

Tutorial on

# Synthetic Healthcare Data Generation and Assessment: Challenges, Methods, and Impact on Machine Learning

Mihaela van der Schaar

Ahmed M. Alaa

University of Cambridge

The Alan Turing Institute

University of California, Los Angeles



[vanderschaar-lab.com](http://vanderschaar-lab.com)



[mv472@cam.ac.uk](mailto:mv472@cam.ac.uk), [ahmedmalaa@ucla.edu](mailto:ahmedmalaa@ucla.edu)



van\_der\_Schaar  
\\ LAB

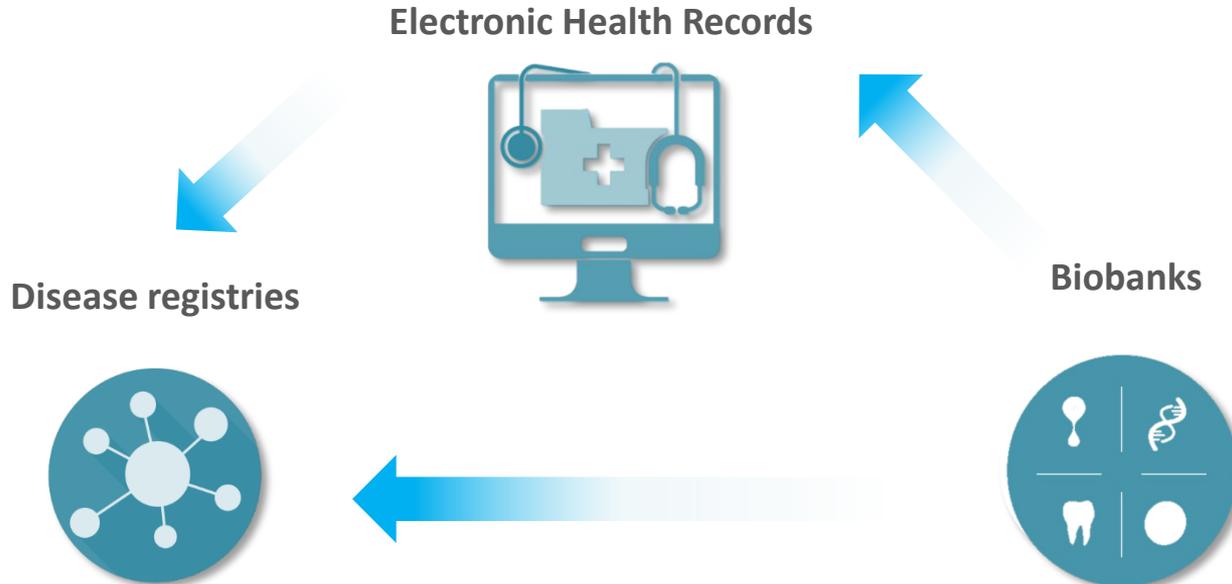


UNIVERSITY OF  
CAMBRIDGE

# Healthcare data: an essential resource

- **Availability of healthcare data resources:**

can catalyze a complete transformation in healthcare using ML – improve clinical practice & clinical workflows, empower patients, enhance drug development, enable medical knowledge discovery etc.



# Healthcare data: not easy to access

- Strict regulations for data access
- ...the result of perfectly valid concerns regarding privacy



- **Lack of high-quality healthcare data: impedes ML research in healthcare!**

# What history teaches us...

- Open access data sets = significant progress!



Technology

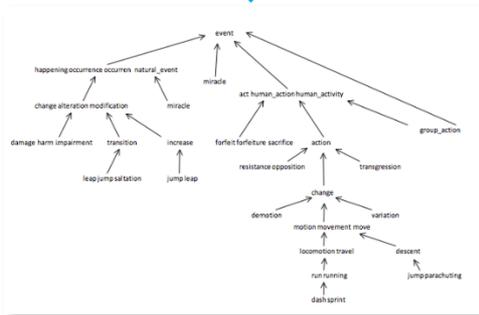
## From not working to neural networking

Special report

Jun 25th 2016 edition >

The artificial-intelligence boom is based on an old idea, but with a modern twist

[C. Fellbaum et al, 1980s]



WordNet

Progress in NLP

[Fei-Fei Li et al, 2006]



ImageNet

Progress in imaging, vision

# The story is more complex for healthcare data...

- Unlike ImageNet, clinical data is about *people and their health*: ethical considerations!
- One dataset is not enough: medicine is complex; many diseases, different types of data (images, genetic, tabular, longitudinal, time-series, ...), diverse populations, different uses, patient characteristics and treatments change over time...etc.
- One of the few initiatives: MIMIC dataset from Beth Israel Deaconess Medical center...
- Companies/organizations are trying to lock up access to data to productize their models!



<sup>1</sup>A. E. Johnson et al, Scientific data, 2016

# De-identified data vs Synthetic data

- **De-identified/anonymized data:** real data with all personal identifiers removed/data fields scrambled

- **Synthetic data:** data **created** from scratch, cannot be synced back to any individual (if modeled properly)



**Requires ML/statistical modelling!**

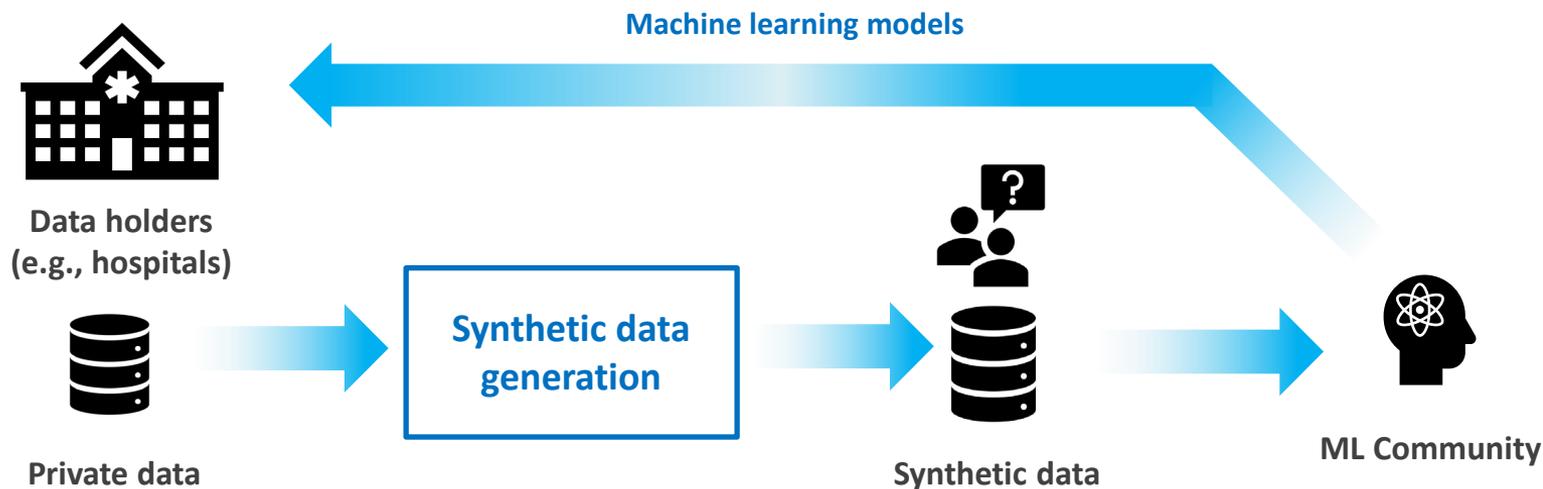
**This tutorial**



**Generating synthetic data to be used for  
machine learning modeling  
is itself a machine learning problem!**

# How can synthetic data help?

- Share a synthetic (proximal) version of the data that resembles real data but contains no real samples for any specific individual...

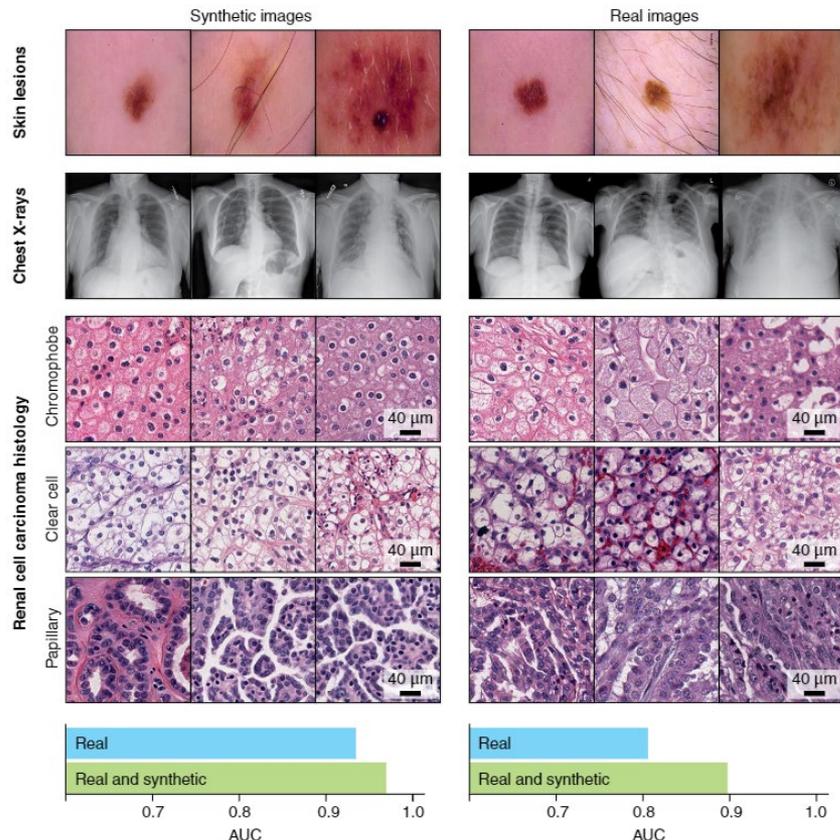


# Use cases for synthetic data

- Developing **analytics**
- Facilitating **reproducibility** of clinical studies and analyses
- **Augmenting** small-sample data sets:
  - Data for rare diseases
  - Data for underrepresented patient subgroups (to guard against model bias)
- Increasing **robustness** and **adaptability** of ML models (transferring across hospitals)
- **Simulating** forward-looking data

# Synthetic clinical data in action: biomedical imaging

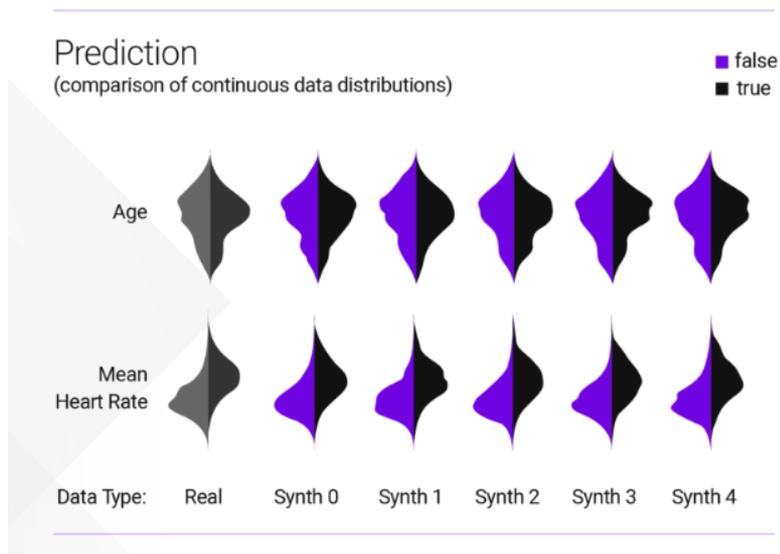
- Synthesizing skin lesion, chest x-rays and histology images using GANs<sup>3</sup>
- A classifier trained on real + synthetic data improved predictions of a rare subtype of renal cell carcinomas
- Even with access to real data, synthetic data can still be used to augment training data.



<sup>3</sup> R. J. Chen et al, Nature Biomedical Engineering, 2021

# Synthetic clinical data in action: COVID-19

- **MDClone**: a synthetic data generation platform used by Sheba Medical Center, Maccabi Institute to accelerate time-to-insight for COVID-19



## THE WALL STREET JOURNAL. The People in This Medical Research Are Fake. The Innovations Are Real.

'Synthetic-data technology,' by creating artificial patient populations has the potential to speed up innovations without compromising privacy



# Privacy concerns are central to clinical data sharing

- Irresponsible sharing of clinical data = legal consequences for researchers, privacy breaches for patients



## May 2021 Healthcare Data Breach Report

POSTED BY HIPAA JOURNAL ON JUN 18, 2021

May was the worst month of 2021 to date for healthcare data breaches. There were 63 breaches of 500 or more records reported to the Department of Health and Human Services' Office for Civil Rights in May. For the past three months, breaches have been reported at a rate of more than 2 per day. The average number of healthcare data breaches per month has now risen to 54.67. May was also the worst month of the year in terms of the severity of breaches. 6,535,130 healthcare records were breached across those 63 incidents. The average number of breached healthcare records each month has now risen to 3,323,116. 17,733,372 healthcare records have now been exposed or impermissibly disclosed so far in 2021 and almost 40 million records (39.87M) have been breached in the past 12 months. Largest Healthcare Data Breaches Reported in April 2021 As was the case in April, there were 19 healthcare data breaches involving 10,000 or more records and 7 of those breaches involved 100,000 or more records. All but one of those breaches was a hacking incident or involved IT systems being compromised by...

## HIPAA AND COMPLIANCE NEWS

### Patient Data Privacy Lawsuit Against Google, UChicago Dismissed

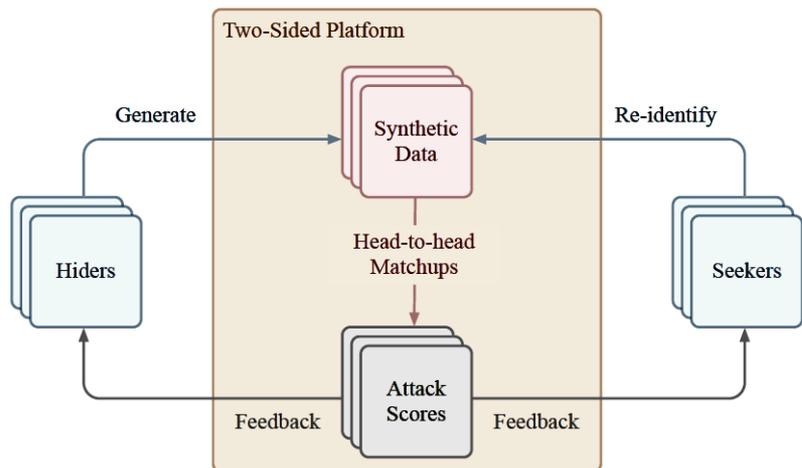
A judge ruled to dismiss the patient data privacy lawsuit brought against Google and UChicago, as the patient failed to adequately demonstrate what damages were caused by the partnership.



# Synthetic clinical data in action: Hide-and-seek competition

## Hide-and-seek privacy challenge

<https://www.vanderschaar-lab.com/privacy-challenge/>



# Synthetic clinical data in action: Hide-and-seeK competition

## Hide-and-seeK privacy challenge

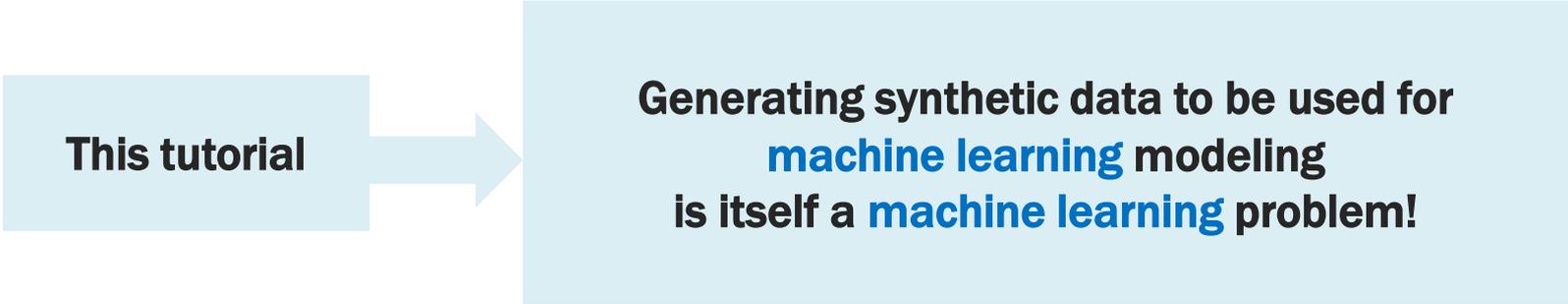
<https://www.vanderschaar-lab.com/privacy-challenge/>

- **Organized by van der Schaar-lab, with support from Amsterdam UMC and Microsoft Research Cambridge**
  - Competitors are either “hidere” aiming to design a model for generating synthetic ICU data or “seekere” aiming to re-identify patients in the original data set.
  - **Key lesson learned:** defining the metrics for evaluating synthetic data and privacy preservation is a tricky problem!

Inspiration Exchange - synthetic data evaluation: [www.youtube.com/watch?v=2FoazjRtTUI](http://www.youtube.com/watch?v=2FoazjRtTUI)

# Desiderata for synthetic data generation

This tutorial

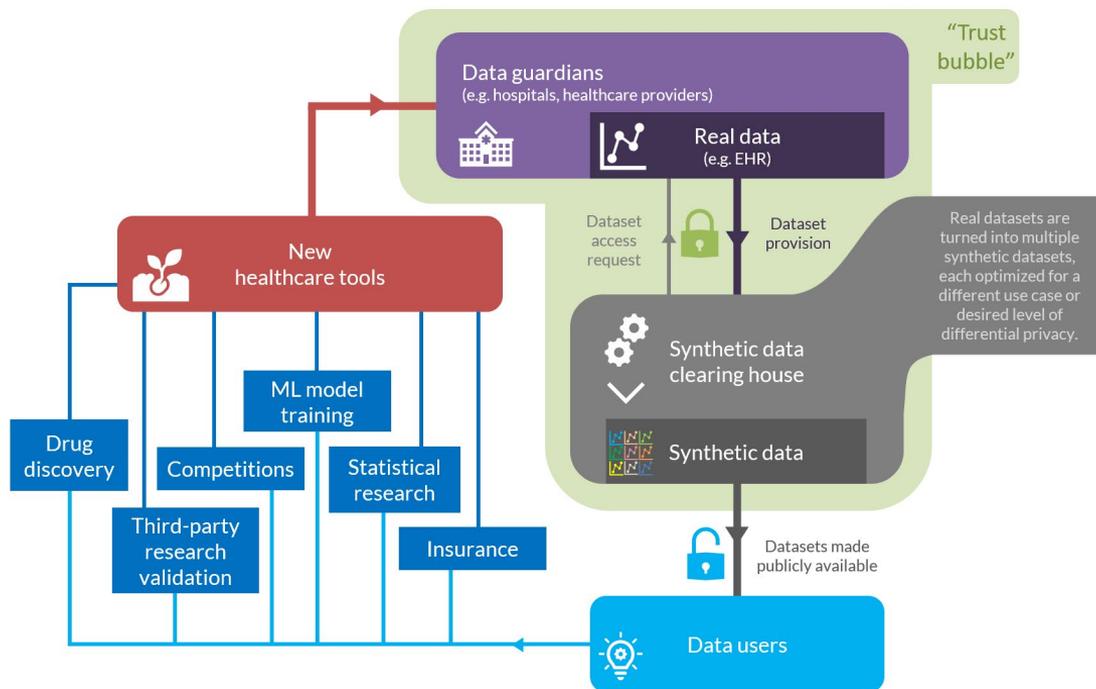


Generating synthetic data to be used for  
**machine learning** modeling  
is itself a **machine learning** problem!

- **Two key questions:**

- How to build a machine learning model to generate synthetic data?
- How to evaluate the quality of a synthetic dataset?

