

Deep kernel-based distances between distributions

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Based on work with:

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What's a kernel again?

- Linear classifiers: $\hat{y}(x) = \text{sign}(f(x)), f(x) = w^\top (x, 1)$

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- Use a “richer” x :

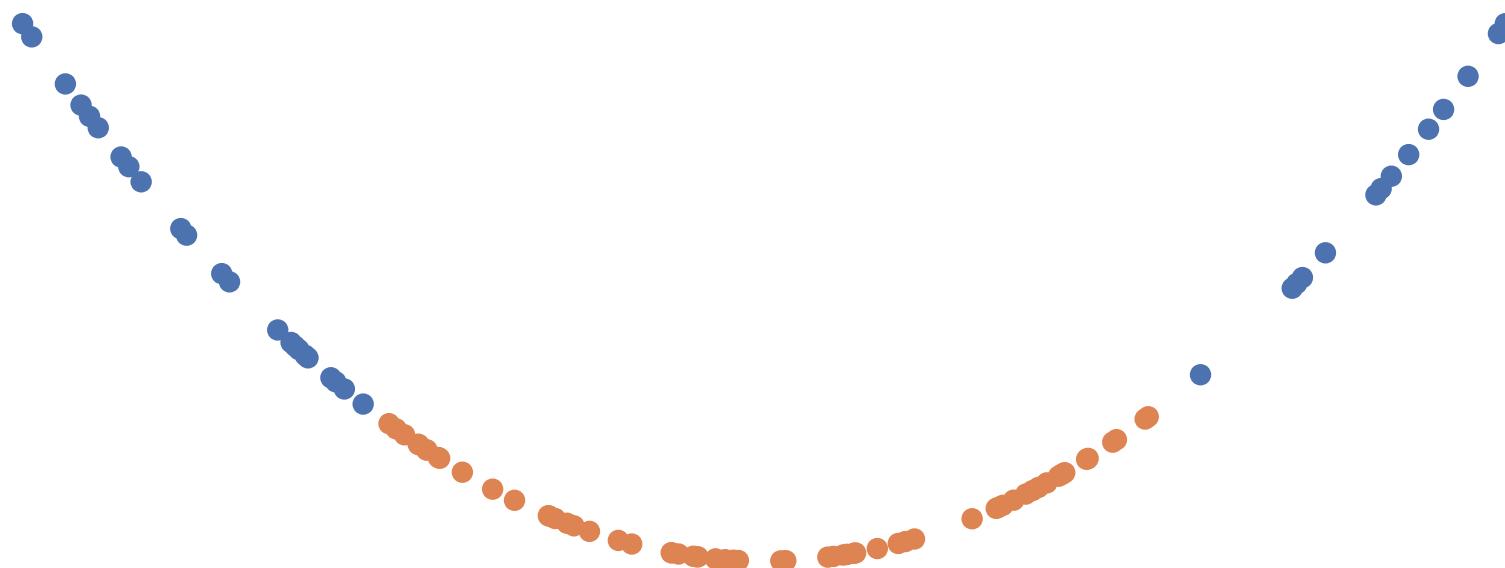
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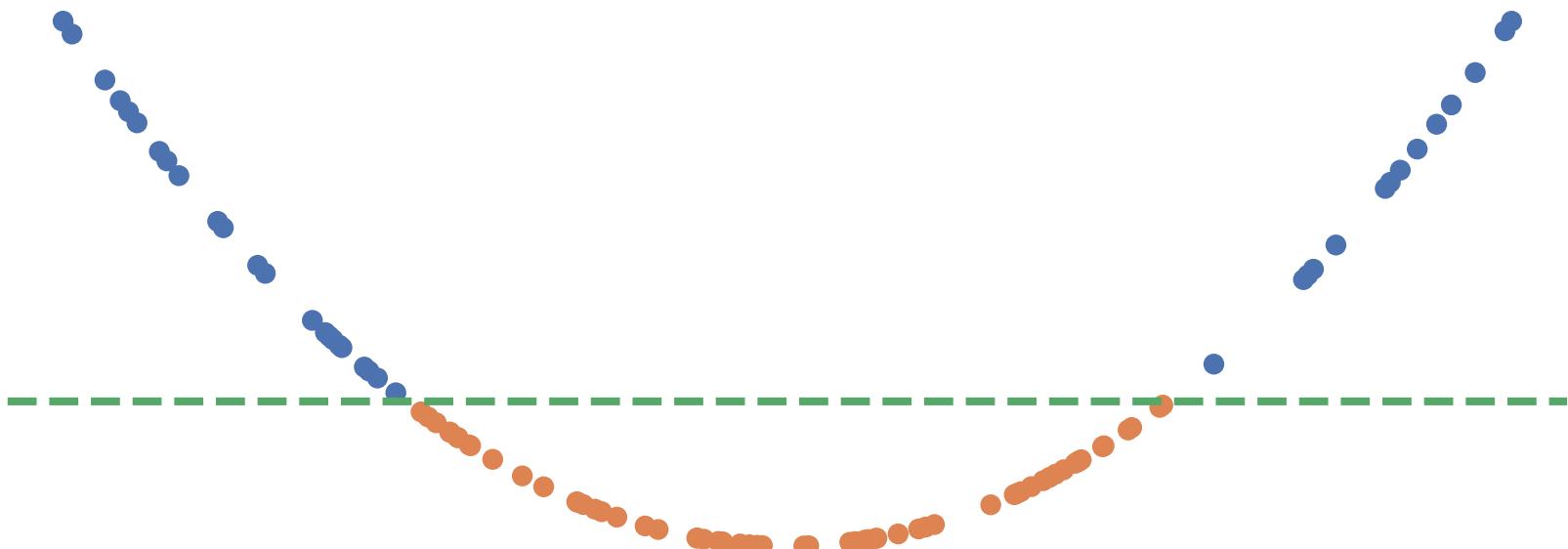
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- Can avoid explicit $\phi(x)$; instead $k(x, y) = \langle \phi(x), \phi(y) \rangle_{\mathcal{H}}$
- “Kernelized” algorithms access data only through $k(x, y)$

$$f(x) = \langle w, \phi(x) \rangle_{\mathcal{H}} = \sum_{i=1}^n \alpha_i k(X_i, x)$$

Reproducing Kernel Hilbert Space (RKHS)

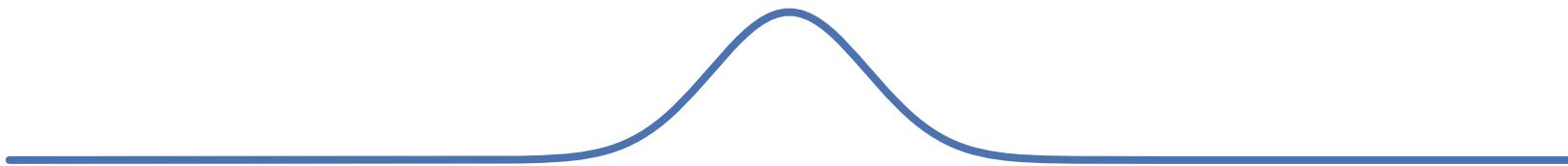
- Ex: Gaussian RBF

$$k(x, y) = \exp\left(-\frac{\|x - y\|^2}{2\sigma^2}\right)$$

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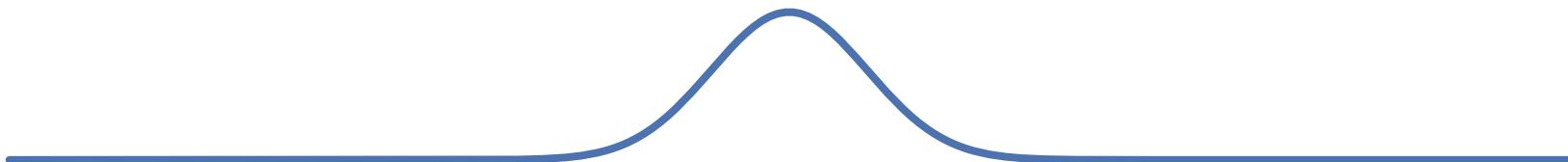
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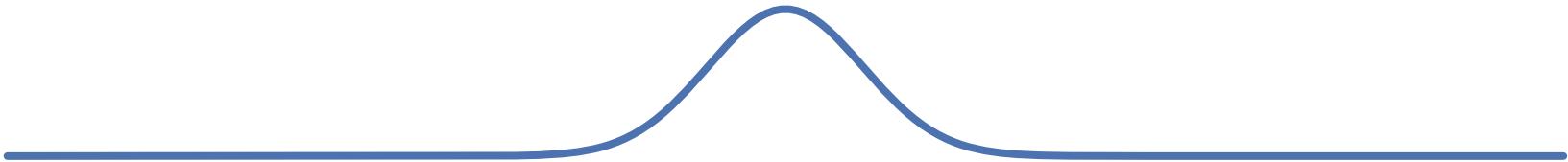


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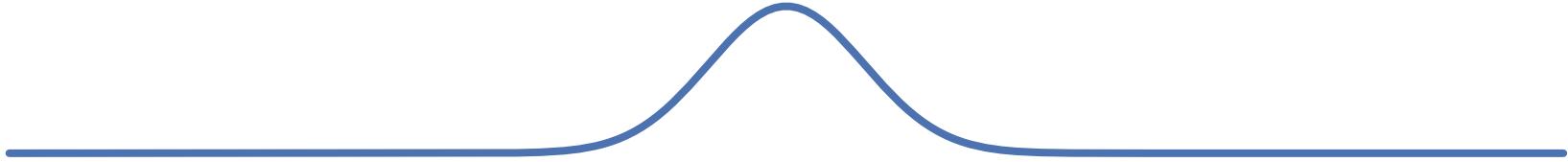


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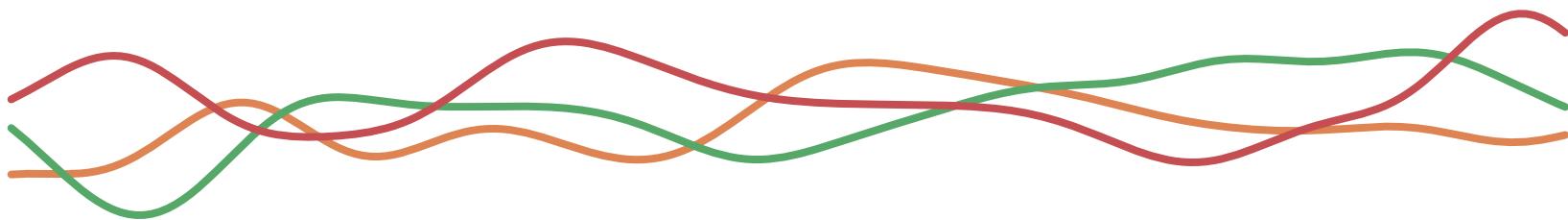


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- $\|\sum_i \alpha_i \phi(X_i)\|_{\mathcal{H}}^2 = \alpha^\top K \alpha$, where $K_{ij} = k(X_i, X_j)$
- $\text{argmin}_{f \in \mathcal{H}} L(f(X_1), \dots, f(X_n)) + \lambda \|f\|_{\mathcal{H}}^2$ is in $\{\sum_{i=1}^n \alpha_i \phi(X_i) \mid \alpha \in \mathbb{R}^n\}$ - the representer theorem

Maximum Mean Discrepancy (MMD)

$$\text{MMD}_k(\mathbb{P}, \mathbb{Q}) = \sup_{\|f\|_{\mathcal{H}} \leq 1} \mathbb{E}_{\mathbf{X} \sim \mathbb{P}} [f(\mathbf{X})] - \mathbb{E}_{\mathbf{Y} \sim \mathbb{Q}} [f(\mathbf{Y})]$$

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MMD as feature matching

$$\text{MMD}_k(\mathbb{P}, \mathbb{Q}) = \left\| \mathbb{E}_{\mathbf{X} \sim \mathbb{P}} [\varphi(\mathbf{X})] - \mathbb{E}_{\mathbf{Y} \sim \mathbb{Q}} [\varphi(\mathbf{Y})] \right\|_{\mathcal{H}}$$

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- Many kernels: **infinite-dimensional** \mathcal{H}

MMD and OT

Entropic Regularization

Schrödinger's problem:

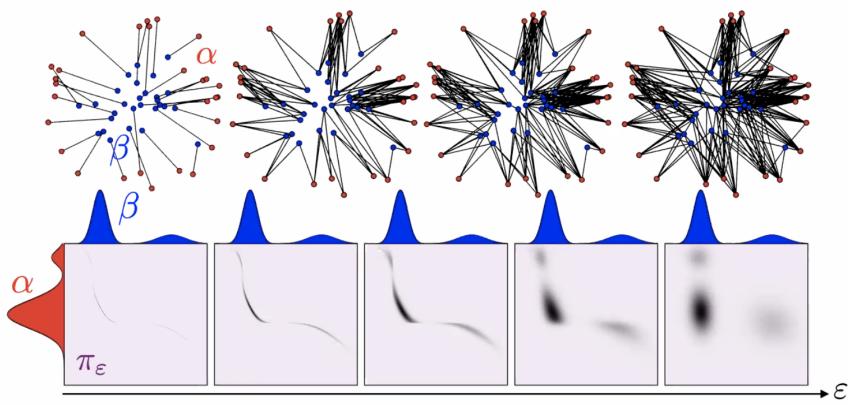
[1931]

$$\min_{\mathbf{P} \mathbf{1} = \mathbf{a}, \mathbf{P}^\top \mathbf{1} = \mathbf{b}} \sum_{i,j} d(\mathbf{x}_i, \mathbf{y}_j)^p \mathbf{P}_{i,j} + \varepsilon \mathbf{P}_{i,j} \log(\mathbf{P}_{i,j})$$



Erwin Schrödinger

$$\pi = \sum_{i,j} \mathbf{P}_{i,j} \delta_{\mathbf{x}_i, \mathbf{y}_j}$$

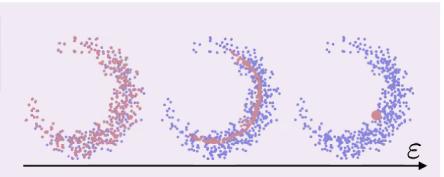


Sinkhorn Divergences

$$W_p^\varepsilon(\alpha, \beta) \stackrel{\text{def.}}{=} \min_{\mathbf{P} \mathbf{1} = \mathbf{a}, \mathbf{P}^\top \mathbf{1} = \mathbf{b}} \sum_{i,j} d(\mathbf{x}_i, \mathbf{y}_j)^p \mathbf{P}_{i,j} + \varepsilon \mathbf{P}_{i,j} \log(\mathbf{P}_{i,j})$$

Problem: $W_p^\varepsilon(\alpha, \alpha) \neq 0$

$$\min_{\alpha} W_p^\varepsilon(\alpha, \beta)$$



$$\overline{W}_p^\varepsilon(\alpha, \beta) \stackrel{\text{def.}}{=} W_p^\varepsilon(\alpha, \beta)^p - \frac{1}{2} W_p^\varepsilon(\alpha, \alpha)^p - \frac{1}{2} W_p^\varepsilon(\beta, \beta)^p$$

[Ramdas, García Trillo, Cuturi, 2017]

$$\text{Theorem: } W_p(\alpha, \beta)^p \xleftarrow[\text{[Léonard 2012]}]{\varepsilon \rightarrow 0} \overline{W}_p^\varepsilon(\alpha, \beta)^p \xrightarrow[\text{[Carlier et al 2017]}]{\varepsilon \rightarrow +\infty} \|\alpha - \beta\|_{-d^p}^2$$

Kernel norms (MMD): $\|\xi\|_{-d^p}^2 \stackrel{\text{def.}}{=} - \int_{\mathcal{X}^2} d(x, y)^p d\xi(x) d\xi(y)$

Proposition: $\|\cdot\|_{-\|\cdot\|^p}$ is a norm for $0 < p < 2$.



Arthur Gretton

Estimating MMD

$$\text{MMD}_k^2(\mathbb{P}, \mathbb{Q}) = \mathbb{E}_{\mathbf{X}, \mathbf{X}' \sim \mathbb{P}} [k(\mathbf{X}, \mathbf{X}')] + \mathbb{E}_{\mathbf{Y}, \mathbf{Y}' \sim \mathbb{Q}} [k(\mathbf{Y}, \mathbf{Y}')] - 2 \mathbb{E}_{\substack{\mathbf{X} \sim \mathbb{P} \\ \mathbf{Y} \sim \mathbb{Q}}} [k(\mathbf{X}, \mathbf{Y})]$$

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$$\widehat{\text{MMD}}_k^2(\mathbf{X}, \mathbf{Y}) = \text{mean}(K_{\mathbf{XX}}) + \text{mean}(K_{\mathbf{YY}}) - 2 \text{mean}(K_{\mathbf{XY}})$$

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—	1.0	0.2	0.6
—	0.2	1.0	0.5
—	0.6	0.5	1.0

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$K_{\mathbf{YY}}$

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—	1.0	0.8	0.7
—	0.8	1.0	0.6
—	0.7	0.6	1.0

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$K_{\mathbf{YY}}$

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$K_{\mathbf{XY}}$

—	0.3	0.1	0.2
—	0.2	0.3	0.3
—	0.2	0.1	0.4

I: Two-sample testing

- Given samples from two unknown distributions

$$X \sim P \quad Y \sim Q$$

- Question: is $P = Q$?

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- Does my generative model Q_θ match P_{data} ?

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$$\textcolor{blue}{X} \sim \mathbb{P} \quad \textcolor{brown}{Y} \sim \mathbb{Q}$$

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- Does presence of this protein affect DNA binding? [[MMDiff2](#)]
- Do these dob and birthday columns mean the same thing?
- Does my generative model \mathbb{Q}_θ match \mathbb{P}_{data} ?
- Independence testing: is $P(\textcolor{blue}{X}, \textcolor{brown}{Y}) = P(\textcolor{blue}{X})P(\textcolor{brown}{Y})$?

