

Domain Generalization with Small Data

International Journal of Computer Vision (IJCV) 2024

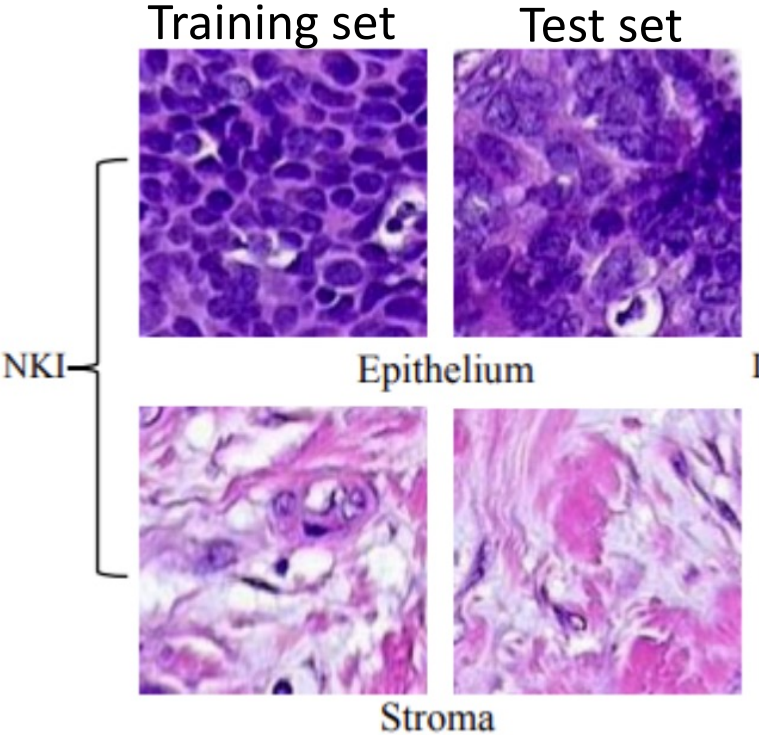
Kecheng Chen¹, Elena Gal², Hong Yan¹, Haoliang Li¹