# A clearinghouse for healthcare data resources

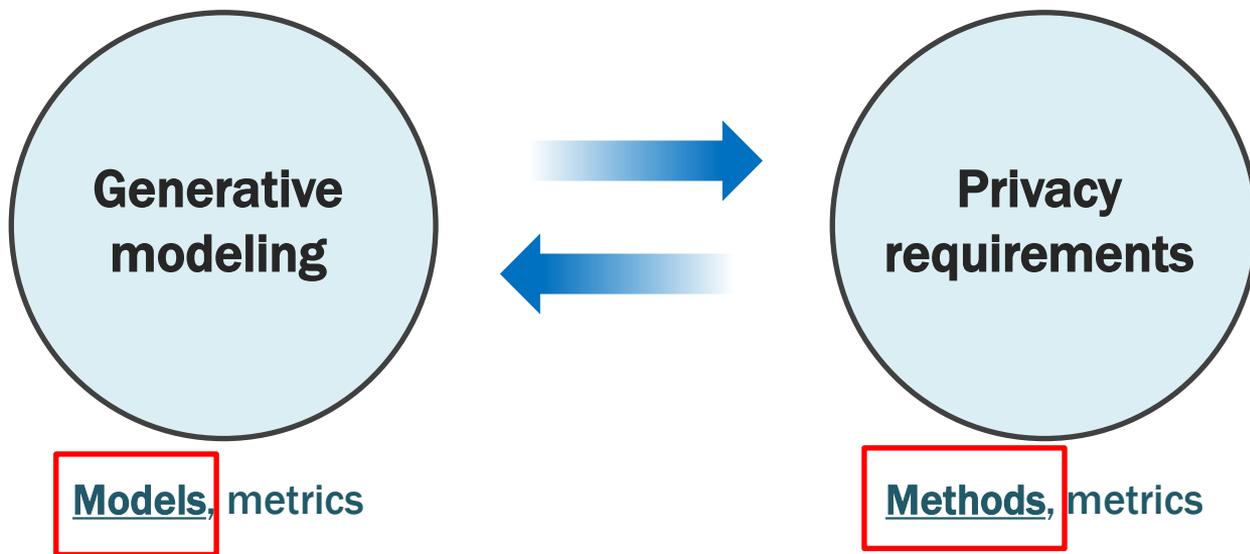


[www.vanderschaar-lab.com/synthetic-data-breaking-the-data-logjam-in-machine-learning-for-healthcare/](http://www.vanderschaar-lab.com/synthetic-data-breaking-the-data-logjam-in-machine-learning-for-healthcare/)

**Synthetic generation of healthcare data:  
A brief technical background**

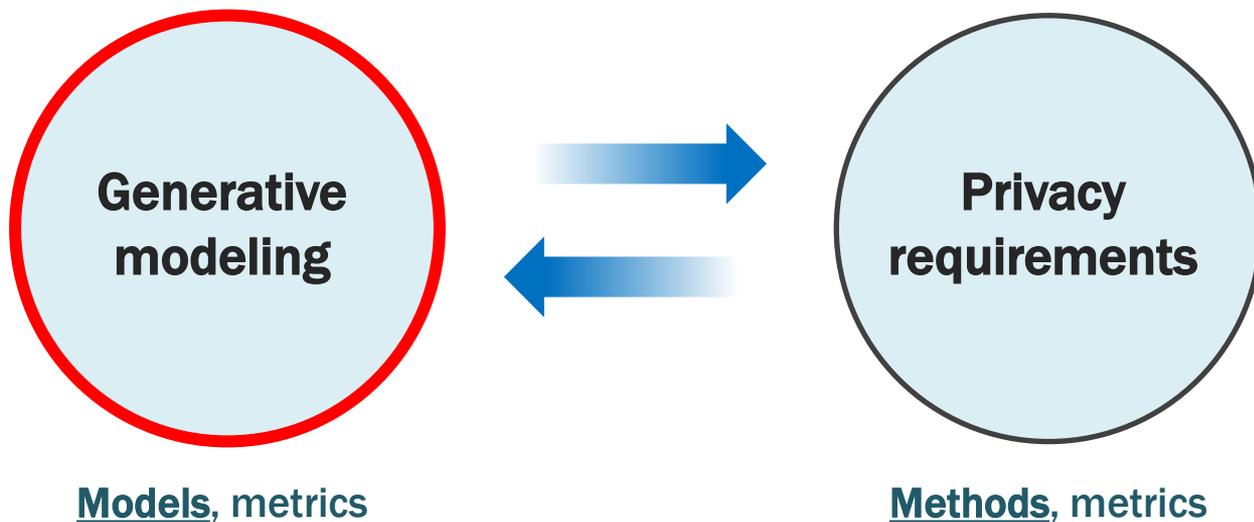
# Desiderata for synthetic data generation

- We want synthetic data to enable learning statistical patterns without compromising the privacy of individual patients in the dataset



# Desiderata for synthetic data generation

- We want synthetic data to enable learning statistical patterns without compromising the privacy of individual patients in the dataset



# Generative modeling

A model that simulates data

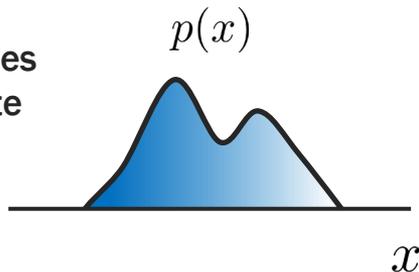
Estimates a (high-dimensional) probability density

Unsupervised

● Generative modeling

Sample feature instances from a density estimate

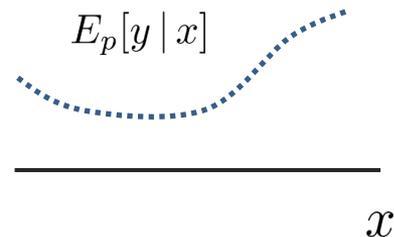
$$x \sim \hat{p}(x)$$



● Discriminative modeling

Given a feature, predict a target output

$$\hat{y} = E_{\hat{p}}[y | x]$$



# Generative modeling for clinical data

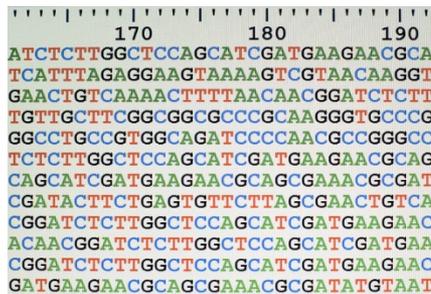
- What makes generation of synthetic **clinical** data different?

- Complex and diverse data structures
- Domain knowledge

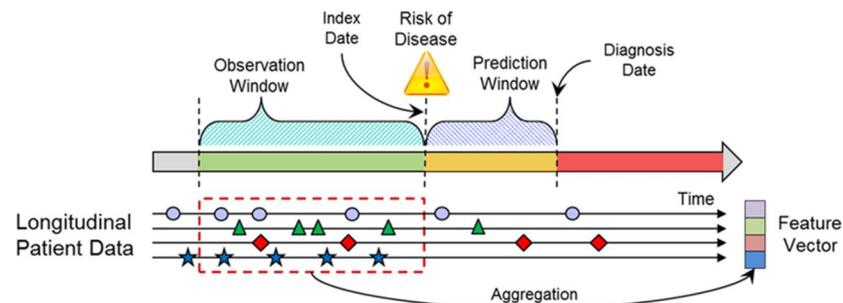
## Clinical variables

Parameter	PRF	Non-PRF
	Patients (n)	Patients (n)
Age (yrs) ranges		
14-20 years	54	62
21-25 years	23	24
26-30 years	5	8
31-35 years	9	2
35-40 years	4	2
40+ years	5	2
Females	54	41
Males	46	59
Oral contraceptive steroid users	11	8
Smokers/oral tobacco users	5	5
Diabetes (insulin dependent)	1	1
Estrogen therapy (HRT)	1	0
Patients receiving additional narcotic Rx's	15	18
Patients receiving additional steroid Rx's	17	11
PreOperative lower Third-Molar Eval.		
History of pericoronitis	3	5
Fully erupted molar	36	16
Soft tissue impacted molar	6	5
Partially bony impacted molar	84	98
Completely bony impacted molar	71	76

## Genetic data



## Electronic health record data



# The generative modeling problem

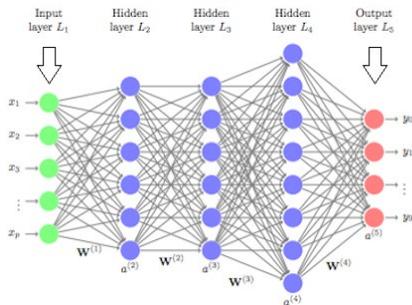
- We have a data set of real patient data:  $\{X_1, \dots, X_N\}$
- A generative model is effectively an estimate  $\hat{P}(X)$  of the real distribution  $P(X)$
- A synthetic data is a sample from the generative model:  $\hat{X} \sim \hat{P}(X)$
- We want the generative model to be:
  - able to handle high-dimensional data
  - easy to train
  - easy to sample from

# Two modeling approaches

## Deep learning

- Rich non-linear models
- Scalable learning, end-to-end training
- Data-driven

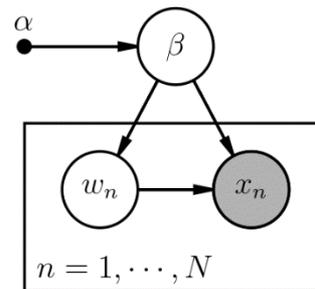
Used for learning complex function with the goal of making predictions



## Probabilistic models

- Simpler, often linear models
- Principled inference, but intractable
- Encodes prior assumptions

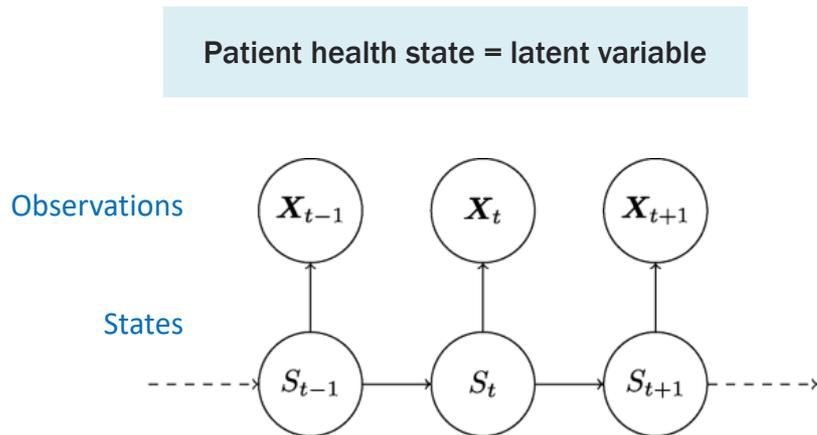
Used for modeling data distributions



# Probabilistic modeling

- Use our intuition about the data to factorize the joint distribution of all variables
- Learn the model using maximum likelihood estimation
- **Example:** Hidden Markov models
  - **Data type:** time-series, sequential
  - **Intuition:** each new observation only depends on the previous observation
  - Data distribution factorizes to:

$$P(X_1, \dots, X_T) = \prod_{t=1}^T P(X_t | S_t) \cdot P(S_t | S_{t-1})$$

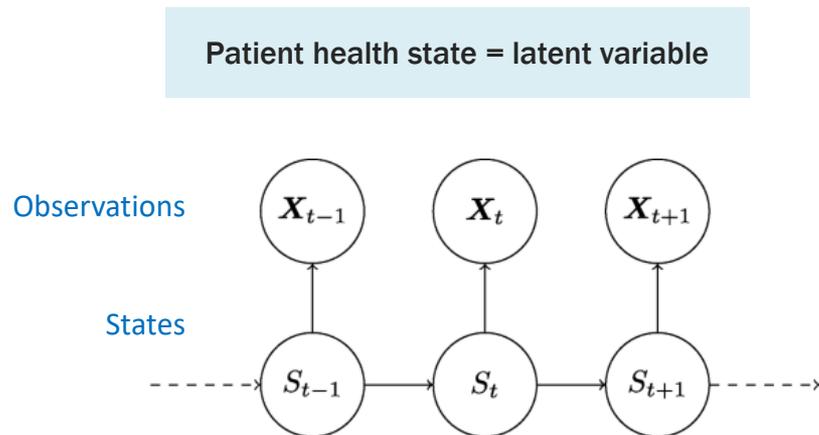


# Probabilistic modeling: Learning

- Analytical derivation of the log-likelihood = depends on the model
- HMMs: no tractable algorithm for maximum likelihood estimation
- **Expectation-Maximization (Baum-Welch) algorithm (approximate inference)**
- HMMs are generative: we can sample synthetic time-series from them

$$S_t \sim P(S_t | S_{t-1})$$

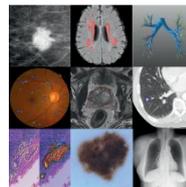
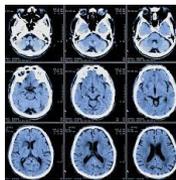
$$X_t \sim P(X_t | S_t)$$



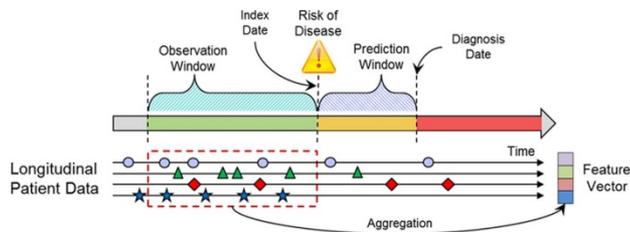
# Why not just use probabilistic models?

- Strong assumption, limited representation complexity, inference routines need to be designed for each modeling scenario...
  - Can we find a fixed factorization of joint pixel distribution for biomedical images?

$$P(X_1, \dots, X_T)$$

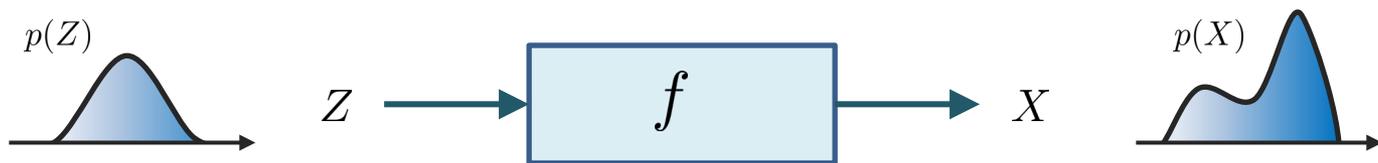


- How can we model unstructured, irregularly sampled EHR data?



# Categorization of modern (deep) generative models

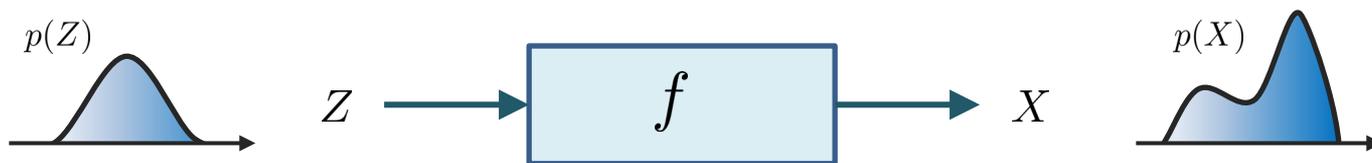
- Data-driven, SGD-based learning, complex representations
- **Key idea:** map a noise variable  $Z$  to a random variable  $X$  through a neural net  $f$



- Different deep generative models specify a different loss function to learn  $f$
- Unlike standard NNs, these are models that we can **sample** data from

# Categorization of modern (deep) generative models

- Data-driven, SGD-based learning, complex representations
- **Key idea:** map a noise variable  $Z$  to a random variable  $X$  through a neural net  $f$



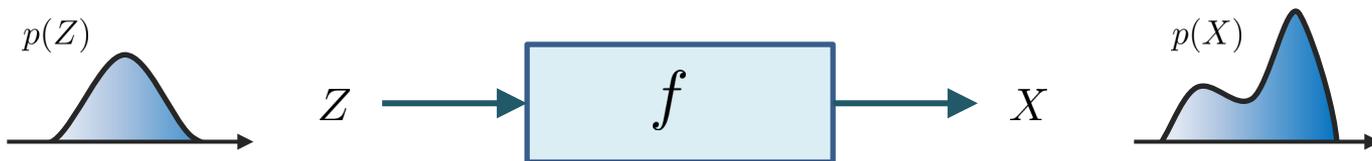
## Implicit-likelihood models

- A model that learns how to sample synthetic data without explicitly defining the likelihood function
- Learns by comparison

## Explicit-likelihood models

- A model that defines the model likelihood and trains via maximum likelihood estimation
- Fits a distribution

# Taxonomy of deep generative models

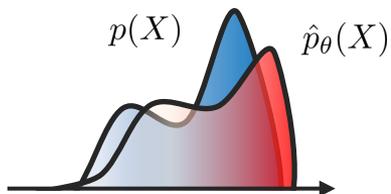


## Generative models

### Explicit-likelihood models

- Maximize likelihood

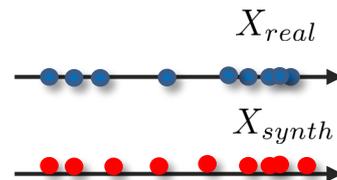
$$\hat{\theta} = \arg \max_{\theta} \log L(X_{real}; \theta)$$