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- Given samples from two unknown distributions

$$X \sim P \quad Y \sim Q$$

- Question: is $P = Q$?
- Hypothesis testing approach:

$$H_0 : P = Q \quad H_1 : P \neq Q$$

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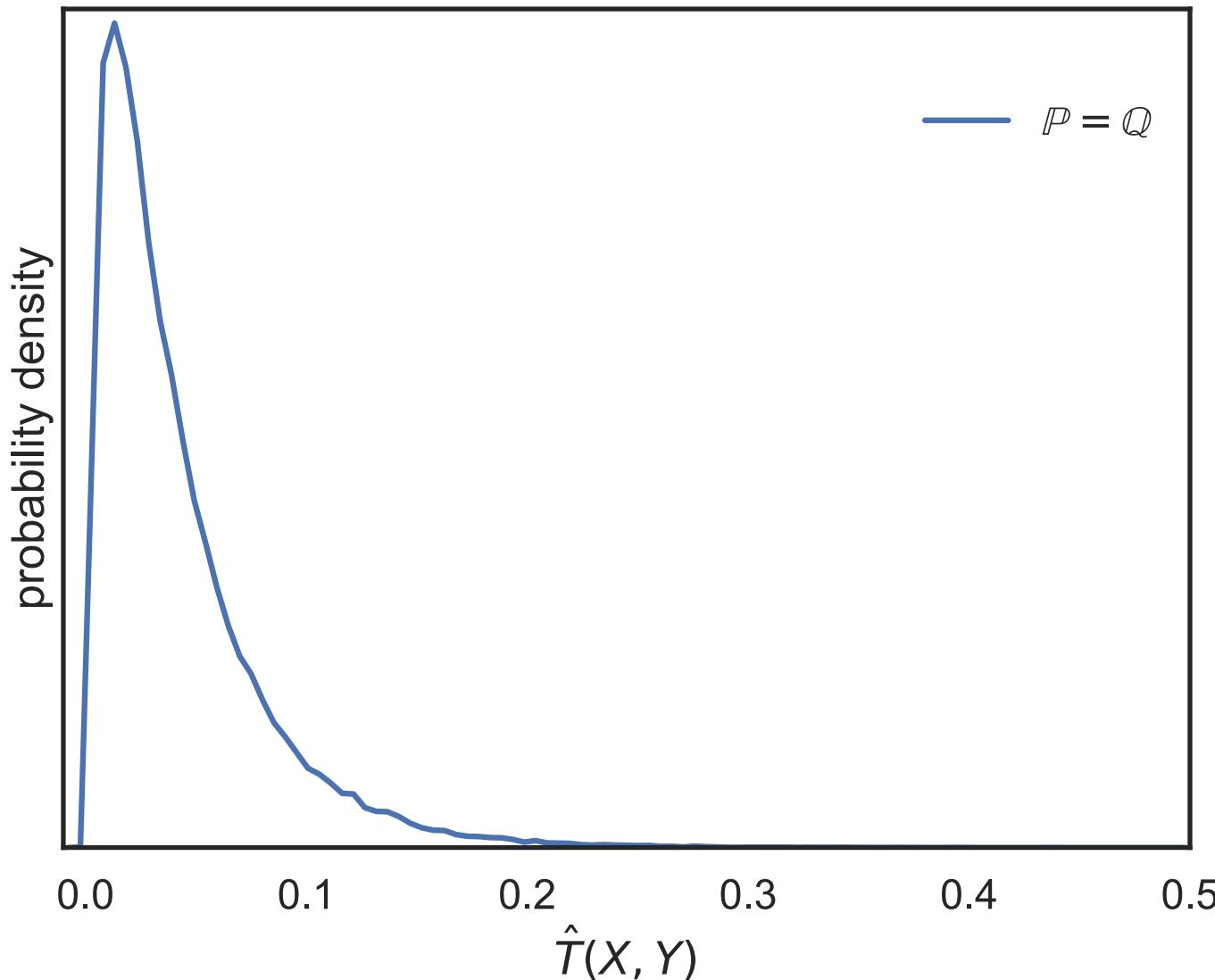
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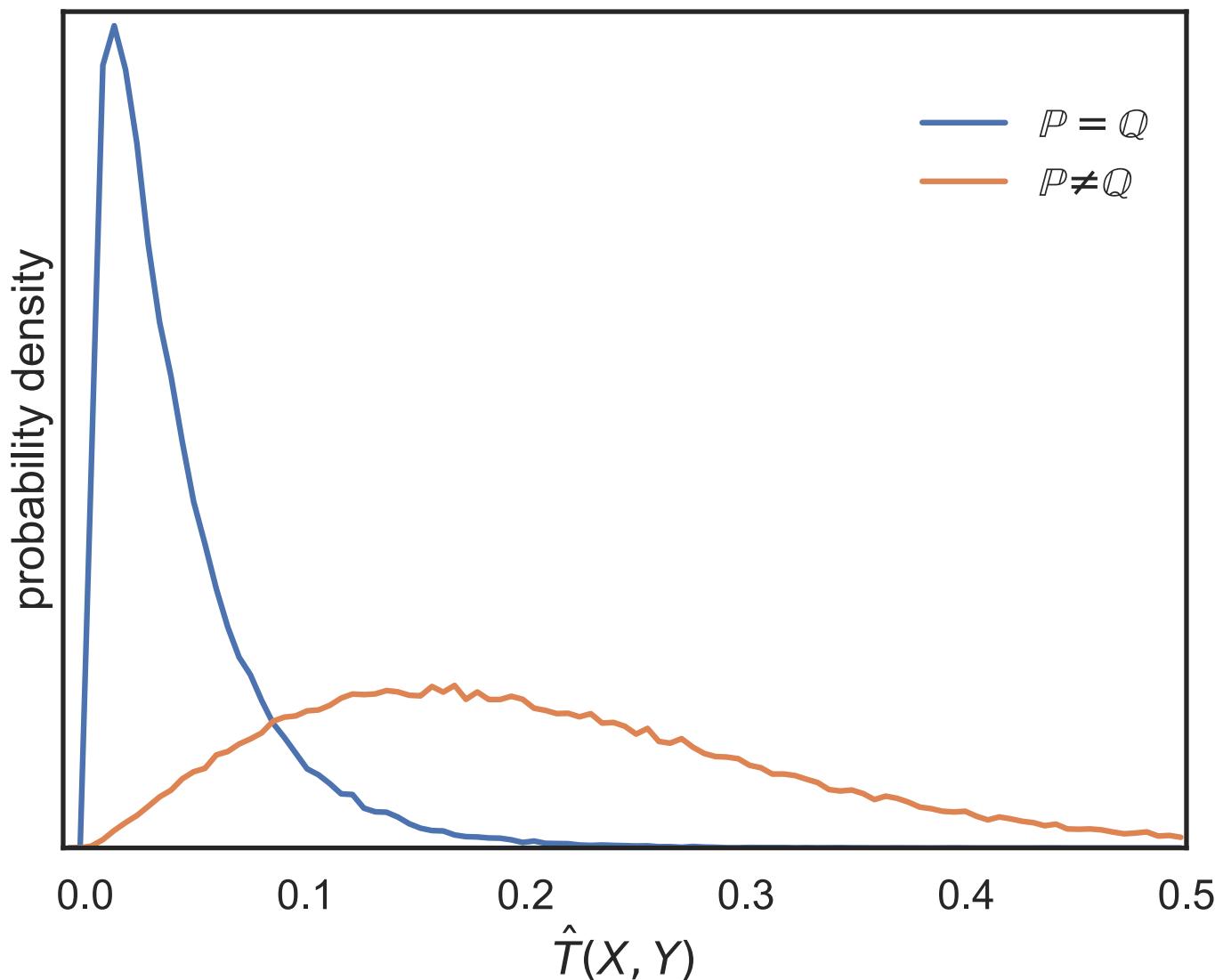
$$H_0 : \mathbb{P} = \mathbb{Q} \quad H_1 : \mathbb{P} \neq \mathbb{Q}$$

- Reject H_0 if test statistic $\hat{T}(X, Y) > c_\alpha$

What's a hypothesis test again?

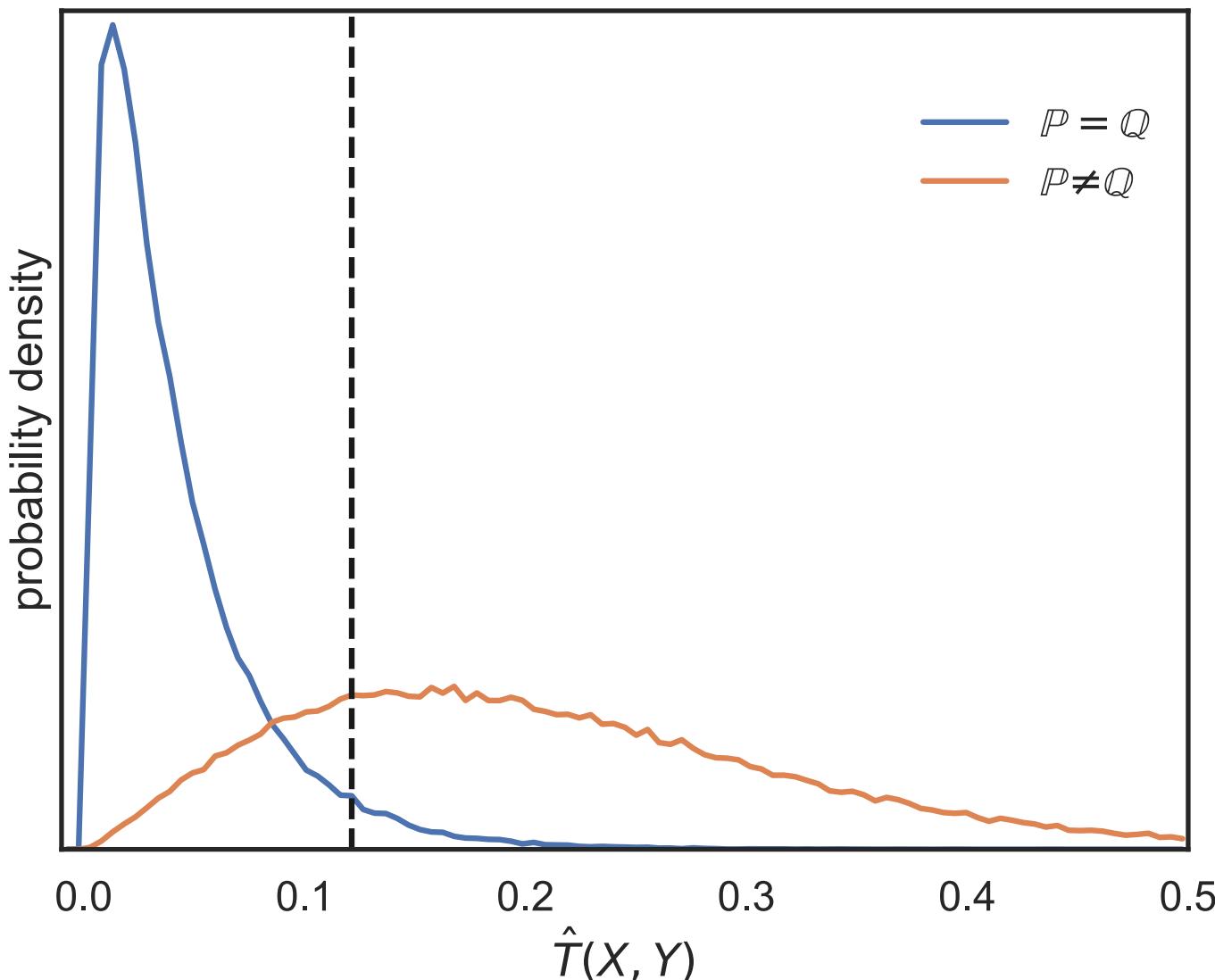


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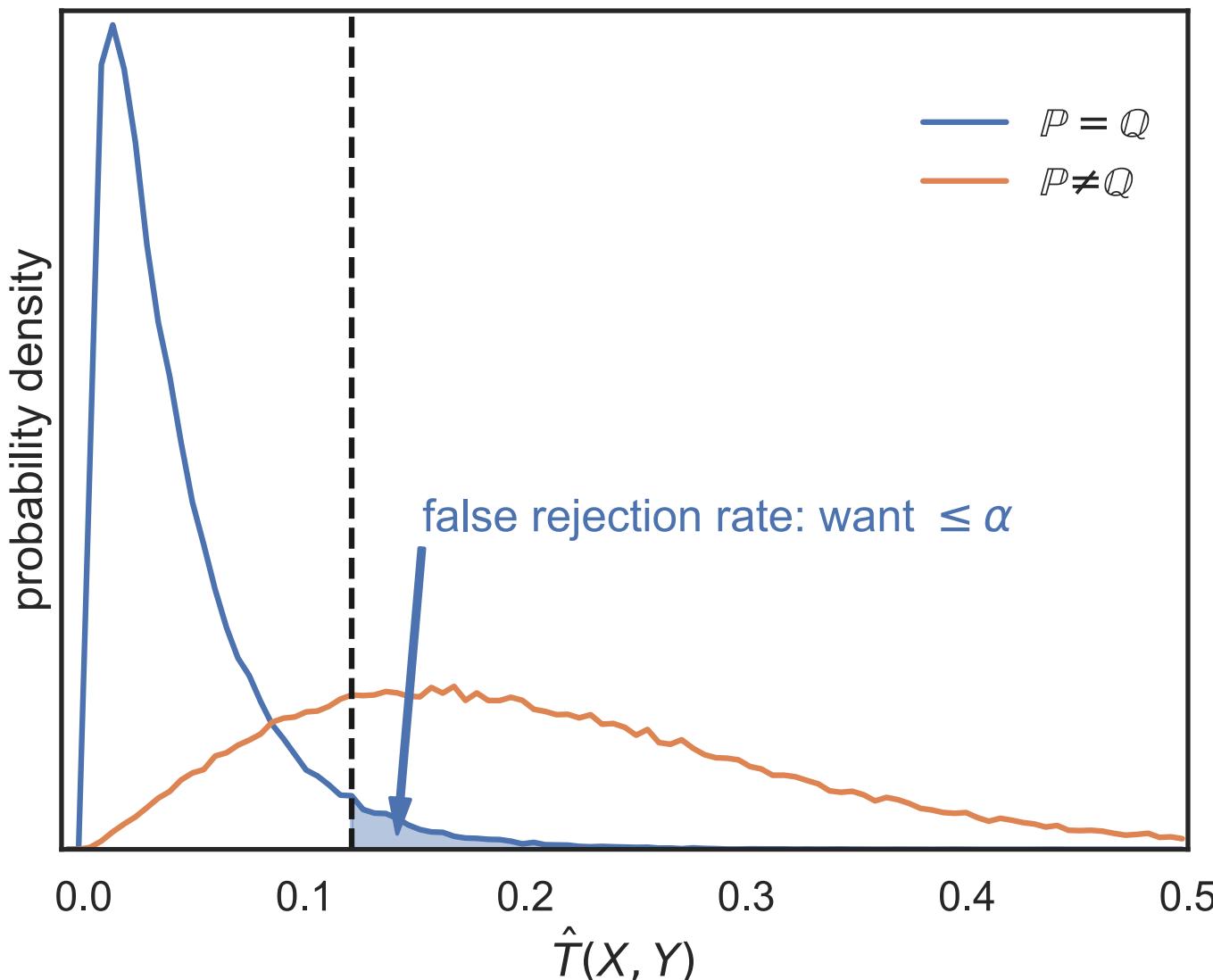
What's a hypothesis test again?

don't reject H_0 c_α reject H_0 (say $P \neq Q$)



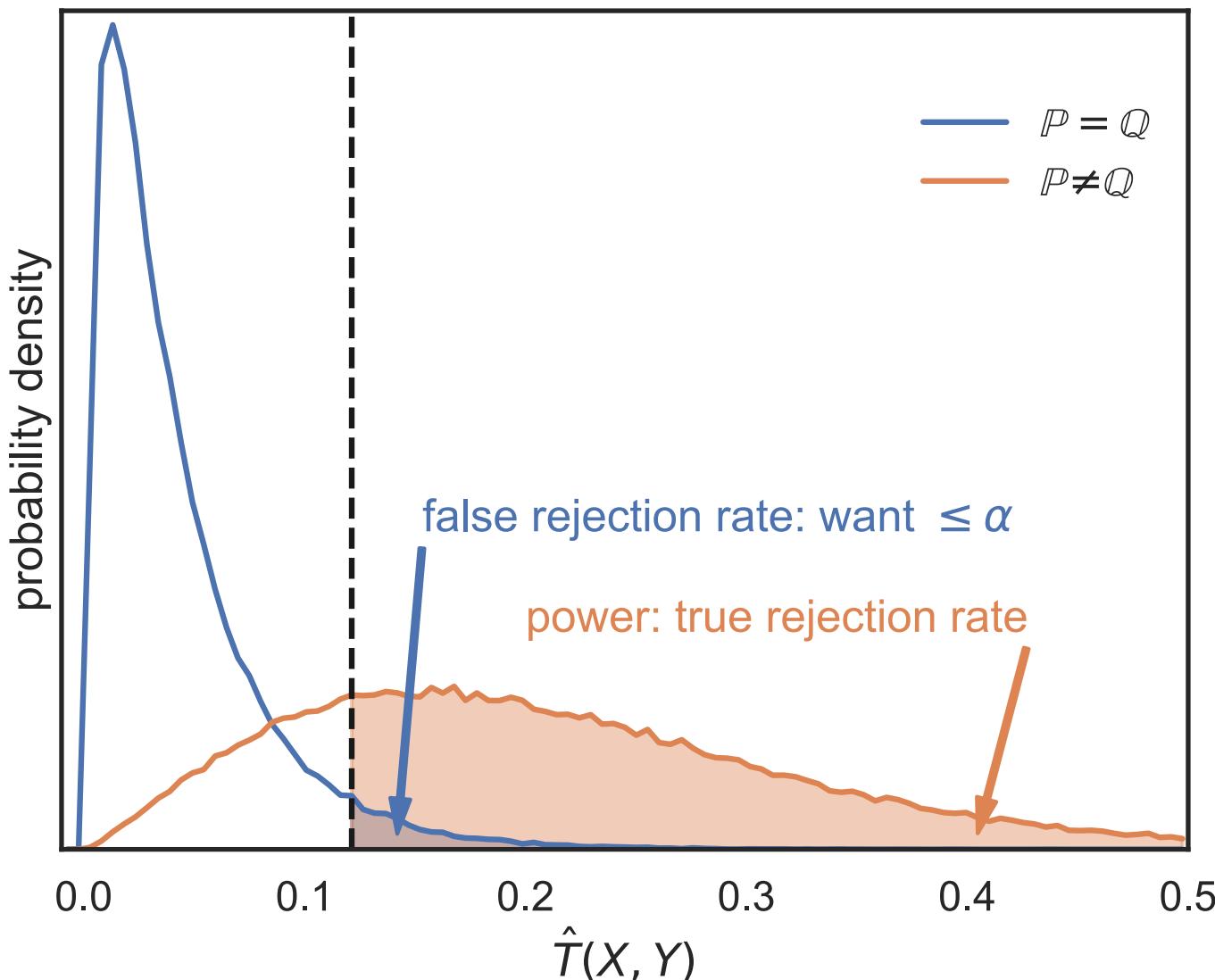
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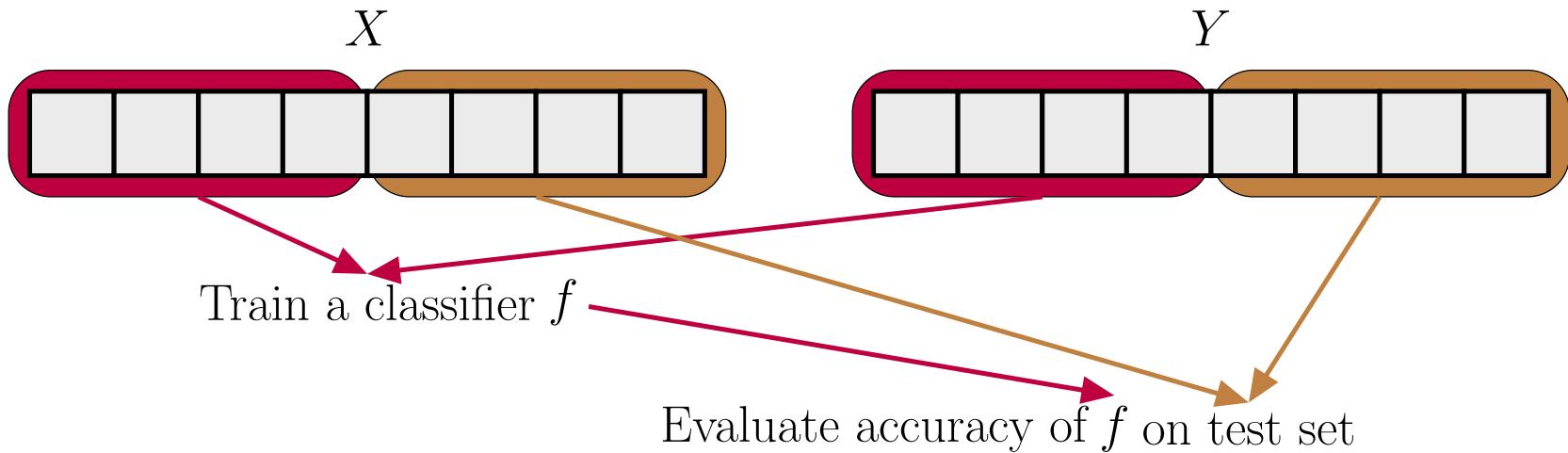
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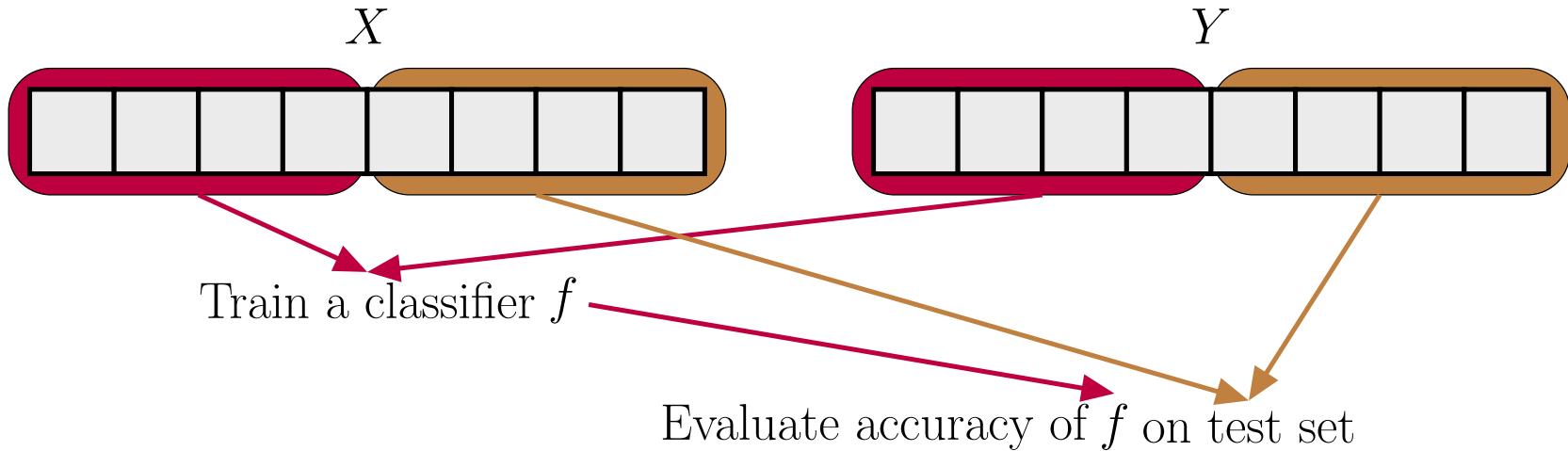
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- Need enormous n if kernel is bad for problem

