

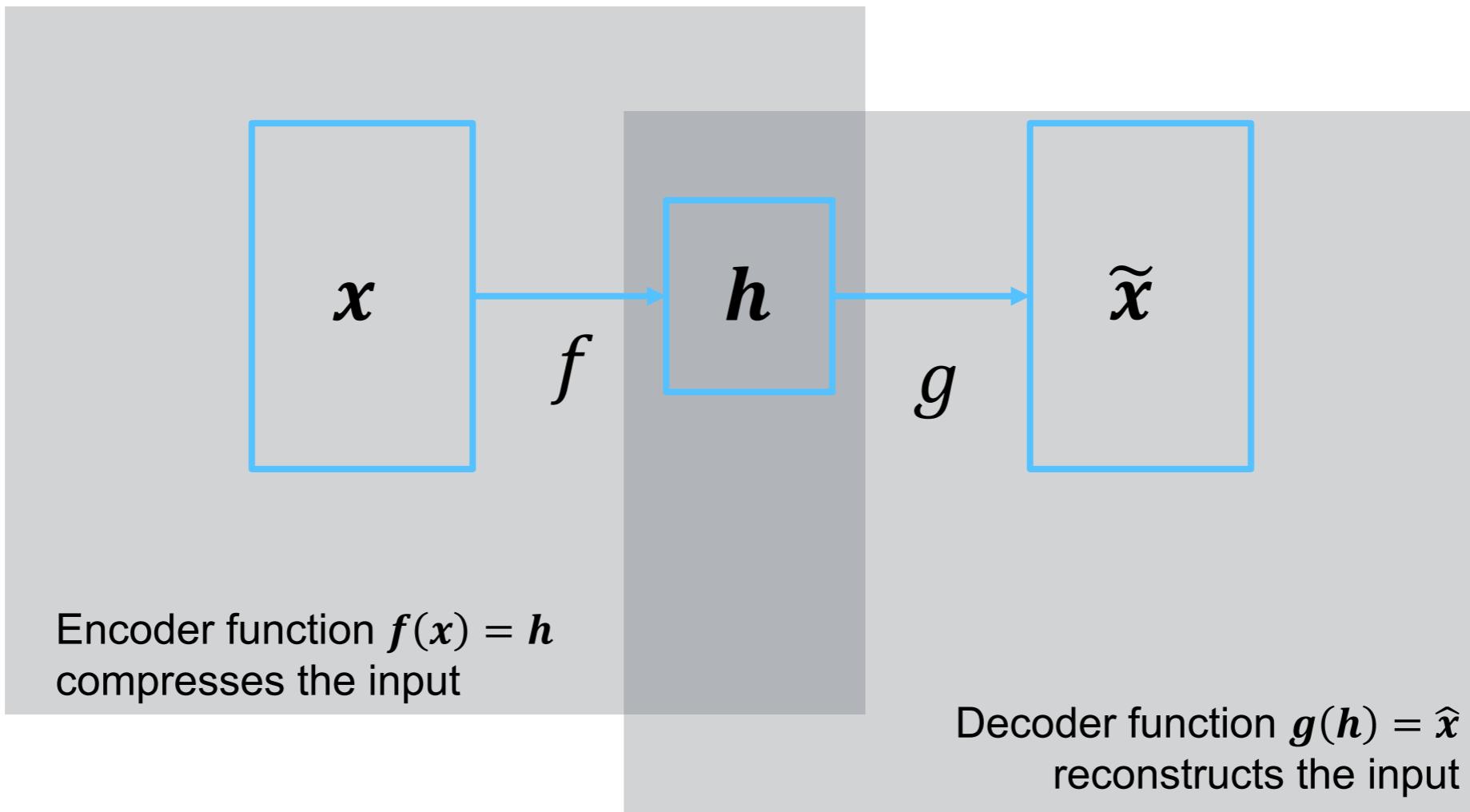
# **Autoencoders** and their **applications** in computational biology

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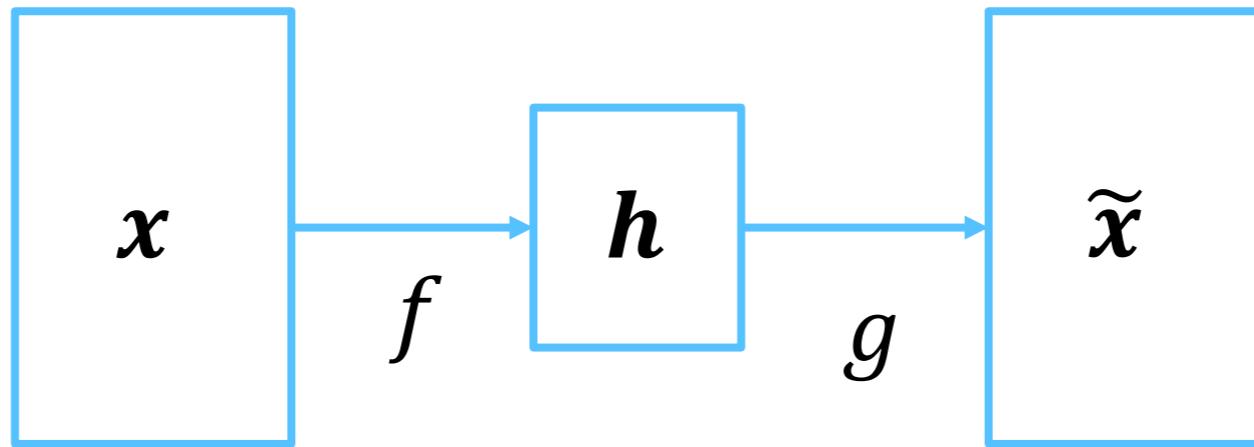
# Overview

- Intro to autoencoders
- Main variations - examples
- Applications in single-cell analysis
- Hands-on exercise