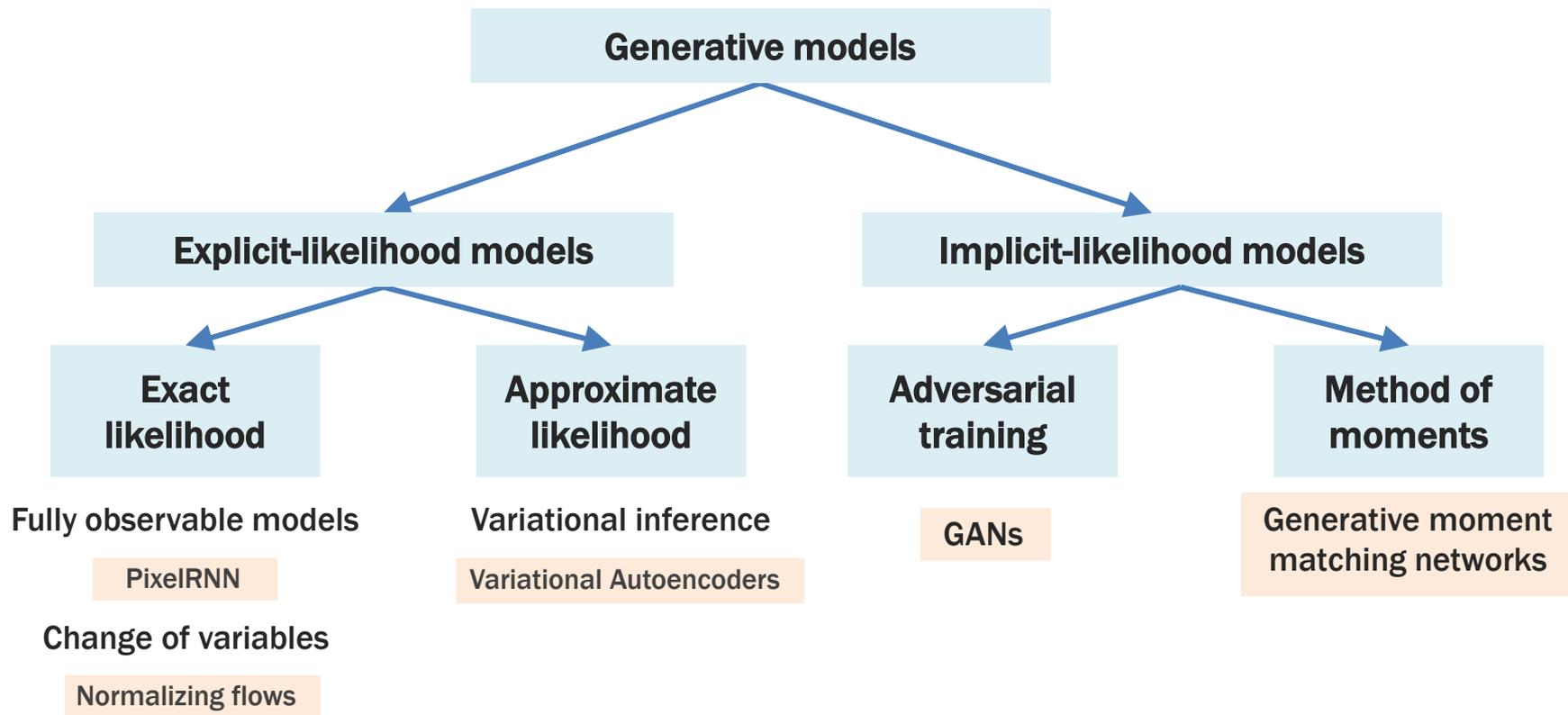
### Implicit-likelihood models

- Two-sample tests, sample comparison

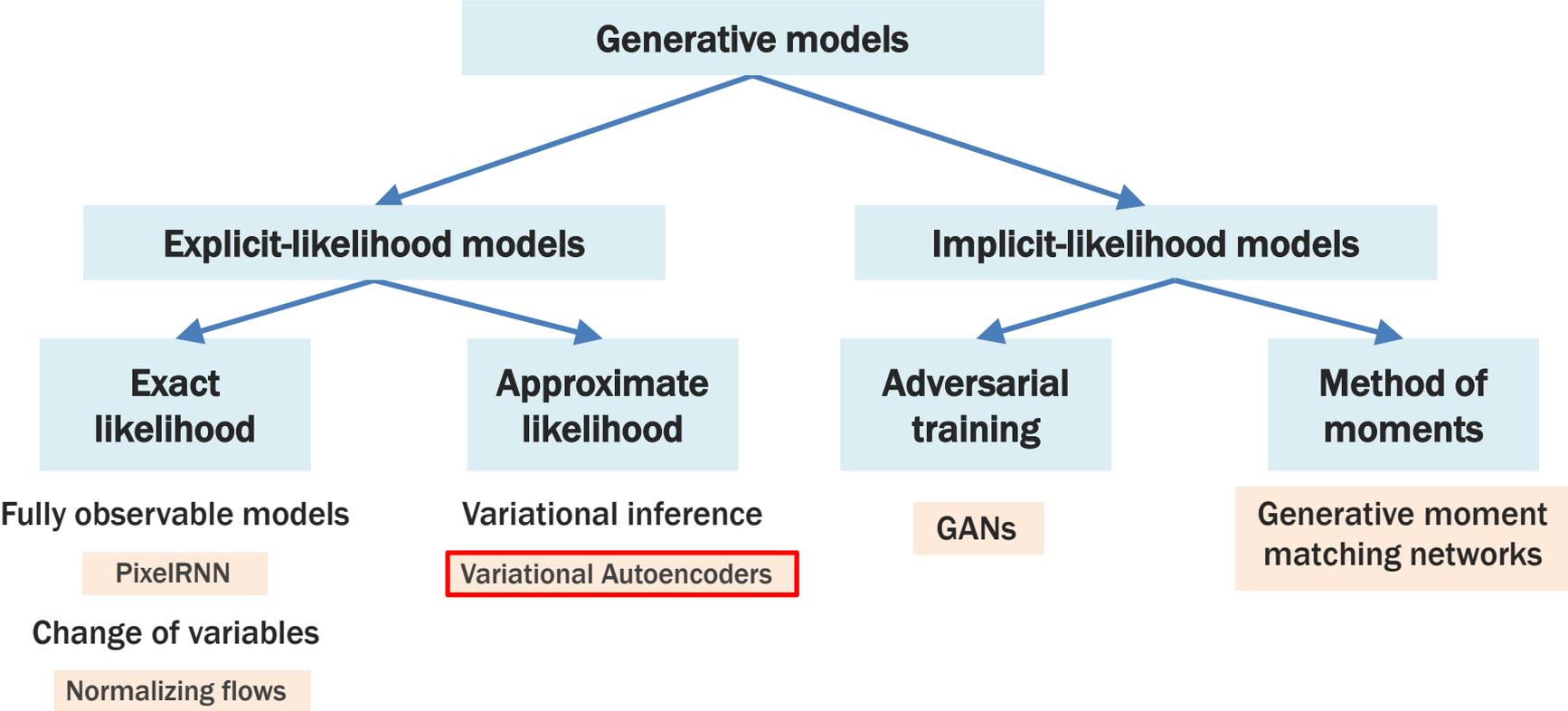
$$L(X_{real}, X_{synth})$$



# Taxonomy of deep generative models



# Taxonomy of deep generative models

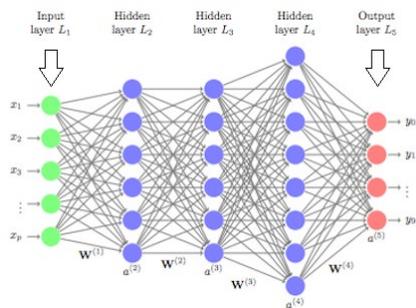


# Explicit density models (I): Variational Autoencoders (VAEs)

- **VAEs:** probabilistic spinoff of Autoencoders, a latent variable model

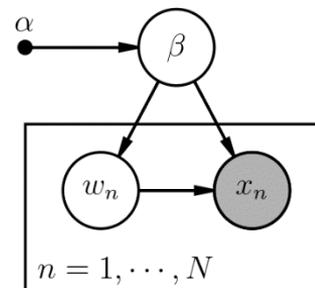
**Autoencoder**

**Deep learning**



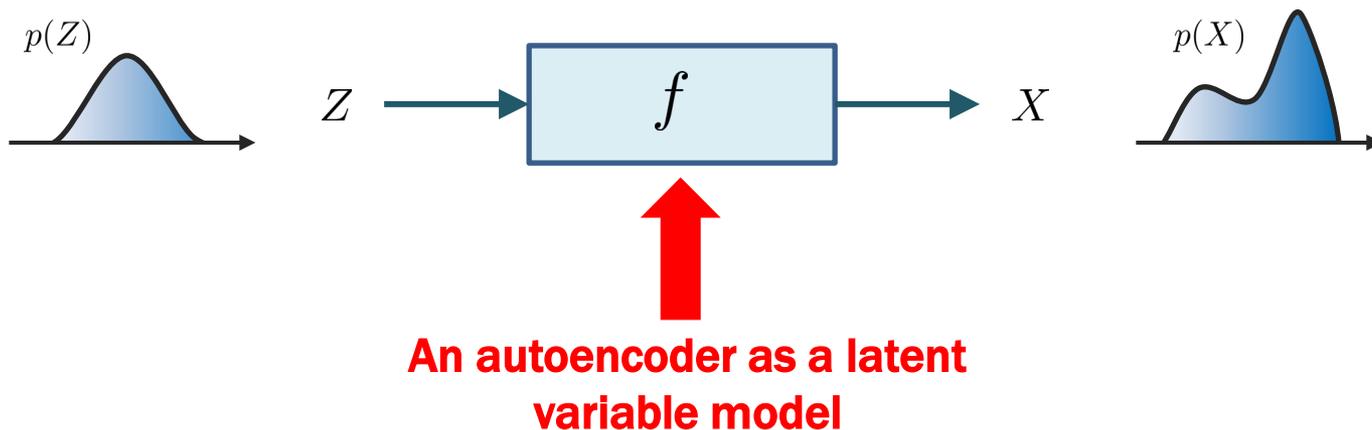
**Variational inference**

**Probabilistic models**



# Explicit density models (I): Variational Autoencoders (VAEs)

- **VAEs:** probabilistic spinoff of Autoencoders, a latent variable model

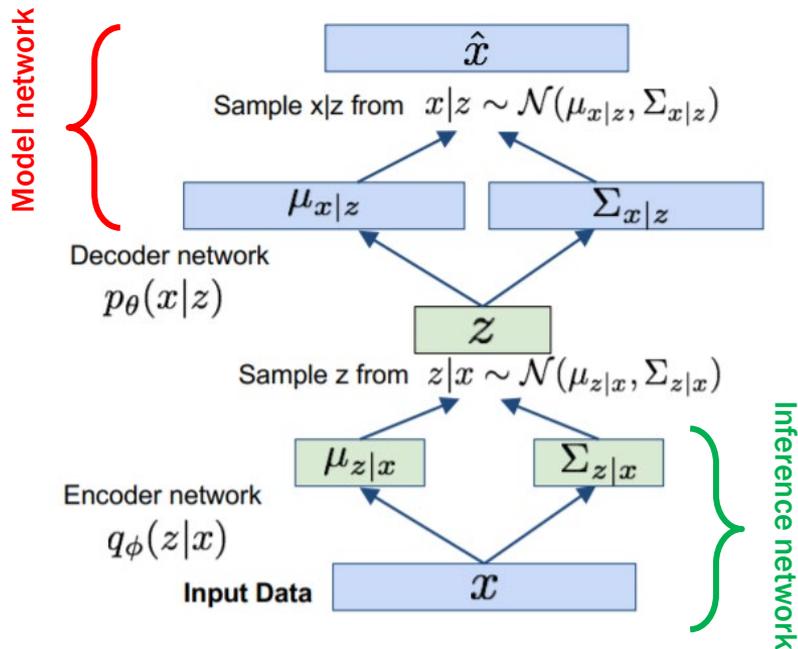


# Variational Autoencoders

- Latent variable model  $\rightarrow$  marginalizing over latent variables  $\rightarrow$  likelihood is intractable
- Optimize Evidence lower bound (ELBO) on model likelihood:

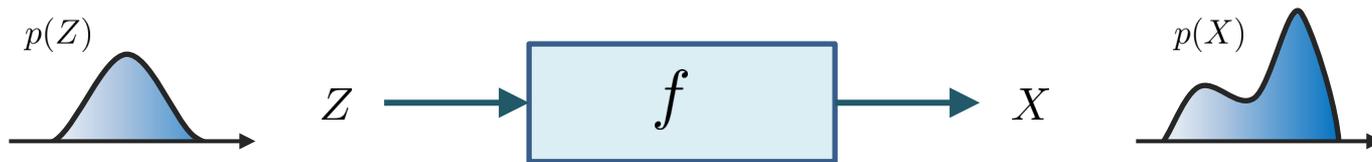
$$\underbrace{\mathbb{E}_z \left[ \log p_\theta(x^{(i)} | z) \right]}_{\text{Model network}} - \underbrace{D_{KL}(q_\phi(z | x^{(i)}) || p_\theta(z))}_{\text{Inference network}}$$

$$\mathcal{L}(x^{(i)}, \theta, \phi)$$

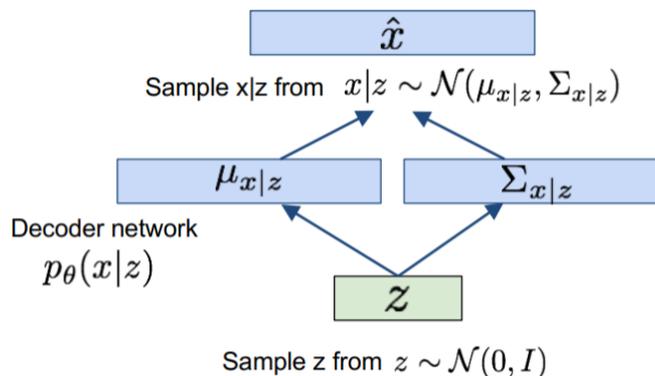


# Sampling from VAEs

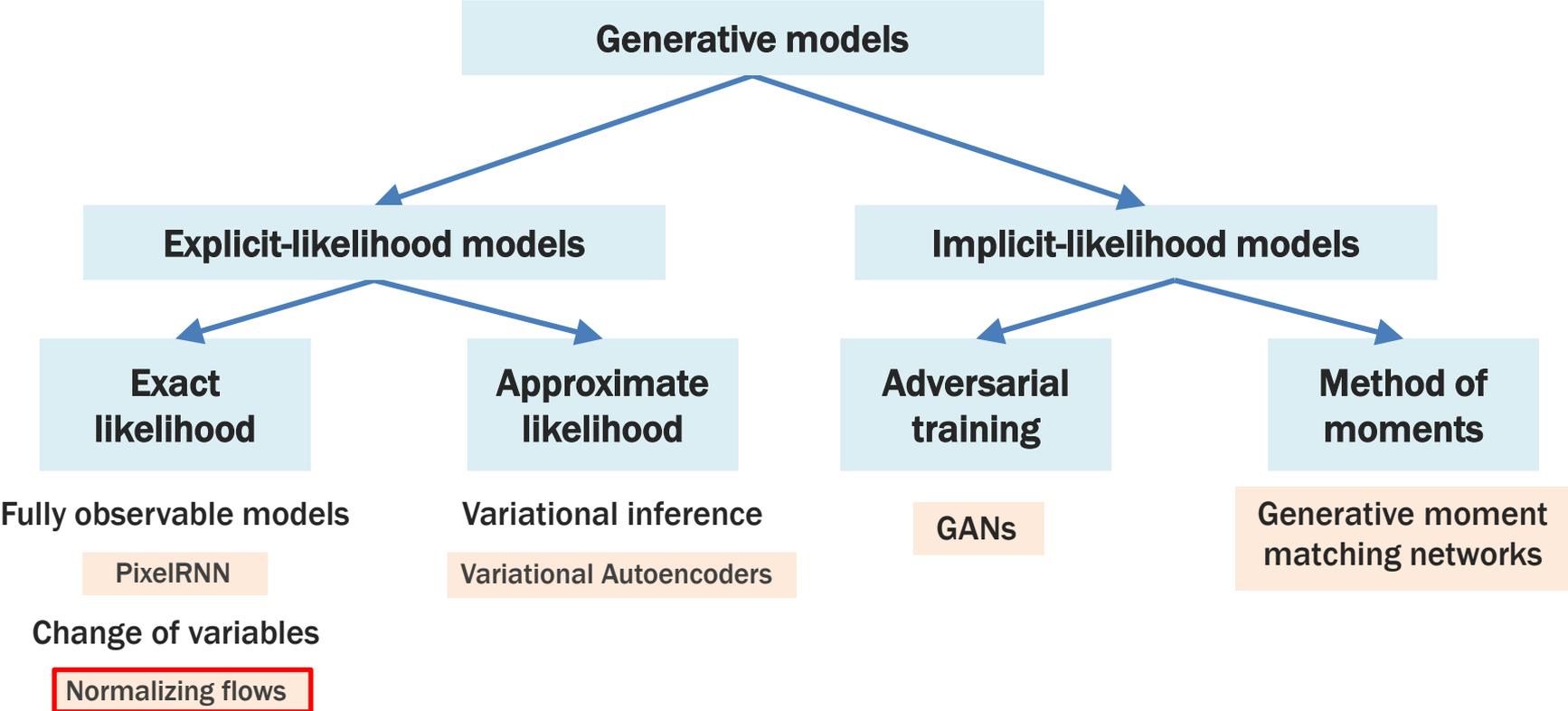
- **Recall key idea:** map a noise variable  $Z$  to a random variable  $X$  through  $f$



- Use decoder network and sample from prior...

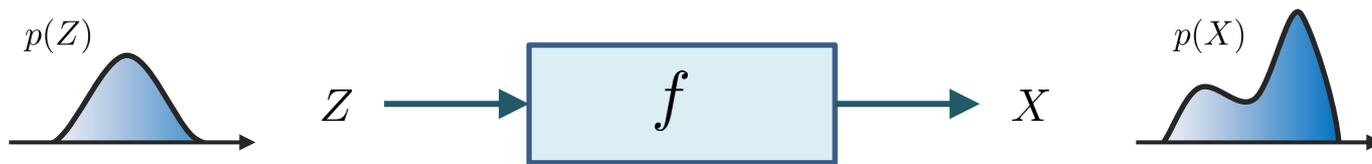


# Taxonomy of deep generative models



## Explicit density models (II): Normalizing flows

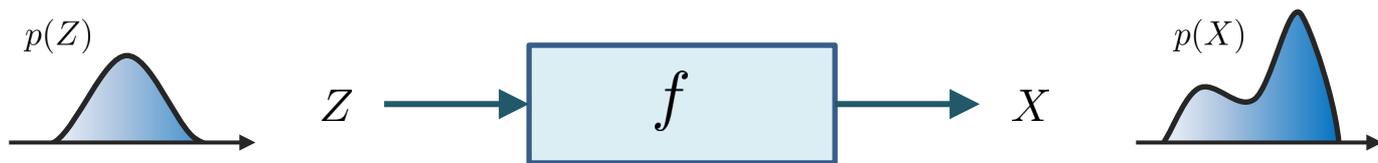
- **Recall key idea:** map a noise variable  $Z$  to a random variable  $X$  through  $f$



**Use an invertible transform +  
change of variables formula**

# Normalizing Flows

- Change of variables formula:



- Distribution of transformed variable:  $p_X(x) = p_Z(f^{-1}(x)) \left| \det \left( \frac{\partial f^{-1}(x)}{\partial x} \right) \right|$

- For high-dimensional random variables:  $p_X(x) = p_Z(f^{-1}(x)) \underbrace{|\det \mathbf{J}[f]|}$

Jacobian matrix

# Normalizing Flows

- For high-dimensional random variables:  $p_X(x) = p_Z(f^{-1}(x)) |\det \mathbf{J}[f]|$

- Flow composition:  $f^{(1)} \circ f^{(2)} \circ \dots \circ f^{(M)}$

- Need to constrain the transformation so that:

- The Jacobean determinant is easy to compute

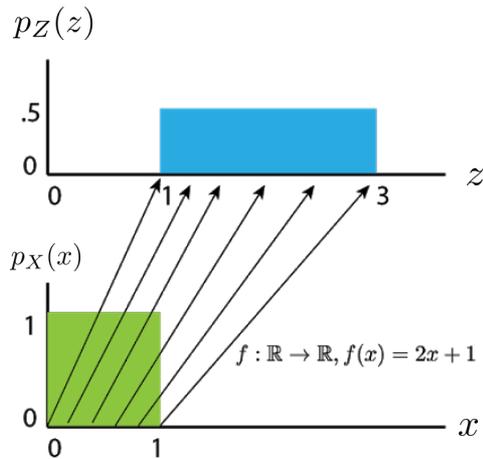
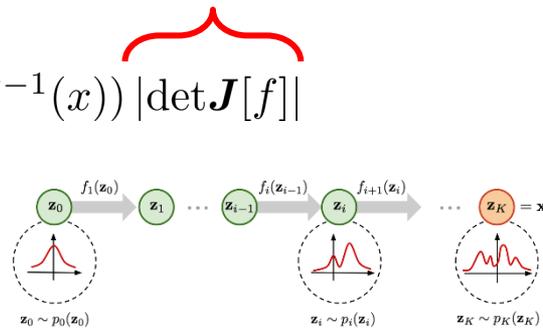
Needed for efficient training

- The forward and inverse map are easy to compute

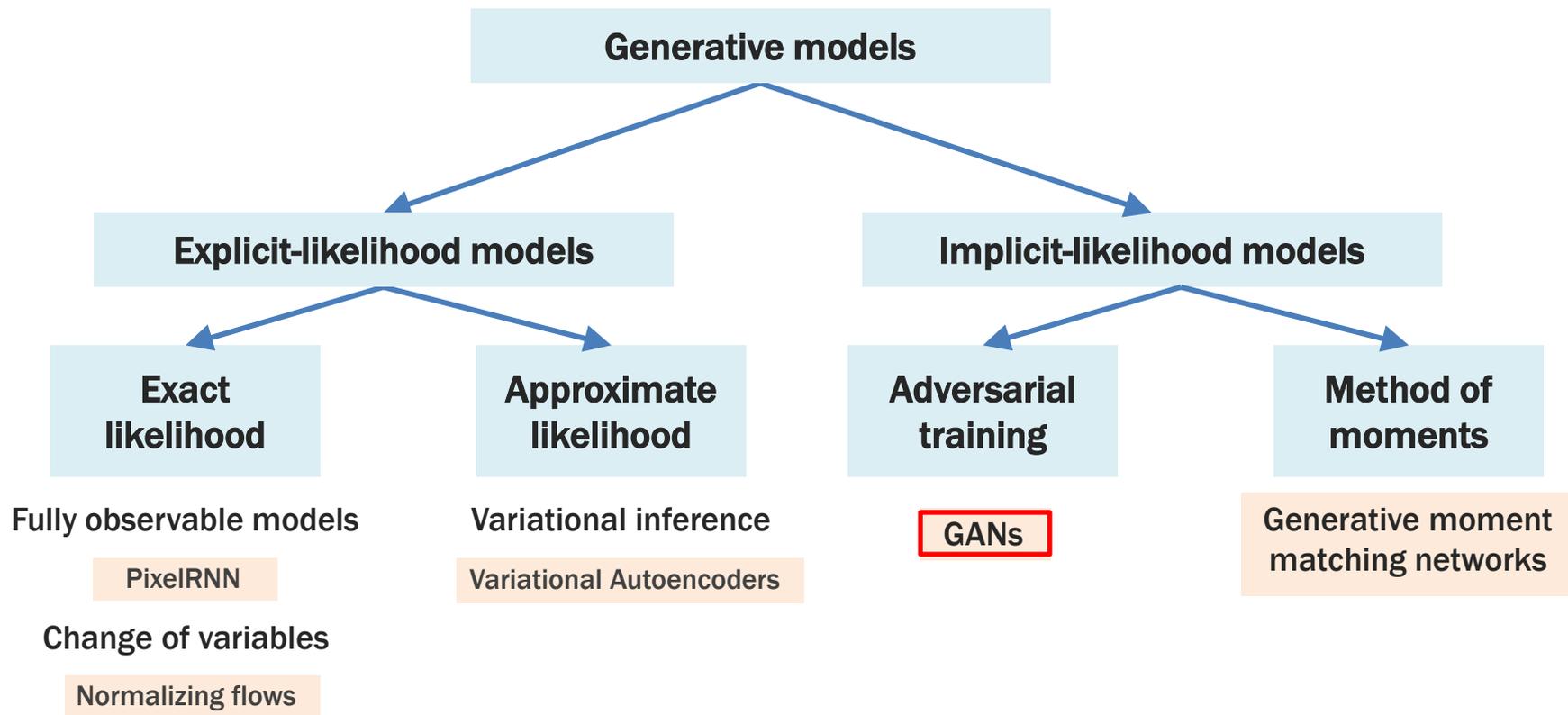
Needed for efficient sampling

**Key advantage:** Exact likelihood for training and evaluation!

Jacobian matrix

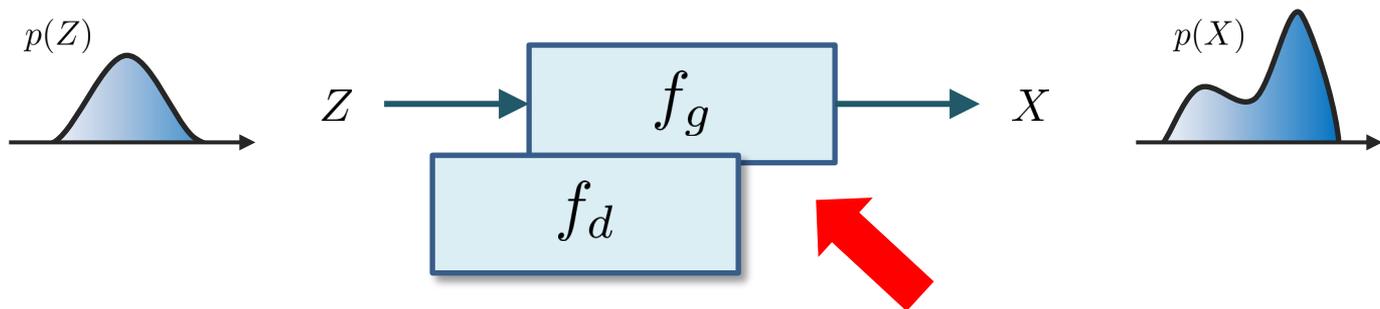


# Taxonomy of deep generative models



# Implicit density models: Generative Adversarial Nets

- **Recall key idea:** map a noise variable  $Z$  to a random variable  $X$  through  $f$



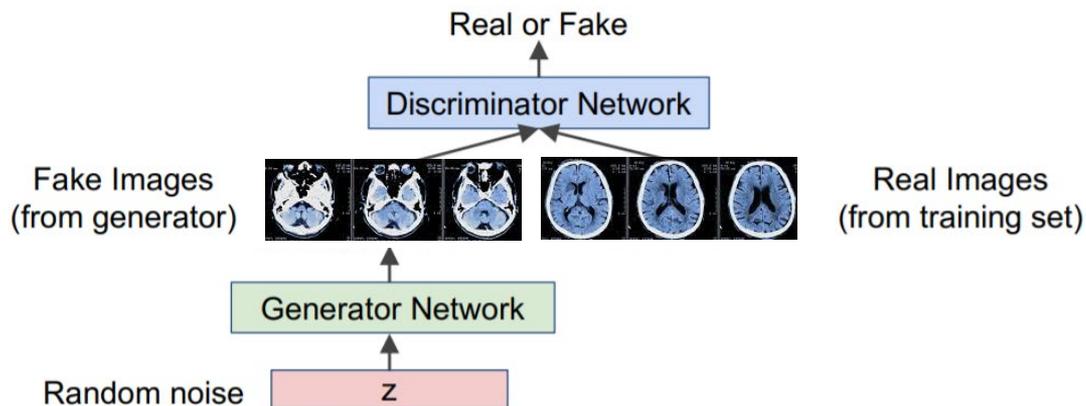
**One player in a 2-player  
minimax game**

- The transformation is optimized with the aid of a second player (discriminator network).

# Generative Adversarial Nets

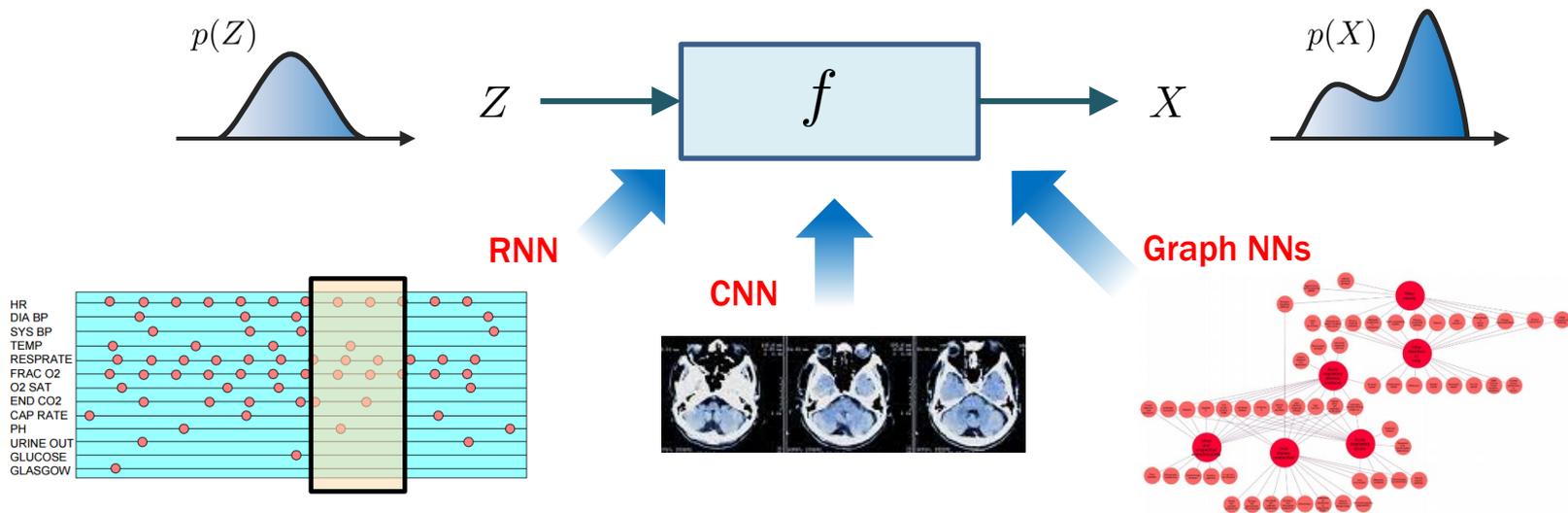
- Minimax loss function

$$\min_{\theta_g} \max_{\theta_d} \left[ \mathbb{E}_{x \sim p_{data}} \log D_{\theta_d}(x) + \mathbb{E}_{z \sim p(z)} \log(1 - D_{\theta_d}(G_{\theta_g}(z))) \right]$$



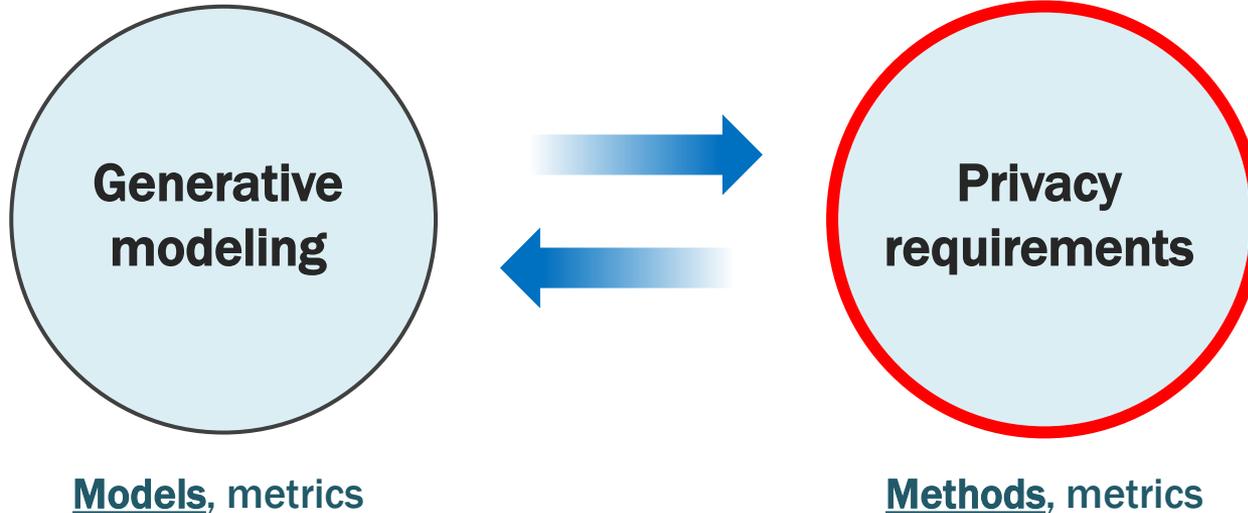
# Adapting deep generative models to your healthcare data

- In most cases, an off-the-shelf generative model will **not** be sufficient
- We need to make **design choices**...