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get $\widehat{\text{MMD}}(\mathbf{X}, \mathbf{Y}) = \left| \hat{T}(\mathbf{X}, \mathbf{Y}) - \frac{1}{2} \right|$

Optimizing test power

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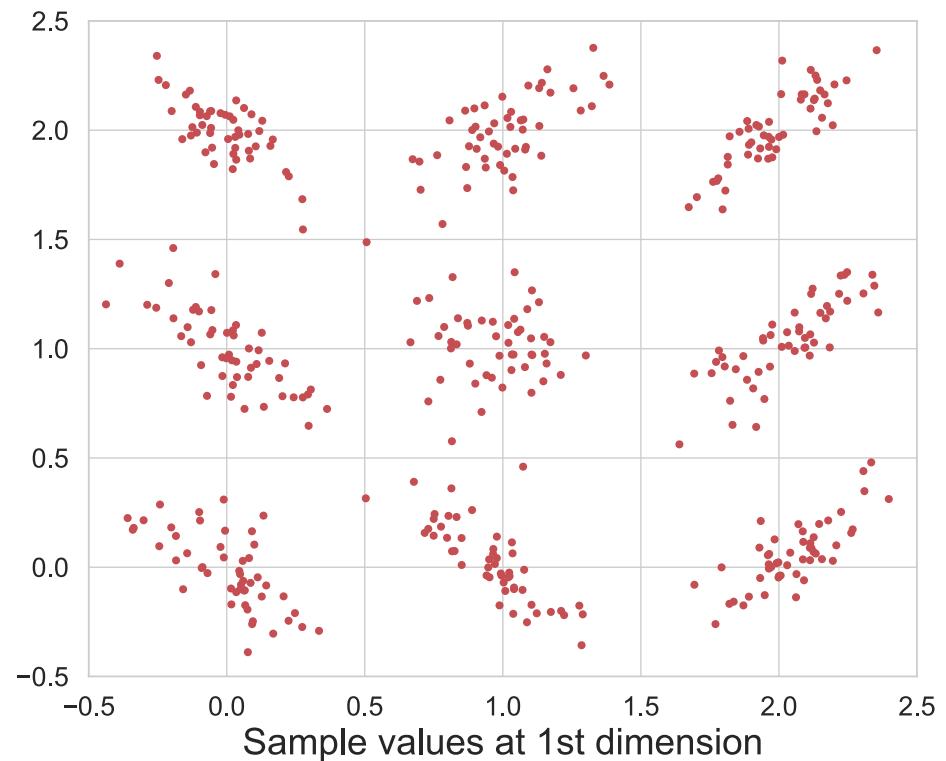
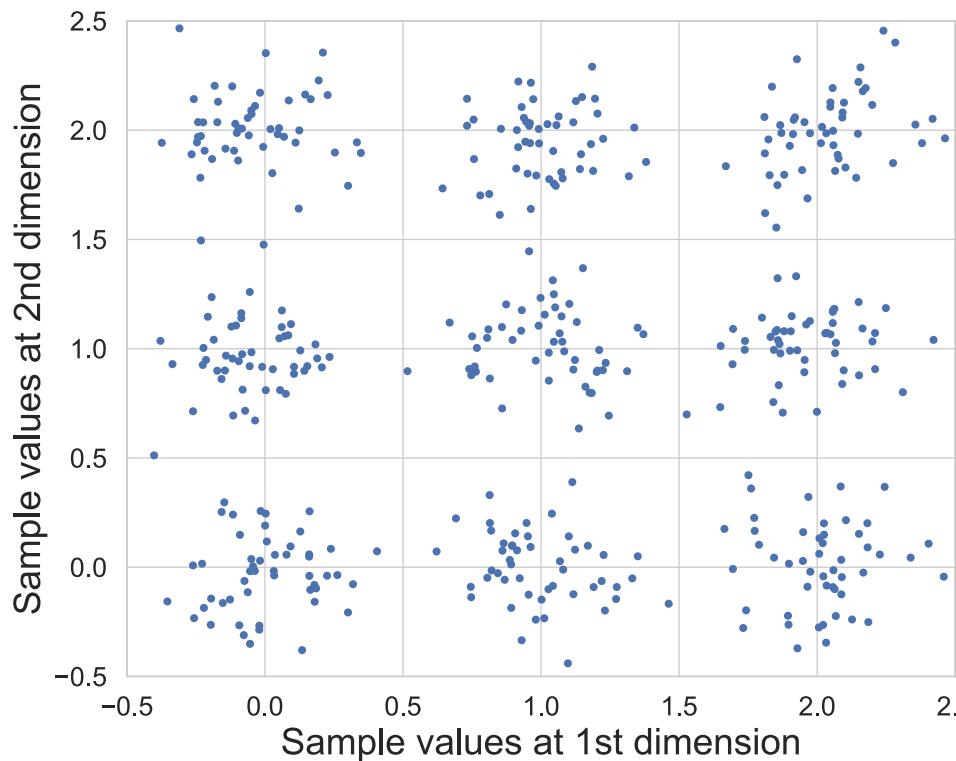
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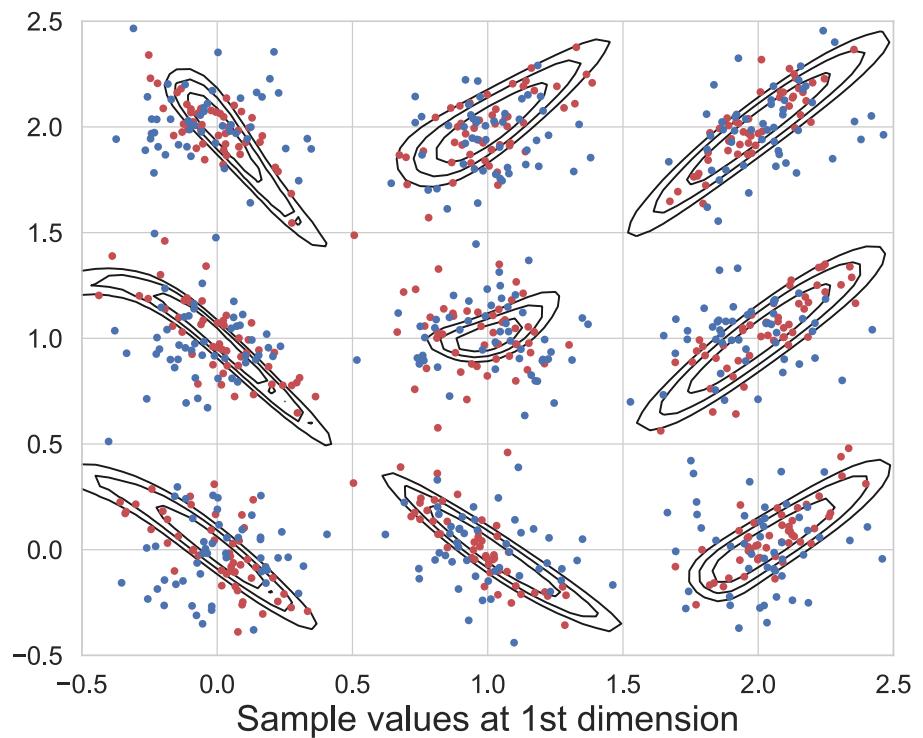
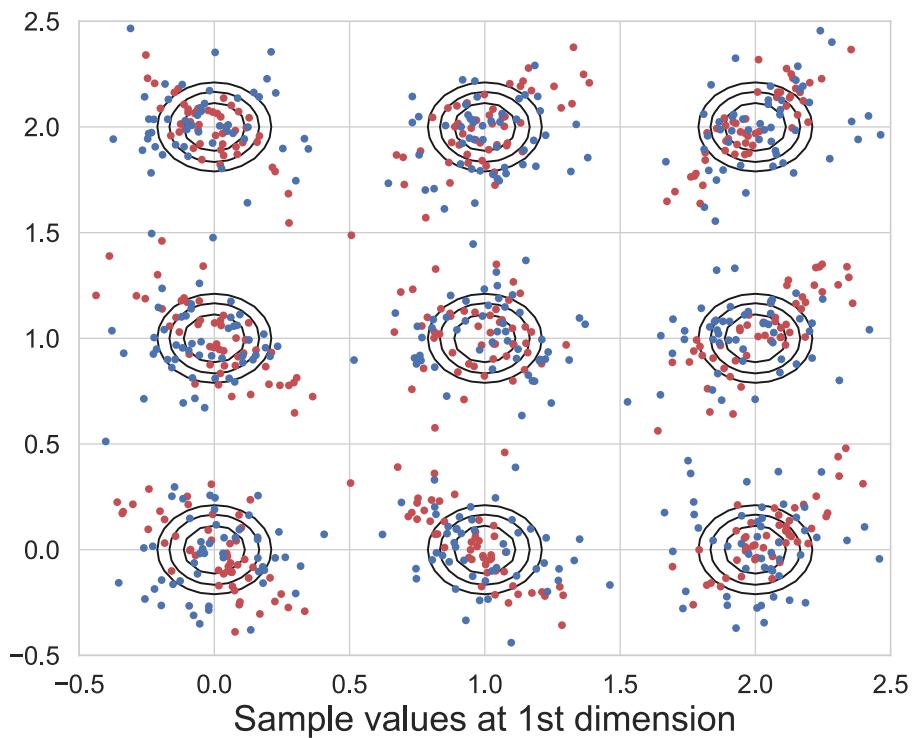
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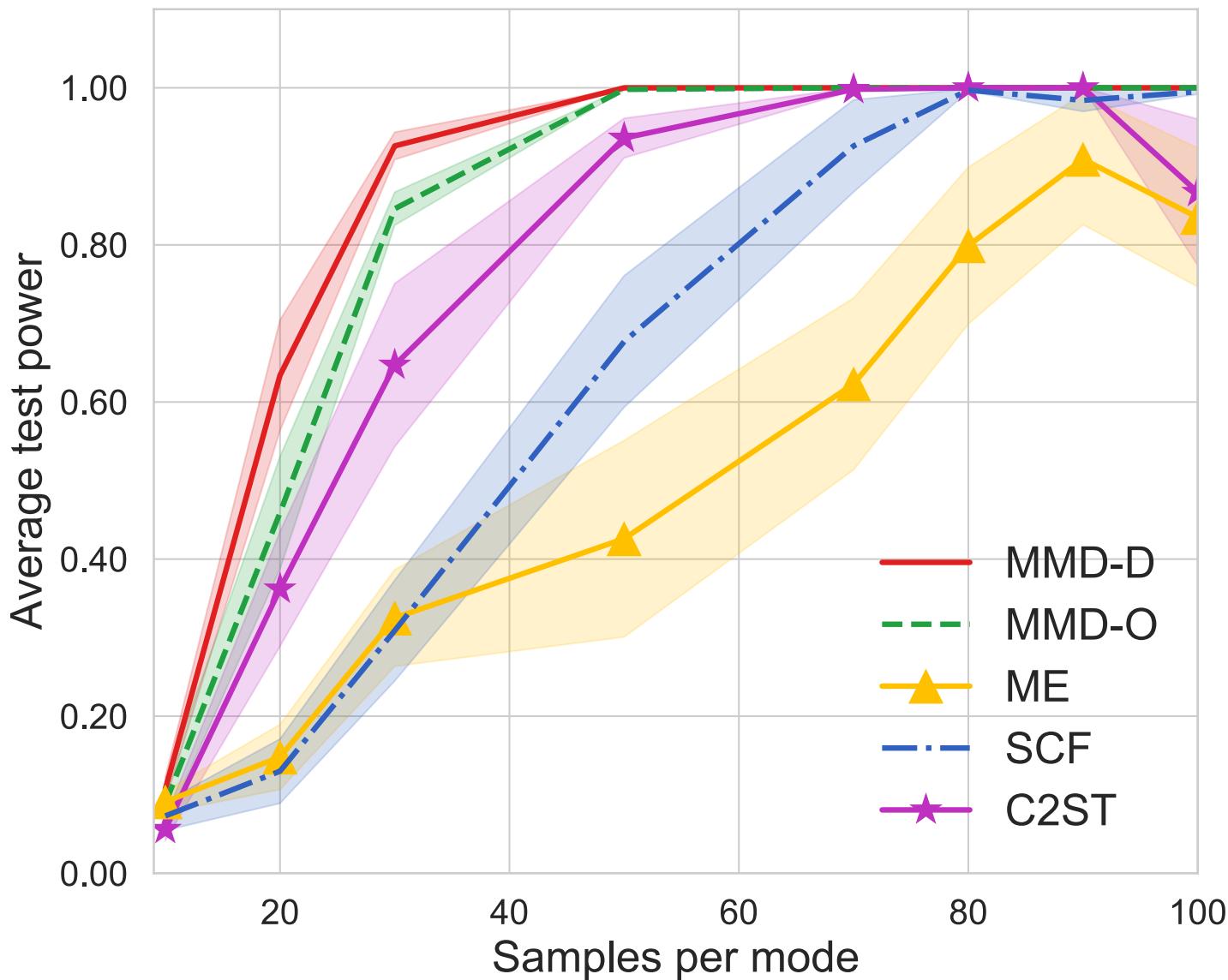
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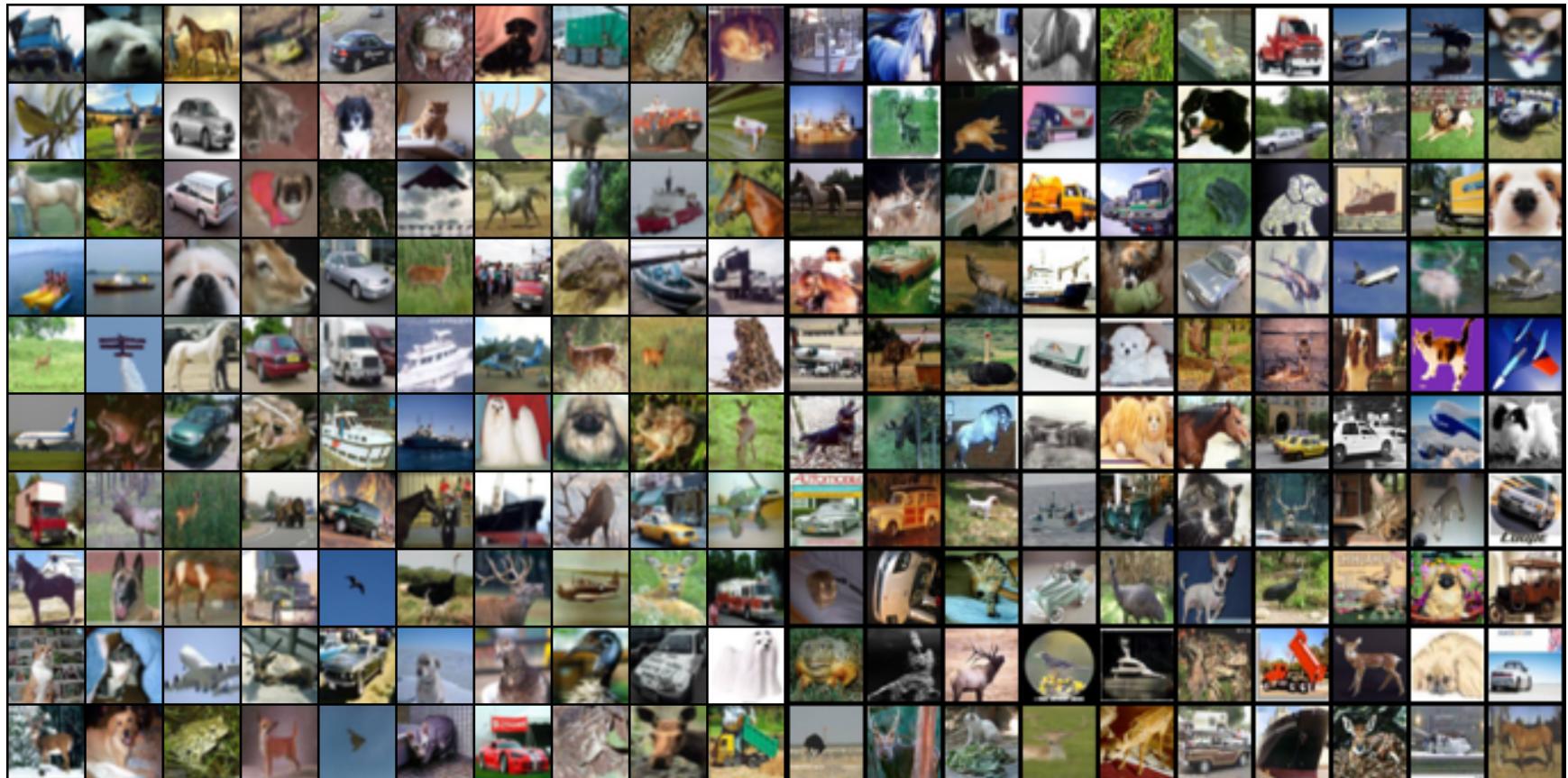
Blobs kernels



Blobs results



CIFAR-10 vs CIFAR-10.1



Train on 1 000, test on 1 031, repeat 10 times. Rejection rates:

ME	SCF	C2ST	MMD-O	MMD-D
0.588	0.171	0.452	0.316	0.744

Ablation vs classifier-based tests

Dataset	Cross-entropy			Max power		
	Sign	Lin	Ours	Sign	Lin	Ours
Blob	0.84	0.94	0.90	-	0.95	0.99
High-d Gauss. mix.	0.47	0.59	0.29	-	0.64	0.66
Higgs	0.26	0.40	0.35	-	0.30	0.40
MNIST vs GAN	0.65	0.71	0.80	-	0.94	1.00

II: Training implicit generative models

Given samples from a distribution \mathbb{P} over \mathcal{X} ,
we want a model that can produce new samples from $\mathbb{Q}_\theta \approx \mathbb{P}$