¹ Department of Electrical Engineering, City University of Hong Kong

² Department of Mathematics, University of Oxford

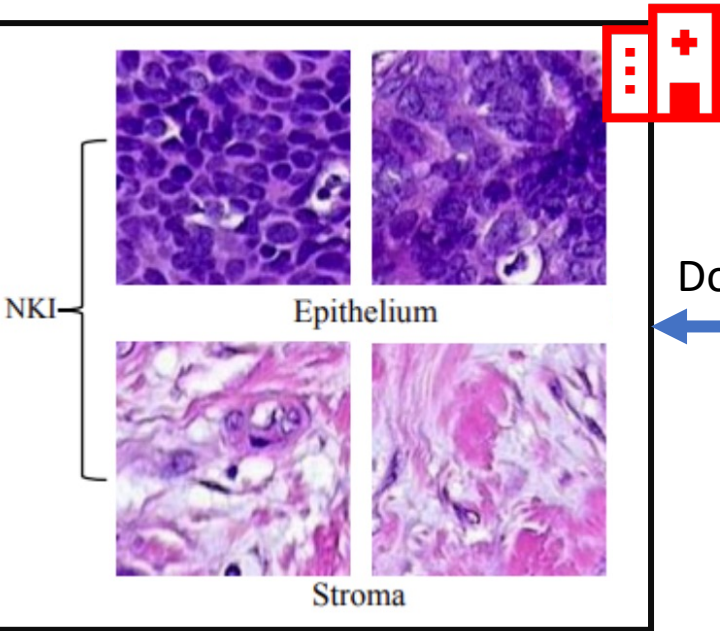
Motivation

Common assumption : iid

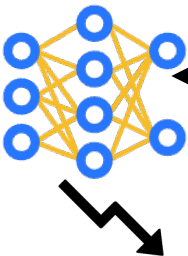


Out of distribution problem

Training set



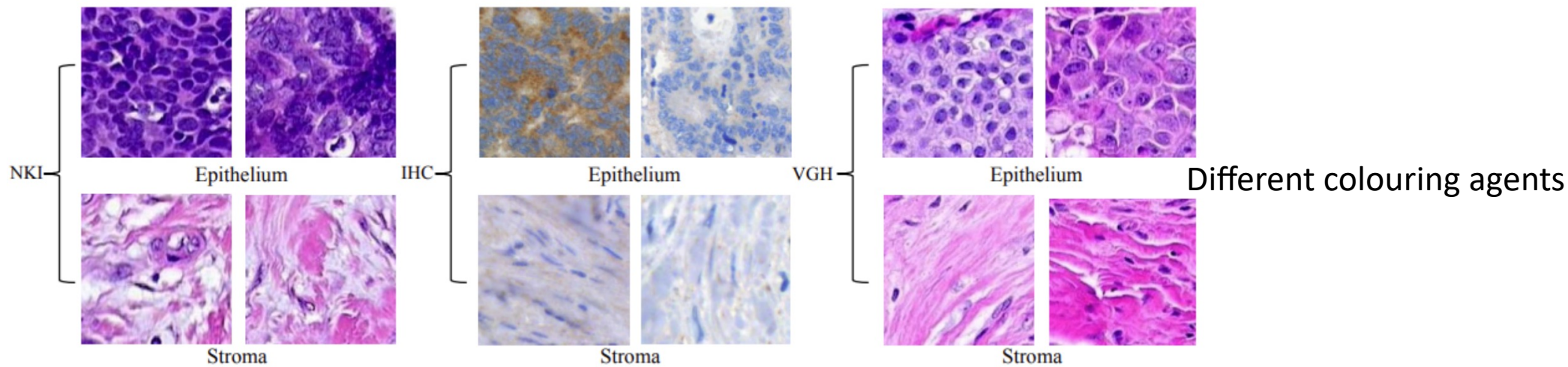