# Autoencoders

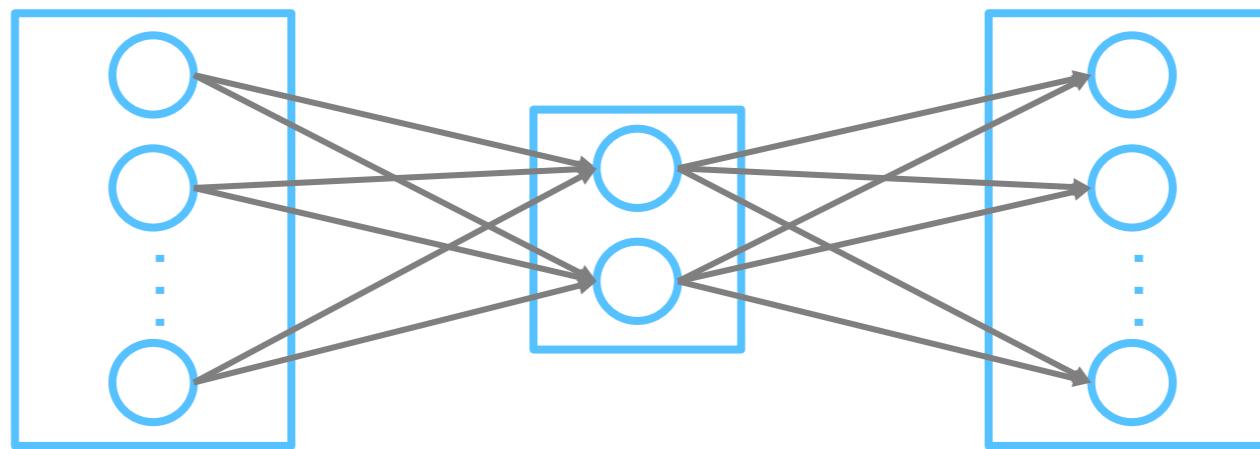


# Autoencoders



- Non-linear activation functions → complex relationships
- Lossy reconstruction → most salient features of the data

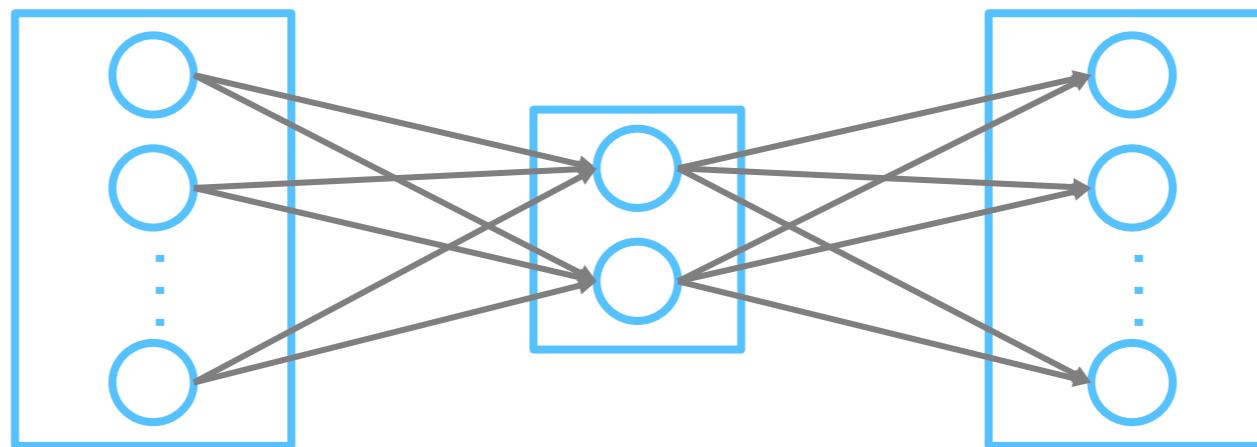
# Autoencoders



Trained using **backpropagation**

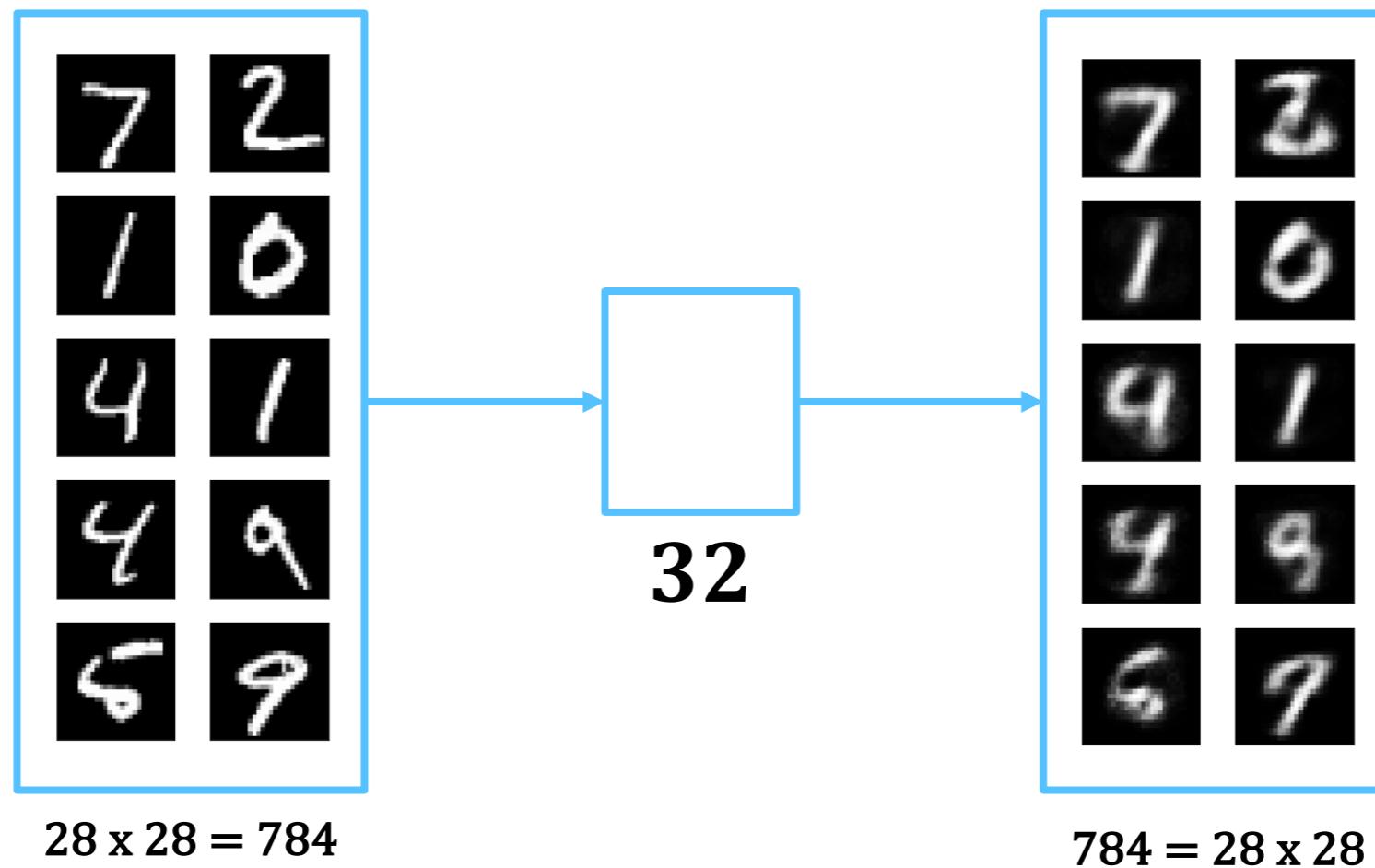
$$mse = \frac{1}{n} \sum_{i=1}^n (x_i - \tilde{x}_i)^2 = \frac{1}{n} \sum_{i=1}^n (x_i - g(f(x_i)))^2$$