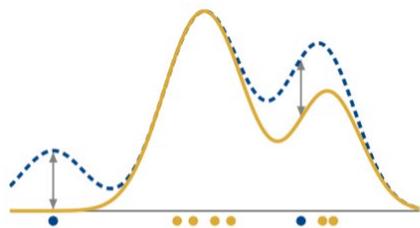
# Desiderata for synthetic data generation

- We want synthetic data to enable learning statistical patterns without compromising the privacy of individual patients in the dataset

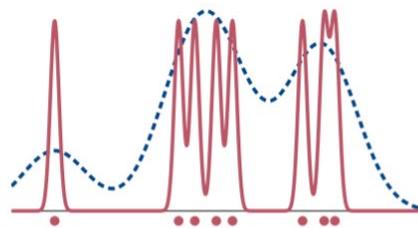


# Memorization and overfitting in generative models

- Synthetic data violates privacy if it copies real data
- Data copying happens when the generative model **memorizes** training data
- Is memorization the same thing as overfitting?



(a) Memorization



(b) Overfitting

# Statistical inference and privacy

- More generally: we want synthetic data to enable learning statistical patterns without compromising the privacy of individual members of the dataset
  - Common mistake: conflating inference with privacy violation



# Statistical inference is not a privacy violation

- We want synthetic data to enable learning statistical patterns without compromising the privacy of individual members of the dataset
  - Privacy in data sharing is a difficult concept to formalize...

Analysis on real data



Smoker → Cancer

Analysis on synthetic data



Mr. X is a Smoker → Mr. X has an elevated risk of cancer

# Differential privacy

## ● Definition

- A randomized mechanism  $\mathcal{M} : \mathcal{X} \rightarrow \mathcal{Y}$  is  $\epsilon$ -differentially private if for all neighbouring inputs and for all sets of outputs  $E \subseteq \mathcal{Y}$  we have

$$\mathbb{P}(\mathcal{M}(x) \in E) \leq e^\epsilon \mathbb{P}(\mathcal{M}(x') \in E)$$

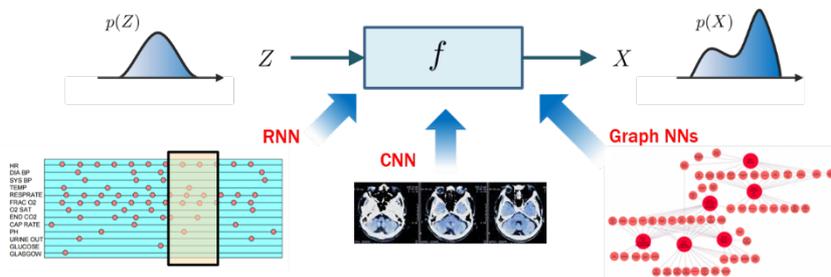
- **Intuition:** the result of an analysis conducted using a data set would not change if any individual (synthetic) patient data point was removed from the data set.

# Incorporating differential privacy into generative models

- Differential privacy is incorporated by adding noise
- Three different approaches:
  - Add noise to the model output
  - Add noise to the model parameters
  - Add noise to the model gradients during training

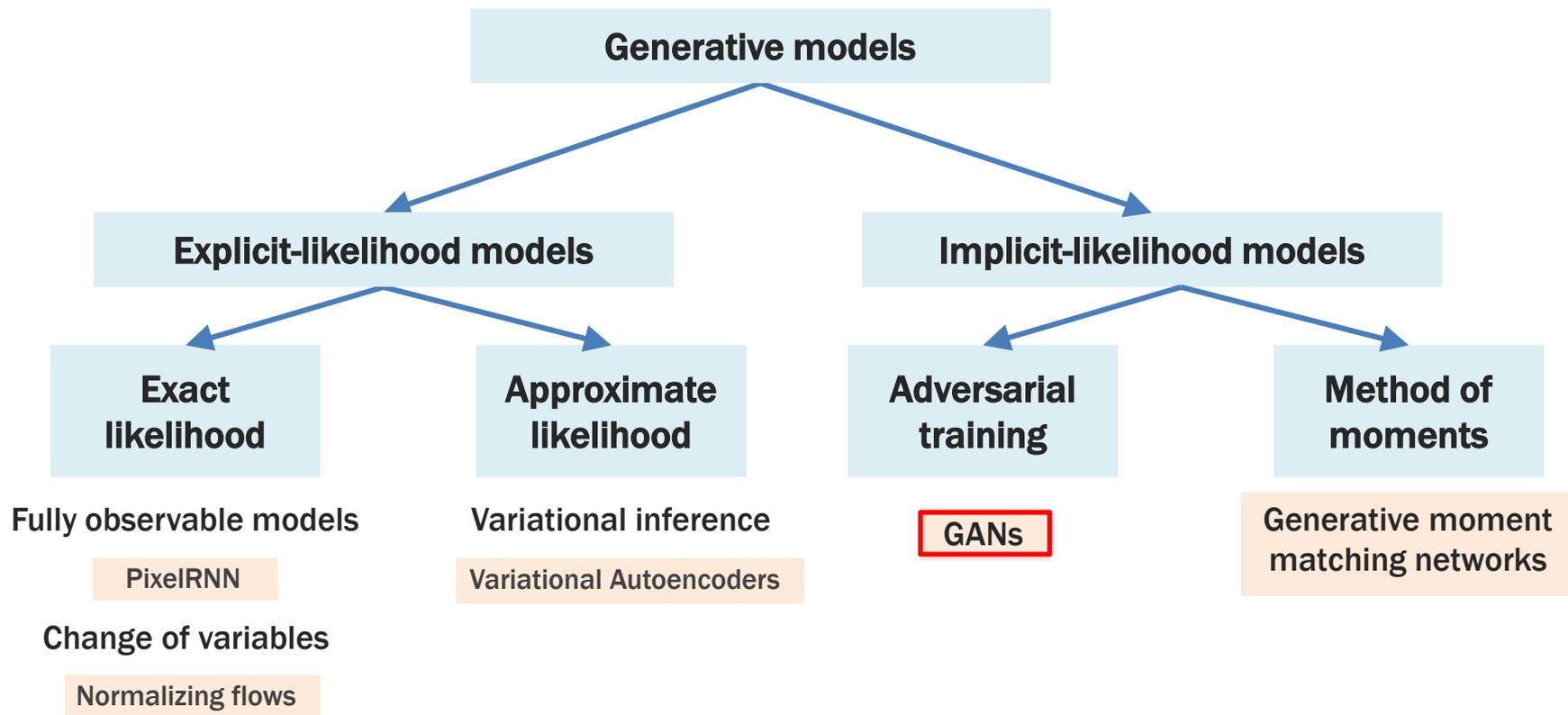
# Recipe for generating synthetic healthcare data

- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, normalizing flows, GANs, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., NNs, RNN, CNN, transfer representations etc.
- **Step 3: Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy**



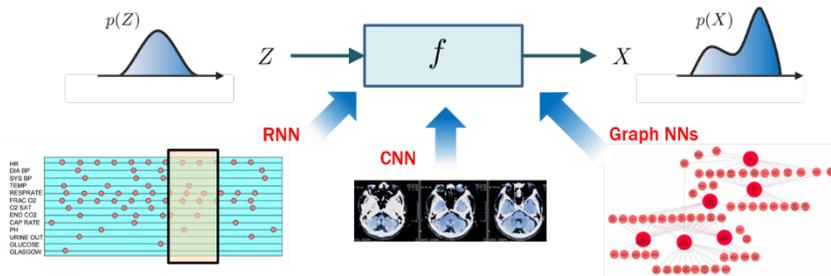
# **Generative models for synthetic tabular data**

# Taxonomy of deep generative models: Focus on GANs



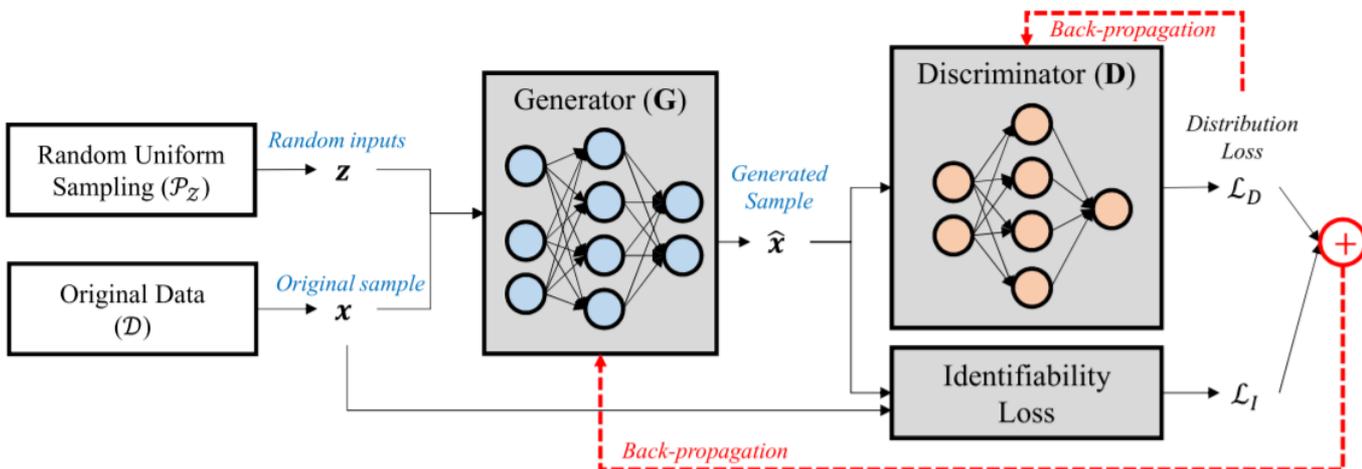
# Recipe for generating synthetic healthcare data

- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, normalizing flows, **GANs**, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., **NNs**, RNN, CNN, transfer representations etc.
- **Step 3: Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy**



# ADS-GAN: Synthetic data fulfilling GDPR privacy requirements

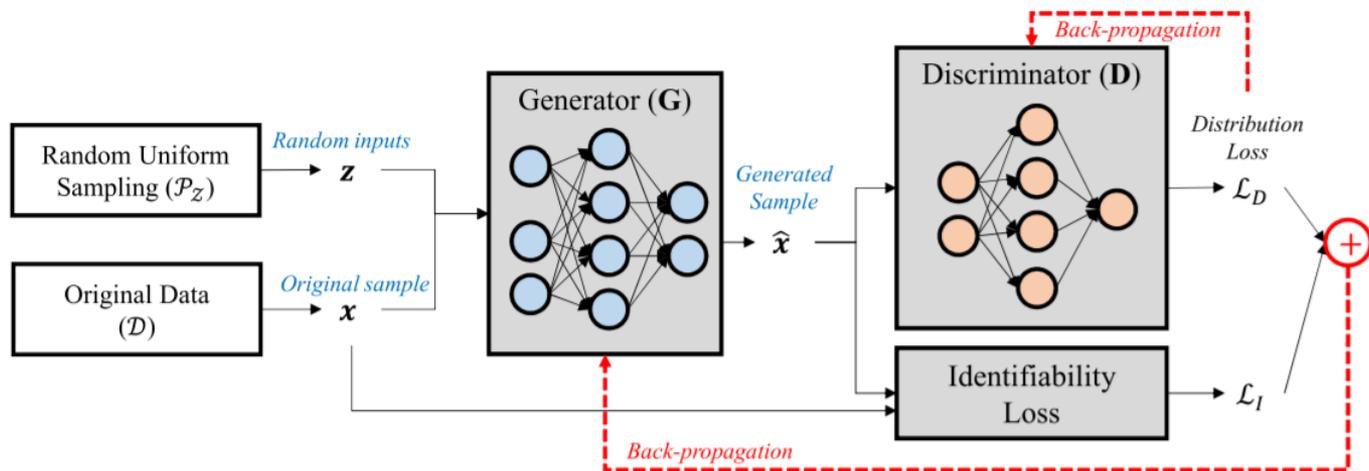
- Generating GDPR-compliant **anonymized** clinical data using **GANs**.
- Can be applied to any clinical datasets with tabular data (e.g. transplantation)



# ADS-GAN: Synthetic data fulfilling GDPR privacy requirements

## ● Privacy

- GDPR requirements are not formally/well-defined – descriptive, not formal
- Formally defining requirements – introduce **Identifiability Metric**



# ADS-GAN: Synthetic data fulfilling GDPR privacy requirements

## ● Privacy

- GDPR requirements are not formally/well-defined – descriptive, not formal
- Formally defining requirements – introduce **Identifiability Metric**

$\hat{\mathcal{D}}$  is  $\epsilon$ -identifiable from  $\mathcal{D}$  if

$$\mathcal{I}(\mathcal{D}, \hat{\mathcal{D}}) = \frac{1}{N} \left[ \mathbb{I}(\hat{r}_i < r_i) \right] < \epsilon$$

where  $\mathbb{I}$  represents the identity function and

$$r_i = \min_{\mathbf{x}_j \in \mathcal{D}/\mathbf{x}_i} \|\mathbf{w} \cdot (\mathbf{x}_i - \mathbf{x}_j)\|$$

$$\hat{r}_i = \min_{\hat{\mathbf{x}}_j \in \hat{\mathcal{D}}} \|\mathbf{w} \cdot (\mathbf{x}_i - \hat{\mathbf{x}}_j)\|$$

# ADS-GAN: Synthetic data fulfilling GDPR privacy requirements

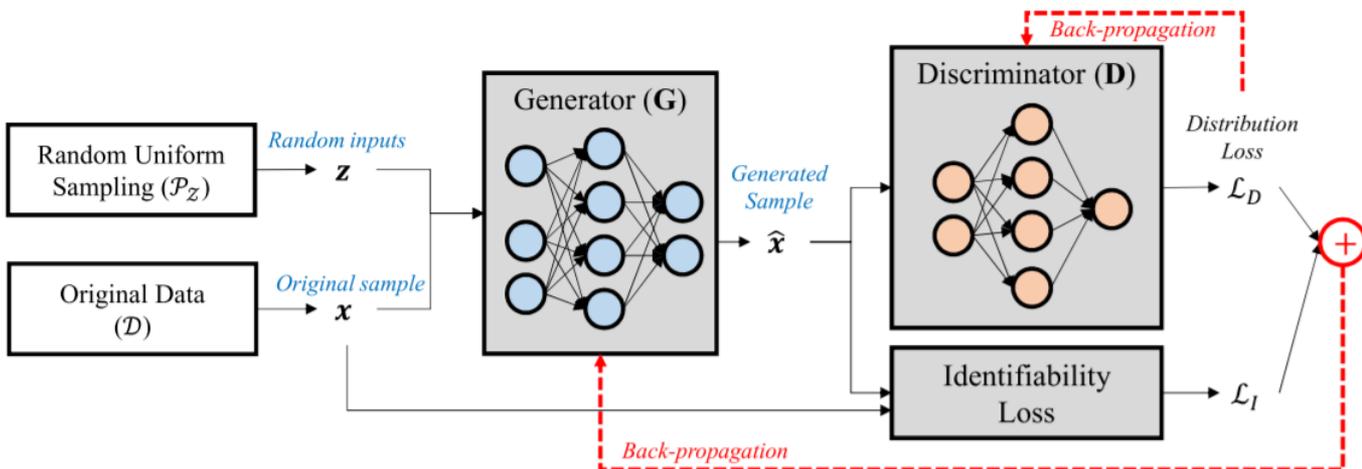
- **Privacy**

- GDPR requirements are not formally/well-defined – descriptive, not formal
- Formally defining requirements – introduce **Identifiability Metric**

- **$\epsilon$ -identifiability** = probability - that the distance to the closest synthetic observation is closer (“not different enough”) than the distance from the closest real observation in  $D$  - is less than  $\epsilon$ .
- ADS-GAN allows us to move away from differential privacy and define identifiability based on the probability of re-identification given the combination of all data on any individual patient.

# ADS-GAN: Synthetic data fulfilling GDPR privacy requirements

- **Fidelity:** unlike conditional GANs (pre-determined variable set), ADS-GAN optimizes a conditioning set per patient and generates all components based on these

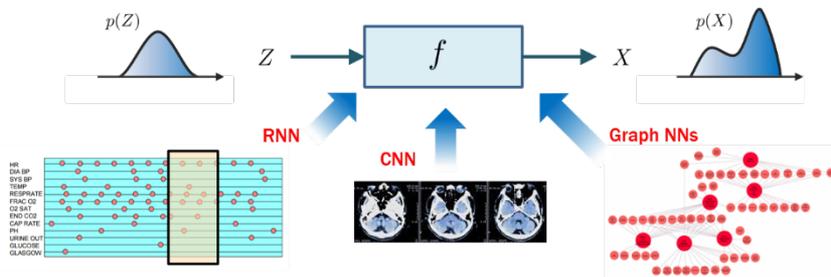


# ADS-GAN: Synthetic data fulfilling GDPR privacy requirements

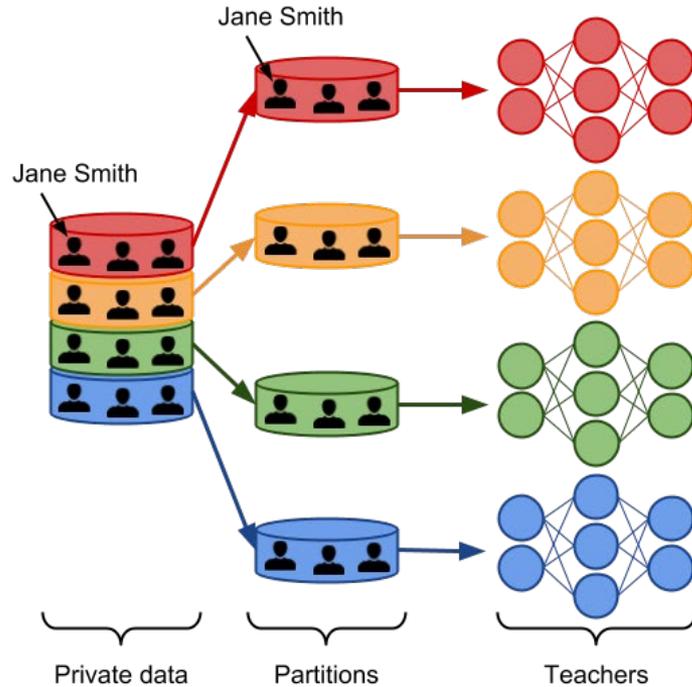
- **Fidelity:** unlike conditional GANs (pre-determined variable set), ADS-GAN optimizes a conditioning set per patient and generates all components based on these
- **Advantages:**
  - Improve quality of synthetic data while ensuring that no feature combination could readily reveal a patient's identity.