Domain/distribution gap



Test set

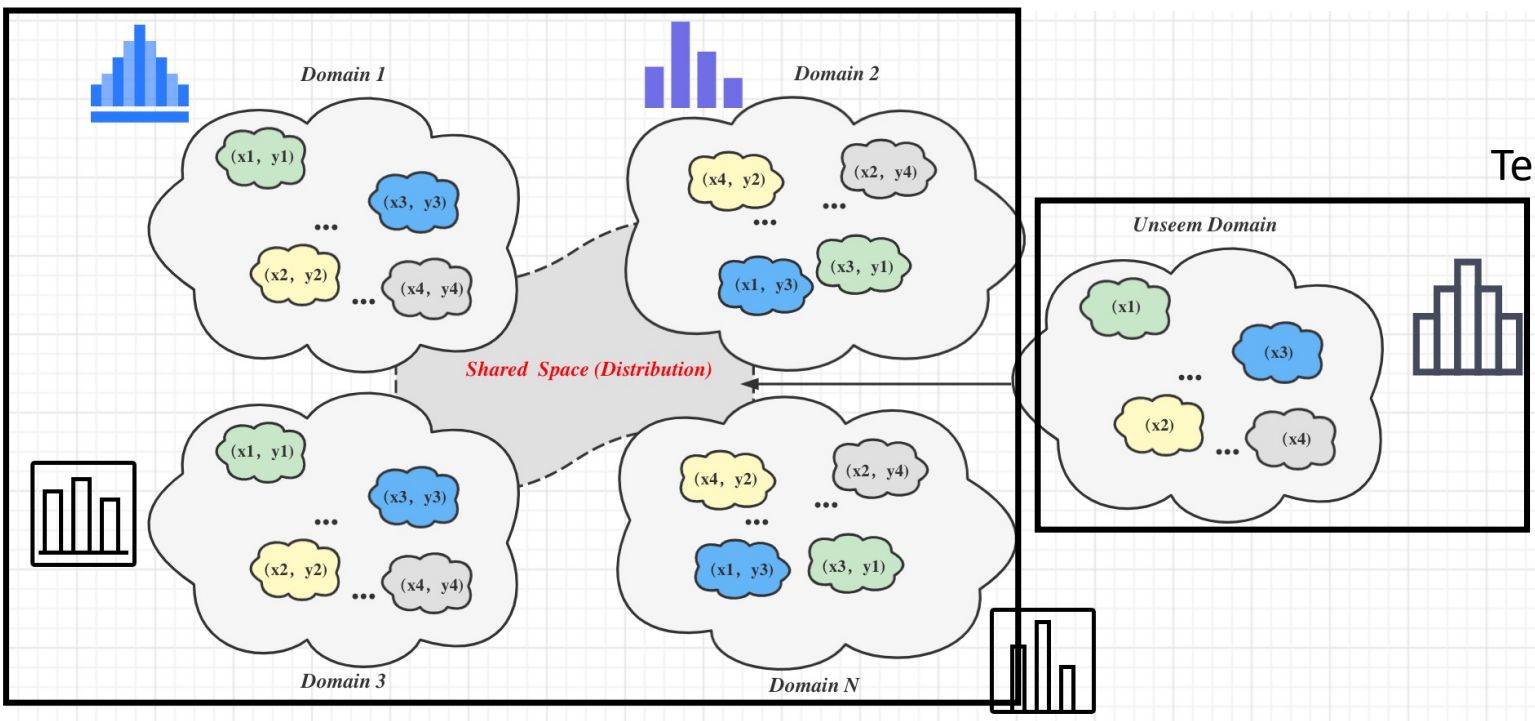
Different colouring agents

What is Domain Generalization (DG) ?

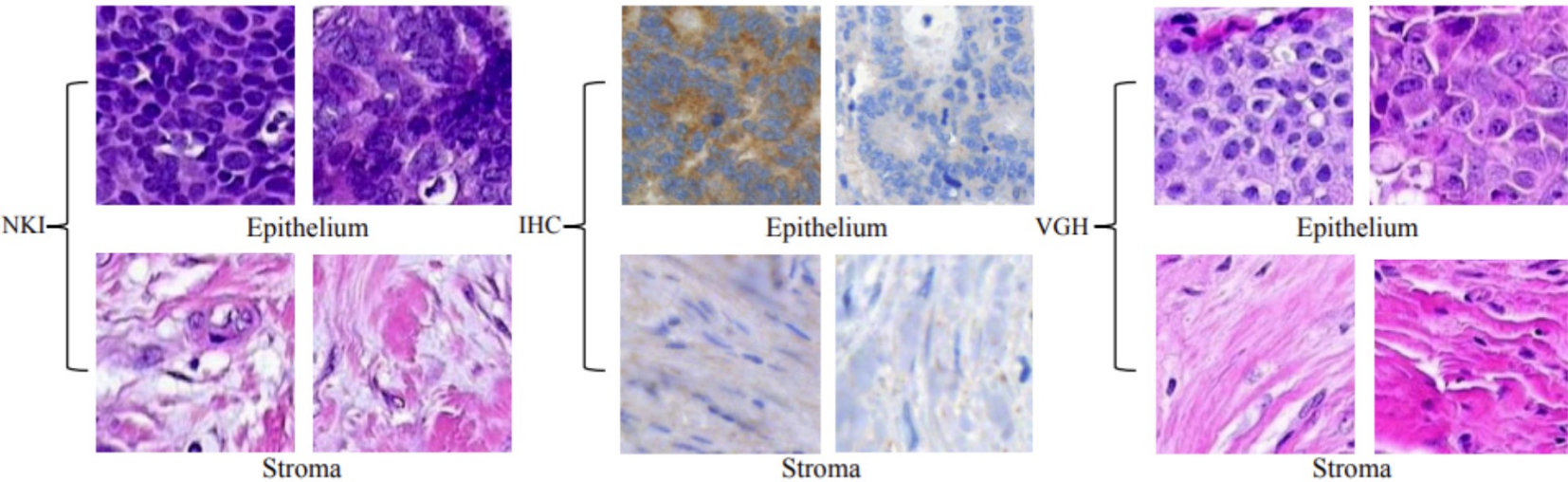


Training set

- 1. Obtain a more robust models
- 2. Annotating the data is expensive



What is DG in the context of small data?