# Autoencoders

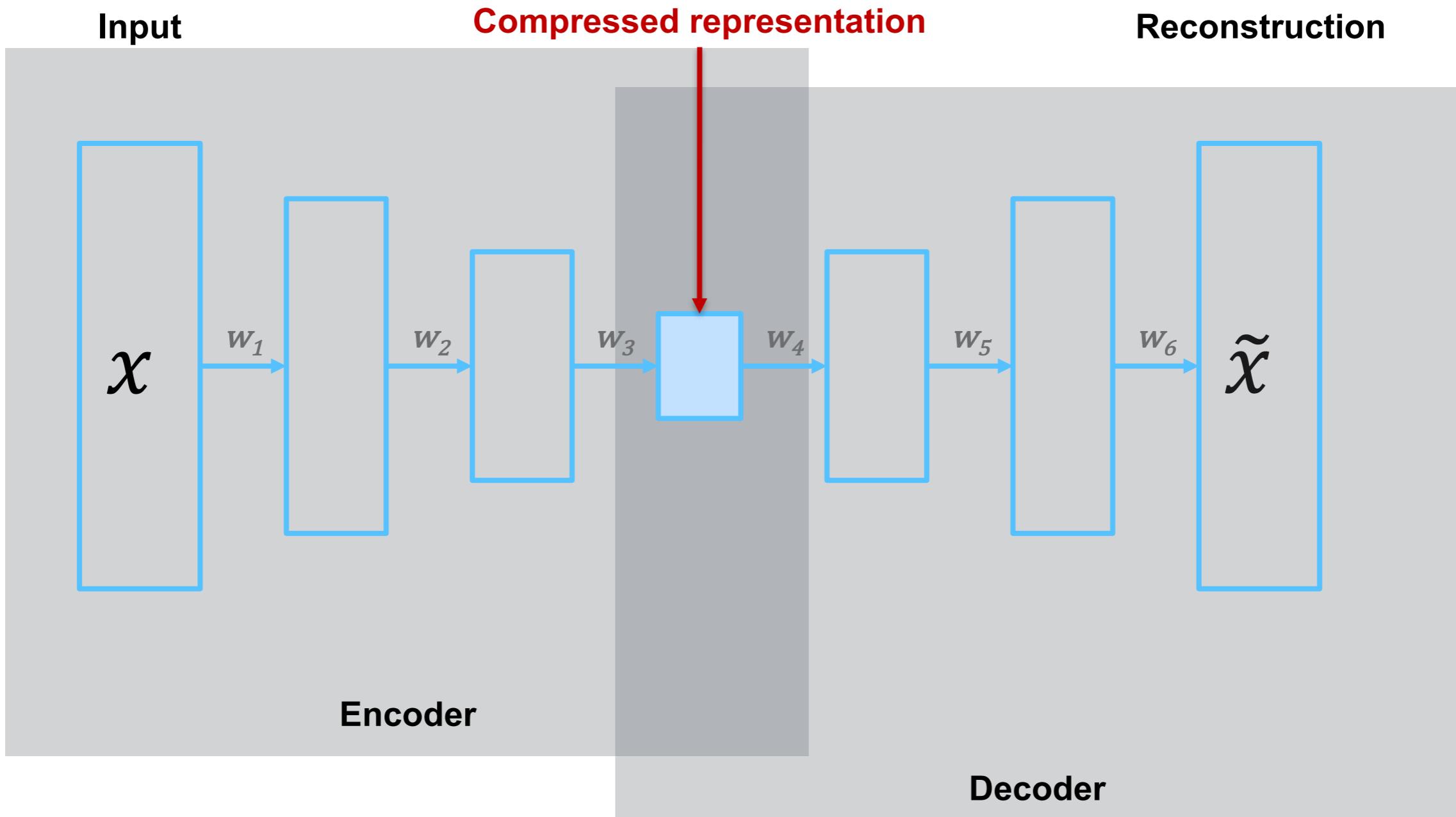


- Data compression
- Experiment reconstruction
- Dimensionality reduction

# Example 1: simple AE

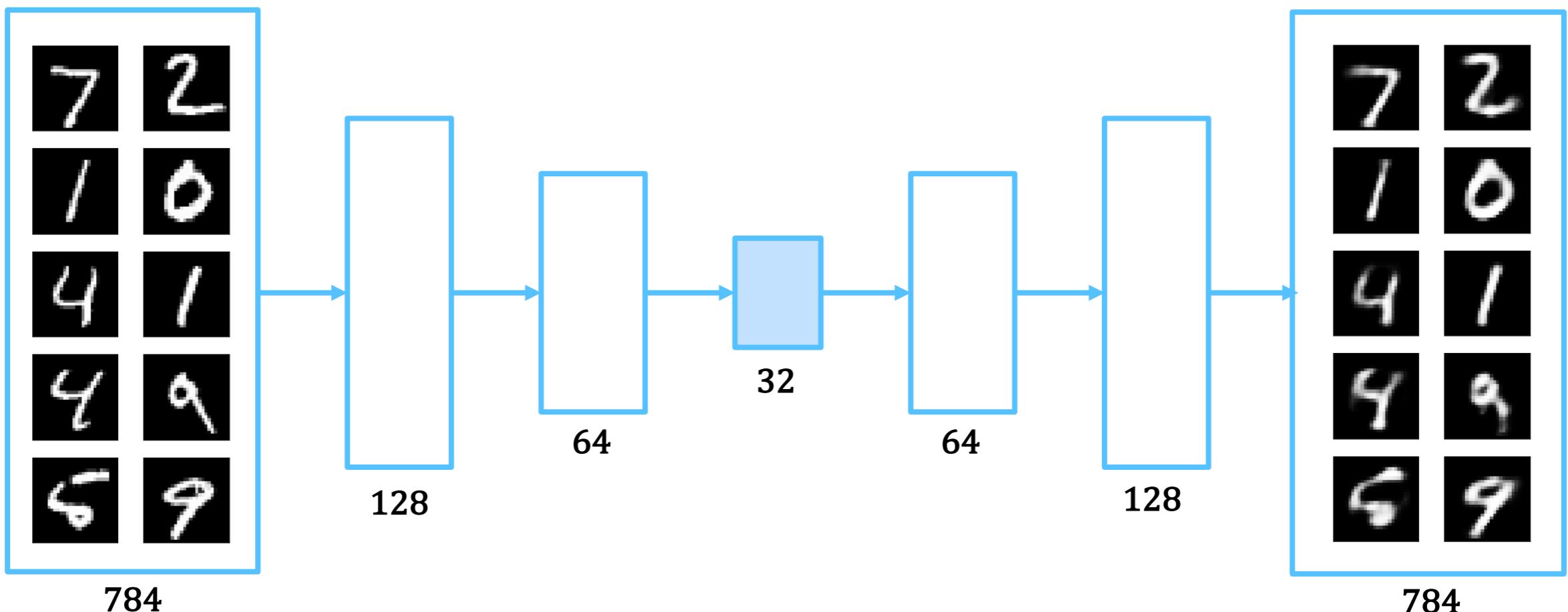


# Deep autoencoders

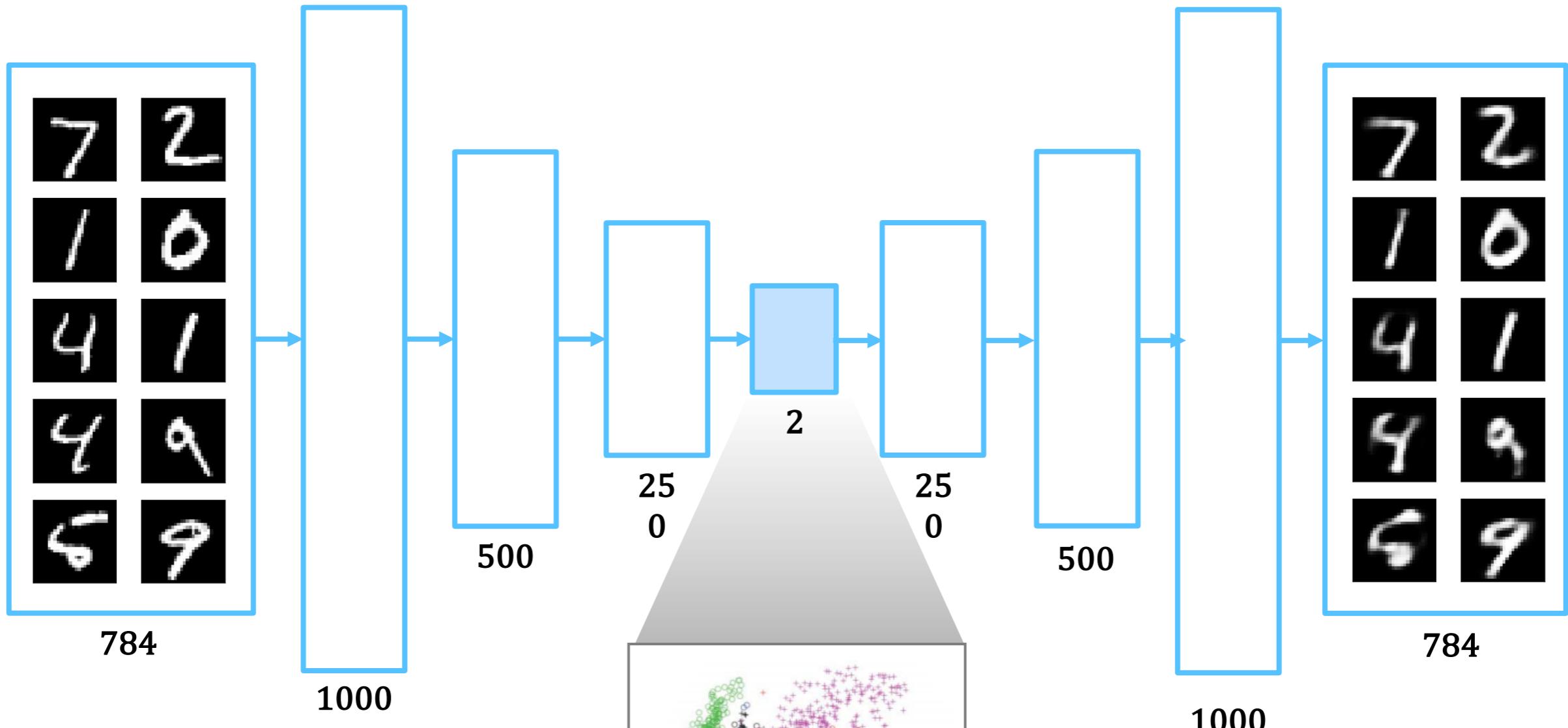


