# **Generative Ratio Matching Networks**

Akash Srivastava $^{*,1,2}$ , Kai Xu $^{*,3}$ , Michael U. Gutmann $^3$ , Charles Sutton $^{3,4,5}$ 

\* denotes equal contributions

To appear in ICLR 2020; OpenReview: https://openreview.net/forum?id=SJg7spEYDS

 $<sup>^1</sup>$ MIT-IBM Watson AI Lab  $^2$ IBM Research  $^3$ University of Edinburgh  $^4$ Google AI  $^5$ Alan Turing Institute

#### Introduction and motivations

Implicit deep generative models:  $x = \mathrm{NN}(z; heta)$  where  $z \sim$  noise

Maximum mean discrepancy networks (MMD-nets)

- X can only work well with low-dimensional data
- **v** are very **stable** to train by avoiding the saddle-point optimization problem

Adversarial generative models (e.g. GANs, MMD-GANs)

- **c**an generate **high-dimensional** data such as natural images
- X are very **difficult** to train due to the saddle-point optimization problem

Q: Can we have two **?**?

A: Yes. Generative ratio matching (GRAM) is a *stable* learning algorithm for *implicit* deep generative models that does **not** involve a saddle-point optimization problem and therefore is easy to train **½**.

## Background: maximum mean discrepancy

The maximum mean discrepancy (MMD) between two distributions p and q is defined as

$$\mathrm{MMD}_{\mathcal{F}}(p,q) = \sup_{f \in \mathcal{F}} \left( \mathbb{E}_p[f(x)] - \mathbb{E}_q[f(x)] 
ight)$$

Gretton et al. (2012) shows that it is sufficient to choose  $\mathcal F$  to be a unit ball in an reproducing kernel Hilbert space (RKHS)  $\mathcal R$  with a characteristic kernel k s.t.

$$\mathrm{MMD}_{\mathcal{F}}(p,q) = 0 \iff p = q$$

The empirical estimate of the (squared) MMD with  $x_i \sim p$  and  $y_j \sim q$  by Monte Carlo is

$$\sqrt{ ext{MMD}_{\mathcal{R}}^2(p,q)} = rac{1}{N^2} \sum_{i=1}^N \sum_{i'=1}^N \underbrace{k(x_i,x_{i'})}_{i'=1} - rac{2}{NM} \sum_{i=1}^N \sum_{j=1}^M \underbrace{k(x_i,y_j)}_{j=1} + rac{1}{M^2} \sum_{j=1}^M \sum_{j'=1}^M \underbrace{k(y_j,y_{j'})}_{j'=1}$$

MMD-nets trains neural generators by minimizing this empirical estimate.

# Background: density ratio estimation via moment matching

Density ratio estimation: find  $\hat{r}(x)pprox r(x)=rac{p(x)}{q(x)}$  with samples from p and q

Finite moments under the fixed design setup gives  $\hat{\mathbf{r}}_q = [\hat{r}(x_1^q),...,\hat{r}(x_M^q)]$  for  $x^q \sim q$ 

$$\min_r \left( \int \underbrace{\phi(x)} p(x) dx - \int \underbrace{\phi(x)} r(x) q(x) dx 
ight)^2$$

Huang et al. (2007) shows that by changing  $\phi(x)$  to k(x;.), where k is a characteristic kernel in RKHS, we can match infinite moments and the optimization below agrees with the true r(x)

$$\min_{r \in \mathcal{R}} \left\| \int \underbrace{k(x;.)p(x)dx} - \int \underbrace{k(x;.)r(x)q(x)dx} 
ight\|_{\mathcal{R}}^2$$

Analytical solution:  $\hat{\mathbf{r}} = \mathbf{K}_{q,q}^{-1}\mathbf{K}_{q,p}\mathbf{1}$ , where  $[\mathbf{K}_{p,q}]_{i,j} = k(x_i^p, x_j^q)$  given samples  $\{x_i^p\}$  and  $\{x_j^q\}$ .