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thispersondoesnotexist.com

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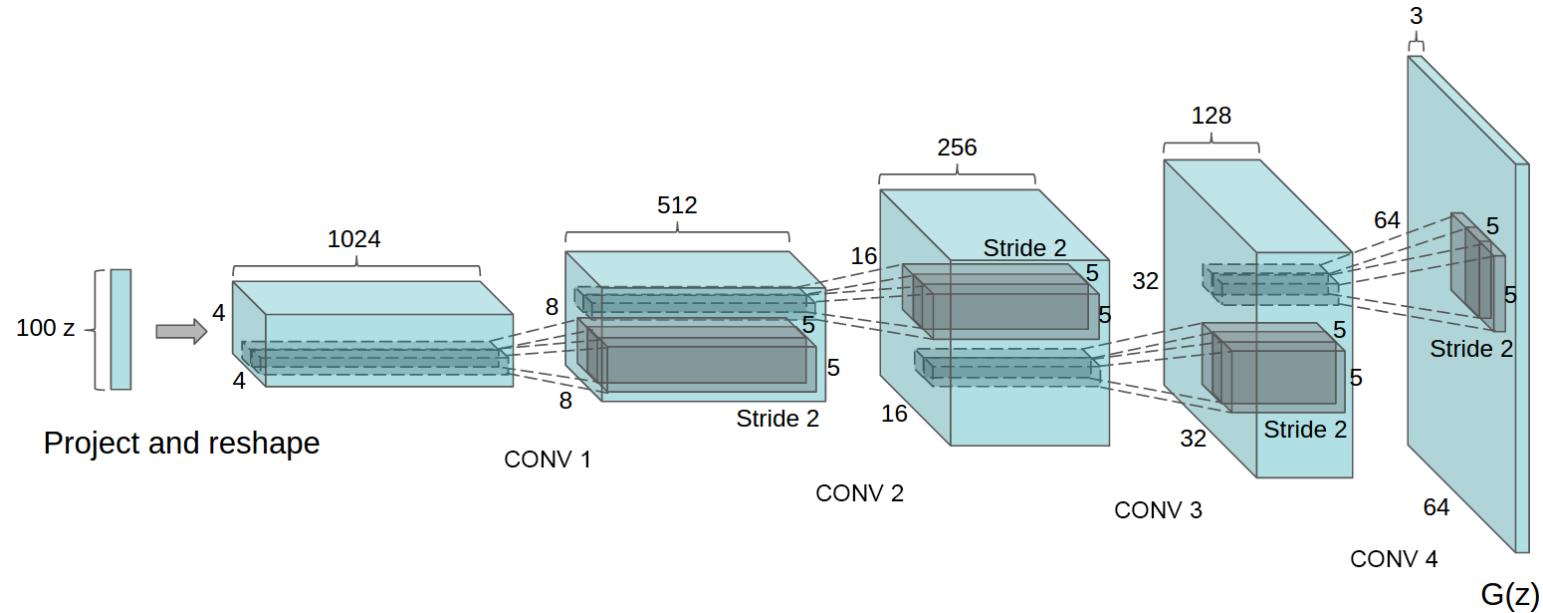
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Generator networks

Fixed distribution of latents: $Z \sim \text{Uniform}([-1, 1]^{100})$

Maps through a network: $G_\theta(Z) \sim Q_\theta$

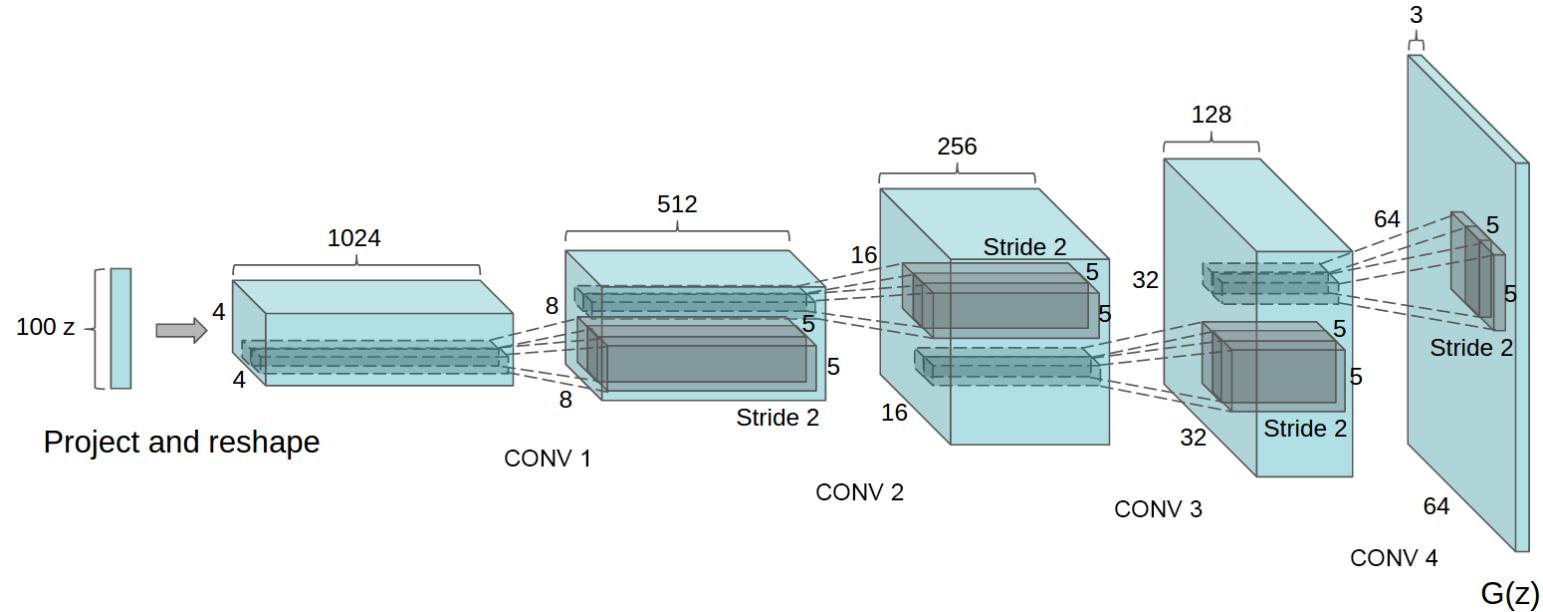


DCGAN generator [Radford+ ICLR-16]

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How to choose θ ?

GANs and their flaws

- GANs [Goodfellow+ NeurIPS-14] minimize discriminator accuracy (like classifier test) between \mathbb{P} and Q_{θ}
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- “Natural image manifold” usually considered low-dim
- Won't align at init, so won't ever align

WGANS and MMD GANs

- Integral probability metrics with “smooth” \mathcal{F} are continuous
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- Some kind of constraint on ϕ_ψ is important!

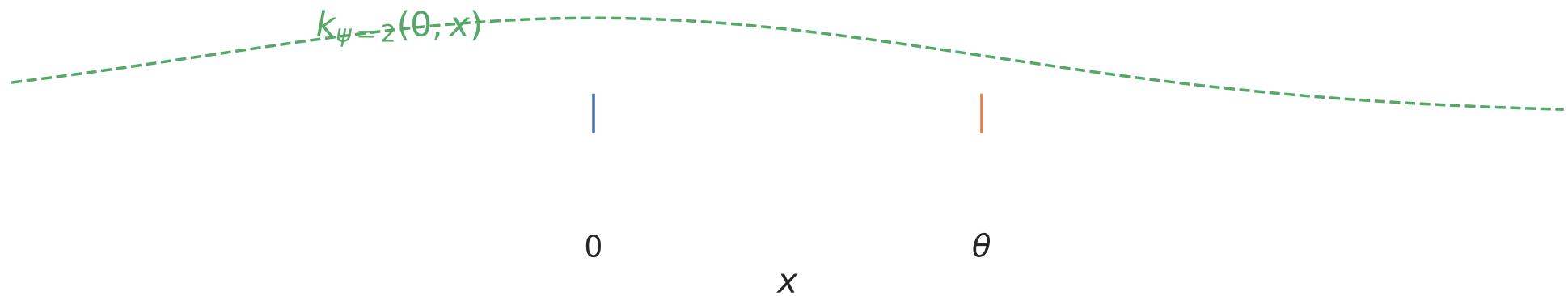
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Illustrative problem in \mathbb{R} , DiracGAN [[Mescheder+ ICML-18](#)]:



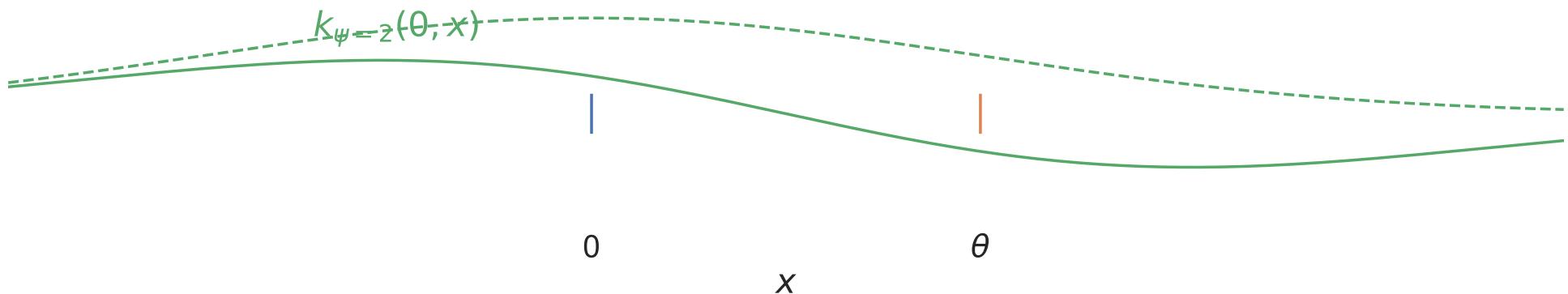
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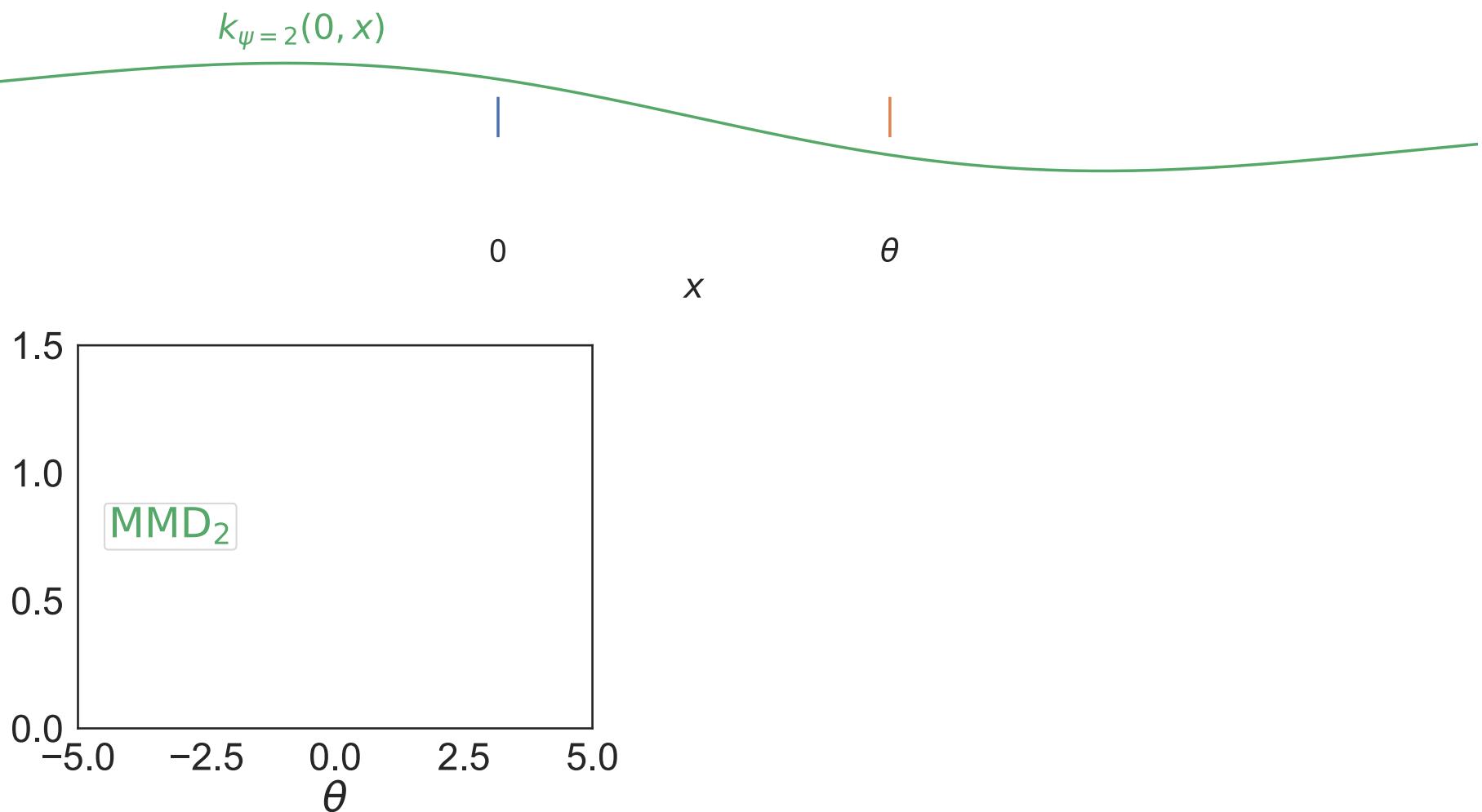
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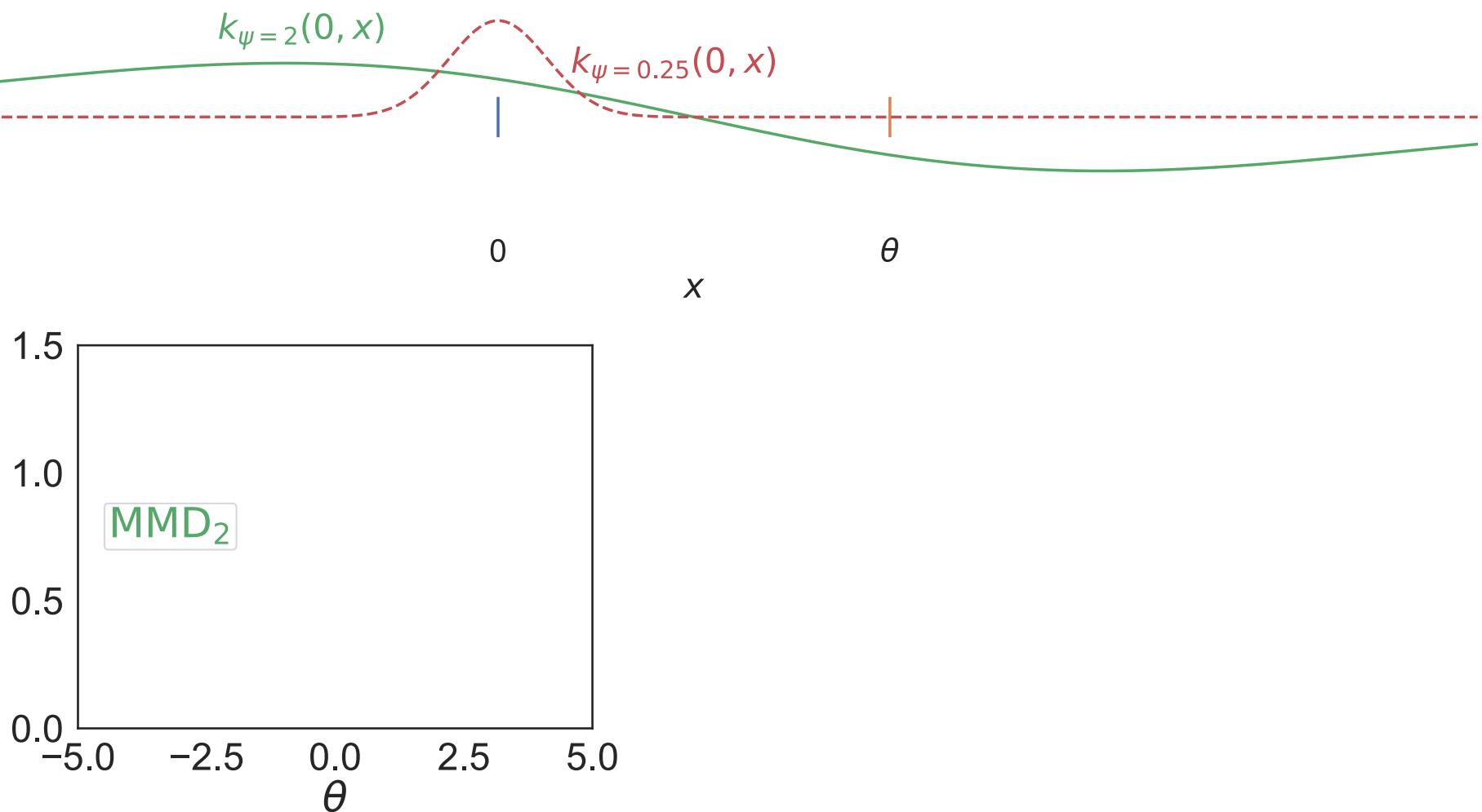
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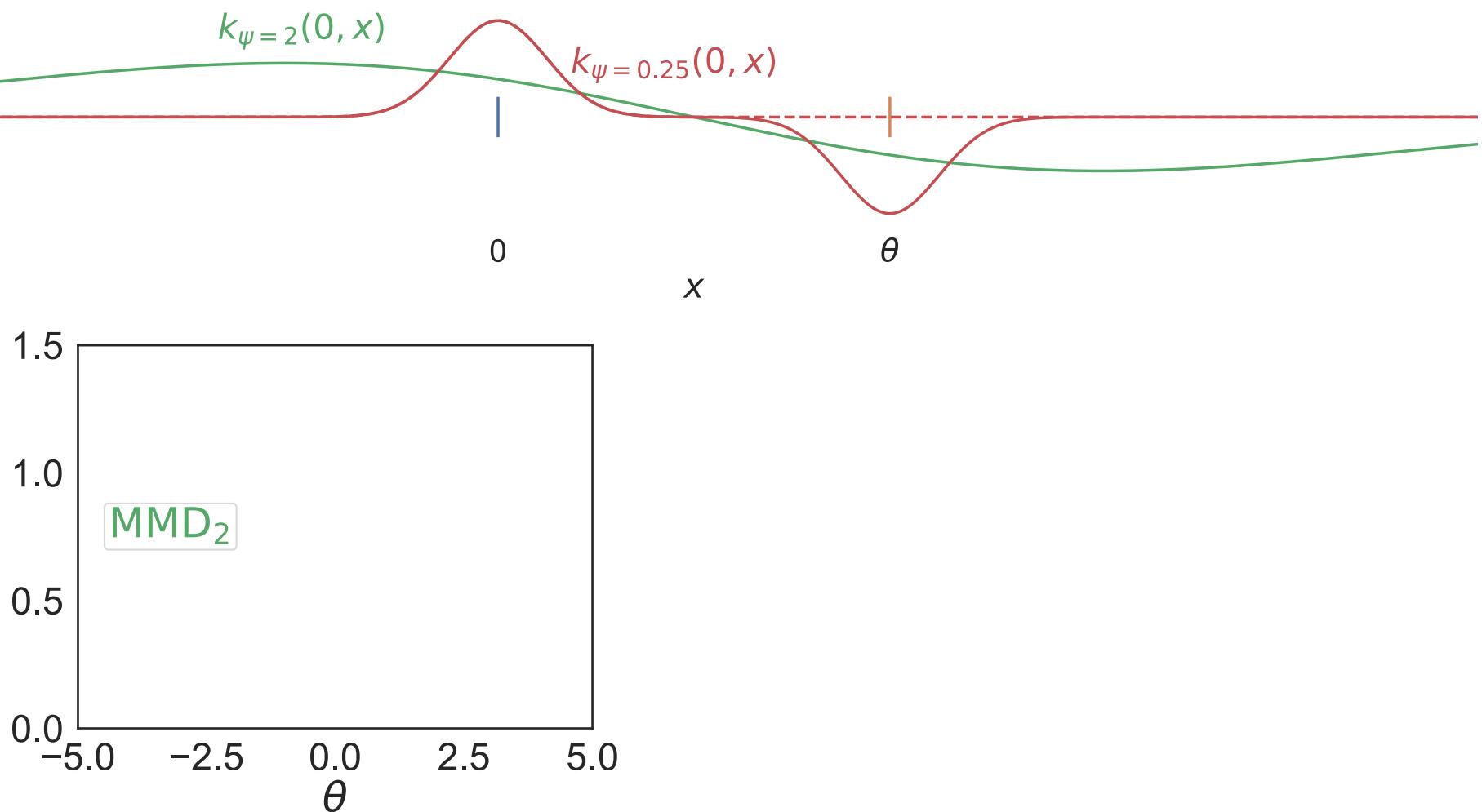
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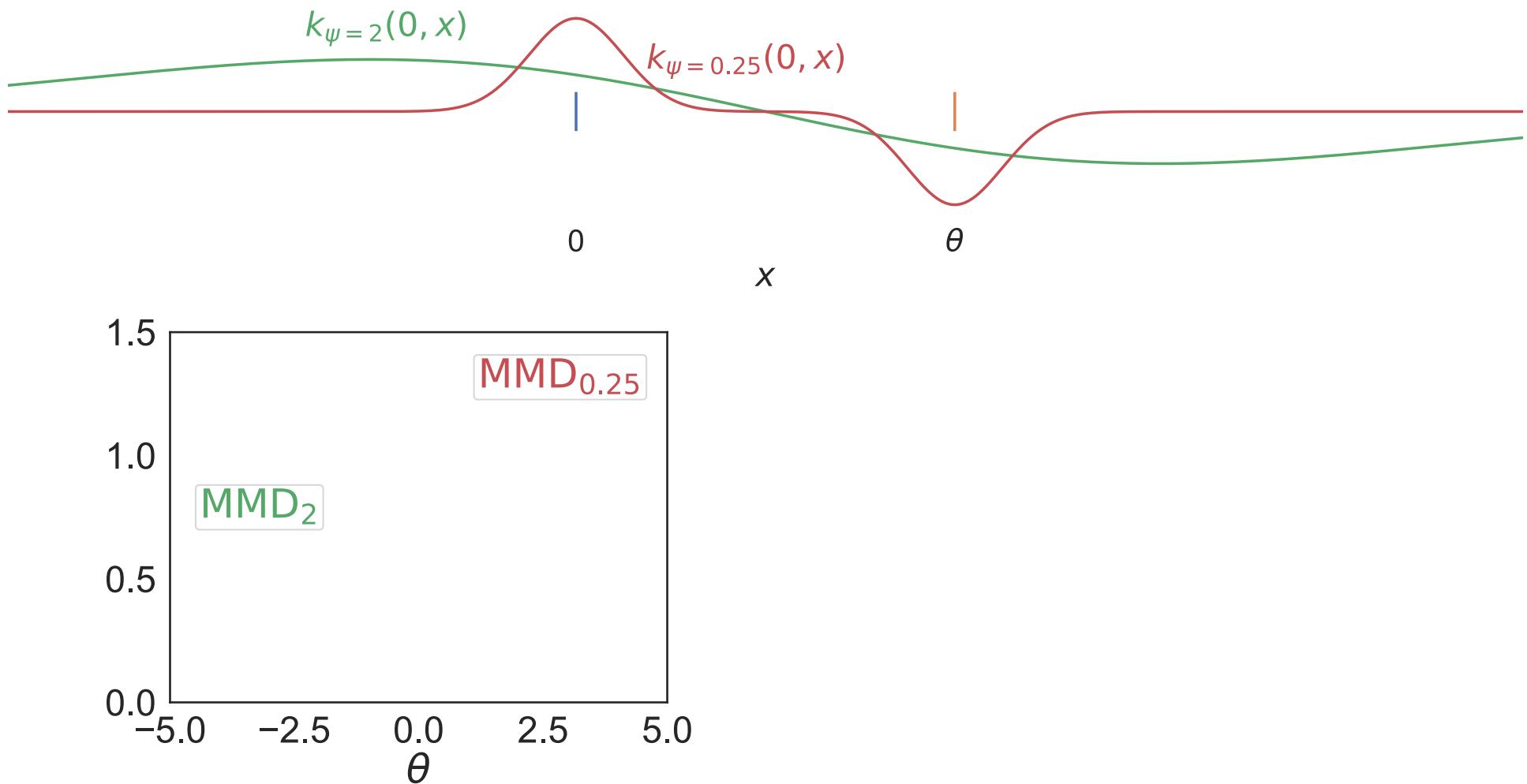
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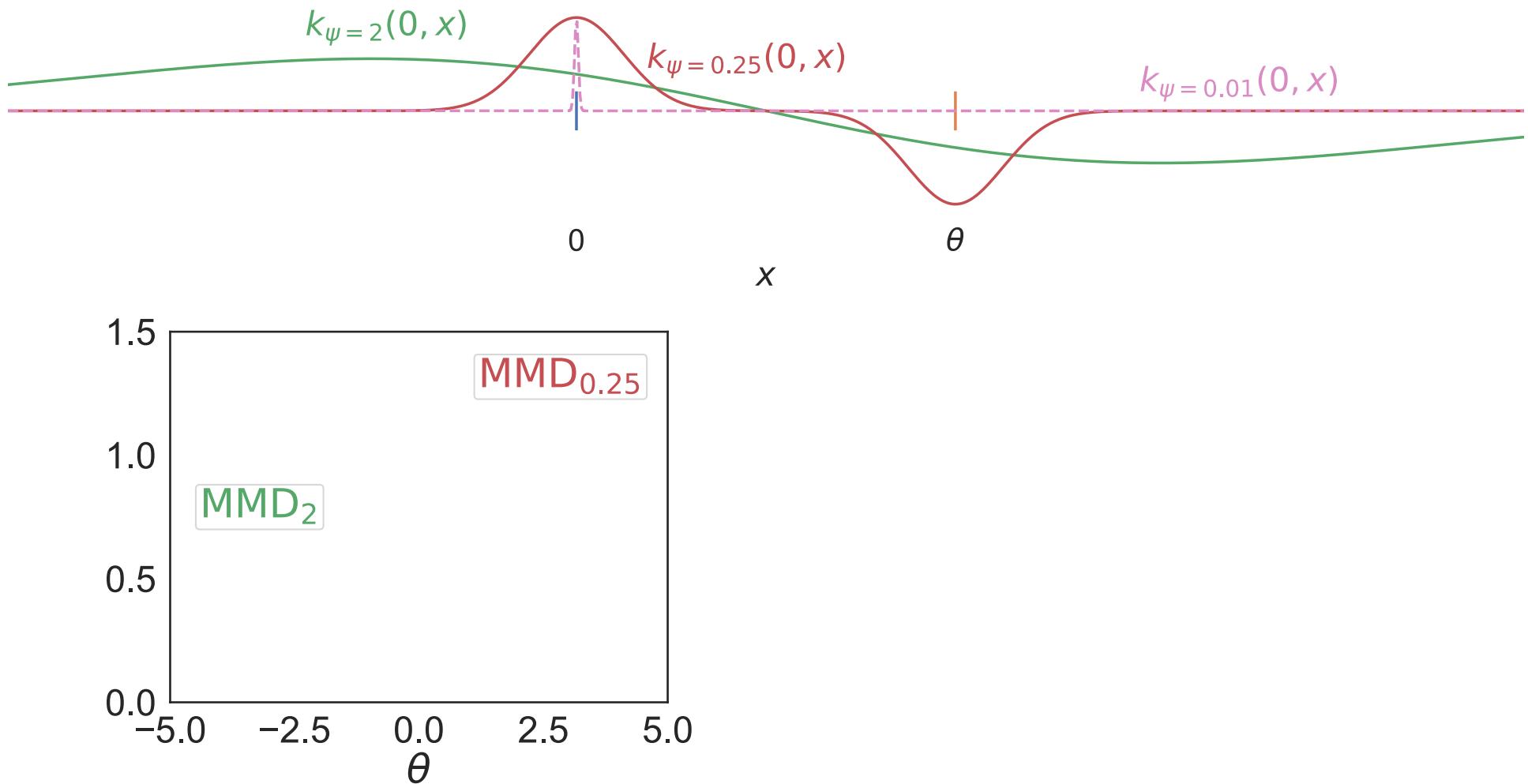
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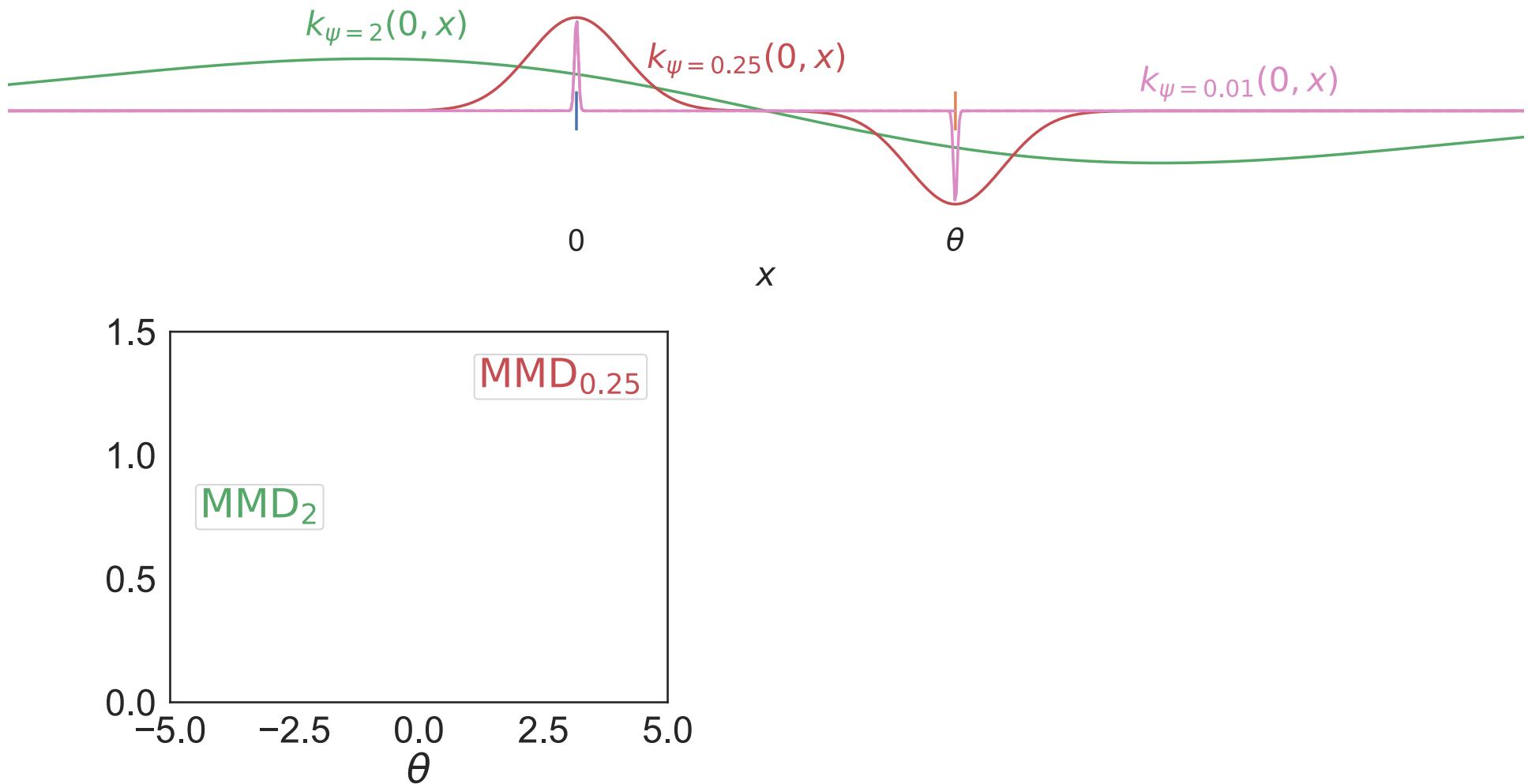
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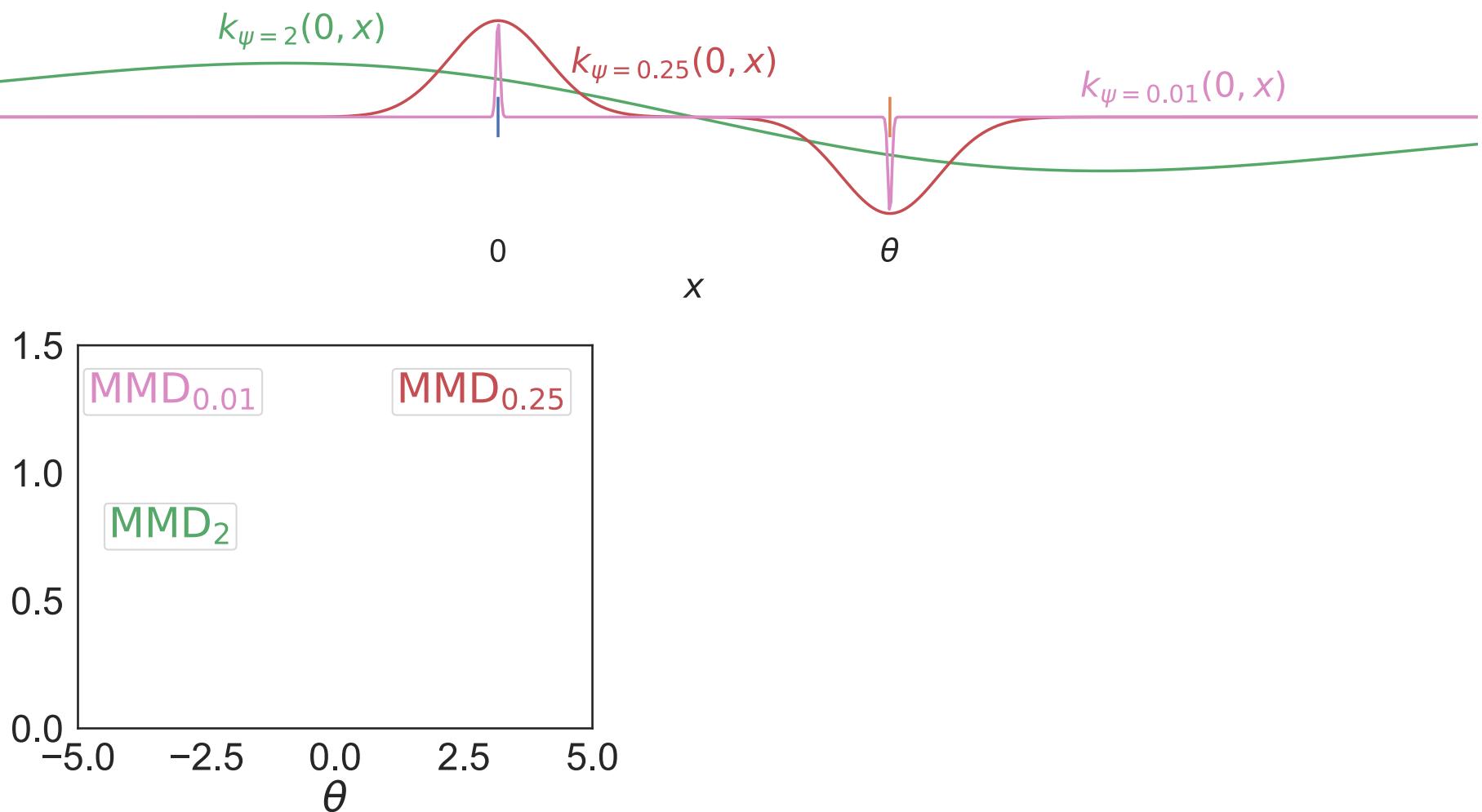
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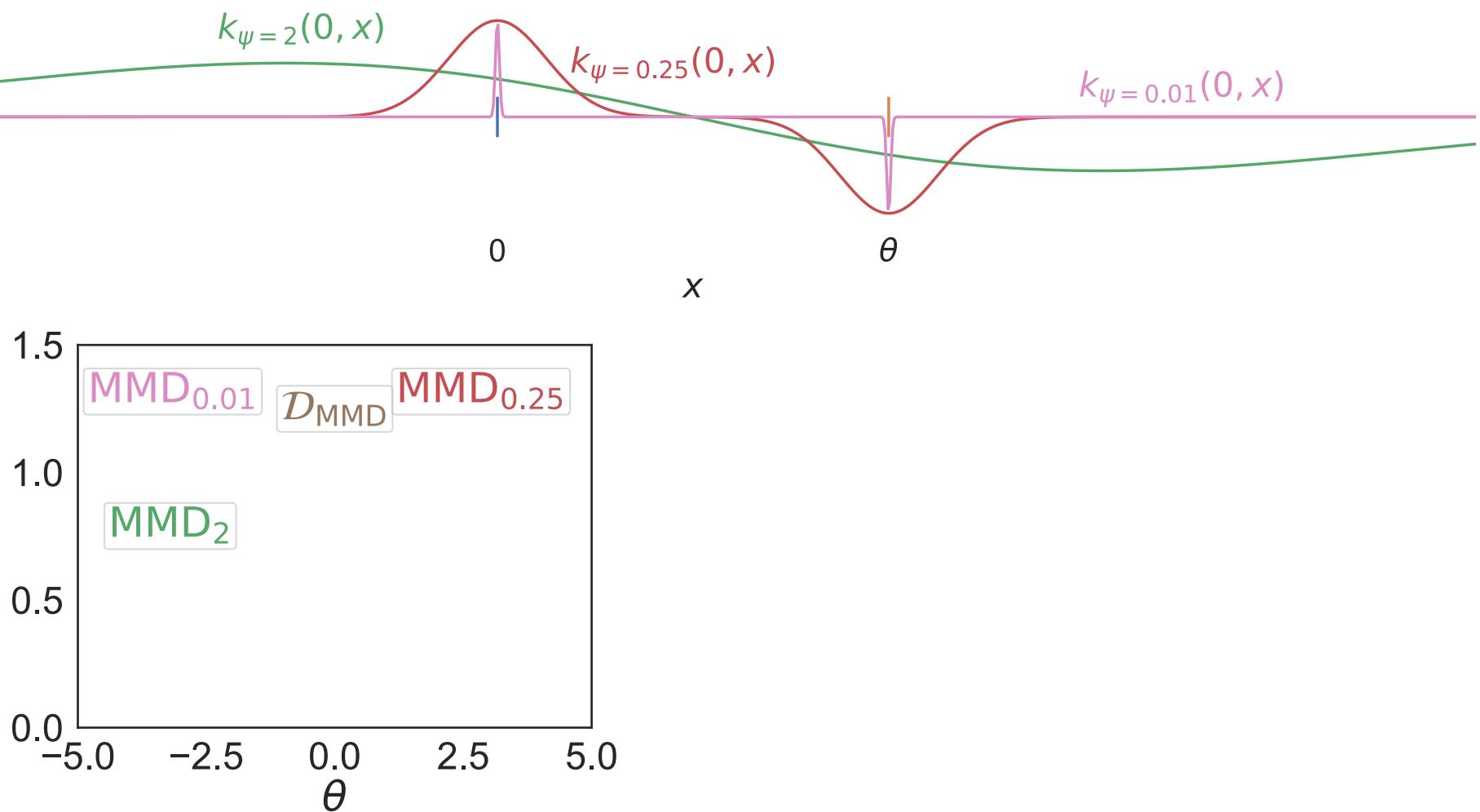
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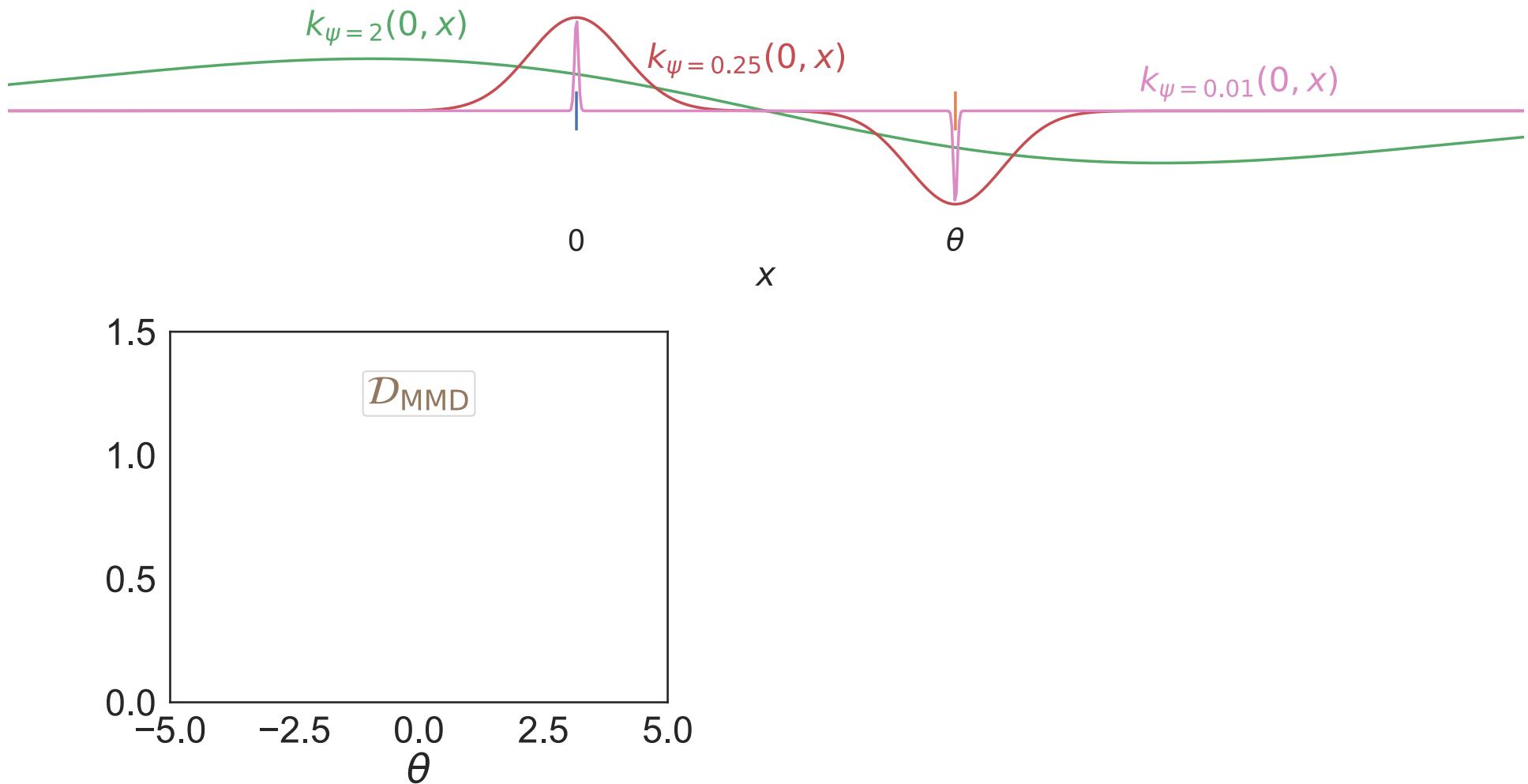