# Recipe for generating synthetic healthcare data

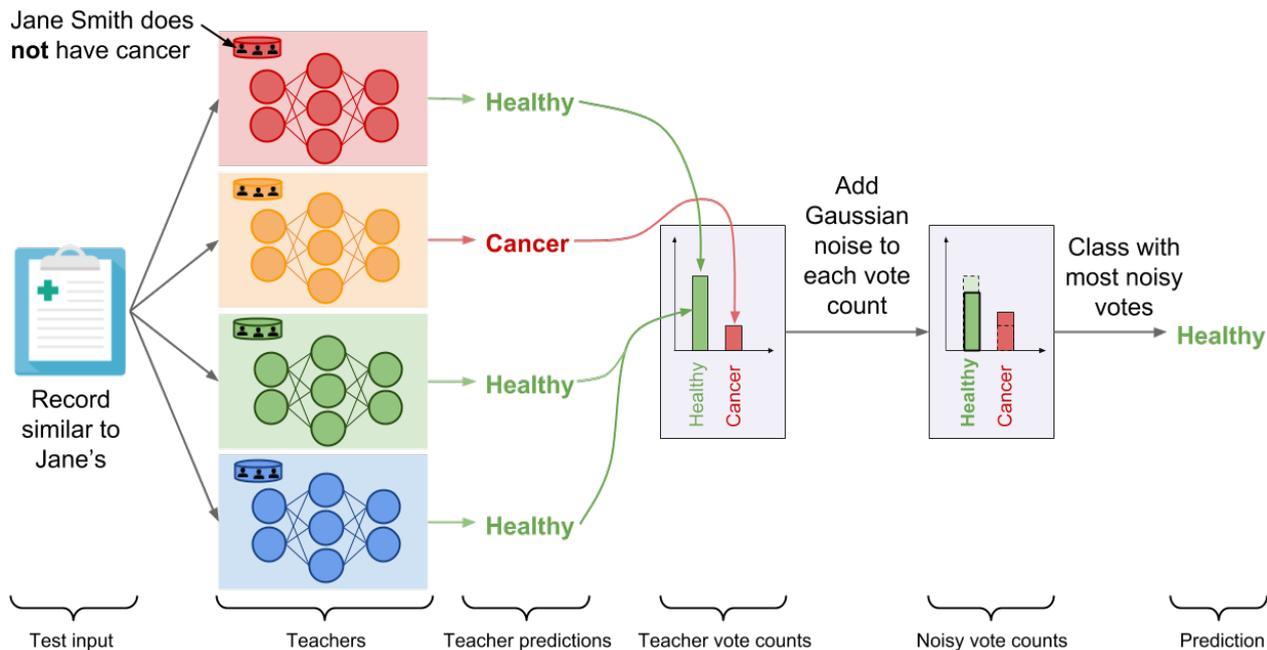
- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, normalizing flows, **GANs**, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., **NNs**, RNN, CNN, transfer representations etc.
- **Step 3: Incorporate **differential privacy** or other privacy notion/ sanitize the data to ensure privacy**



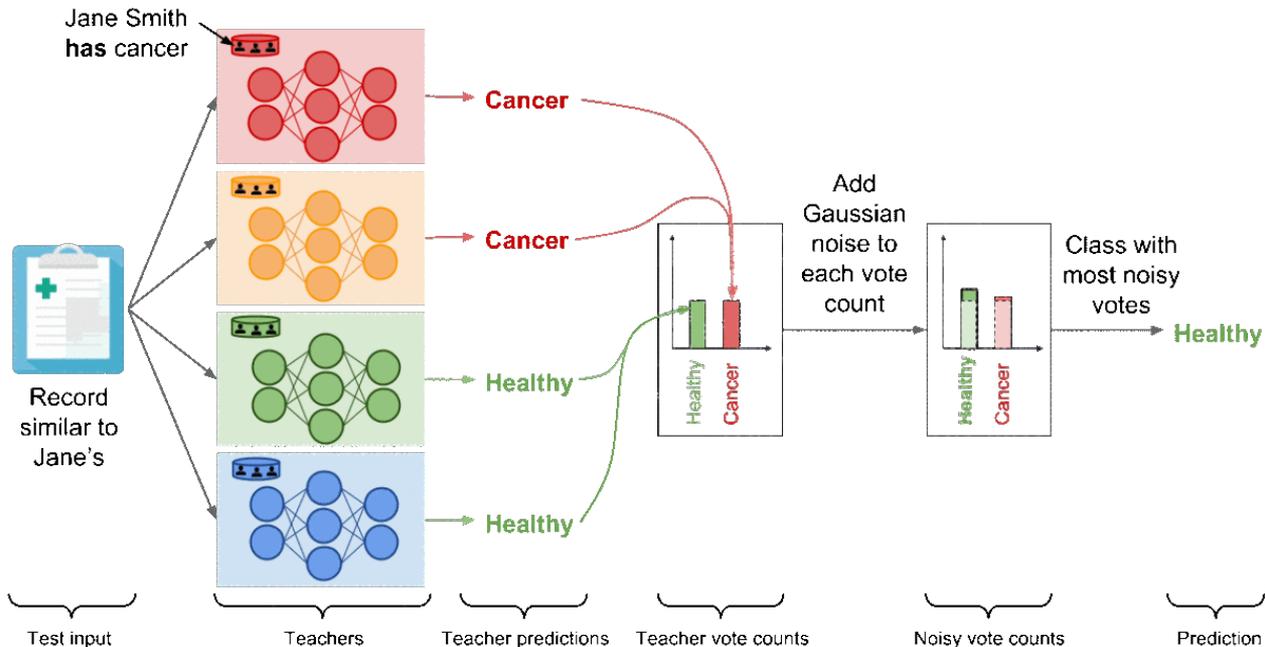
# PATE: Private Aggregations of Teacher Ensembles



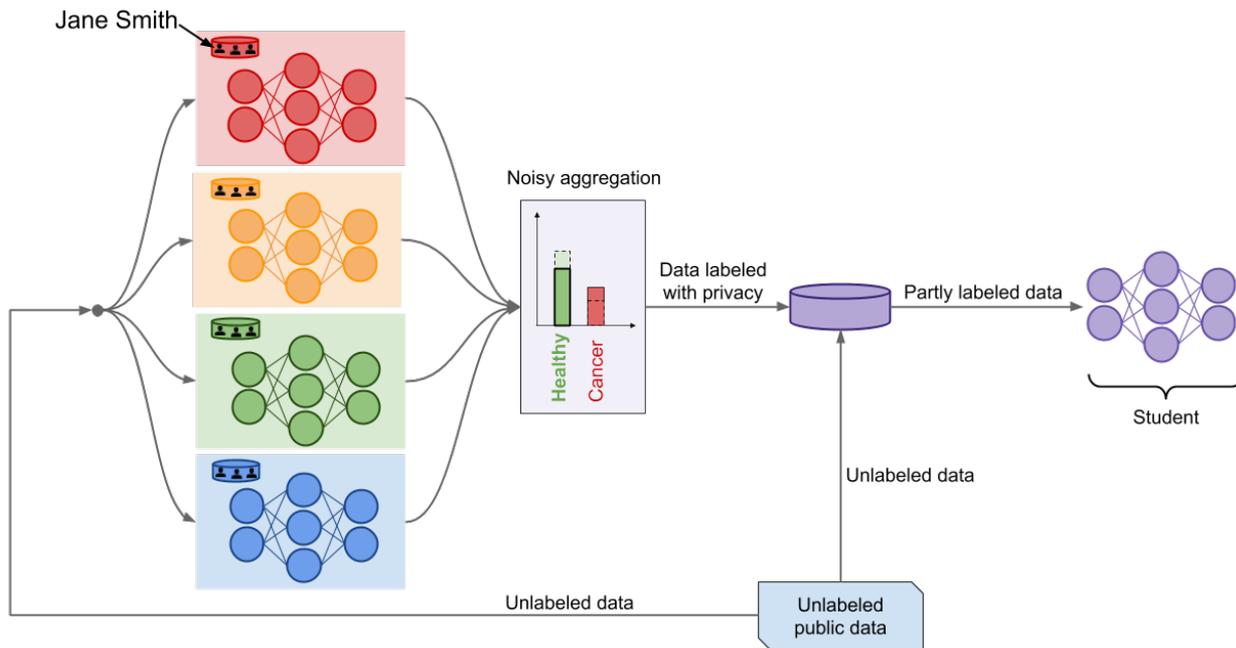
# PATE: Private Aggregations of Teacher Ensembles



# PATE: Private Aggregations of Teacher Ensembles



# PATE: Private Aggregations of Teacher Ensembles



# PATE: Differential Privacy

Formally, given the  $k$  teachers,  $m$  possible classes and an input feature vector,  $\mathbf{x}$ , set

$$n_j(\mathbf{x}) = |\{T_i : T_i(\mathbf{x}) = j\}| \text{ for } j = 1, \dots, m$$

so that  $n_j(\mathbf{x})$  is the number of teachers that output class  $j$  for  $\mathbf{x}$ . The output of the  $\text{PATE}_\lambda$  mechanism for input  $\mathbf{x}$  is then defined as

$$\text{PATE}_\lambda(\mathbf{x}) = \arg \max_{j \in [m]} (n_j(\mathbf{x}) + Y_j)$$

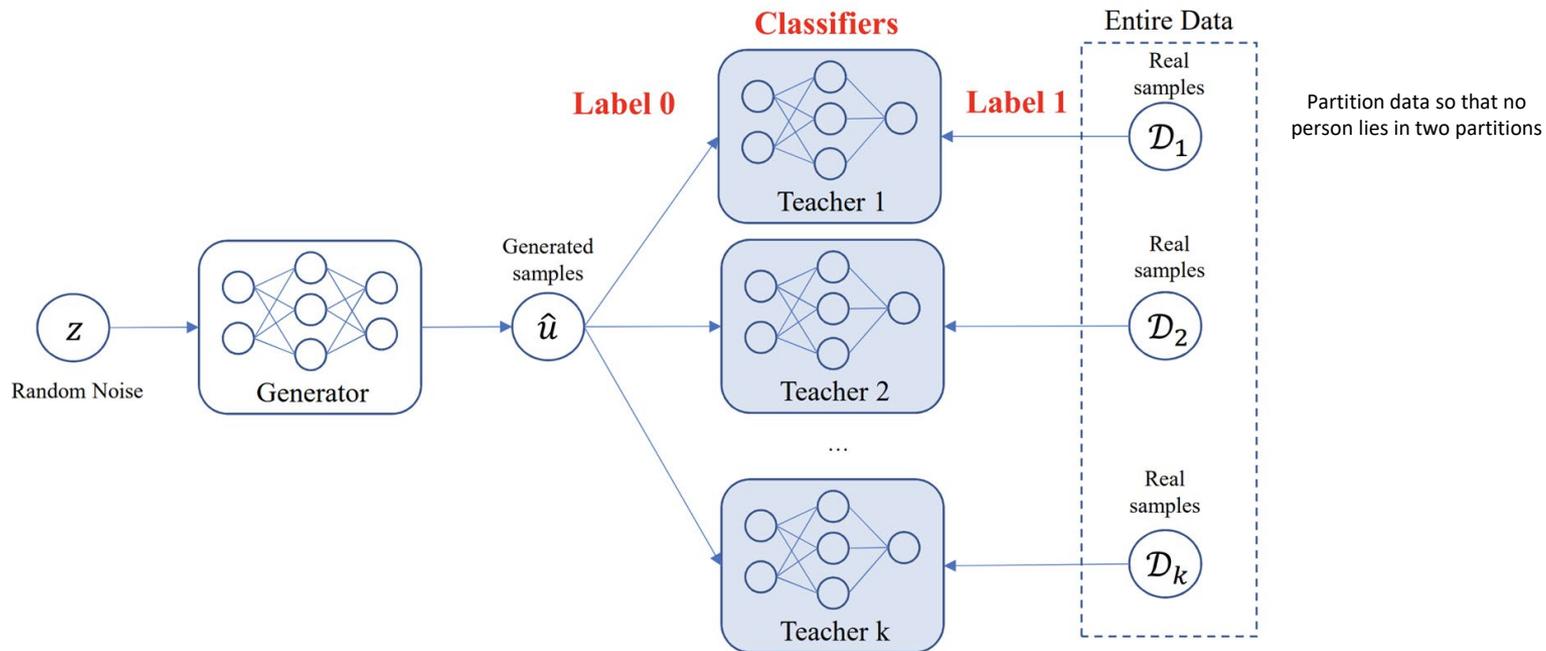
where  $Y_1, \dots, Y_m$  are i.i.d.  $Lap(\lambda)$  random variables. The following result, found in [25], follows from [12].

**Theorem.** *The output of a single query to the  $\text{PATE}_\lambda$  mechanism is  $(\frac{1}{\lambda}, 0)$ -differentially private.*

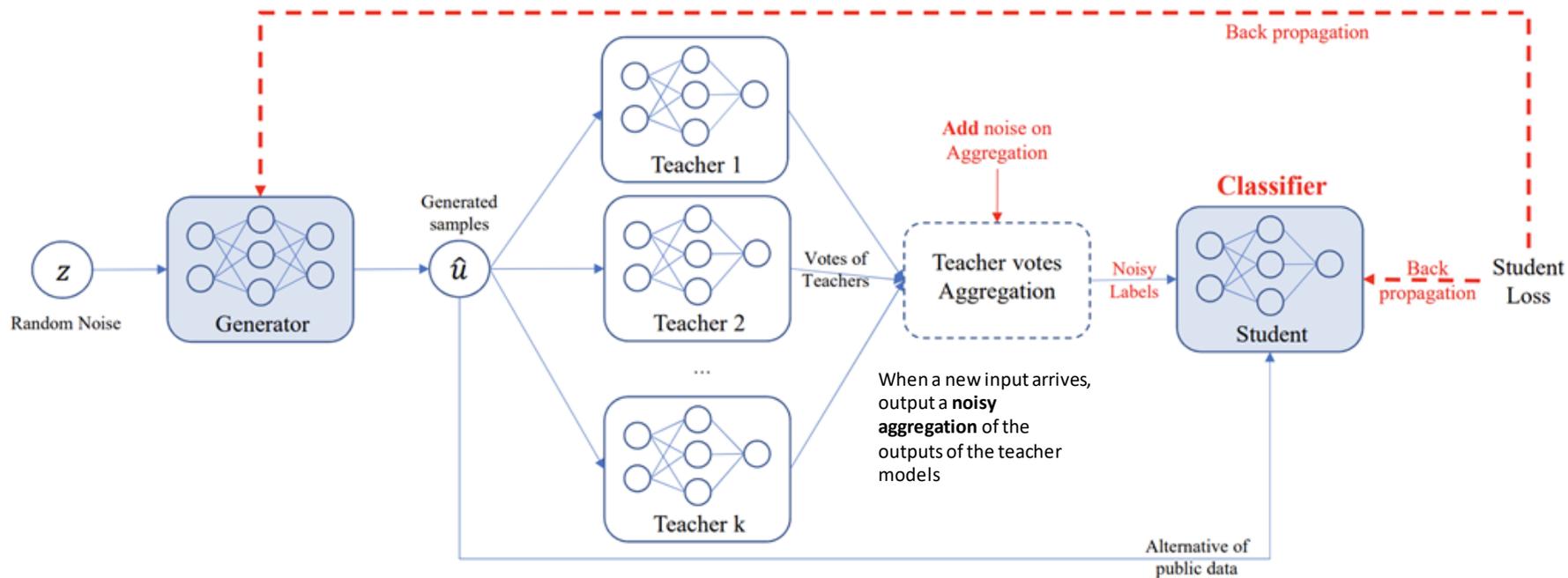
# PATE + GAN framework

- PATE framework is only applicable to **discriminative models**
- We need to extend the **PATE framework to generative models**
- We combine the state-of-the-art generative models (**GAN**) with the state-of-the-art DP framework (**PATE**)
- If we train the discriminator in a differentially private manner, then the generator will be differentially private by **post-processing theorem**
- A differentially private discriminator is **sufficient** but it may not be **necessary**.

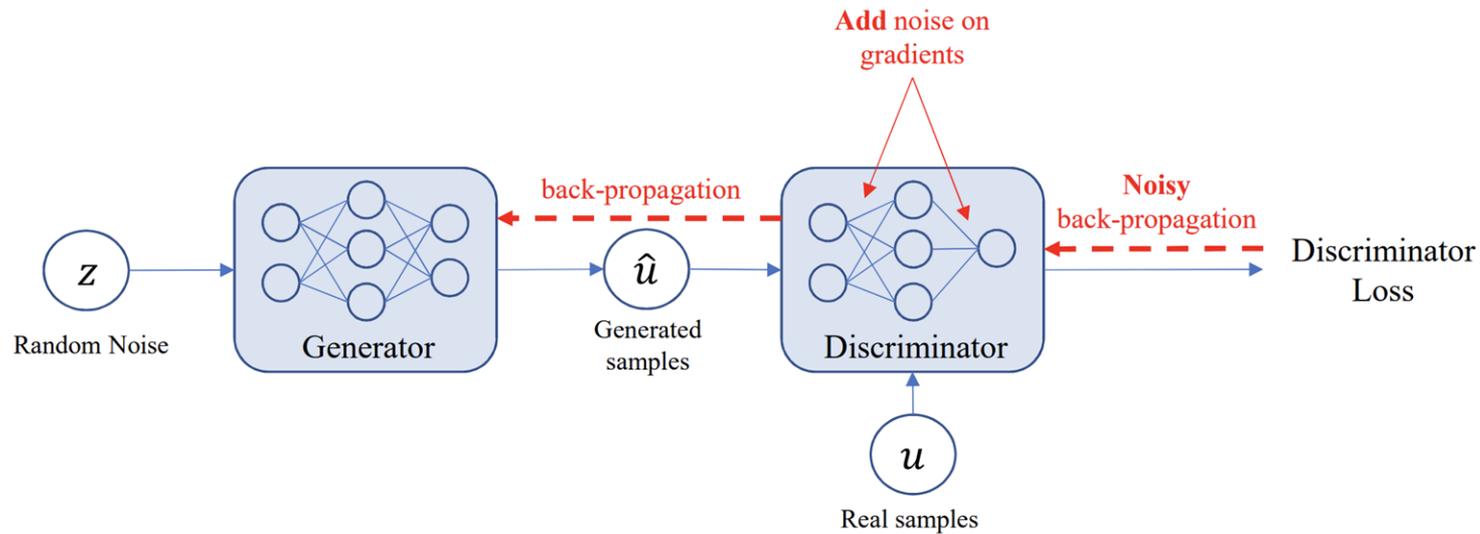
# PATE-GAN teacher



# PATE-GAN framework

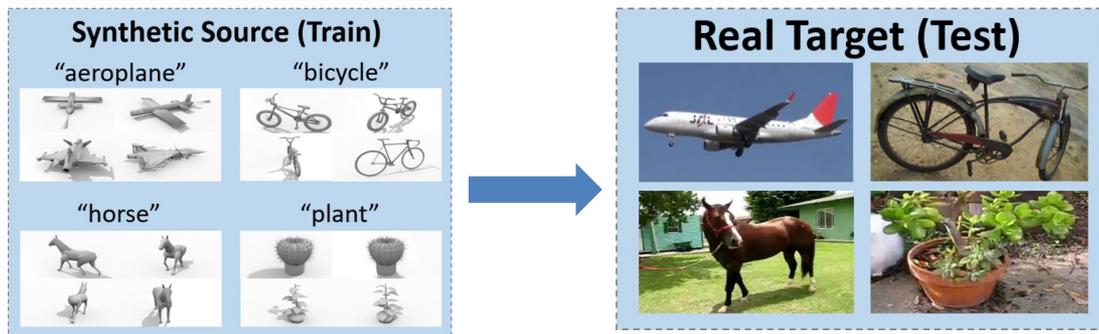


# Baseline: DP-GAN



# Evaluations: How to Evaluate Synthetic Data?

- **Predictivity:** samples should be **just as useful as** real data when used for the same predictive purposes (i.e. train on synthetic data, test on real data)
- **Experimental settings:**
  - **Setting A:** Train on Real, Test on Real
  - **Setting B:** Train on Synthetic, Test on Real
  - **Setting C:** Train on Synthetic, Test on Synthetic



# Evaluations: Datasets

- **Predictivity**: samples should be **just as useful as** real data when used for the same predictive purposes (i.e. train on synthetic data, test on real data)

Datasets	No of samples	No of features	AUROC	AUPRC
Kaggle Credit	284807	29	0.9438	0.7020
MAGGIC	30389	29	0.7069	0.3638
UNOS	23706	20	0.6416	0.6677
Kaggle Cervical cancer	858	35	0.9354	0.6314
UCI ISOLET	7797	617	0.9671	0.8758
UCI Epileptic Seizure Recognition	11500	179	0.9809	0.9511

# Evaluations: Setting B with different models

	AUROC			AUPRC		
	GAN	PATE-GAN	DPGAN	GAN	PATE-GAN	DPGAN
Logistic Regression	0.8950	0.8728	0.8720	0.4069	0.3907	0.3923
Random Forests [5]	0.9075	0.8980	0.8730	0.3219	0.3157	0.2926
Gaussian Naive Bayes [29]	0.8861	0.8817	0.8522	0.1963	0.1858	0.1601
Bernoulli Naive Bayes [29]	0.8997	0.8968	0.8891	0.2169	0.2099	0.2069
Linear SVM [10]	0.7611	0.7523	0.7502	0.4473	0.4466	0.4464
Decision Tree [28]	0.9102	0.9011	0.8647	0.4071	0.3978	0.3672
LDA [3]	0.8710	0.8510	0.8487	0.1956	0.1852	0.1788
AdaBoost [17]	0.9143	0.8952	0.8809	0.4530	0.4366	0.4234
Bagging [4]	0.8951	0.8877	0.8657	0.3303	0.3221	0.3073
GBM [18]	0.8848	0.8709	0.8499	0.3057	0.2974	0.2773
Multi-layer Perceptron	0.9086	0.8925	0.8787	0.4790	0.4693	0.4600
XgBoost [8]	0.9058	0.8904	0.8637	0.3837	0.3700	0.3440
<b>Average</b>	<b>0.8866</b>	<b>0.8737</b>	<b>0.8578</b>	<b>0.3453</b>	<b>0.3351</b>	<b>0.3219</b>

Table 1: Performance comparison of 12 different predictive models in Setting B (trained on synthetic, tested on real) in terms of AUROC and AUPRC (the generators of PATE-GAN and DPGAN are  $(1, 10^{-5})$ -differentially private).

# Evaluations: Setting B with different datasets

Datasets	AUROC			AUPRC		
	GAN	PATE-GAN	DPGAN	GAN	PATE-GAN	DPGAN
Kaggle Credit	0.8866	0.8737	0.8578	0.3453	0.3351	0.3219
MAGGIC	0.6574	0.6446	0.6286	0.3054	0.2952	0.2820
UNOS	0.6277	0.5996	0.5552	0.6554	0.6282	0.5862
Kaggle Cervical Cancer	0.9268	0.9108	0.8699	0.5994	0.5460	0.4851
UCI ISOLET	0.8171	0.6399	0.5577	0.5561	0.2953	0.2146
UCI Epileptic Seizure Recognition	0.9173	0.7681	0.6718	0.8133	0.6512	0.5369

Table 2: Performance comparison of 12 different predictive models in Setting B (trained on synthetic, tested on real) in terms of AUROC and AUPRC (the generators of PATE-GAN and DPGAN are  $(1, 10^{-5})$ -differentially private) over 6 different datasets. GAN is  $(\infty, \infty)$ -differentially private and is given to indicate an upper bound of PATE-GAN and DPGAN.

# Evaluations: Setting B with Different Privacy Budget

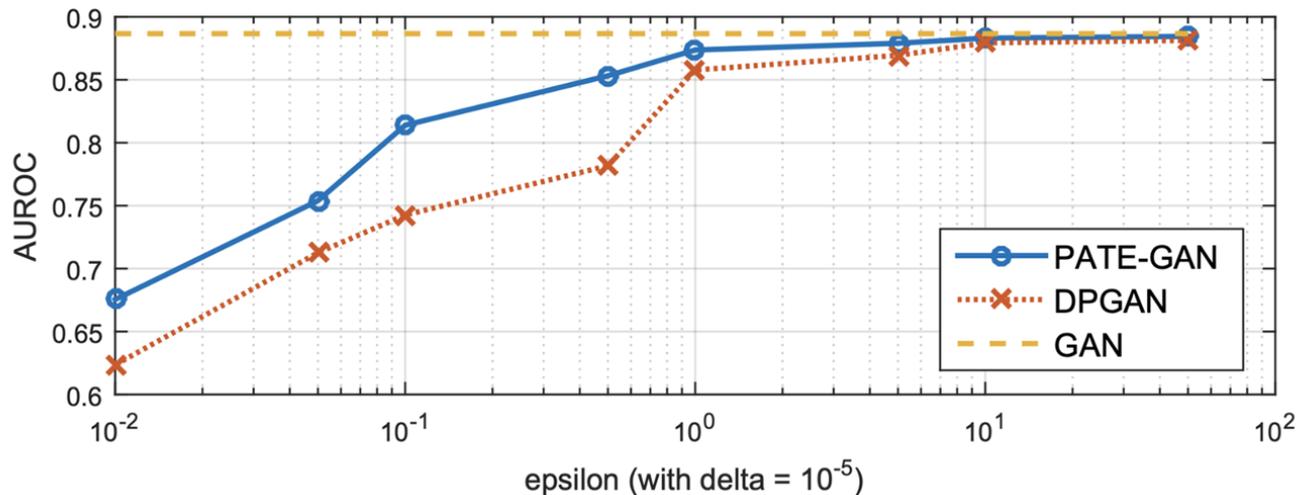


Figure 1: Average AUROC performance across 12 different predictive models trained on the synthetic dataset generated by PATE-GAN and DPGAN with various  $\epsilon$  (with  $\delta = 10^{-5}$ ) (Setting B).