Hierarchy of representation  
Stacking – pretraining\*

## Example 2: deep AE



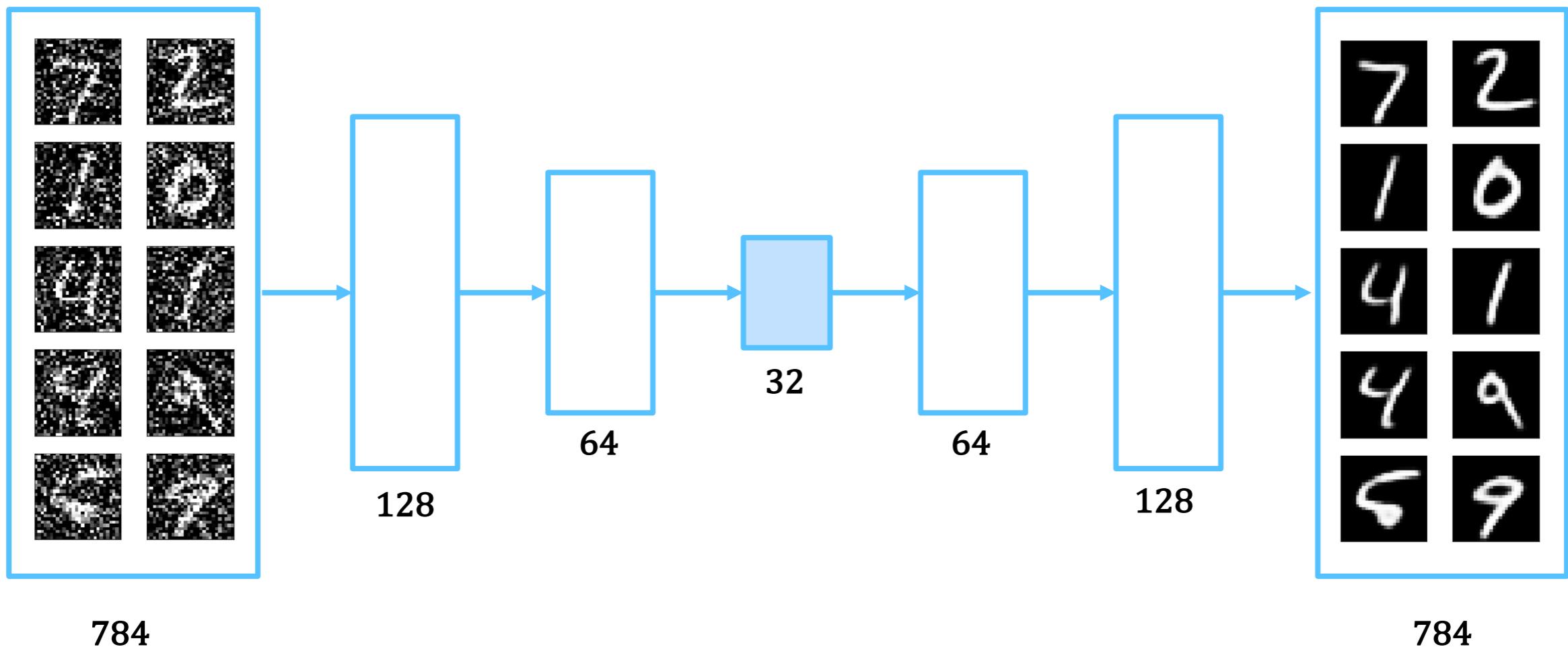
# Example 3: deep AE + dimensionality reduction



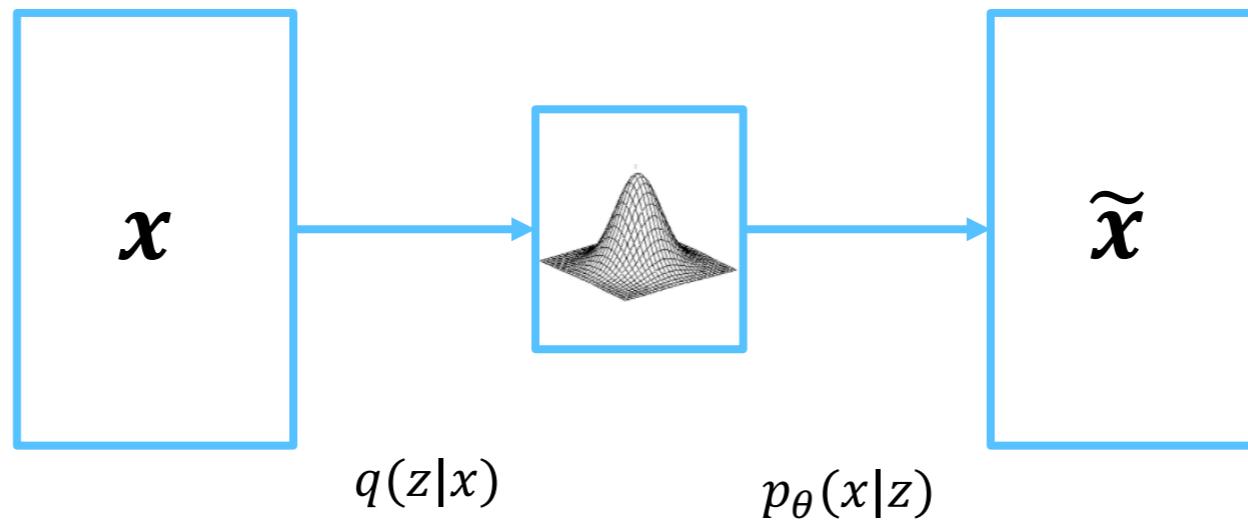
# Different flavors

- **Undercomplete:** the “vanilla” flavor
- **Convolutional:** convolutions as hidden layers
- **Sparse:** impose sparsity constraint on hidden units
- **Denoising:** corrupt input with noise to increase robustness
- **Variational:** generative models, probabilistic spin