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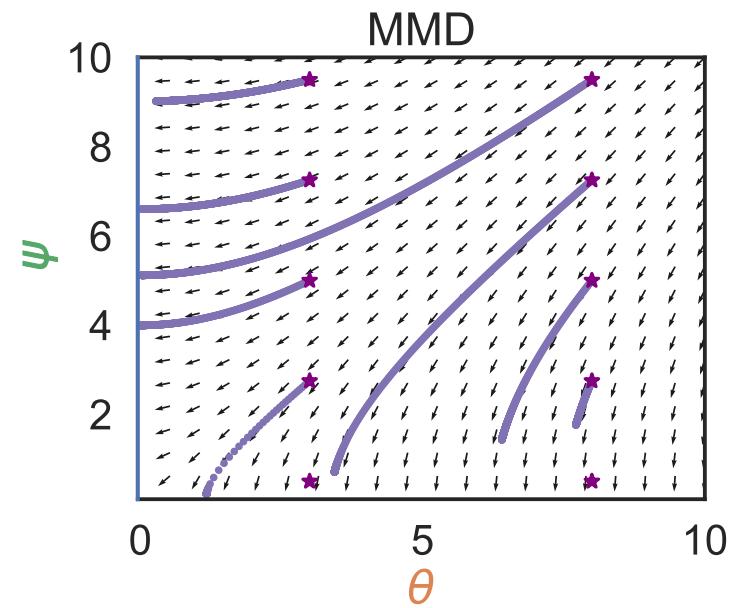
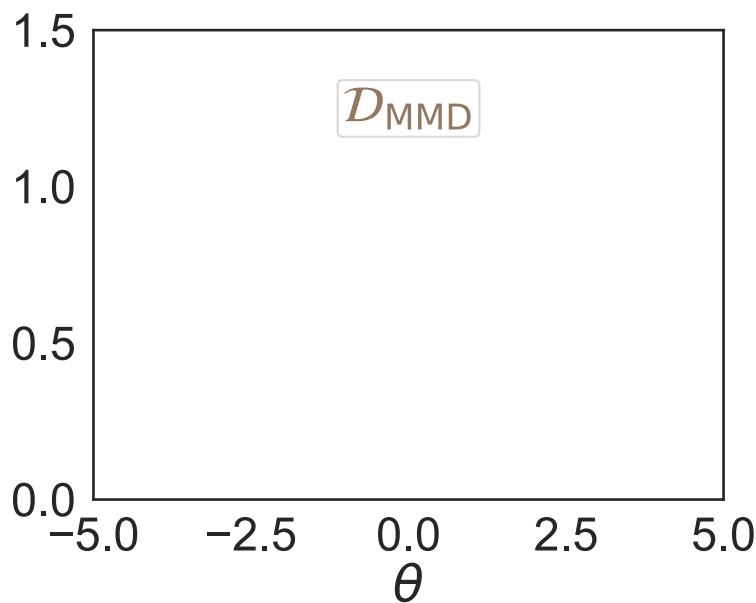
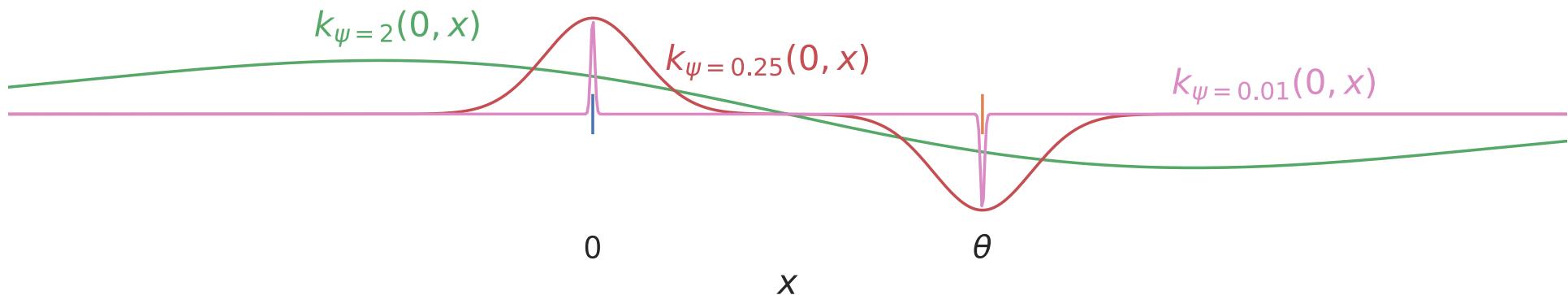
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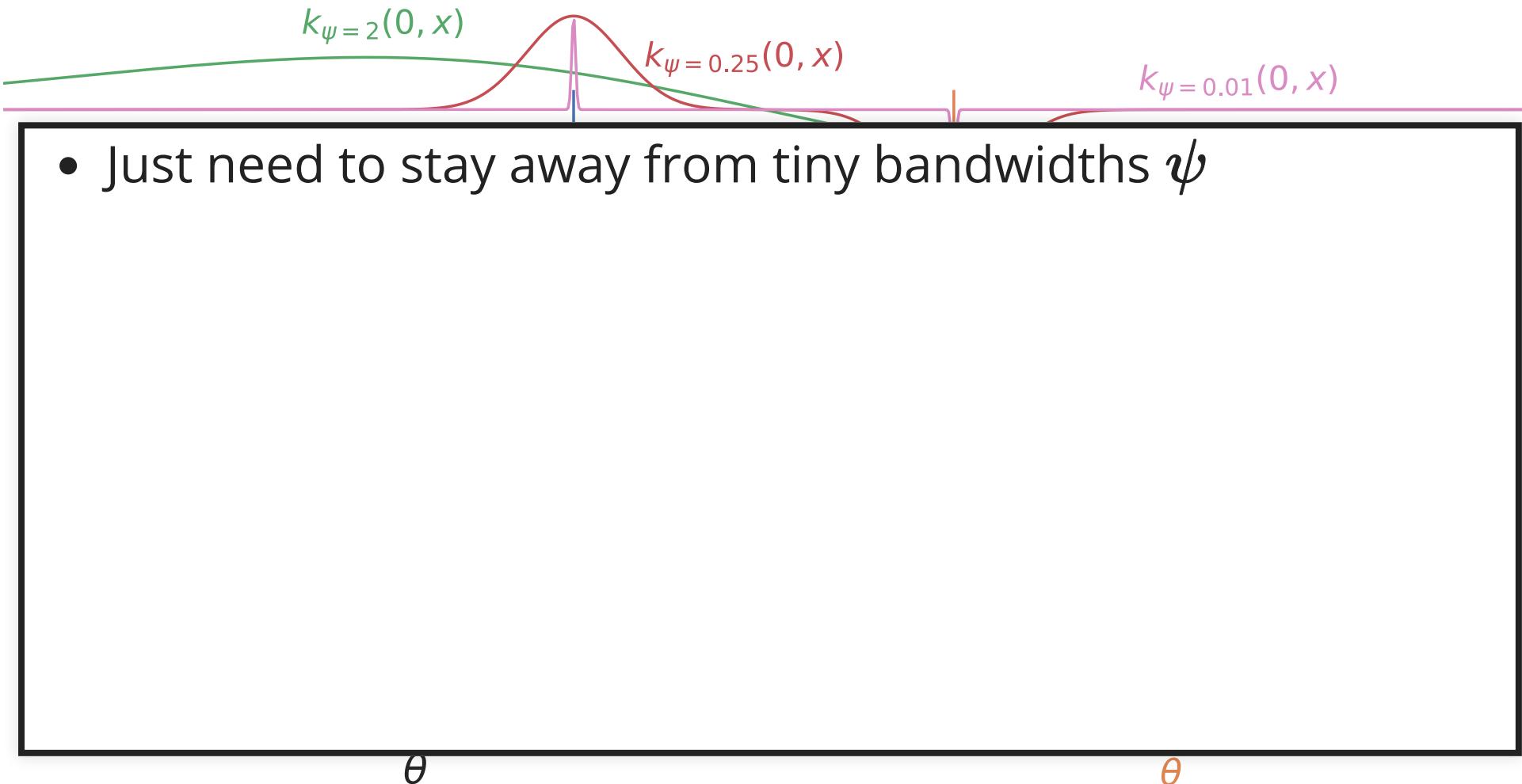
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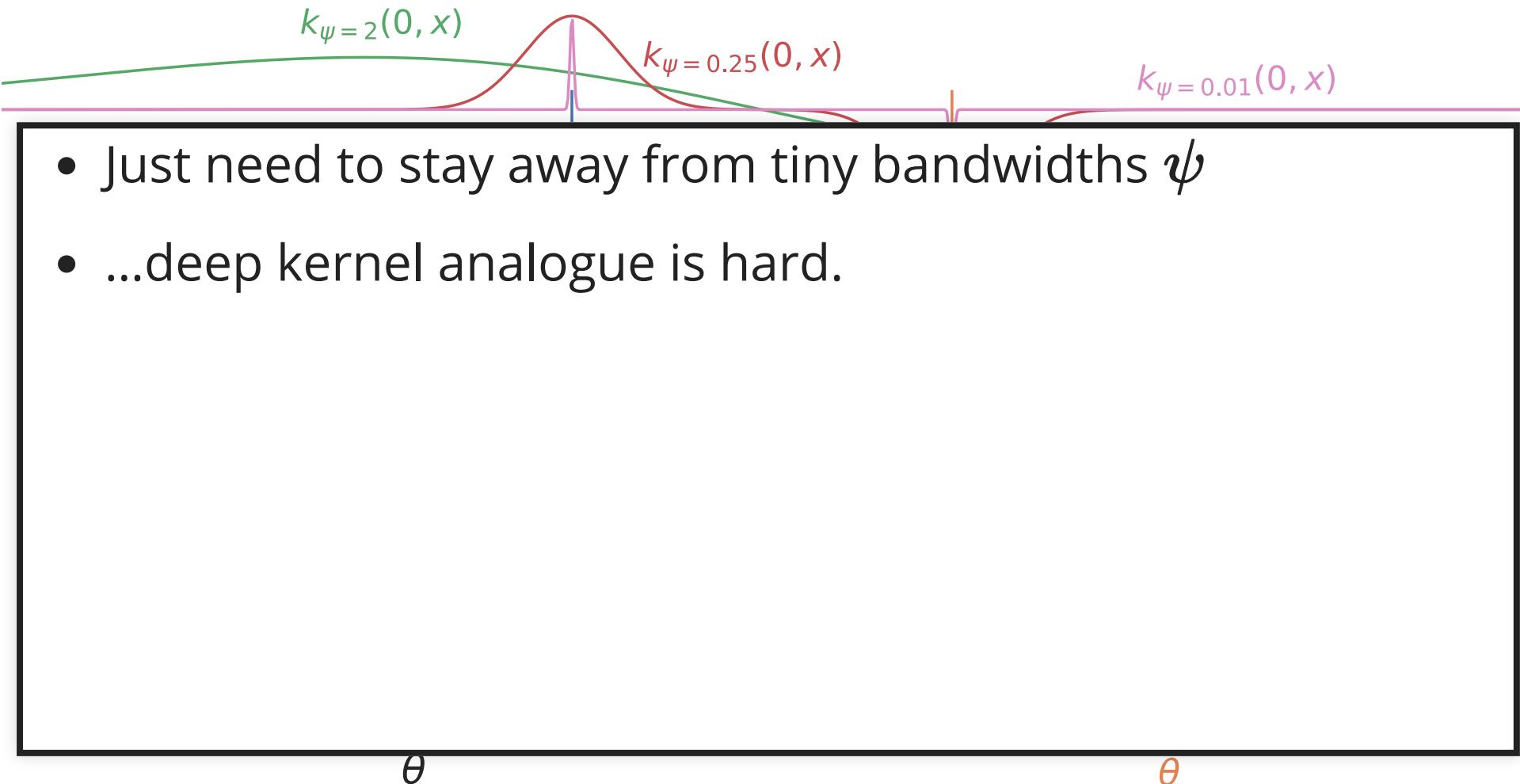
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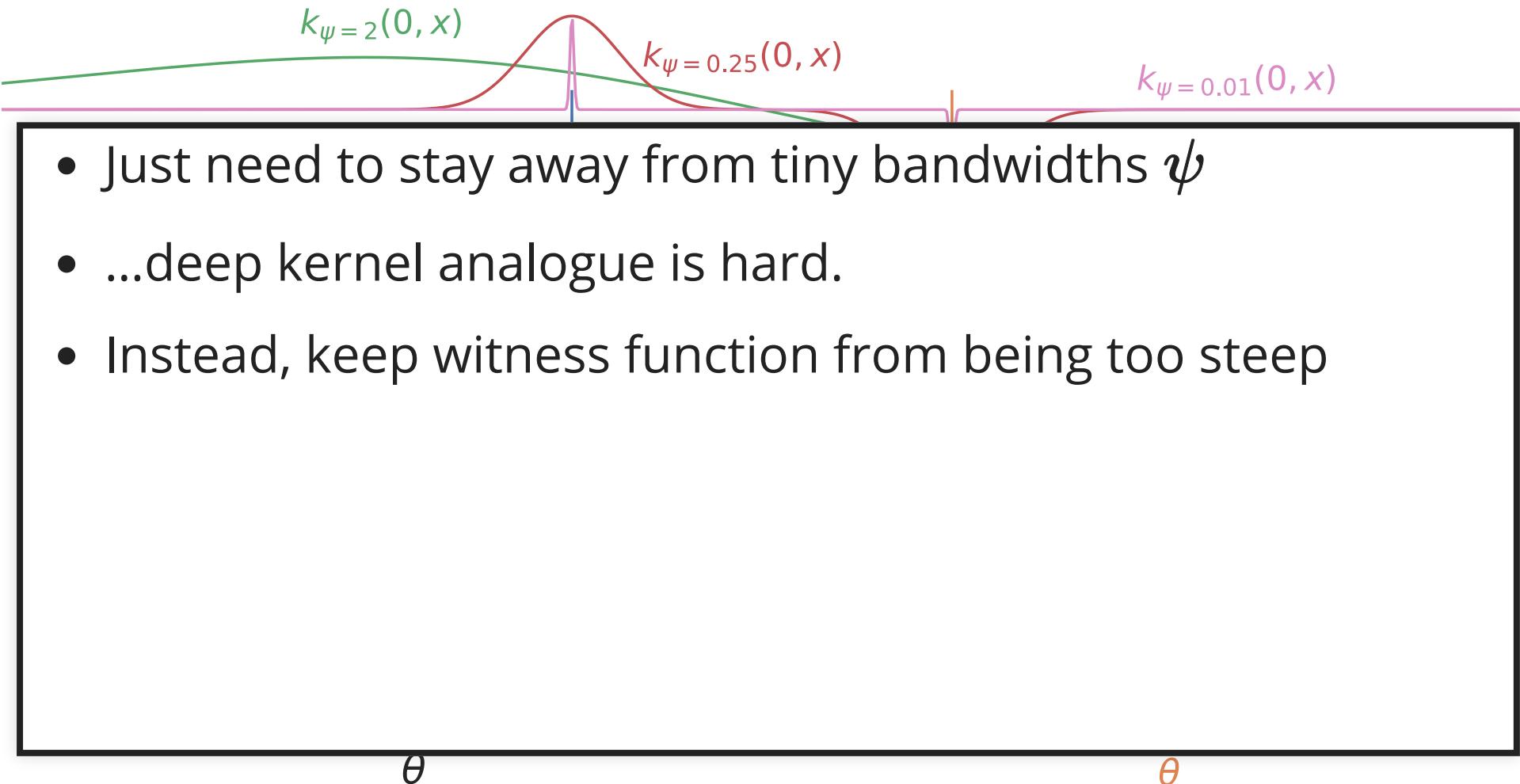
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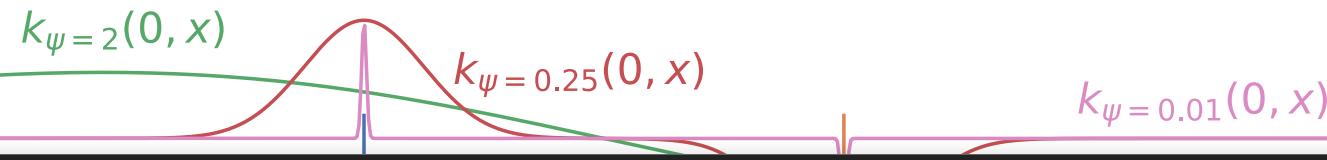
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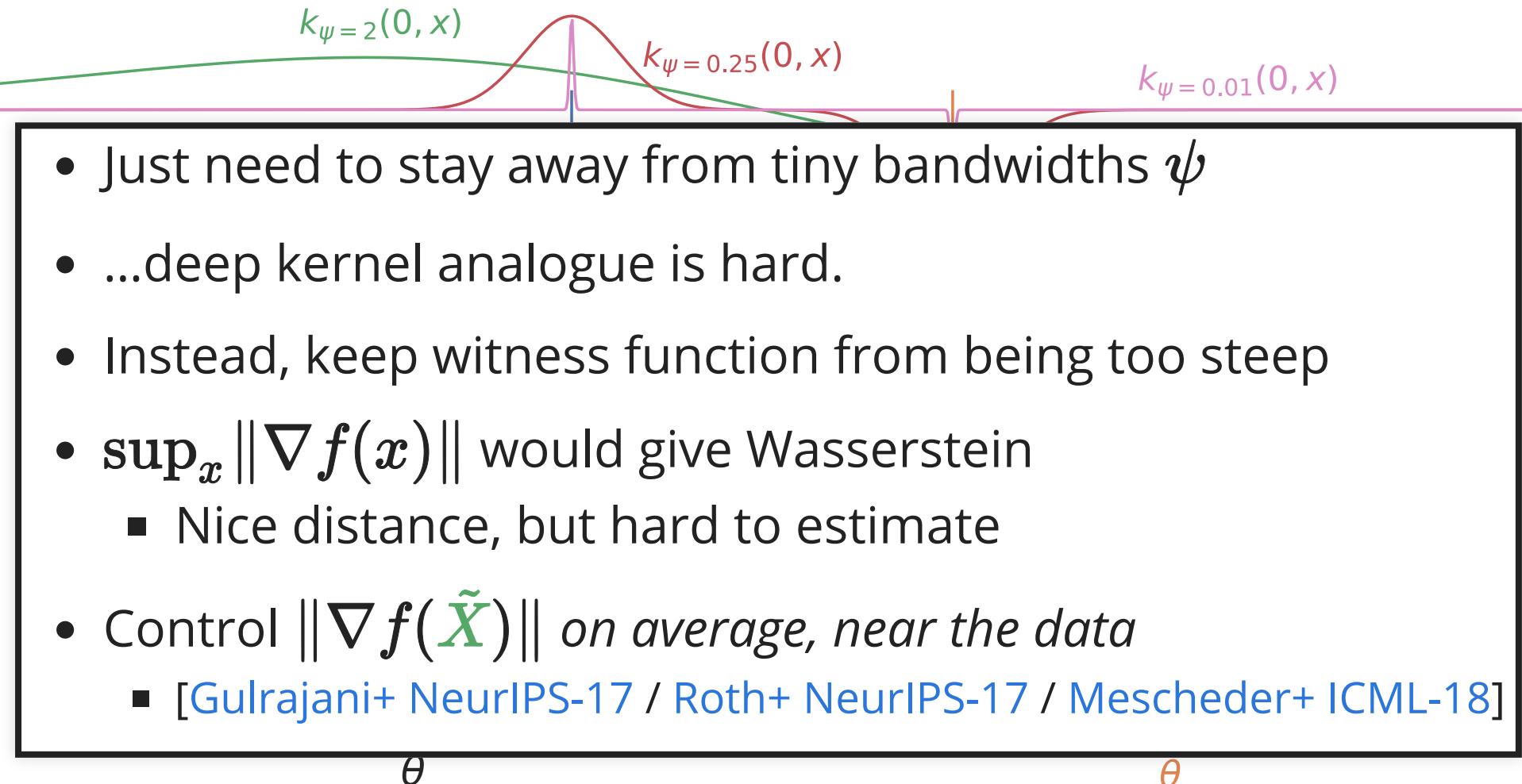
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- Just need to stay away from tiny bandwidths ψ
- ...deep kernel analogue is hard.
- Instead, keep witness function from being too steep
- $\sup_x \|\nabla f(x)\|$ would give Wasserstein
 - Nice distance, but hard to estimate