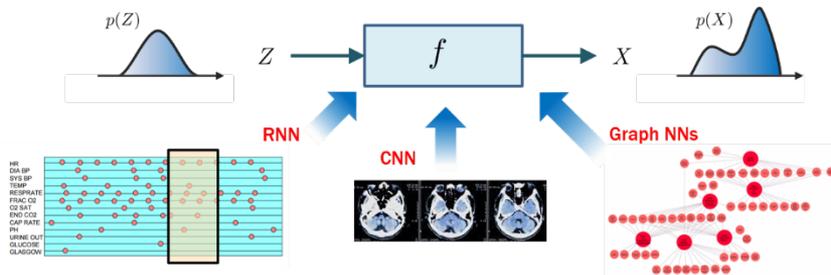
## Evaluations: Setting C for model ranking

PATE-GAN   DPGAN		PATE-GAN   DPGAN			
$\epsilon = 0.01$	0.6909	0.5273	$\epsilon = 1$	0.8364	0.8000
$\epsilon = 0.05$	0.7455	0.6909	$\epsilon = 5$	0.8909	0.8364
$\epsilon = 0.1$	0.7818	0.7455	$\epsilon = 10$	0.9091	0.8909
$\epsilon = 0.5$	0.8000	0.7818	$\epsilon = 50$	0.9091	0.9091

Table 3: Synthetic Ranking Probability of PATE-GAN and the benchmark when comparing Setting A and Setting C for various  $\epsilon$  (with  $\delta = 10^{-5}$ ) in terms of AUROC. The Synthetic Ranking Agreement of Original GAN is 0.9091, which is also attained by both PATE-GAN and DPGAN for  $\epsilon = 50$ .

# Recipe for generating synthetic healthcare data

- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, normalizing flows, **GANs**, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., NNs, RNN, CNN, **transfer representations** etc.
- **Step 3: Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy**



# Generating synthetic data for multiple hospitals



The image is a screenshot of a news article on the NHS Digital website. At the top left is the NHS Digital logo. To its right is a search bar with the text 'Search'. Below the logo and search bar is a breadcrumb trail: 'NHS Digital > News and events'. The main content area has a dark blue background with white text. It starts with the word 'News' in a smaller font, followed by a large, bold headline: 'Trials begin of machine learning system to help hospitals plan and manage COVID-19 treatment resources developed by NHS Digital and University of Cambridge'. Below the headline is a paragraph of text: 'Trials have begun of a system that will use machine learning to help predict the upcoming demand for intensive care (ICU) beds and ventilators needed to treat patients with COVID-19 at individual hospitals and across regions in England.' At the bottom left of the article is the label 'Date:' followed by the date '20 April 2020'.

**NHS**  
Digital

Search

NHS Digital > News and events

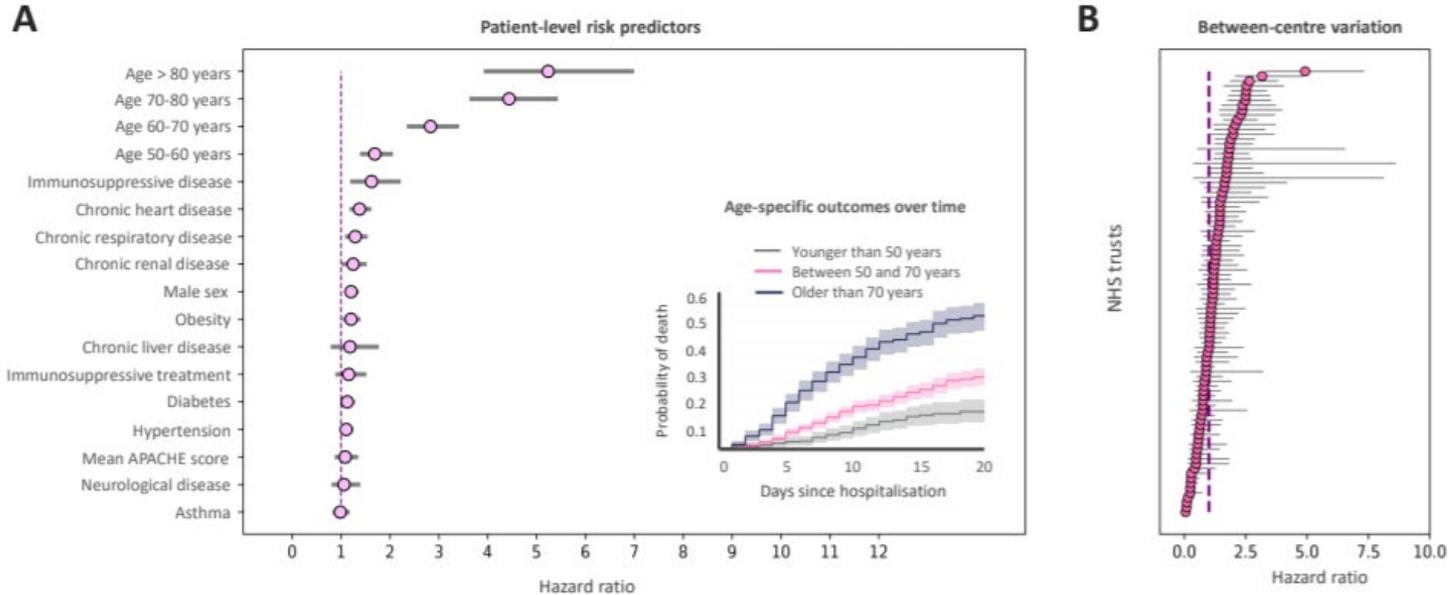
News

## Trials begin of machine learning system to help hospitals plan and manage COVID-19 treatment resources developed by NHS Digital and University of Cambridge

Trials have begun of a system that will use machine learning to help predict the upcoming demand for intensive care (ICU) beds and ventilators needed to treat patients with COVID-19 at individual hospitals and across regions in England.

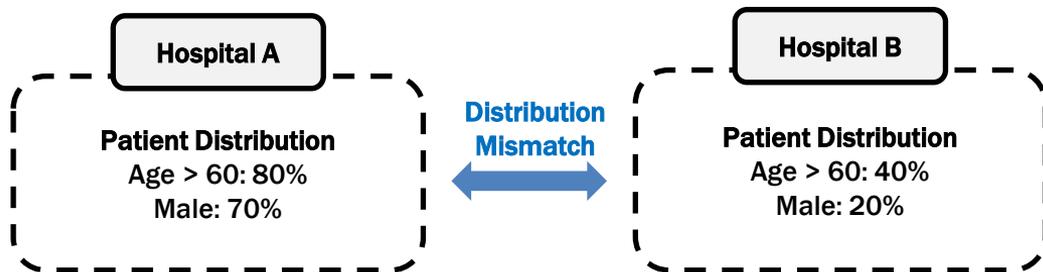
Date: 20 April 2020

# Between-center differences for COVID-19 ICU mortality from early data in England

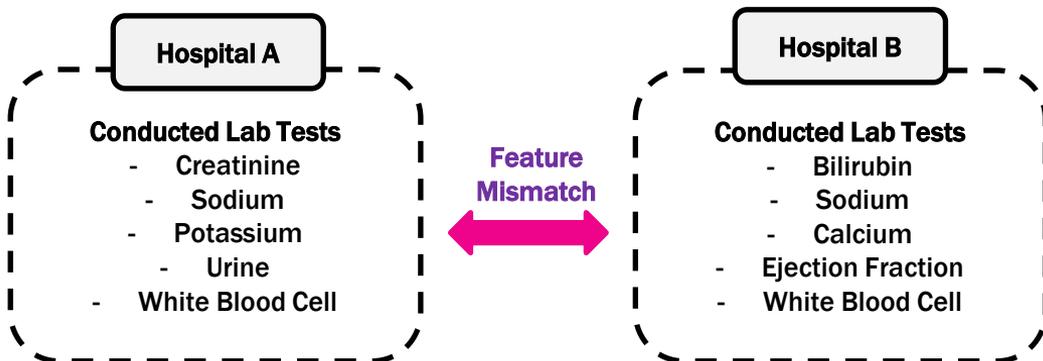


# Transferring what we learned to other jurisdictions

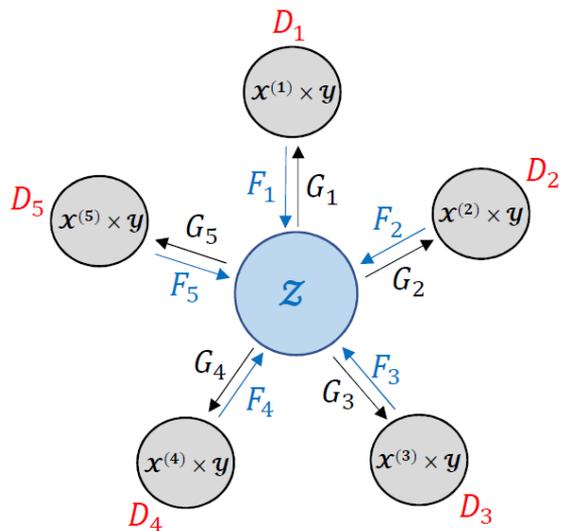
- **Distribution Mismatch:** Auxiliary data does not come from the same distribution as target data



- **Feature Mismatch:** Different data collectors collect different pieces of information for each sample

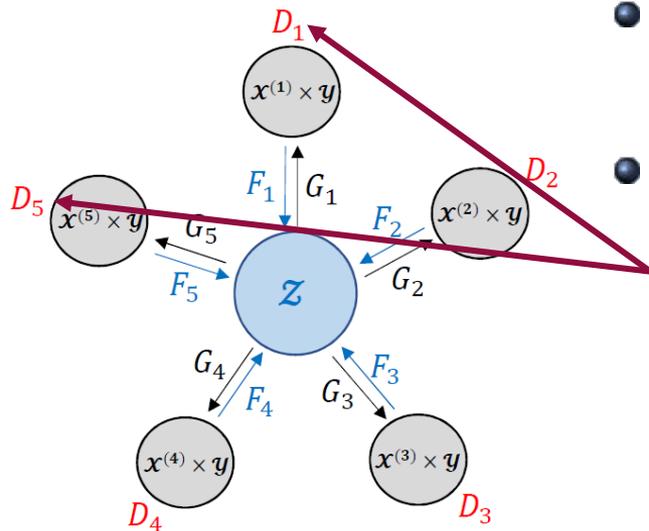


# RadialGAN



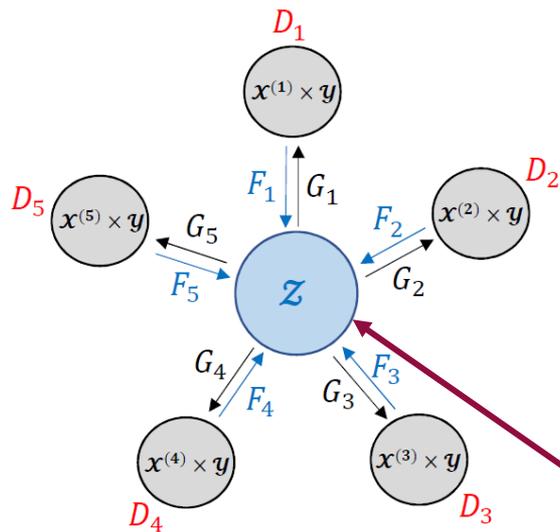
- Use **multiple GAN architectures** to “translate” the data from one dataset to another

# RadialGAN



- Use **multiple GAN architectures** to “translate” the data from one dataset to another
- **Distribution Mismatch** is dealt with by the **adversarial framework** which ensures that “translation” respects the **target distribution**

# RadialGAN



- Use **multiple GAN architectures** to “translate” the data from one dataset to another
- **Distribution Mismatch** is dealt with by the **adversarial framework** which ensures that “translation” respects the **target distribution**
- **Feature mismatch** is dealt with by introducing a **latent space** through which all samples are mapped

# RadialGAN

## MAGGIC Dataset – Heart Failure

- A collection of **different medical studies**
- Label is set as **1-year all-cause mortality**
- Total number of **features across all studies is 216**
  - (1) Average number of features in each study: **66**
  - (2) Average number of **shared features: 35 (53.8%)**

Algorithm	$M = 3$		$M = 5$		$M = 7$	
	AUC	APR	AUC	APR	AUC	APR
<b>RadialGAN</b>	.0154±.0091	.0243±.0096	.0292±.0009	.0310±.0096	.0297±.0071	.0287±.0073
Simple-combine	.0124±.0020	.0110±.0016	.0132±.0020	.0118±.0026	.0135±.0017	.0156±.0025
Co-GAN	.0058±.0028	.0085±.0026	.0094±.0018	.0139±.0036	<b>-.0009±.0015</b>	<b>-.0013±.0027</b>
StarGAN	.0119±.0015	.0150±.0013	.0150±.0025	.0191±.0013	.0121±.0020	.0160±.0021
Cycle-GAN	<b>-.0228±.0112</b>	<b>-.0306±.0085</b>	<b>-.0177±.0082</b>	<b>-.0196±.0085</b>	<b>-.0076±.0022</b>	<b>-.0168±.0030</b>
(Wiens et al., 2014)	<b>-.0314±.0075</b>	<b>-.0445±.0125</b>	<b>-.0276±.0057</b>	<b>-.0421±.0052</b>	<b>-.0292±.0054</b>	<b>-.0411±.0063</b>

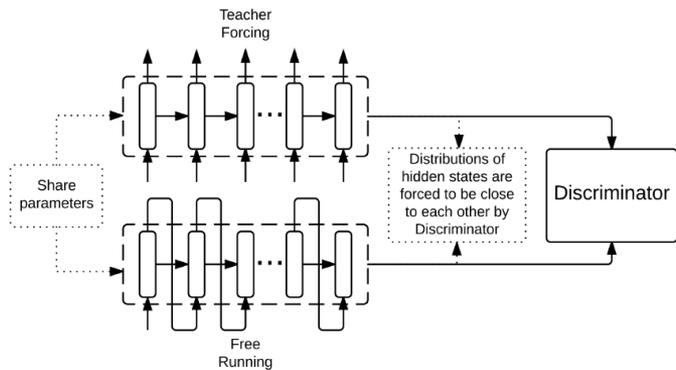
# **Generative models for synthetic time-series data**

# Time-series generation

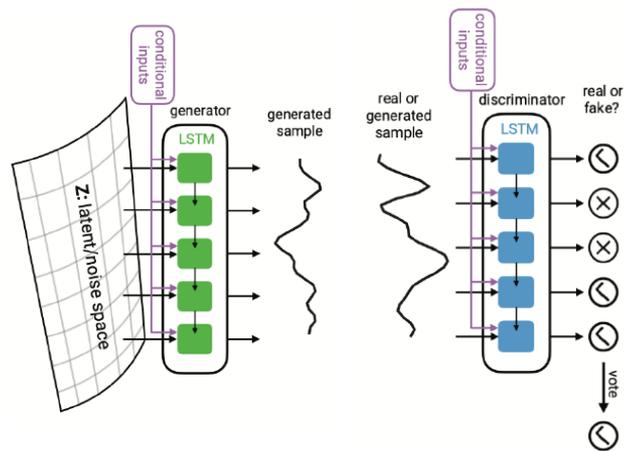
- **Objective:** To generate time-series data with **preserving temporal dynamics**
- **Key Example:** **Synthetic time-series healthcare data generation**
- **Challenges:** Capture the distributions of features **within each time point** as well as complex dynamics of those variables **across time points**

# Time-series generation approaches

## Autoregressive model

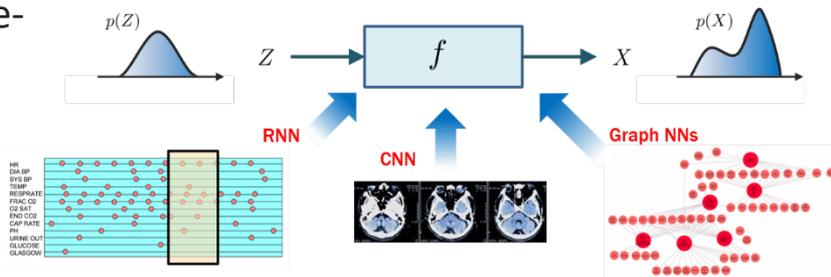


## Recurrent generative model



# Recipe for generating synthetic healthcare data

- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, normalizing flows, **GANs**, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., Autoregressive, attention, latent state-space, **RNN representations** spectral, etc.
- **Step 3: Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy**



# Problem formulation

- Consider tuples of the form  $(S, X_{1:T})$  with some joint distribution  $p$ , where
  - **Static features:**  $S \in \mathcal{S}$
  - **Temporal features:**  $X \in \mathcal{X}$

## Objective

Given training data, learn a density  $\hat{p}(\mathbf{S}, \mathbf{X}_{1:T})$  that best approximates  $p(\mathbf{S}, \mathbf{X}_{1:T})$ .

- **Desiderata**
  - **Fidelity:** samples should be **indistinguishable** from real data
  - **Diversity:** samples should be **distributed to cover** that of real data
  - **Predictivity:** samples should be **just as useful as** real data when used for the same predictive purposes (i.e. train on synthetic data, test on real data)

# Two objectives

## Global (sequence-level)

Matching the joint distribution...

$$\min_{\hat{p}} D\left(p(\mathbf{S}, \mathbf{X}_{1:T}) \parallel \hat{p}(\mathbf{S}, \mathbf{X}_{1:T})\right) \quad (1)$$

...requires a perfect adversary.

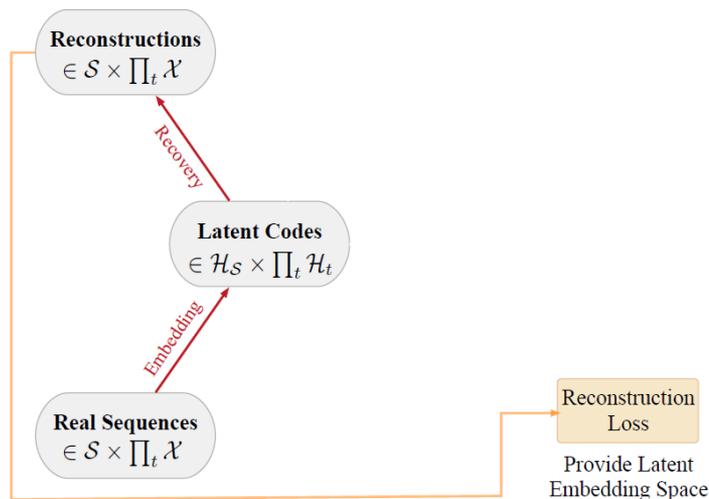
## Local (stepwise)

Matching the conditionals...

$$\min_{\hat{p}} D\left(p(\mathbf{X}_t | \mathbf{S}, \mathbf{X}_{1:t-1}) \parallel \hat{p}(\mathbf{X}_t | \mathbf{S}, \mathbf{X}_{1:t-1})\right) \quad (2)$$

...requires ground-truth sequences.

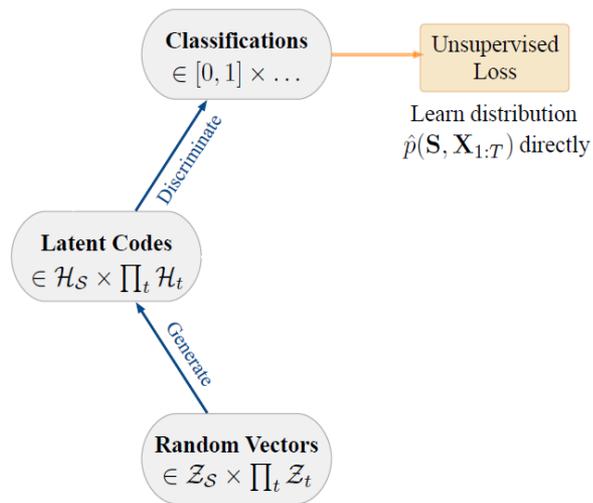
# TimeGAN: Encode, Generate, and Iterate



- Provide mapping between the **feature space** and **latent space**, where the adversarial network learns the underlying **temporal dynamics** of the data

$$\mathcal{L}_R = \mathbb{E}_{\mathbf{s}, \mathbf{x}_{1:T} \sim p} [\|\mathbf{s} - \tilde{\mathbf{s}}\|_2 + \sum_t \|\mathbf{x}_t - \tilde{\mathbf{x}}_t\|_2]$$

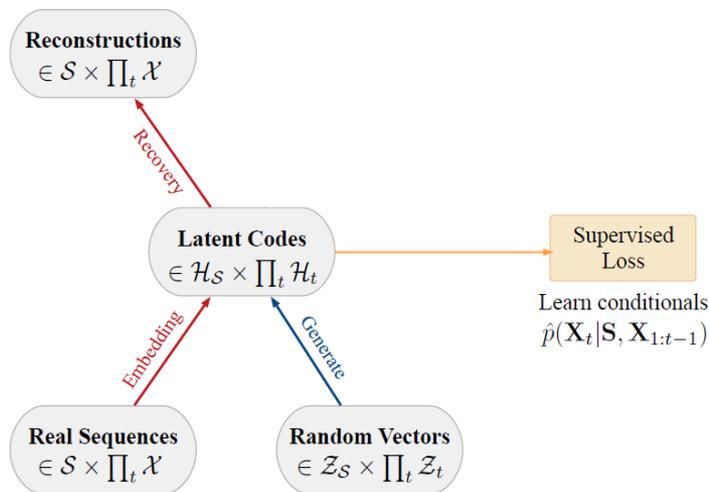
# TimeGAN: Encode, Generate, and Iterate



- The generator **produces synthetic outputs** through the latent space, and the discriminator operates on the basis of **real vs. synthetic embeddings**.

$$\mathcal{L}_U = \mathbb{E}_{\mathbf{s}, \mathbf{x}_{1:T} \sim p} [\log y_S + \sum_t \log y_t] + \mathbb{E}_{\mathbf{s}, \mathbf{x}_{1:T} \sim \hat{p}} [\log(1 - \hat{y}_S) + \sum_t \log(1 - \hat{y}_t)]$$