### **GRAM:** an overview

Two targets in the training loop

- 1. Learning a projection function  $f_{\theta}$  that maps the data space into a low-dimensional manifold which preserves the density ratio between data and model.
  - $\circ$  "Preserves":  $\left| rac{ar{p}_x(x)}{ar{q}_x(x)} 
    ight| = \left| rac{ar{p}(f_{ heta}(x))}{ar{q}(f_{ heta}(x))} 
    ight|$ , measured by  $D( heta) = \int q_x(x) \left( rac{ar{p}_x(x)}{ar{q}_x(x)} rac{ar{p}(f_{ heta}(x))}{ar{q}(f_{ heta}(x))} 
    ight)^2 dx$
  - $\circ$  ?  $\frac{p_x(x)}{q_x(x)}$  is hard to estimate in the high-dimensional space ...
- 2. Matching the model  $G_\gamma$  to data in the low-dimensional manifold by minimizing MMD
  - h MMD works well in low dimensional space
  - $\circ \ \ \underline{\mathrm{MMD}} = 0 \ leftharpoonup rac{ar{p}(f_{ heta}(x))}{ar{q}(f_{ heta}(x))} = 1 \ leftharpoonup rac{p_x(x)}{q_x(x)} = 1$

Both with empirical estimates based on samples from the data  $\{x_i^p\}$  and the model  $\{x_j^q\}$ .

 $f_{ heta}$  and  $G_{\gamma}$  are simultaneously updated.

## **GRAM: tractable ratio matching**

lacktriangledown Learning the projection function  $f_{ heta}(x)$  by minimizing the squared difference

$$D(\theta) = \int \underline{q_x(x)} \left( \frac{p_x(x)}{q_x(x)} - \frac{\bar{p}(f_{\theta}(x))}{\bar{q}(f_{\theta}(x))} \right)^2 dx$$

$$= C - 2 \int p_x(x) \frac{\bar{p}(f_{\theta}(x))}{\bar{q}(f_{\theta}(x))} dx + \int q_x(x) \left( \frac{\bar{p}(f_{\theta}(x))}{\bar{q}(f_{\theta}(x))} \right)^2 dx$$

$$= C - 2 \int \bar{p}(f_{\theta}(x)) \frac{\bar{p}(f_{\theta}(x))}{\bar{q}(f_{\theta}(x))} df_{\theta}(x) + \int \bar{q}(f_{\theta}(x)) \left( \frac{\bar{p}(f_{\theta}(x))}{\bar{q}(f_{\theta}(x))} \right)^2 df_{\theta}(x)$$

$$= C' - \left( \int \bar{q}(f_{\theta}(x)) \left( \frac{\bar{p}(f_{\theta}(x))}{\bar{q}(f_{\theta}(x))} \right)^2 df_{\theta}(x) - 1 \right) = C' - \text{PD}(\bar{q}, \bar{p})$$

... or by equivalently maximizing the Pearson divergence 😄.

A reminder on LOTUS:  $\int p(x)g(f(x))dx = \int p(f(x))g(f(x))df(x)$ 

[1]: A derivation of the reverse order for a special case of projection functions was also shown in (Sugiyama et al., 2011).

## **GRAM: Pearson divergence maximization**

Monte Carlo approximation of PD

$$ext{PD}(ar{q},ar{p}) = \int ar{q}(f_{ heta}(x)) \left(rac{ar{p}(f_{ heta}(x))}{ar{q}(f_{ heta}(x))}
ight)^2 df_{ heta}(x) - 1 pprox rac{1}{N} \sum_{i=1}^N \left(rac{ar{p}(f_{ heta}(x_i^q))}{ar{q}(f_{ heta}(x_i^q))}
ight)^2 - 1$$

where  $x_i^q \sim q_x$  or equivalently  $f_{ heta}(x_i^q) \sim ar{q}$ .

Given samples  $\{x_i^p\}$  and  $\{x_j^q\}$ , we use the density ratio estimator based on infinite moments matching (Huang et al., 2007, Sugiyama et al., 2012) under the fixed-design setup

$$\hat{\mathbf{r}}_{q,_{ heta}} = \mathbf{K}_{q,q}^{-1}\mathbf{K}_{q,p}\mathbf{1} = [\hat{r}_{ heta}(x_1^q),...,\hat{r}_{ heta}(x_M^q)]^ op$$

where  $[\mathbf{K}_{p,q}]_{i,j}=k(f_{ heta}(x_i^p),f_{ heta}(x_j^q))$  and  $r_{ heta}(x)=rac{ar{p}(f_{ heta}(x))}{ar{q}(f_{ heta}(x))}.$ 

### GRAM: matching projected model to projected data

2 Minimizing the empirical estimator of MMD in the low-dimensional manifold

$$egin{aligned} \min_{\gamma} \left[ rac{1}{N^2} \sum_{i=1}^{N} \sum_{i'=1}^{N} k(f_{ heta}(x_i), f_{ heta}(x_{i'})) - rac{2}{NM} \sum_{i=1}^{N} \sum_{j=1}^{M} k(f_{ heta}(x_i), f_{ heta}(G_{\gamma}(z_j))) 
ight. \ \left. + rac{1}{M^2} \sum_{j=1}^{M} \sum_{j'=1}^{M} k(f_{ heta}(G_{\gamma}(z_j)), f_{ heta}(G_{\gamma}(z_{j'}))) 
ight] \end{aligned}$$

with respect to its parameters  $\gamma$ .