Non-smoothness of plain MMD GANs

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MMD-GAN with gradient control

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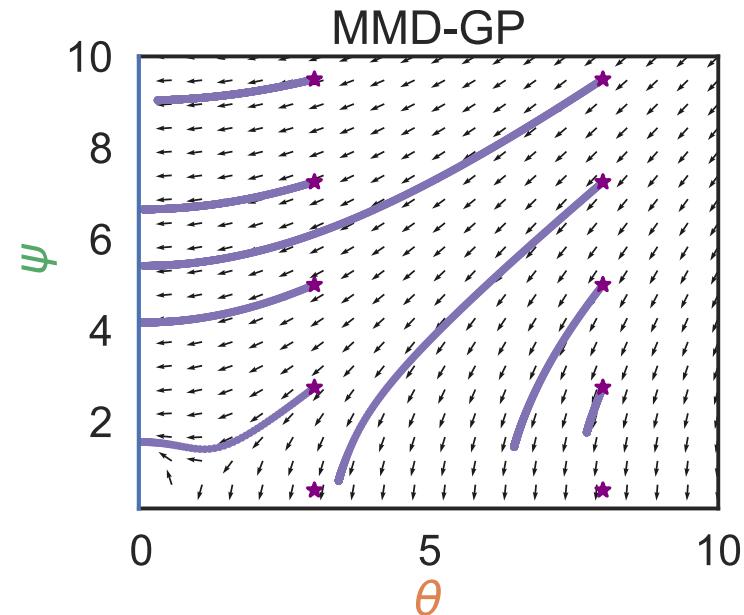
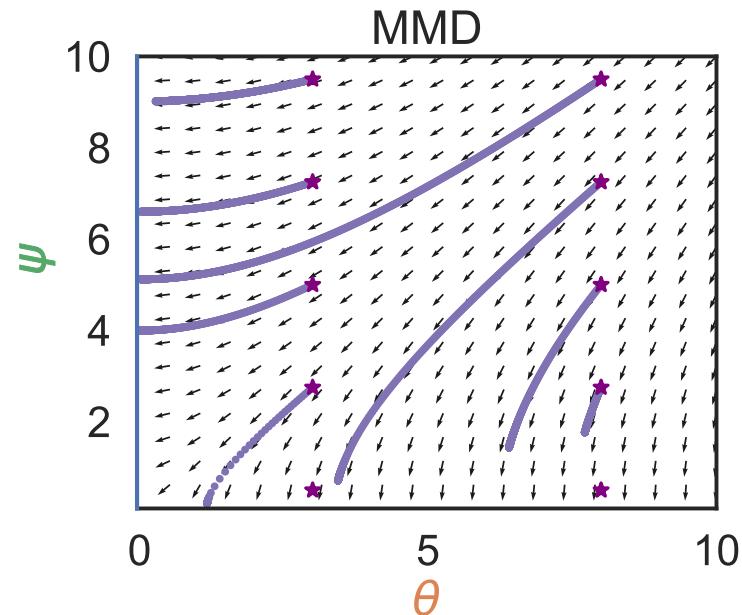
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Gives distance $\text{SMMD}_{\mathbb{S}, k, \lambda}(\mathbb{P}, \mathbb{Q}) = \sigma_{\mathbb{S}, k, \lambda} \text{MMD}_k(\mathbb{P}, \mathbb{Q})$

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$$\sigma_{\mathbb{S}, k, \lambda} := \left(\lambda + \mathbb{E}_{\tilde{\mathbf{X}} \sim \mathbb{S}} [k(\tilde{\mathbf{X}}, \tilde{\mathbf{X}}) + [\nabla_1 \cdot \nabla_2 k](\tilde{\mathbf{X}}, \tilde{\mathbf{X}})] \right)^{-\frac{1}{2}}$$

Gives distance $\text{SMMD}_{\mathbb{S}, k, \lambda}(\mathbb{P}, \mathbb{Q}) = \sigma_{\mathbb{S}, k, \lambda} \text{MMD}_k(\mathbb{P}, \mathbb{Q})$

$\mathcal{D}_{\text{MMD}}^{\Psi}$ has $\mathcal{F} = \bigcup_{\psi \in \Psi} \left\{ f : \|f\|_{\mathcal{H}_{\psi}} \leq 1 \right\}$

$\mathcal{D}_{\text{SMMD}}^{\mathbb{S}, \Psi, \lambda}$ has $\mathcal{F} = \bigcup_{\psi \in \Psi} \left\{ f : \|f\|_{\mathcal{H}_{\psi}} \leq \sigma_{\mathbb{S}, k, \lambda} \right\}$

Deriving the Scaled MMD

$$\mathbb{E}_{\tilde{X} \sim \mathbb{S}} [\|\nabla f(\tilde{X})\|^2] \leq 1$$

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$$\mathbb{E}_{\tilde{X} \sim \mathbb{S}} [f(\tilde{X})^2] + \mathbb{E}_{\tilde{X} \sim \mathbb{S}} [\|\nabla f(\tilde{X})\|^2] + \lambda \|f\|_{\mathcal{H}}^2 \leq 1$$

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Deriving the Scaled MMD

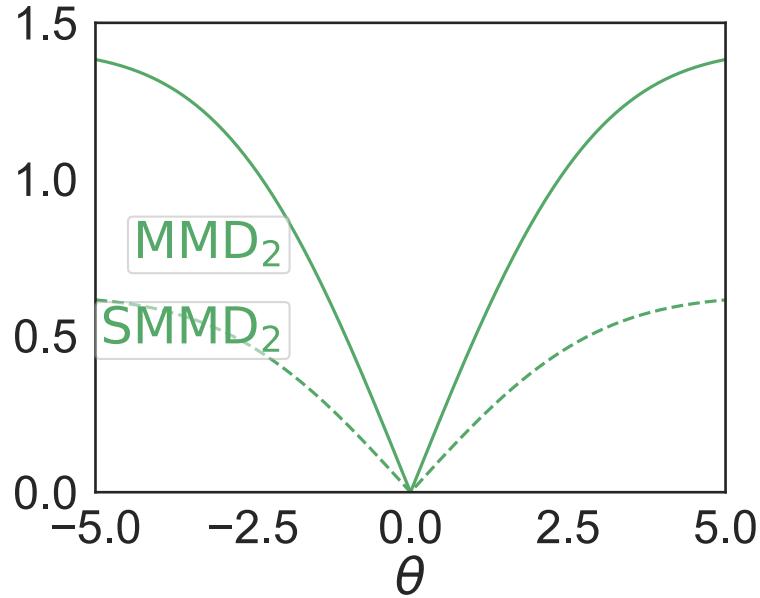
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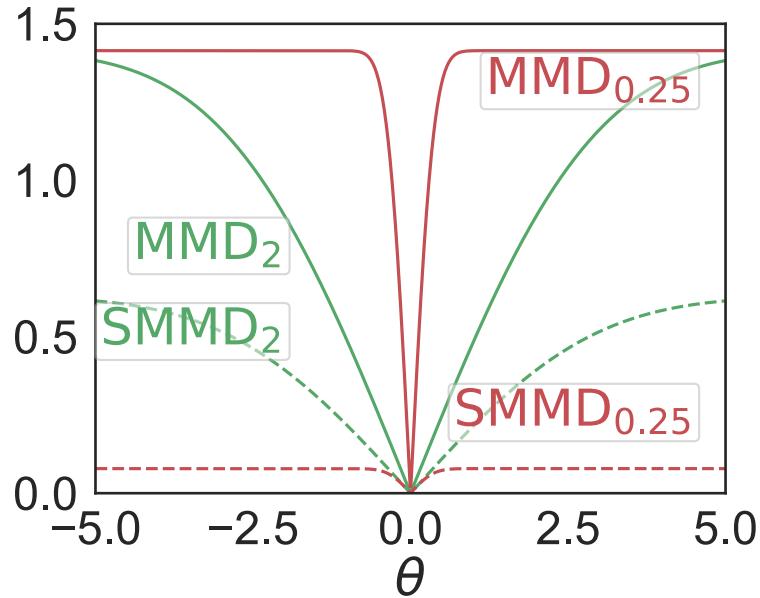
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$$\langle f, D_\lambda f \rangle \leq \|D_\lambda\| \|f\|_{\mathcal{H}}^2 \leq \sigma_{\mathbb{S}, k, \lambda}^{-2} \|f\|_{\mathcal{H}}^2$$

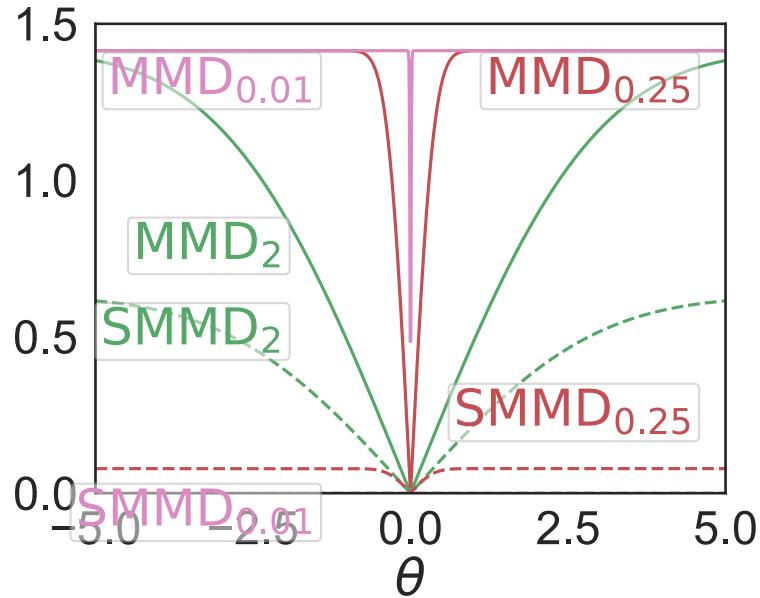
Smoothness of $\mathcal{D}_{\text{SMMD}}$



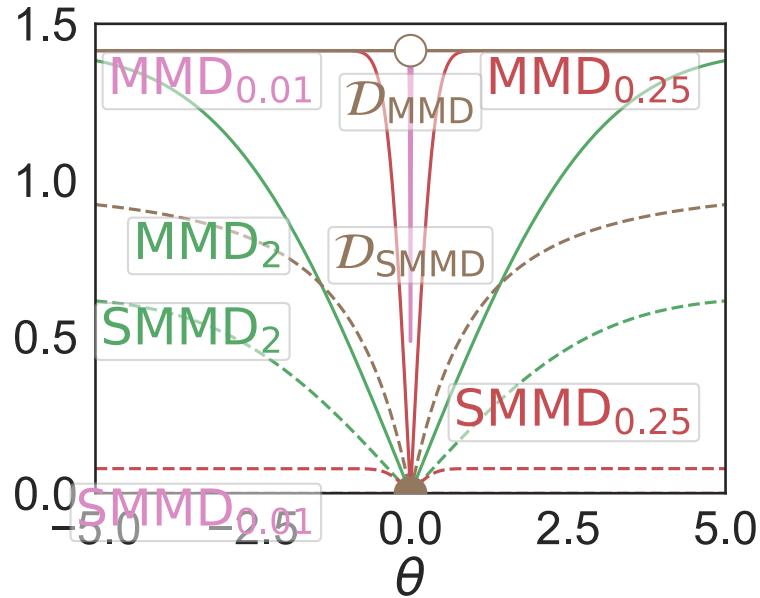
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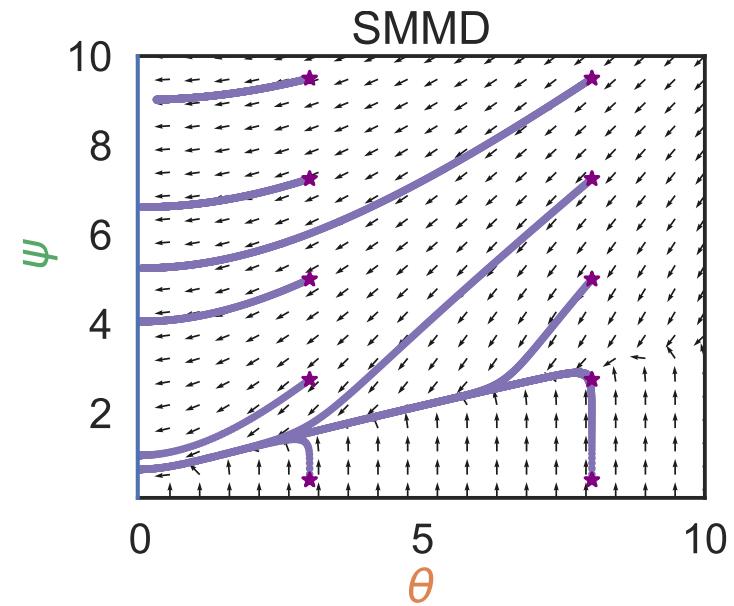
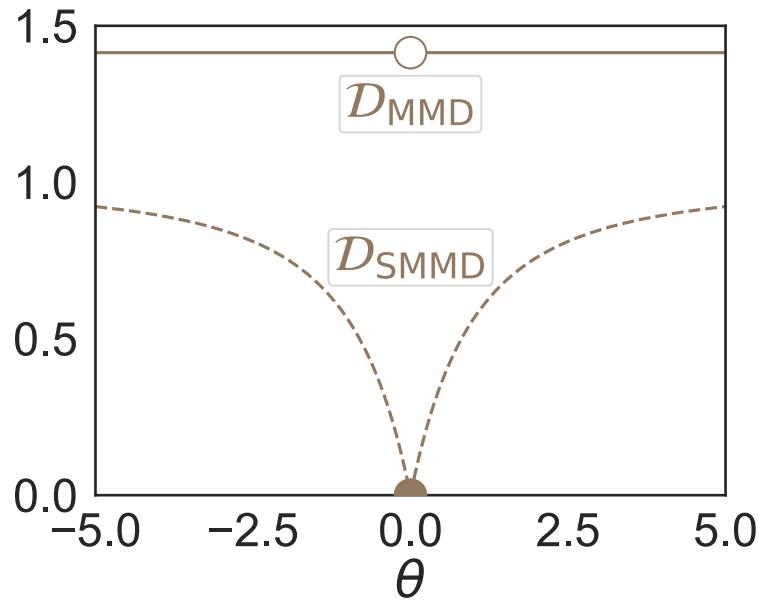
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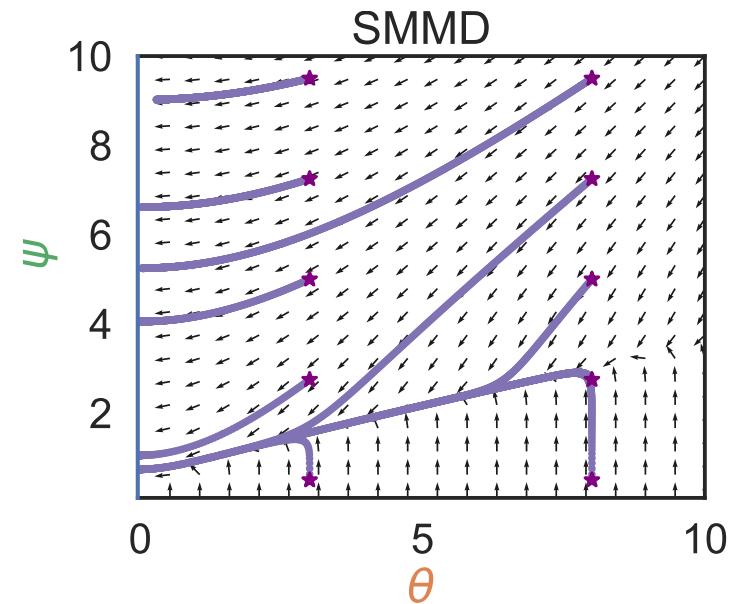
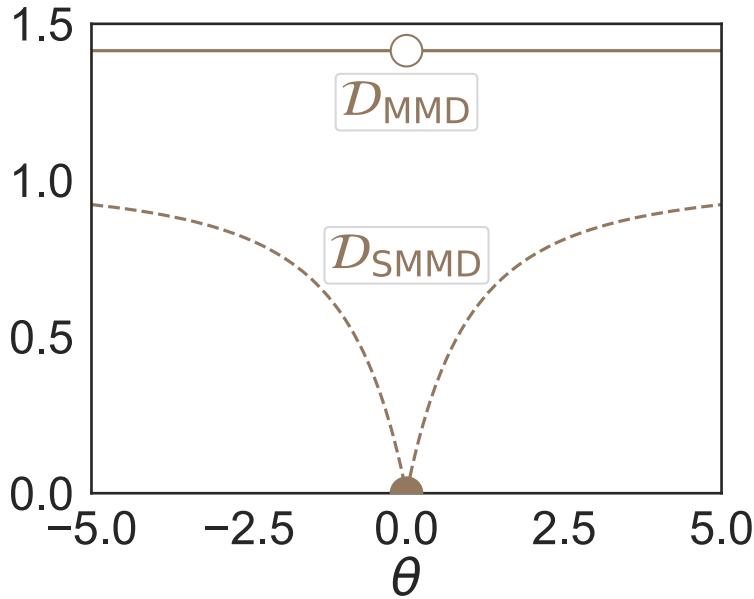
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Theorem: $\mathcal{D}_{\text{SMMD}}^{\mathbb{S}, \Psi, \lambda}$ is continuous.