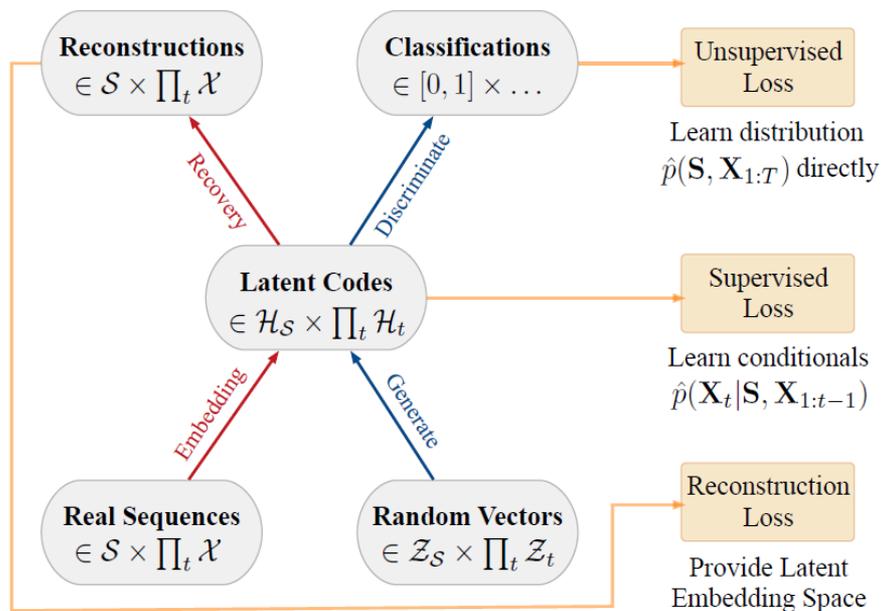
# TimeGAN: Encode, Generate, and Iterate



- The generator receives sequences of embeddings of actual data to generate the next latent vector.

$$\mathcal{L}_S = \mathbb{E}_{\mathbf{s}, \mathbf{x}_{1:T} \sim p} \left[ \sum_t \|\mathbf{h}_t - g_{\mathcal{X}}(\mathbf{h}_S, \mathbf{h}_{t-1}, \mathbf{z}_t)\|_2 \right]$$

# TimeGAN: Jointly optimize



$$\min_{\theta_e, \theta_r} (\lambda \mathcal{L}_S + \mathcal{L}_R)$$

and

$$\min_{\theta_g} (\eta \mathcal{L}_S + \max_{\theta_d} \mathcal{L}_U)$$

# How to evaluate synthetic time-series data?

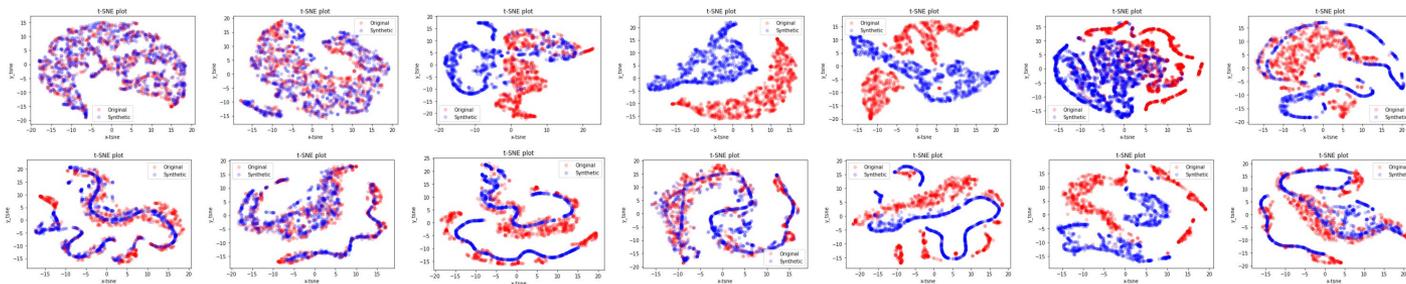
- **Fidelity**: samples should be **indistinguishable** from real data

<i>Metric</i>	<i>Method</i>	Sines	Stocks	Energy	Events
Discriminative Score	TGAN	<b>.011±.008</b>	<b>.102±.021</b>	<b>.236±.012</b>	<b>.161±.018</b>
	RCGAN	.022±.008	.196±.027	.336±.017	.380±.021
	C-RNN-GAN	.229±.040	.399±.028	.499±.001	.462±.011
	T-Forcing	.495±.001	.226±.035	.483±.004	.387±.012
	P-Forcing	.430±.027	.257±.026	.412±.006	.489±.001
	WaveNet	.158±.011	.232±.028	.397±.010	.385±.025
	WaveGAN	.277±.013	.217±.022	.363±.012	.357±.017

Table: Results on Multiple Time-Series Datasets (Bold indicates best).

# How to evaluate synthetic time-series data?

- **Diversity**: samples should be distributed to **cover** the real data



(a) TimeGAN (b) RCGAN (c) CRNNGAN (d) T-Forcing (e) P-Forcing (f) WaveNet (g) WaveGAN

# How to evaluate synthetic time-series data?

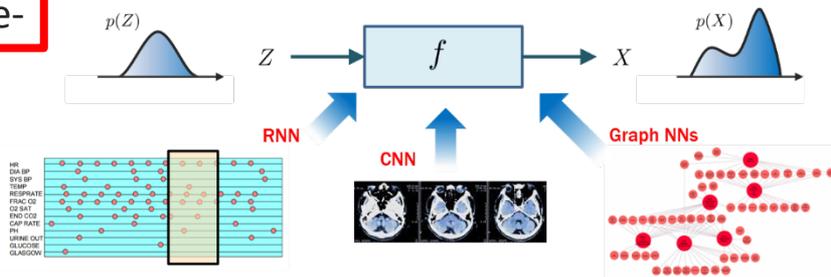
- **Predictivity**: Samples should be **just as useful as** real data when used for the same predictive purposes (i.e. train on synthetic, test on real)

<i>Metric</i>	<i>Method</i>	Sines	Stocks	Energy	Events
Predictive Score	TGAN	<b>.093±.019</b>	<b>.038±.001</b>	<b>.273±.004</b>	<b>.303±.006</b>
	RCGAN	.097±.001	.040±.001	.292±.005	.345±.010
	C-RNN-GAN	.127±.004	<b>.038±.000</b>	.483±.005	.360±.010
	T-Forcing	.150±.022	<b>.038±.001</b>	.315±.005	.310±.003
	P-Forcing	.116±.004	.043±.001	.303±.006	.320±.008
	WaveNet	.117±.008	.042±.001	.311±.005	.333±.004
	WaveGAN	.134±.013	.041±.001	.307±.007	.324±.006
	Original	.094±.001	.036±.001	.250±.003	.293±.000

Table: Results on Multiple Time-Series Datasets (Bold indicates best).

# Recipe for generating synthetic healthcare data

- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, normalizing flows, GANs, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., Autoregressive attention, latent state-space, RNN representations, spectral, etc.
- **Step 3: Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy**



# Attentive state-space models

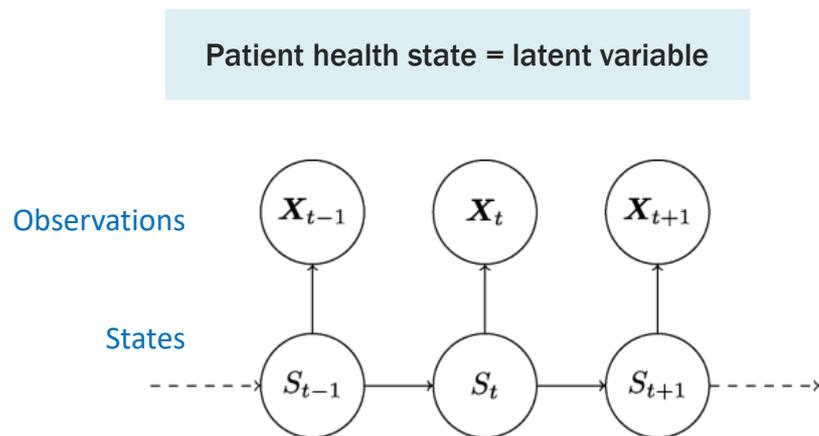
- Latent variable models for sequential data → **state-space models**

- A sequence of variational autoencoders

- **Rationale:**

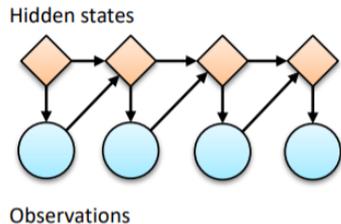
- Interpretable: can discover knowledge
- Can incorporate structure and domain knowledge

- **Unlike other models: learning and inference need to be tailored to the model**

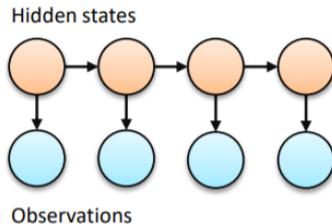


# Attentive state-space models

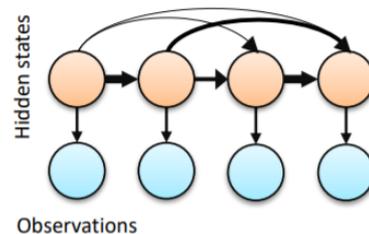
- **Key idea:** non-Markovian, non-stationary state transition



(a) RNN



(b) HMM

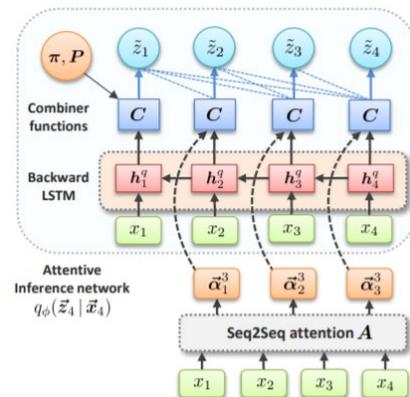
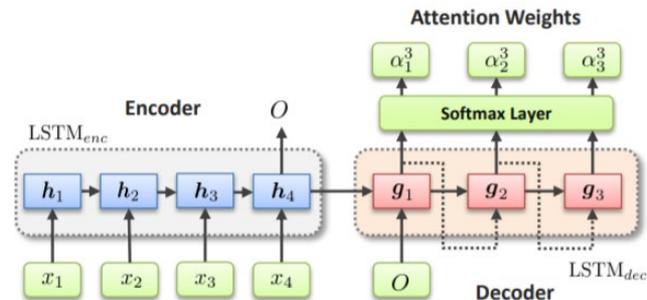


(c) Attentive state space

- **Attention mechanism:** assign different weights to previous states when computing transition probabilities to a new state at each time step

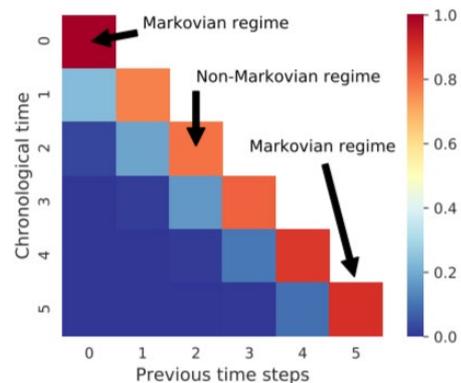
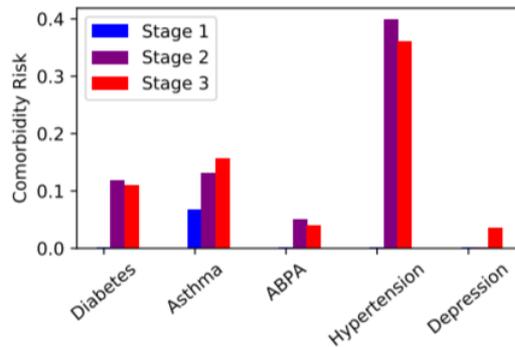
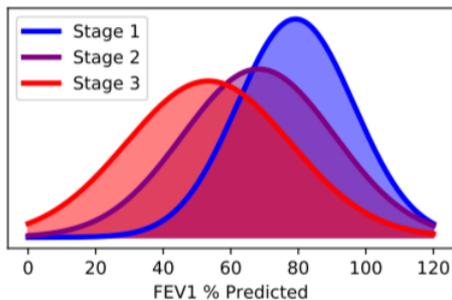
# Attentive state-space models

- **Attention mechanism:** assign different weights to previous states when computing transition probabilities to a new state at each time step
- **Encoder-decoder architecture**
- **Variational inference:** inference network needs to be tailored to this particular model design...



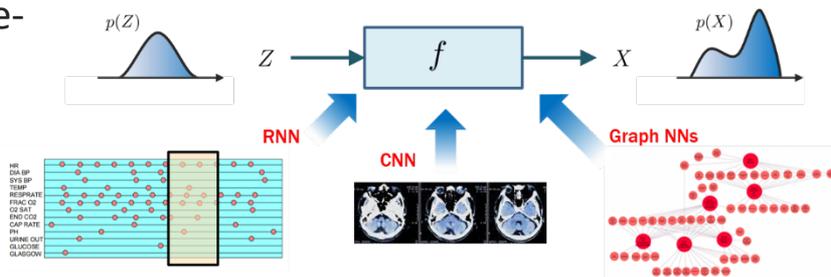
# Attentive state-space models: Synthetic Cystic Fibrosis data

- Not only able to generate synthetic data, but also explain disease progression dynamics both on a population level and patient level.



# Recipe for generating synthetic healthcare data

- **Step 1: Decide the generative modeling approach to use...**
  - Variational auto-encoders, **normalizing flows**, GANs, etc.
- **Step 2: Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).**
  - E.g., Autoregressive, attention, latent state-space, RNN representations, **spectral**, etc.
- **Step 3: Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy**



# Fourier Flows

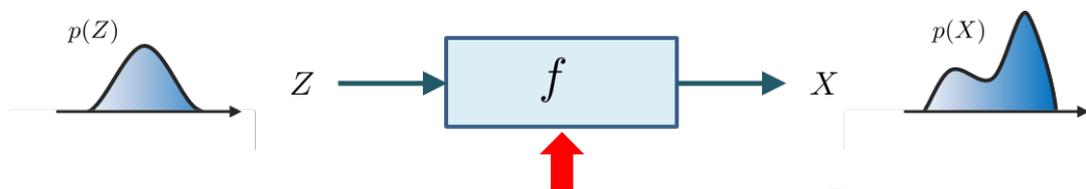
- Recall: for normalizing flows, need to constrain the transformation so that:

- The Jacobean determinant is easy to compute

Needed for efficient training

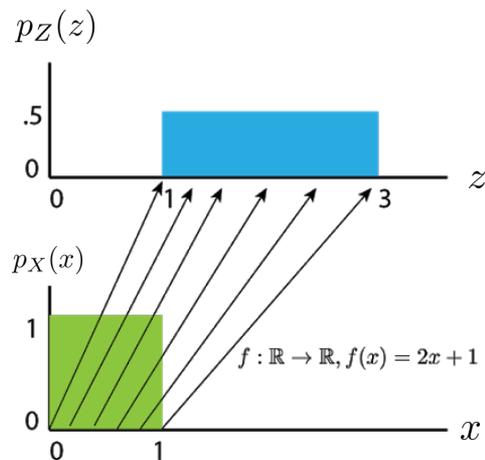
- The forward and inverse map are easy to compute

Needed for efficient sampling



Fourier transform

$$X_k = \sum_{t=0}^{T-1} x_t \cdot e^{-2\pi j \cdot \frac{kt}{T}}, \forall 1 \leq k \leq T-1$$



# Fourier Flows

- Fourier transform has various favorable properties:

- DFT matrix

$$\bar{\mathbf{X}}^d = W \bar{\mathbf{x}}^d, \quad \omega = e^{-2\pi j/N}$$

$$W = \frac{1}{\sqrt{N}} \begin{bmatrix} 1 & 1 & 1 & \dots & 1 \\ 1 & \omega & \omega^2 & \dots & \omega^{N-1} \\ 1 & \omega^2 & \omega^4 & \dots & \omega^{2(N-1)} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & \omega^{N-1} & \omega^{2(N-1)} & \dots & \omega^{(N-1)(N-1)} \end{bmatrix}$$

- Jacobean of the DFT matrix

$$\begin{aligned} |\det(\mathbf{J}[W])| &= |\det(W)| \\ &= \left| \left( \frac{1}{\sqrt{N}} \right)^N \prod_{1 < n < m \leq N} (\omega^m - \omega^n) \right| = 1 \end{aligned}$$

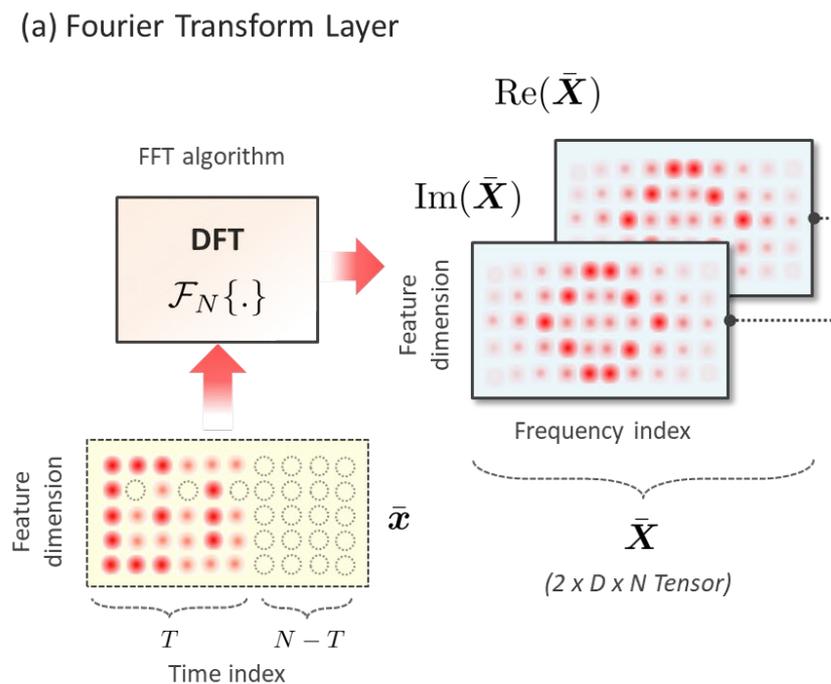
- Convolution property

$$\mathbf{x}_1 \otimes \mathbf{x}_2 \iff \mathbf{X}_1 \odot \mathbf{X}_2$$

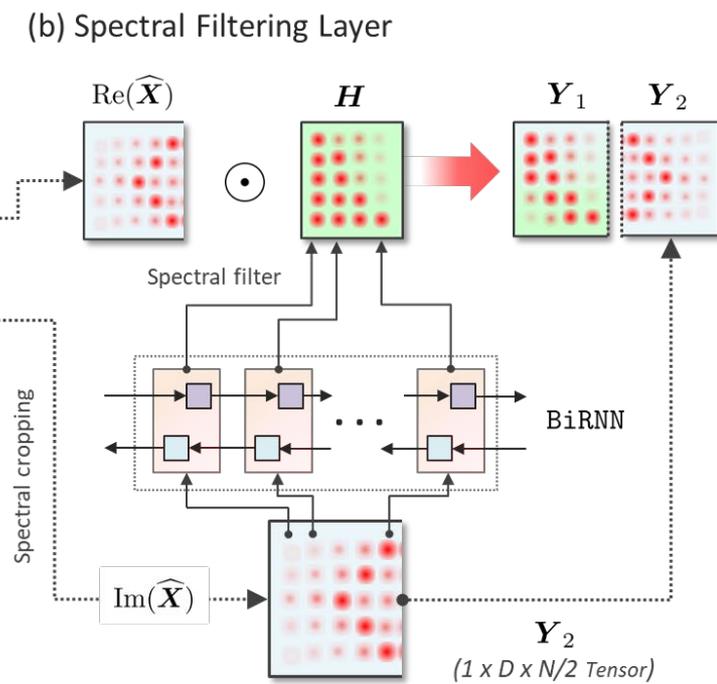
- Handles variable-length time-series, variable sampling rates naturally

# Fourier Flows

(a) Fourier Transform Layer



(b) Spectral Filtering Layer



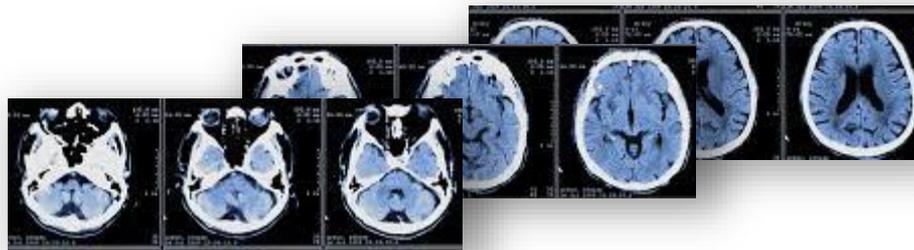
## Different modeling choices are appropriate for synthesizing different types of time-series data...

<b>TimeGAN</b>	<b>Attentive State-space models</b>	<b>Fourier flows</b>
Data-driven, high-dimensional data	Interpretable, handles domain knowledge	Periodic data (e.g., ECG), irregular and variable-length time-series

# Evaluating synthetic healthcare data

# How to measure the quality of synthetic data sets?

- We have followed the recipe and generated the desired synthetic data...

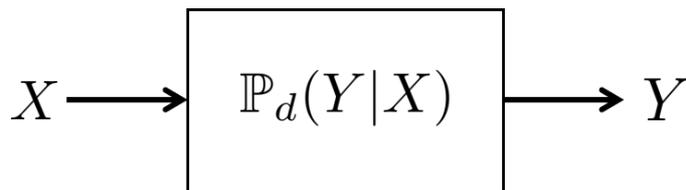


- How do we know if the synthetic data is of a high quality? What does “quality” mean?
  - Inspect individual samples? We may have generated millions!
  - Train on synthetic, test on real? Does not tell us the full picture...
- What makes a good synthetic dataset? How do we define “quality”?

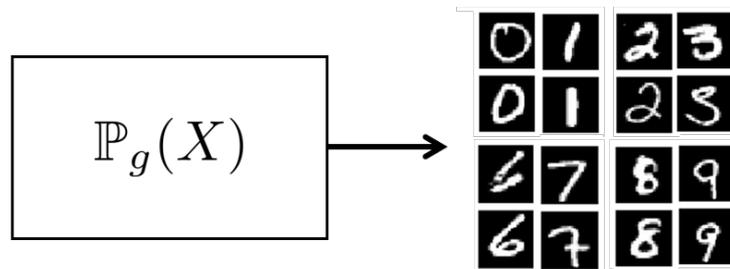
# Evaluating generative models is tricky...

- Accuracy of **discriminative models** is easy to evaluate by simply assessing prediction accuracy on test data (e.g., cross-validation).
- **Generative models**: unsupervised, **no ground-truth**.