# Example 4: denoising AE



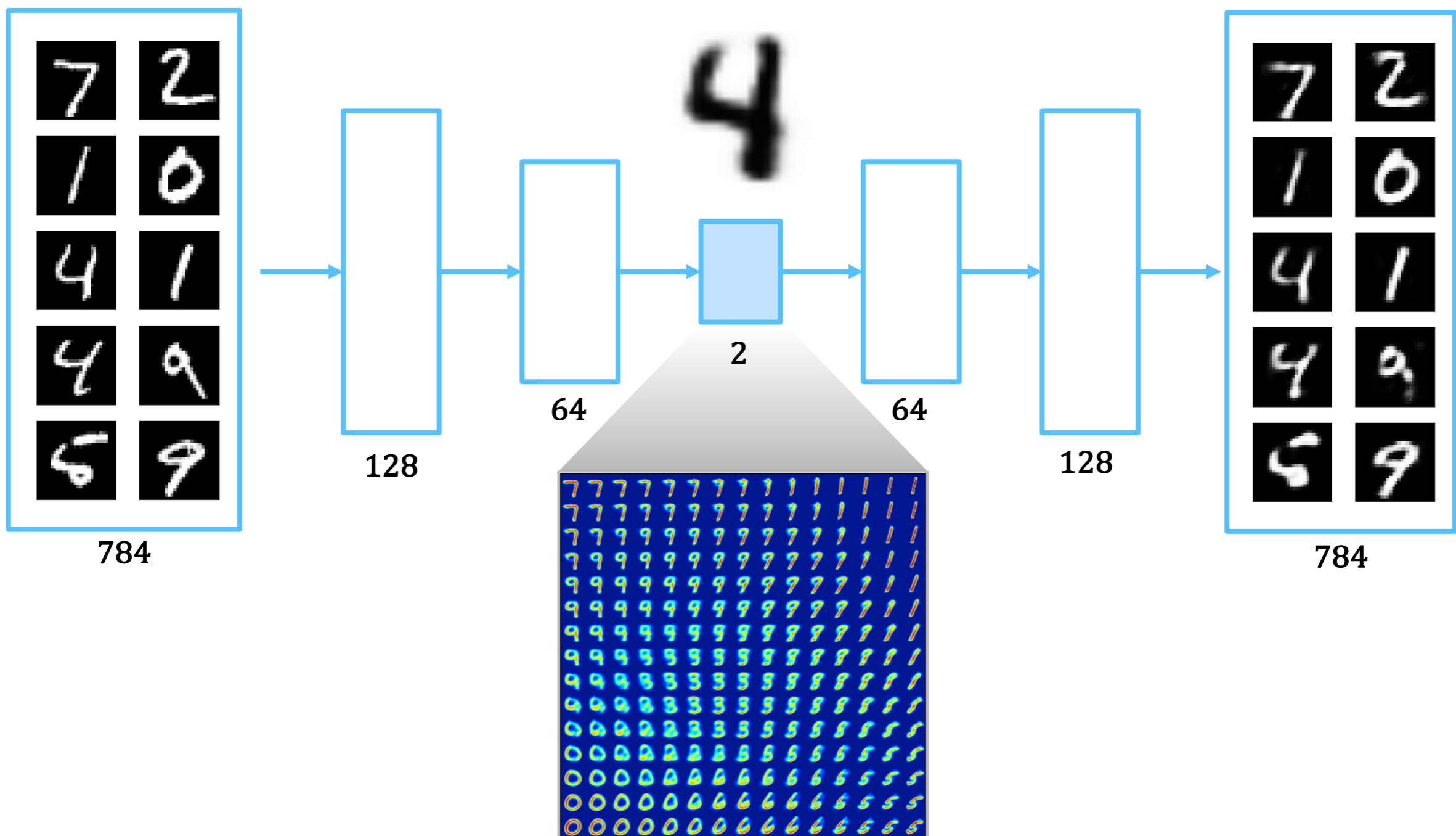
# Variational Autoencoders



**Encoder:** maps input to posterior distributions over latent space

**Decoder:** maps coordinates back to distributions over the original space

# Example 5: variational AE

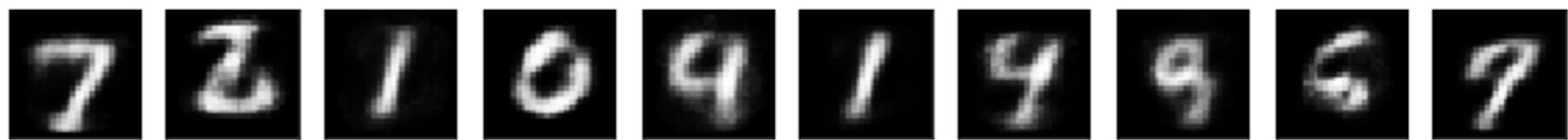


# Comparison

Initial data



AE with 1 hidden layer



AE with 5 hidden layers



Denoising AE with 5  
hidden layer

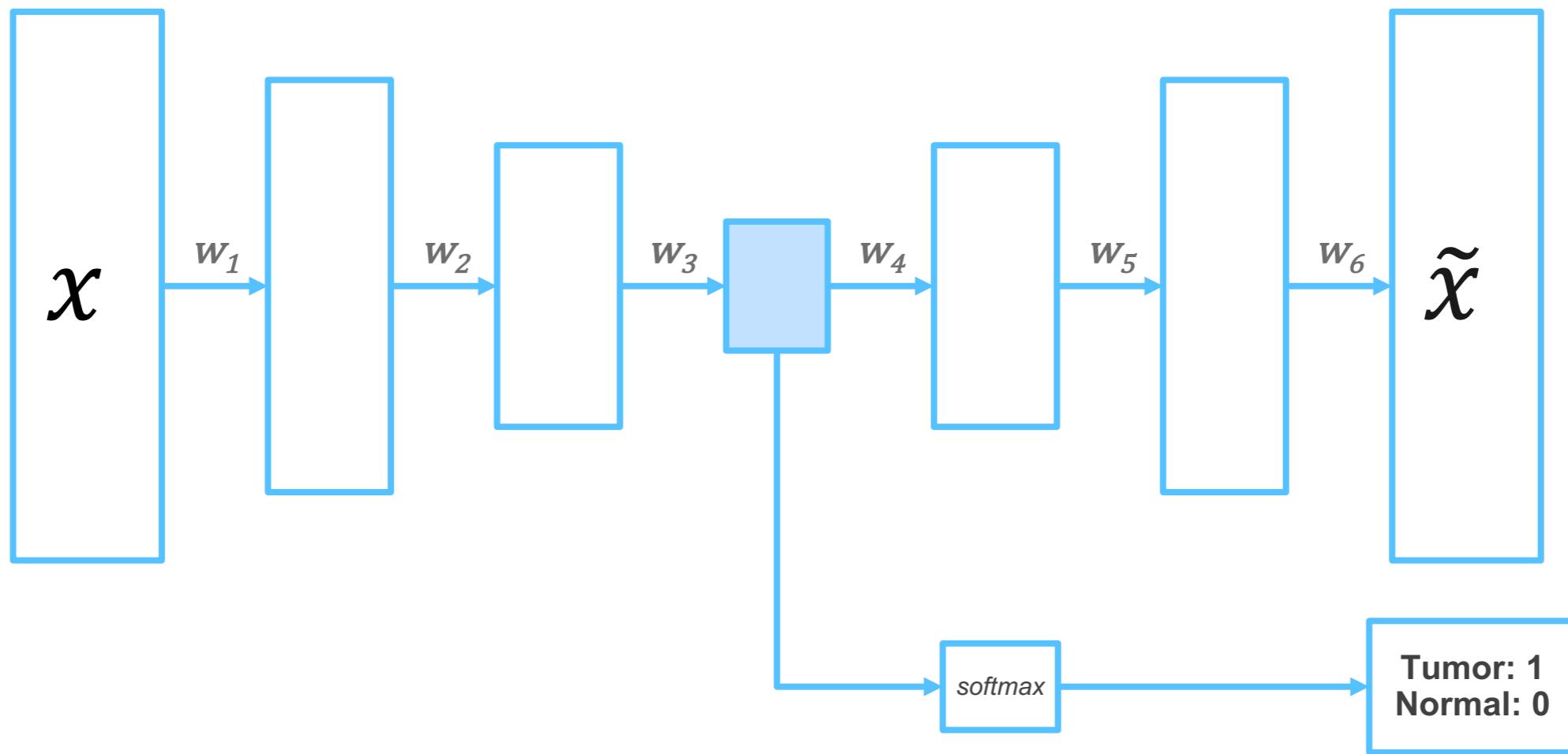


Variational



# Extensions

Modified network architectures allow for hybrid unsupervised and supervised learning