### GRAM: the complete algorithm

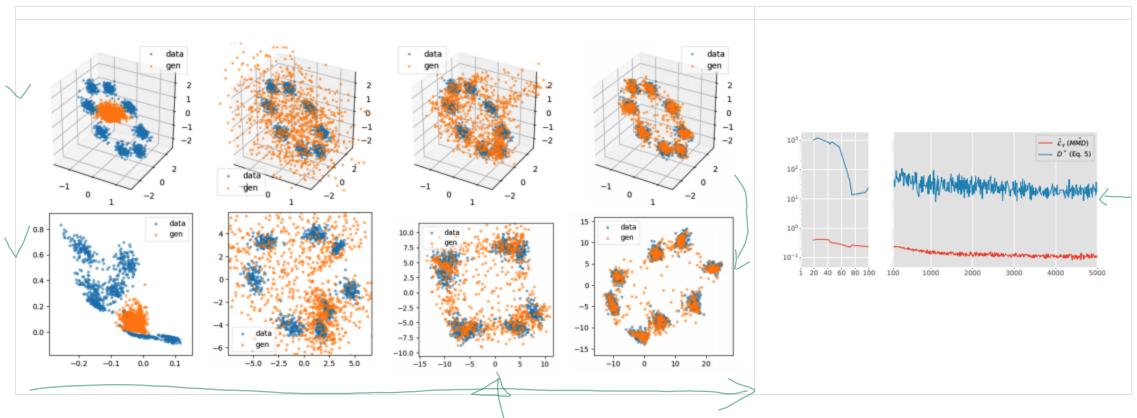
#### Loop until convergence

- 1. Sample a minibatch of data and generate samples from  $G_{\gamma}$
- 2. Project data and generated samples using  $f_{ heta}$
- 3. Compute the kernel Gram matrices using Gaussian kernels in the projected space
- 4. Compute the objectives for  $f_{ heta}$  and  $G_{\gamma}$  using the same kernel Gram matrices
- 5. Backprop two objectives to get the gradients for heta and  $\gamma$
- 6. Perform gradient update for heta and  $\gamma$
- Fun fact: the objectives in our GRAM algorithm both heavily relies on the use of kernel Gram matrices.

# How do GRAM-nets compare to other deep generative models

GAN	MMD-net	MMD-GAN	GRAM-net
$z \sim p_z$ $\downarrow^{\gamma}$ $x^q$ $x^p \sim p_x$ $\downarrow^{\theta}$ $\downarrow^{\theta}$ $\downarrow^{\theta}$ $\downarrow^{\theta}$ $\downarrow^{\phi}$	$egin{array}{cccccccccccccccccccccccccccccccccccc$	$z \sim p_z  x^p \sim p_x$ $\downarrow^{\gamma}  \downarrow^{ heta}$ $x^q  f_{ heta}(x^p)$ $\downarrow^{ heta}$ $f_{ heta}(x^q) \longrightarrow \mathbf{K}$ $\mathcal{L}_{\gamma} \stackrel{\smile}{\smile} \mathcal{L}_{ heta}$	$egin{array}{cccccccccccccccccccccccccccccccccccc$