(a) Discriminative models



(b) Generative models



# Model-dependent or domain-specific...

## Likelihood and statistical divergence

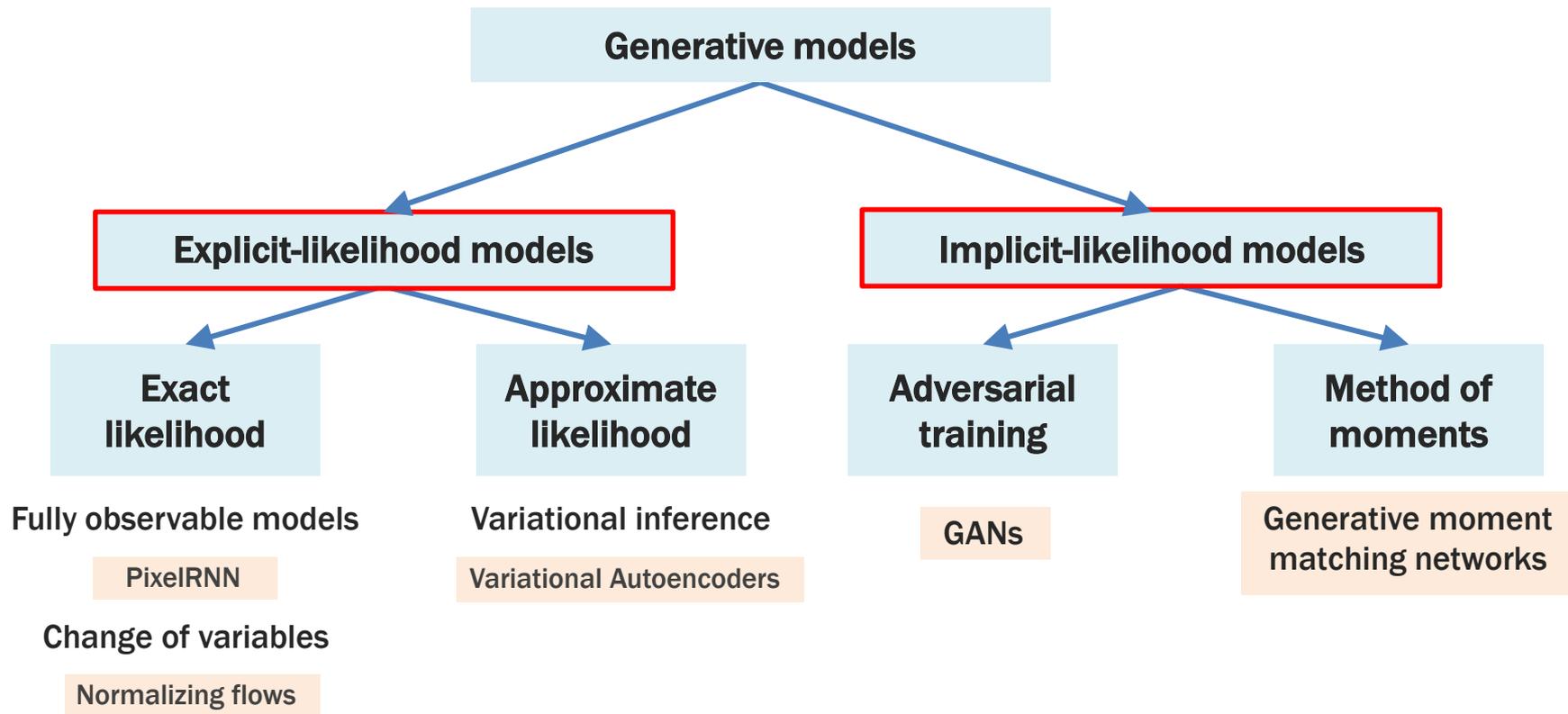
$$\log \mathbb{P}_g(X) \quad D(\mathbb{P}_g \parallel \mathbb{P}_r)$$

- State-of-the-art models do not have tractable likelihood (GANs, VAE, etc)
- Scale badly with high dimensions
- Single number that does not distinguish different modes of failure

## Domain-specific scores

- Measures of the quality of images or audio
- Expert opinion
- Pre-trained representations on ImageNet (e.g. Fréchet Inception distance)

# Recall: Not all models have explicit likelihoods!



# Model likelihood is not the right measure...

- Likelihood is uninterpretable, does not evaluate individual samples and collapses all modes of failure into a single measure...
- Likelihood does not scale well with high-dimensional data...

- Great likelihood and poor samples: samples from a mixture of true model & noise

$$0.01p(\mathbf{x}) + 0.99q(\mathbf{x})$$

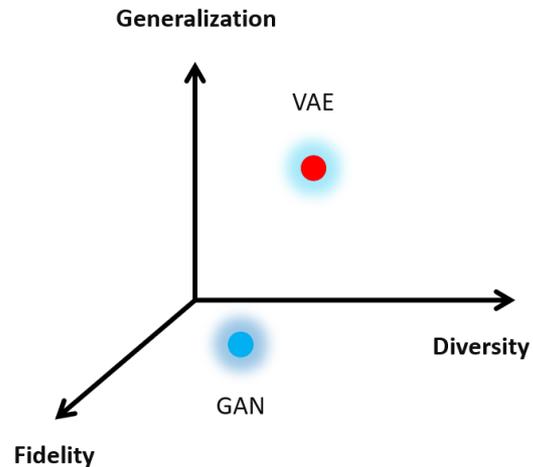
will have likelihood close to true model for high-dimensional data

$$\log [0.01p(\mathbf{x}) + 0.99q(\mathbf{x})] \geq \log [0.01p(\mathbf{x})] = \log p(\mathbf{x}) - \log 100$$

- Poor likelihood and great samples: counter-examples exist.

# Different ways in which a generative model may fail

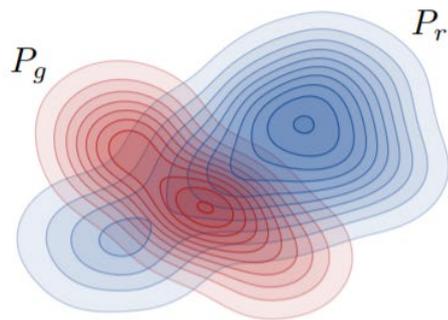
- A single-dimensional metric is not enough...
- Every model's performance can be viewed as a point in a 3D space
  - **Fidelity:** How “good” the synthetic samples are?
  - **Diversity:** How much of the real data is covered?
  - **Generalization:** How often does the model copy training data?
- **Need probabilistic, interpretable, multi-dimensional quantities**



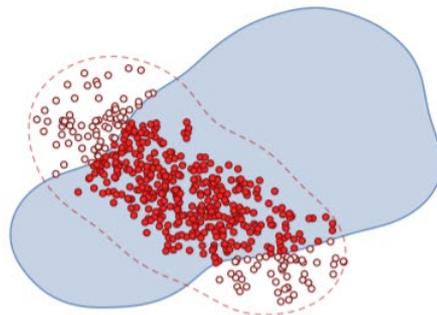
# Precision and Recall analysis

- **Precision:** the fraction of synthetic samples that look realistic (fidelity)
- **Recall:** fraction of real samples that the generative model can synthesize (diversity)

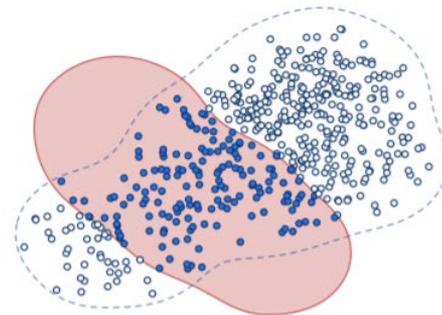
Need to estimate the support of real and synthetic distributions



(a) Example distributions



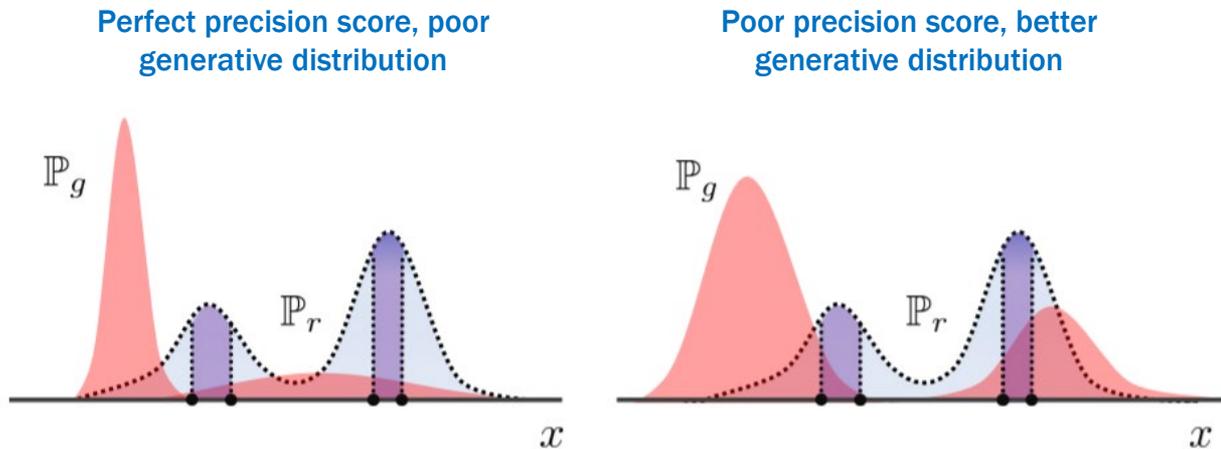
(b) Precision



(c) Recall

# Refined Precision and Recall analysis

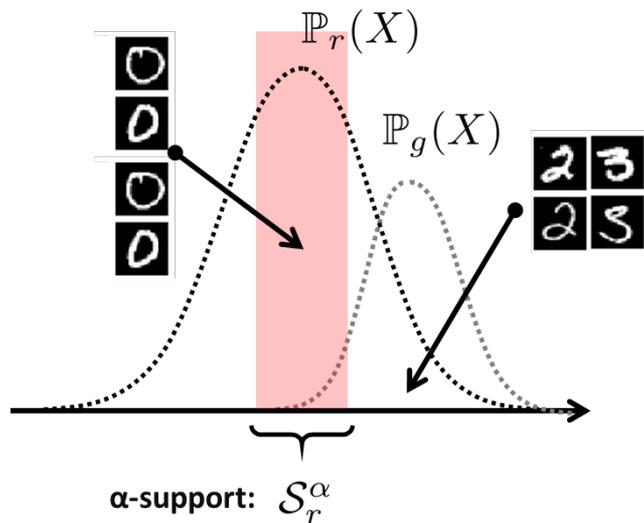
- **Problem with standard precision-recall analysis:**
  - What if the generative model only generates outliers in real distribution?
  - Can we detect mode collapse? Mode invention, etc?



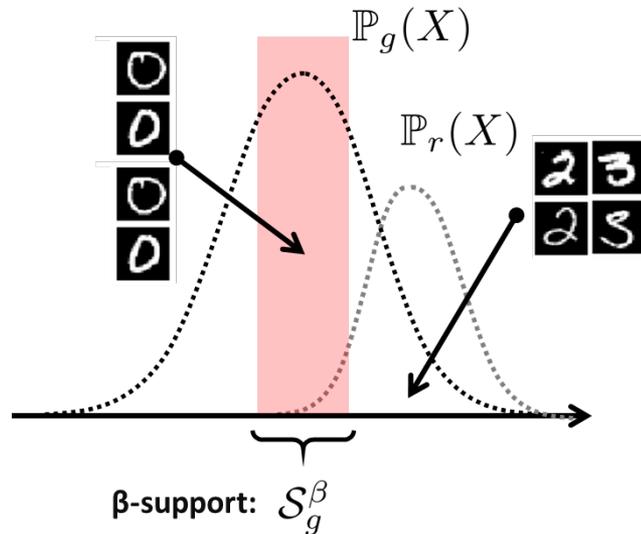
# Refined Precision and Recall analysis

- Use a more refined definition of the support of a distribution...

■  $\alpha$ -Precision measures sample *fidelity*.

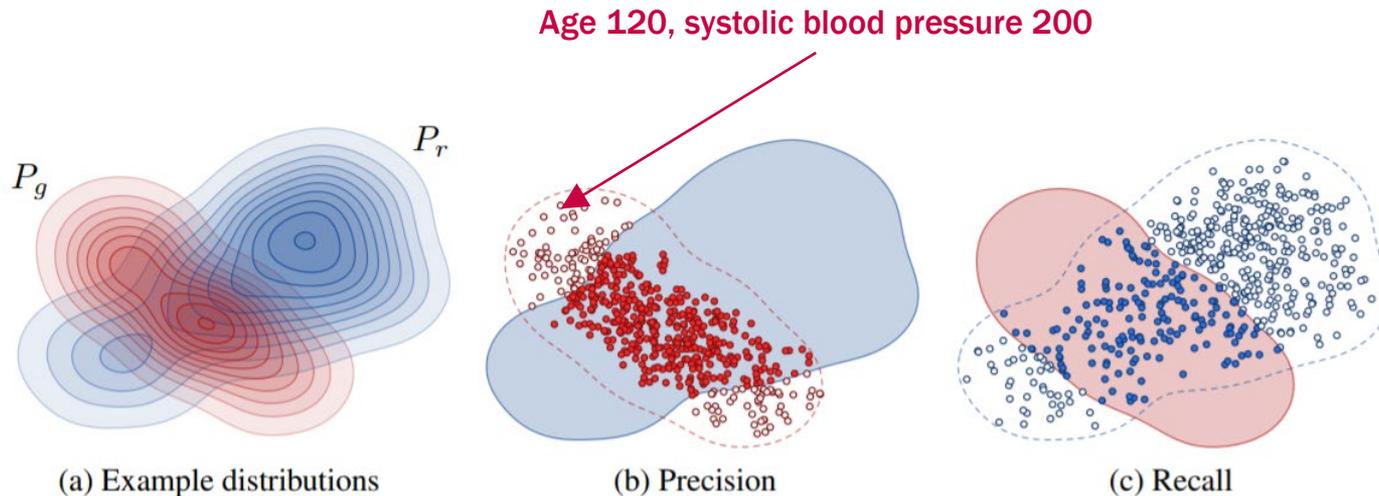


■  $\beta$ -Recall measures sample *diversity*.



# Is my synthetic data clinically sensible?

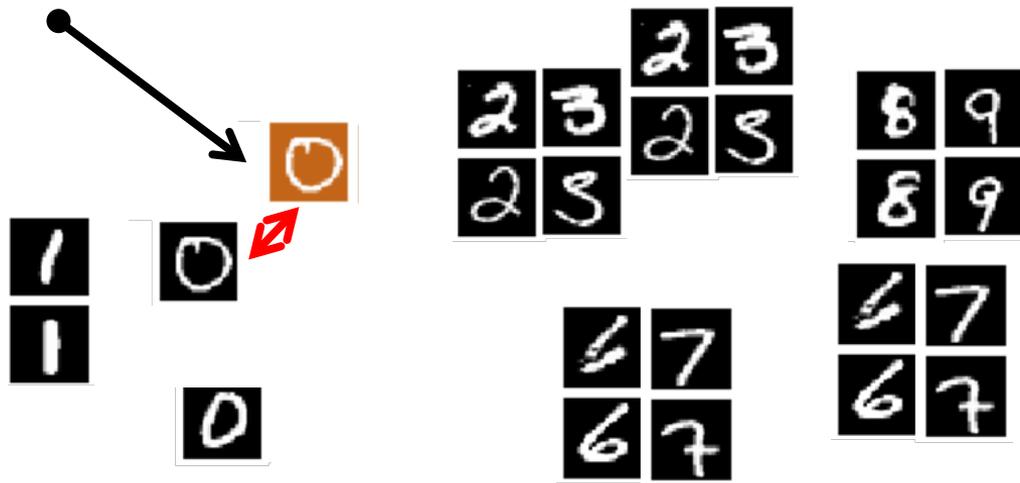
- Precision automatically evaluates if each sample is “clinically realistic”



# How to evaluate privacy preservation in synthetic data?

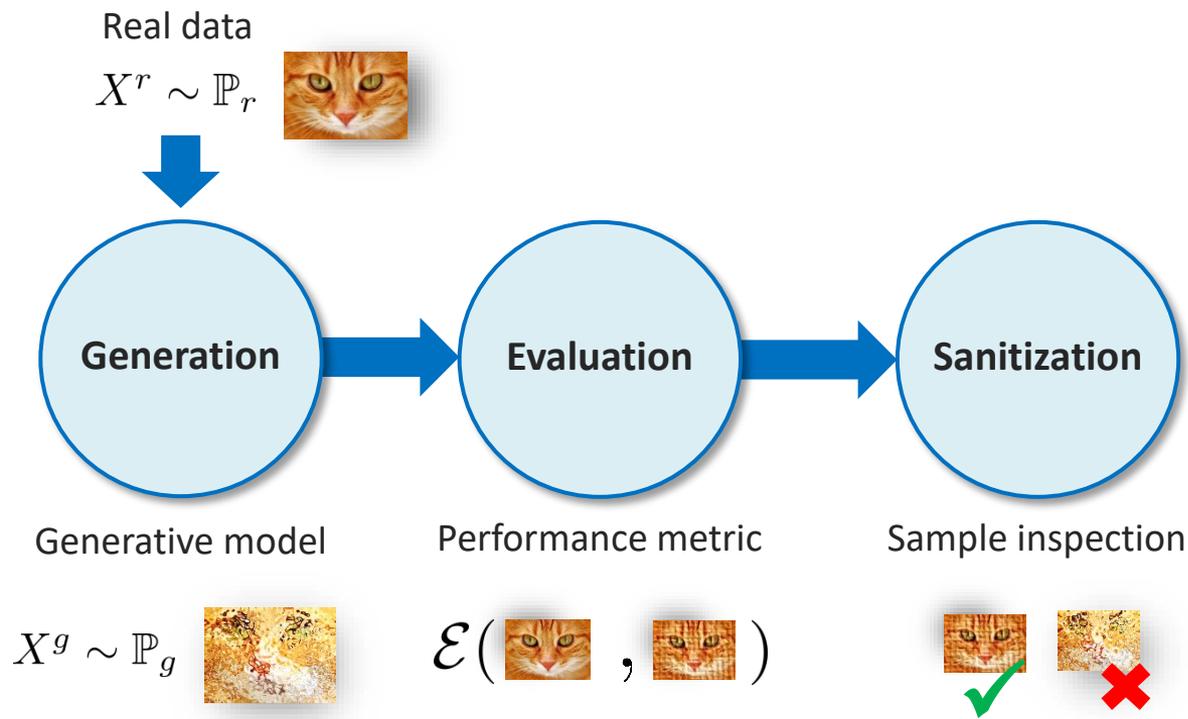
- Are their samples closer to training data than expected?

Synthetic  
sample



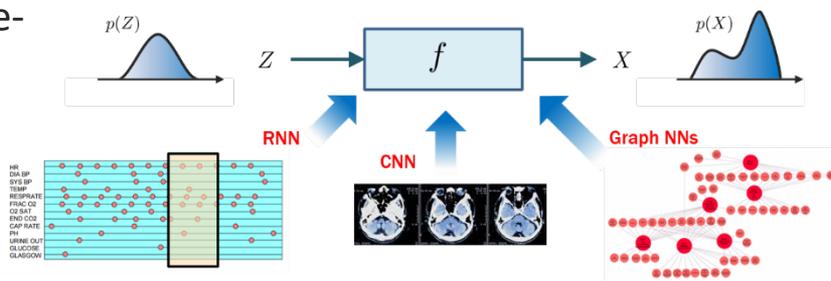
# Sample-level metrics: a fourth step in the recipe

- **Sanitization:** Remove samples that are copied or not precise



# Sample-level metrics: a fourth step in the recipe

- **Step 1:** Decide the generative modeling approach to use...
  - Variational auto-encoders, normalizing flows, GANs, etc.
- **Step 2:** Construct an appropriate representation/structure for the type of healthcare data under consideration (time-series, images, notes, bio-markers, etc).
  - E.g., Autoregressive, attention, latent state-space, RNN representations, spectral, etc.
- **Step 3:** Incorporate differential privacy or other privacy notion/ sanitize the data to ensure privacy
- **Step 4:** Evaluate the model using sample-level metrics, remove “bad” samples...



## **Future directions**

## Future directions

- Synthetic multi-modal data (genetic, images, time-series, etc.).
- Generative models for asynchronous, sparse follow-up clinic visits.
- Evaluating fairness and bias in synthetic data.
- Domain and disease-specific evaluation metrics.
- **Disentangling clinical policies from real observational data.**

# Medkit – Synthetic Data for Decision Modelling

More than “just” synthetic data:  
A full **testing suite** for decision modelling.

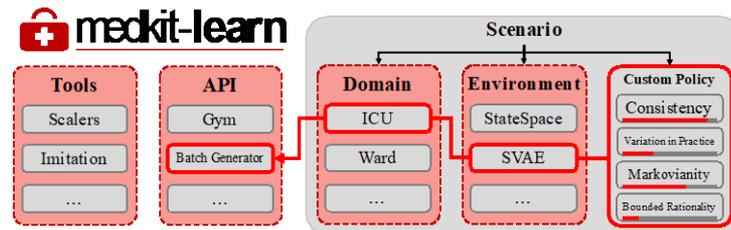
Challenges in healthcare:

- Fully **offline** with limited batch datasets
- Modern time-series generation methods don't **disentangle** environment and policy

Desiderata:

- A collection of **realistic** environment models
- With a variety of expressive and **customizable** policy models

Achieved: Provide ground truth knowledge in complicated and realistic settings, ready to test decision making modelling tools (policies).



# Why important?

Without ground-truth policy inference **cannot** be validated

Medkit provides policies learnt **based on clinical behaviour** but with **customizable** parameters, structured as:

$$Q_{\pi}^{\Omega}(y_t | \vec{x}_t, \vec{y}_{t-1}) = \sum_i w_i \frac{e^{\beta_i q_i(y_t | g_i(\vec{x}_t \langle \mathcal{X}' \rangle_i, \vec{y}_{t-1}))}}{\sum_{y \in \mathcal{Y}} e^{\beta_i q_i(y | g_i(\vec{x}_t \langle \mathcal{X}' \rangle_i, \vec{y}_{t-1}))}}$$

Where users can alter:

- **Ground-truth Structure**
- **Markovianity**
- **Bounded Rationality**
- **Individual Consistency**
- **Variation in Practice**

Or:

Bring your own **completely custom** policy!

**Customizable Policies for Inference**

## Other Resources

- **Vision:** [www.vanderschaar-lab.com/synthetic-data-breaking-the-data-logjam-in-machine-learning-for-healthcare/](http://www.vanderschaar-lab.com/synthetic-data-breaking-the-data-logjam-in-machine-learning-for-healthcare/)
- **Papers:** [www.vanderschaar-lab.com/publications/synthetic-data](http://www.vanderschaar-lab.com/publications/synthetic-data)
- **Software:** [www.vanderschaar-lab.com/software/](http://www.vanderschaar-lab.com/software/)



Engagement  
sessions

## Inspiration Exchange

Themed discussion sessions specifically for machine learning students (particularly masters, Ph.D., and post-docs).

We would like to:

- discuss machine learning models and techniques
- share ideas about how machine learning can revolutionize healthcare
- spark new projects and collaborations
- raise awareness about this unique and exciting area of machine learning.

**Join us!**

[www.vanderschaar-lab.com/engagement-sessions/inspiration-exchange/](http://www.vanderschaar-lab.com/engagement-sessions/inspiration-exchange/)