# Autoencoders for automatic gating

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## DeepCyTOF: Automated Cell Classification of Mass Cytometry Data by Deep Learning and Domain Adaptation

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Huamin Li <sup>1,\*</sup>; Uri Shaham <sup>2,\*</sup>; Yi Yao <sup>3</sup>, Ruth Montgomery <sup>3</sup>, and Yuval Kluger <sup>1,4,5†</sup>

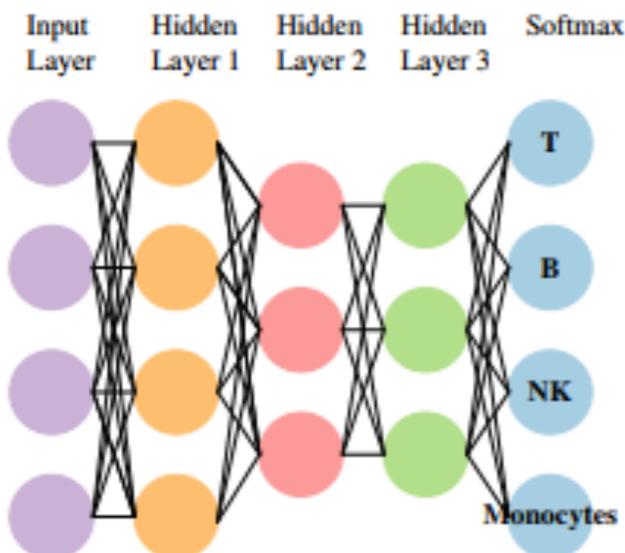


Figure 1: Stacked autoencoder for gating cell populations

Table 2: Summary of results for the cell identification challenge. The numbers in parentheses represent 95% confidence intervals

