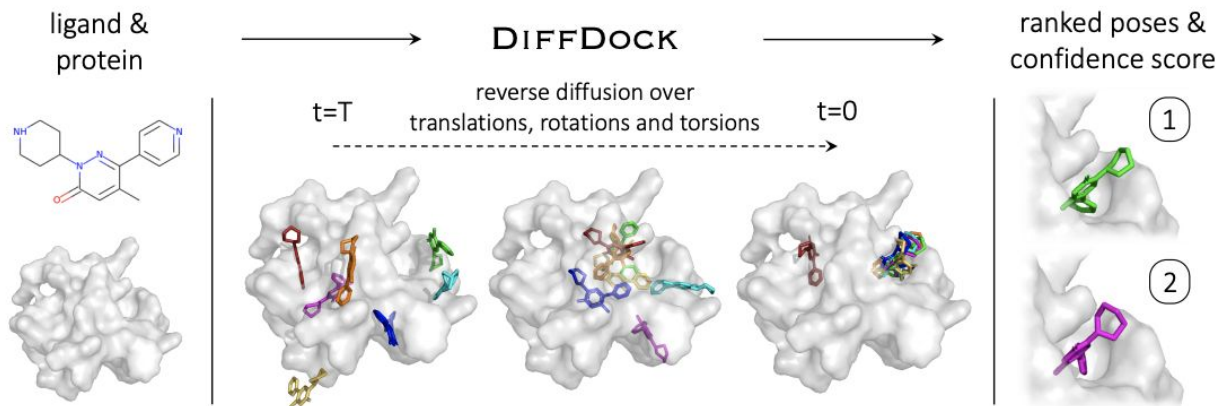
[10] Igashov et al. (2024) Equivariant 3D-conditional diffusion model for molecular linker design,, *Nature Machine Intelligence*.



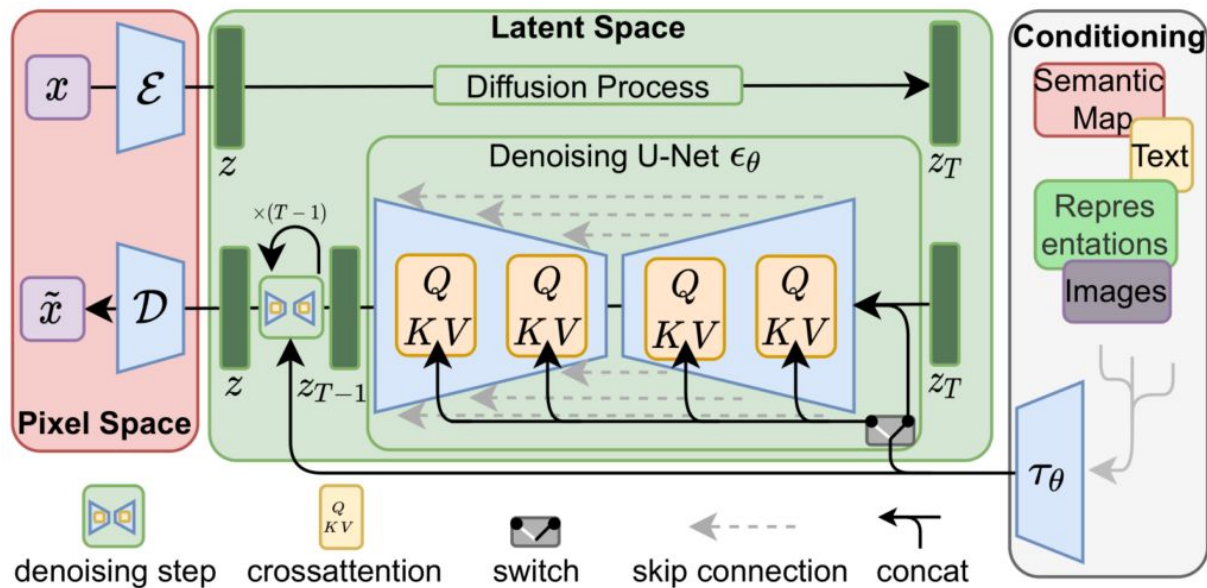
# Diffusion in Biology

Applications:

- Protein and molecule design: TopoDiff, DiffLinker, ...
- **Protein-ligand interaction** modeling: **DiffDock**, ...
- ...



# Latent Diffusion



Rombach et al. High-Resolution Image Synthesis with Latent Diffusion Models. CVPR 2022.

# Big generative AI

The **downside** for us:

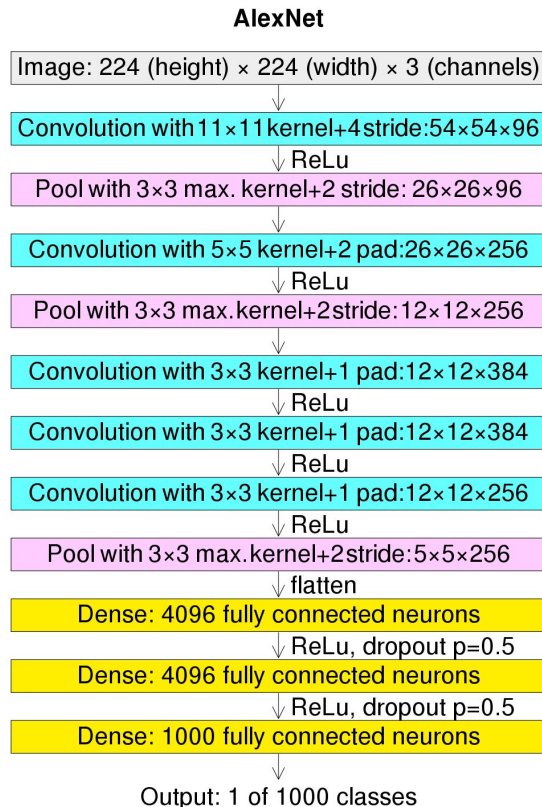
These big models need

a ton of **compute!!!**

AlexNet (2015):

62.3 M parameters

trained on 2 GPUs



# Big generative AI

The **downside for us:**

These big models need

a ton of **compute!!!**

Llama3 (2024):

8 B - 400 B parameters

trained on 16K H100 GPUs