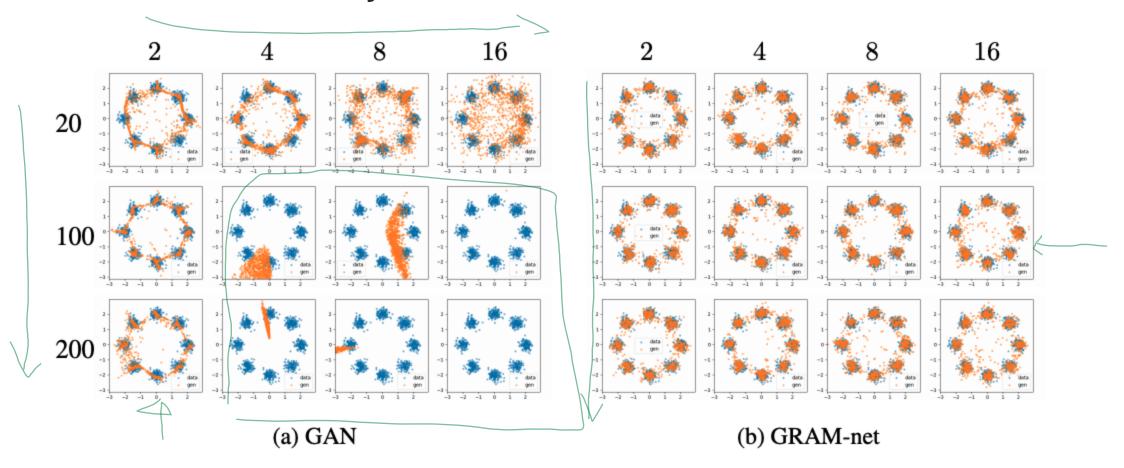
# Illustration of GRAM training



Blue: data, Orange: samples

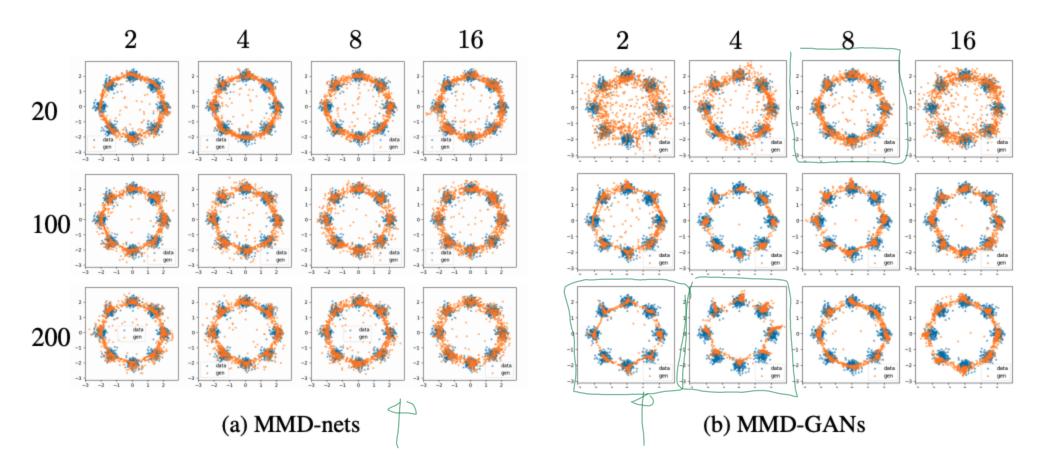
Top: original, Bottom: projected

# **Evaluations: the stability of models**



x-axis = noise dimension and y-axis = generator layer size

# **Evaluations: the stability of models (continued)**



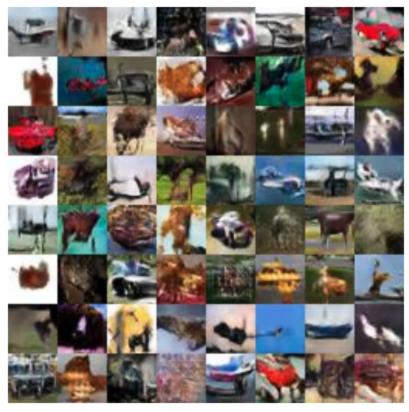
x-axis = noise dimension and y-axis = generator layer size

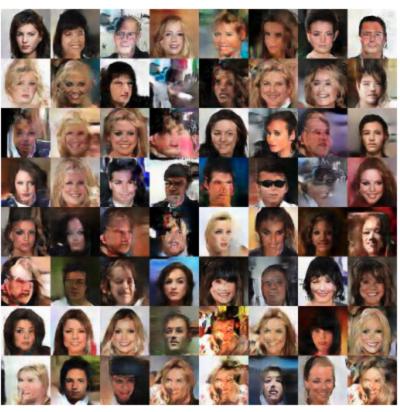
# Quantitative results: sample quality

Table 1: Sample quality (measured by FID; lower is better) of GRAM-nets compared to GANs.

Arch.	Dataset	MMD-GAN	GAN	GRAM-net
DCGAN Weaker DCGAN	Cifar10 Cifar10 CelebA	$40.00 \pm 0.56$ $210.85 \pm 8.92$ $41.105 \pm 1.42$	$26.82 \pm 0.49 31.64 \pm 2.10 30.97 \pm 5.32$	$24.85 \pm 0.94 \ 24.82 \pm 0.62 \ 27.04 \pm 4.24$

# **Qualitative results: random samples**





(a) CIFAR10 (b) CelebA

The end