If \mathbb{S} has a density; k_{top} is Gaussian/linear/...;
 ϕ_ψ is fully-connected, Leaky-ReLU, non-increasing width;
all weights in Ψ have bounded condition number; then
 $\mathcal{W}(\mathbb{Q}_n, \mathbb{P}) \rightarrow 0$ implies $\mathcal{D}_{\text{SMMD}}^{\mathbb{S}, \Psi, \lambda}(\mathbb{Q}_n, \mathbb{P}) \rightarrow 0$.

Results on 160×160 CelebA

SN-SMMD-GAN



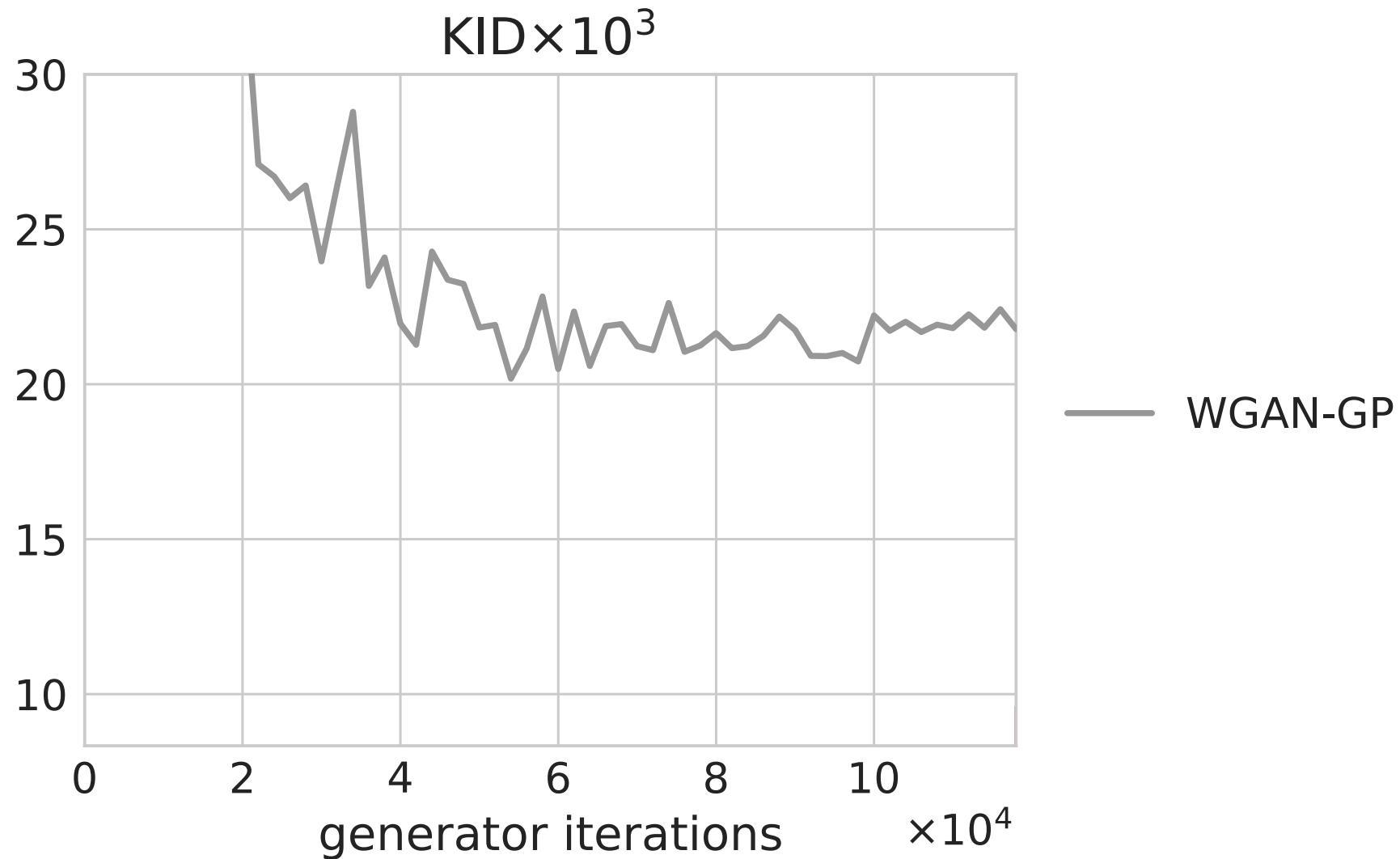
KID: 0.006

WGAN-GP

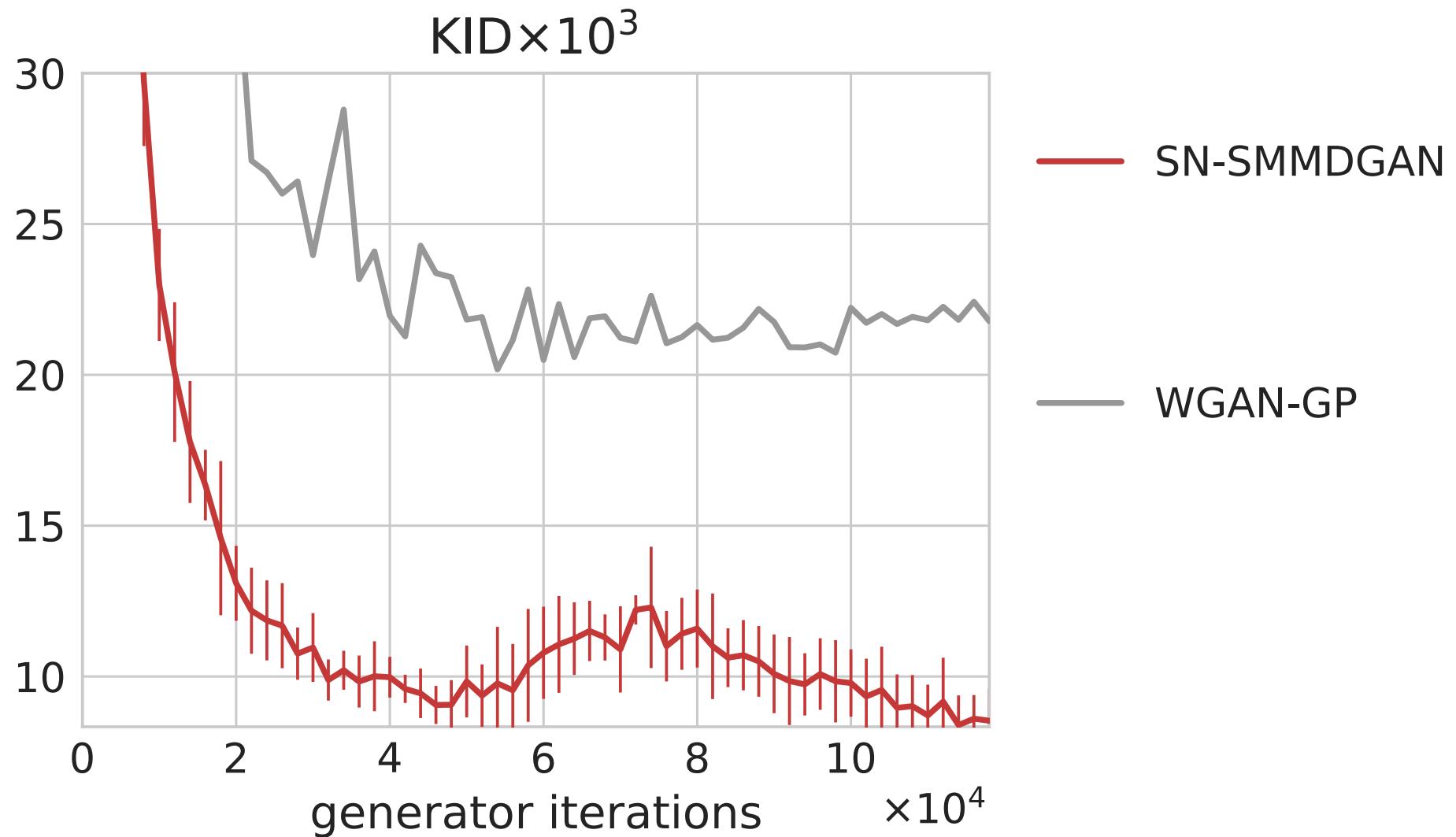


KID: 0.022

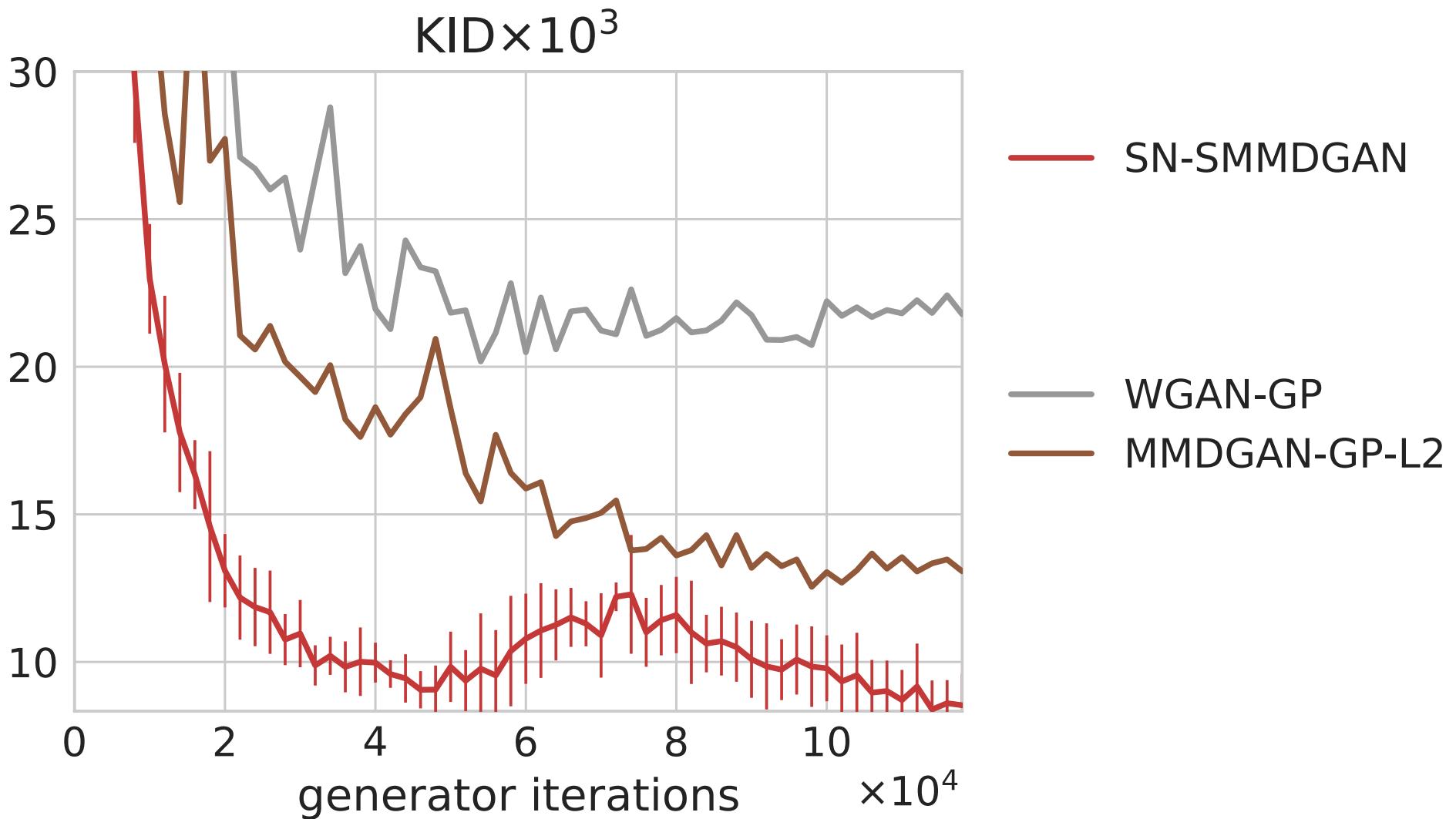
Training process on CelebA



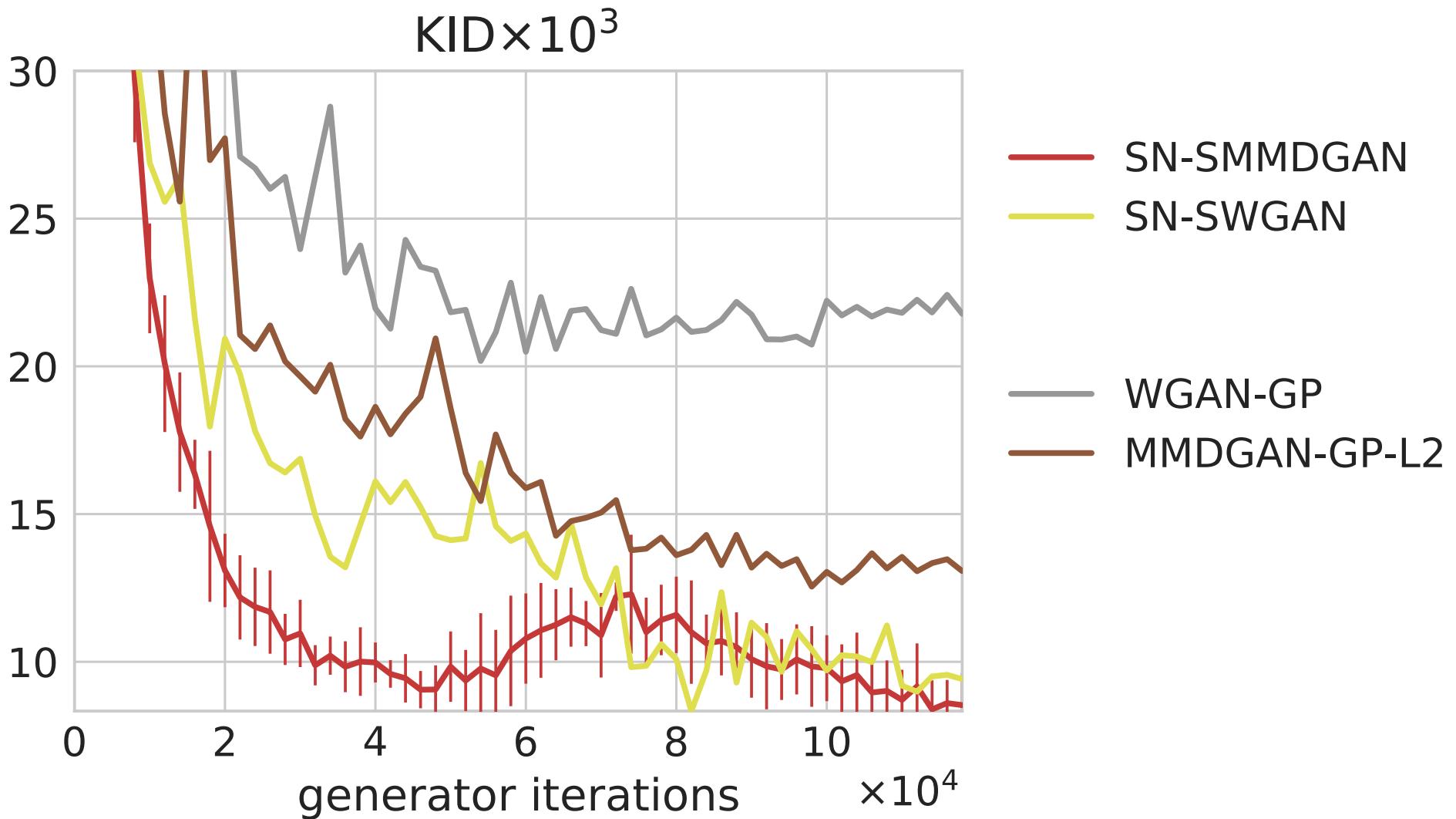
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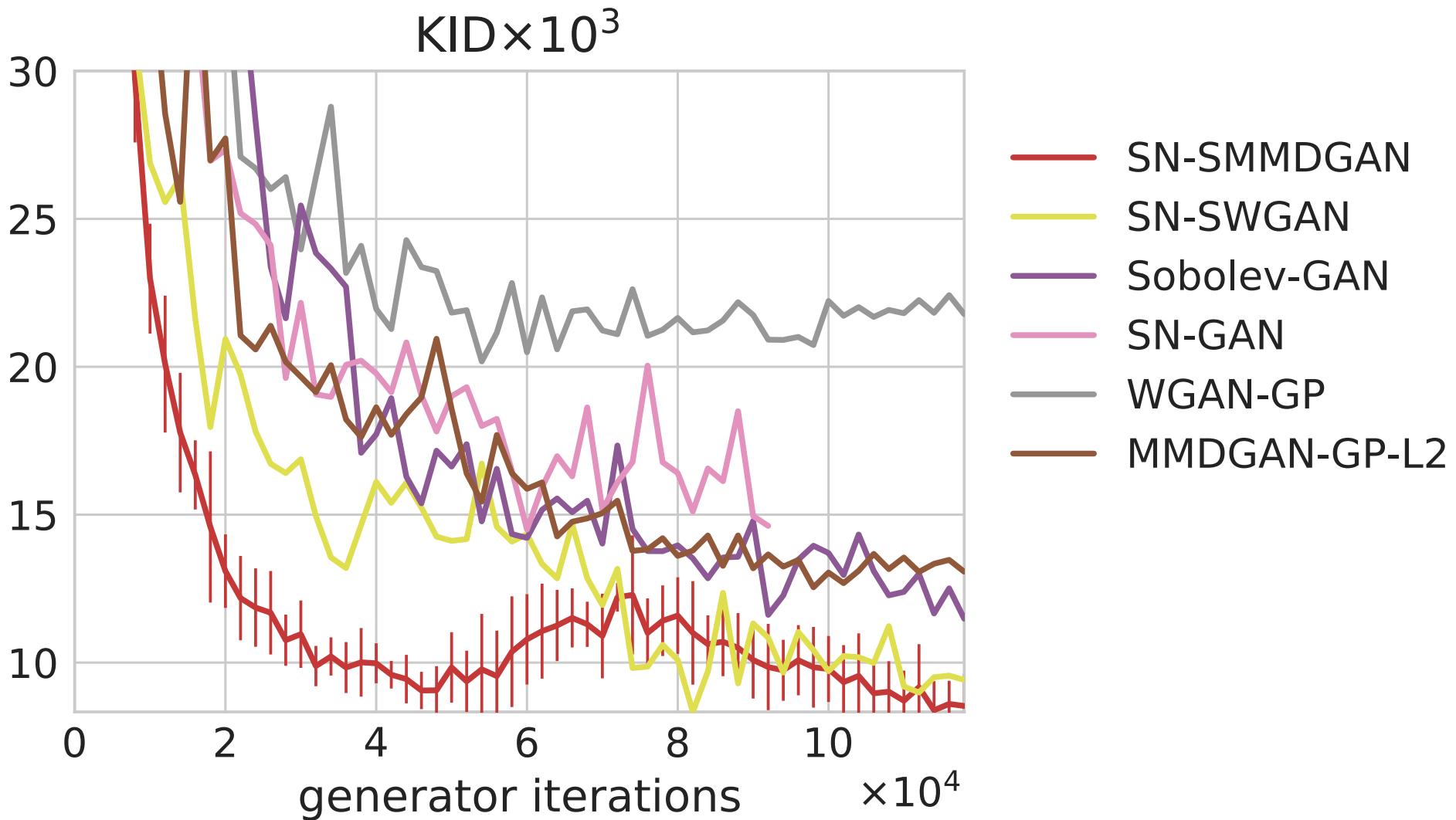
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- Our KID: MMD^2 instead. Unbiased, asymptotically normal

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- Two-sample testing [[ICLR-17](#), [ICML-20](#)]
 - Choose ψ to maximize power criterion
 - Exploit closed form of f_{ψ}^* for permutation testing
- Generative modeling with MMD GANs [[ICLR-18](#), [NeurIPS-18](#)]
 - Need a smooth loss function for the generator
 - Better gradients for generator to follow (?)

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