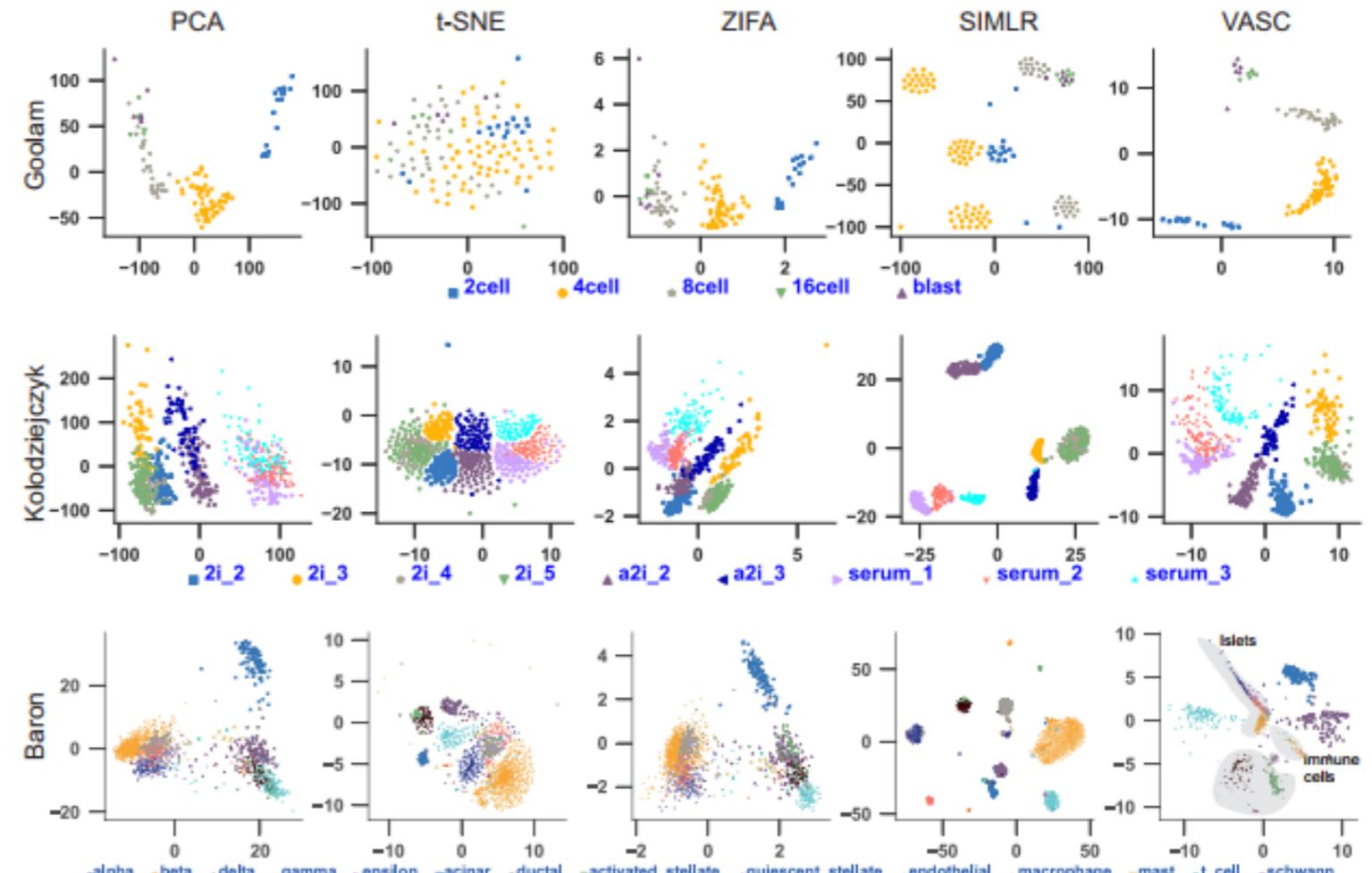
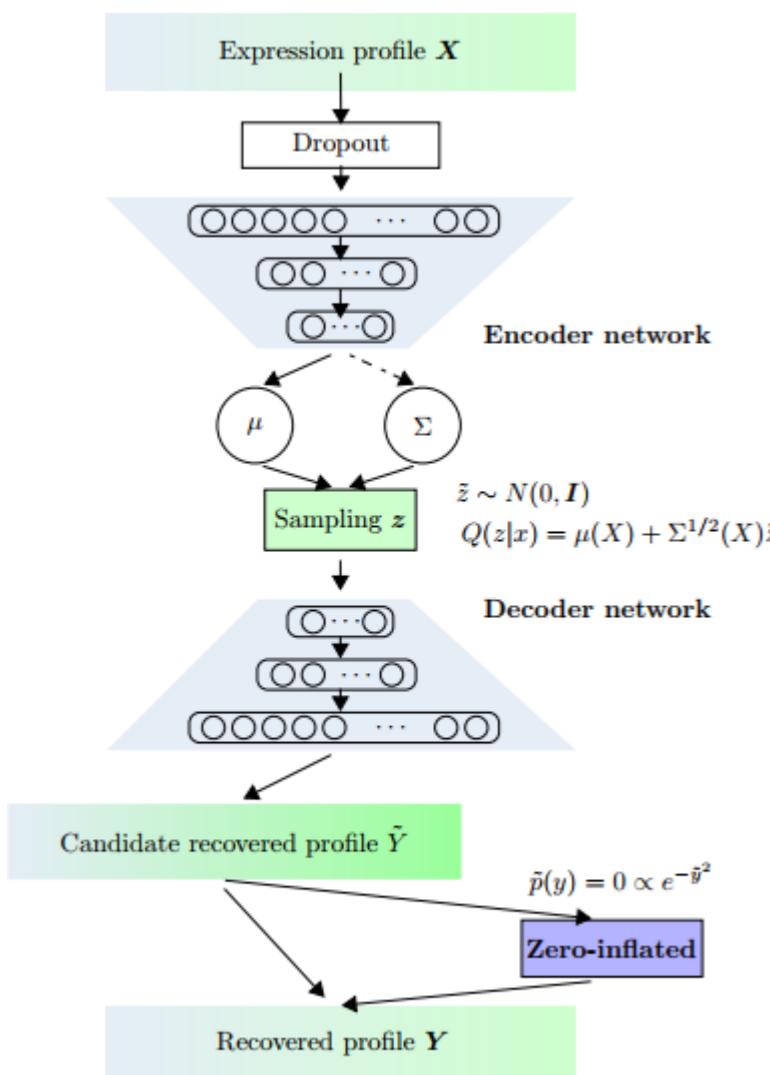
$F = \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}}$	Stacked autoencoder	Competition's winner
GvHD <sup>a</sup>	0.98 (0.97, 0.99)	0.92 (0.88, 0.95)
DLBCL	0.97 (0.95, 0.99)	0.95 (0.93, 0.97)
HSCT	0.98 (0.96, 0.99)	0.98 (0.96, 0.99)
WNV	0.98 (0.97, 0.99)	0.96 (0.94, 0.97)
ND	0.98 (0.96, 0.99)	0.94 (0.92, 0.95)

<sup>a</sup> Datasets: graft-versus-host disease (GvHD); diffuse large B-cell lymphoma (DLBCL); symptomatic West Nile virus (WNV); normal donors (ND); hematopoietic stem cell transplant (HSCT).

# Autoencoders for unsupervised learning

## VASC: dimension reduction and visualization of single cell RNA sequencing data by deep variational autoencoder

Dongfang Wang<sup>1</sup>, Jin Gu<sup>1,\*</sup>



$$\text{Loss}(X, Y) = \text{binary\_entropy}(X, Y) + \text{KL}(Q(z|X) || P(z))$$

# Hands-on exercise

- Characterizing cell populations from single-cell mas cytometry data
- Open your jupyter notebook **ae.ipynb**

# Learning resources

## Papers and blogs:

- Review: <http://msb.embopress.org/content/12/7/878>
- Awesome list: <https://github.com/terryum/awesome-deep-learning-papers>
- Variational Bayes: <https://arxiv.org/pdf/1312.6114.pdf>
- Sparse autoencoders: <https://web.stanford.edu/class/cs294a/sparseAutoencoder.pdf>
- Colah's blog: <http://colah.github.io>

## Tutorials:

- <https://blog.keras.io/building-autoencoders-in-keras.html>

## Courses:

- <http://cs231n.github.io/neural-networks-1/>
- <https://stats385.github.io/readings>
- <http://slazebni.cs.illinois.edu/spring17/#resources>
- <https://www.udacity.com/course/deep-learning-nanodegree-foundation--nd101>