Healthcare Data due to potential privacy concerns or rare diseases



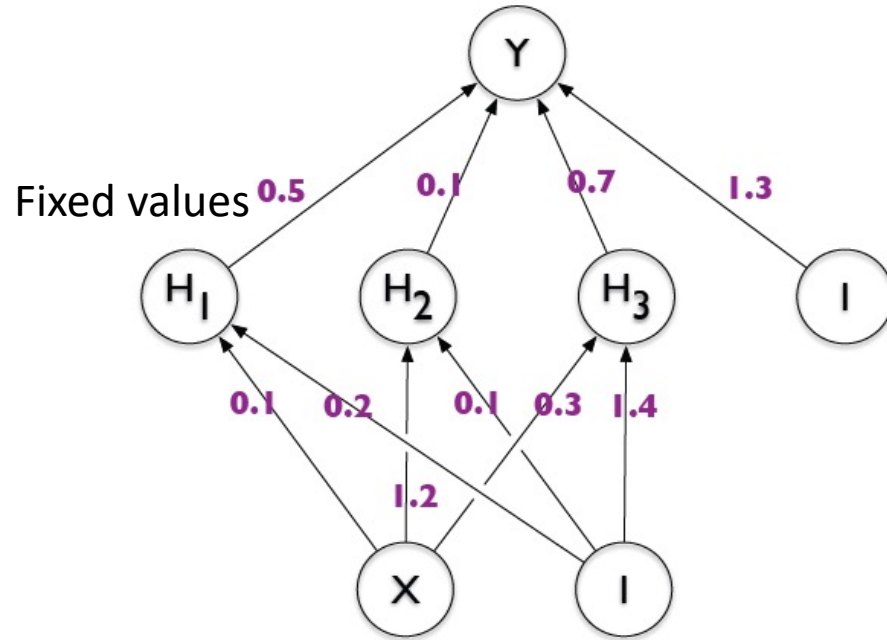
Chip design data due to IP protection

DG with Small Data

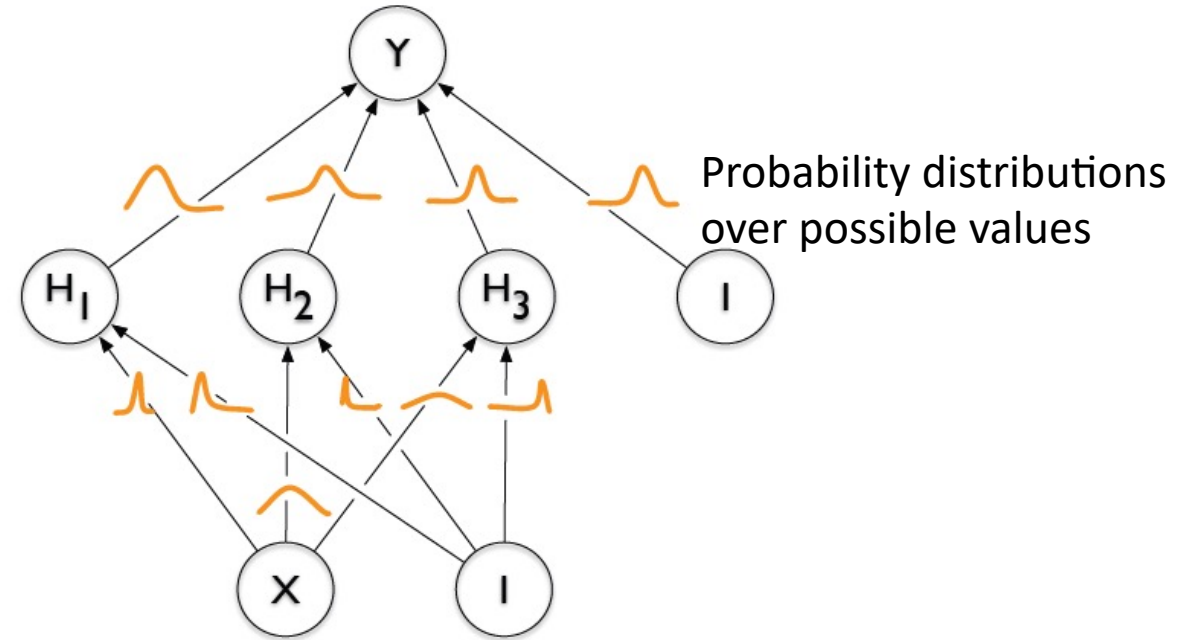


Make the backbone more adaptive to small data scenarios

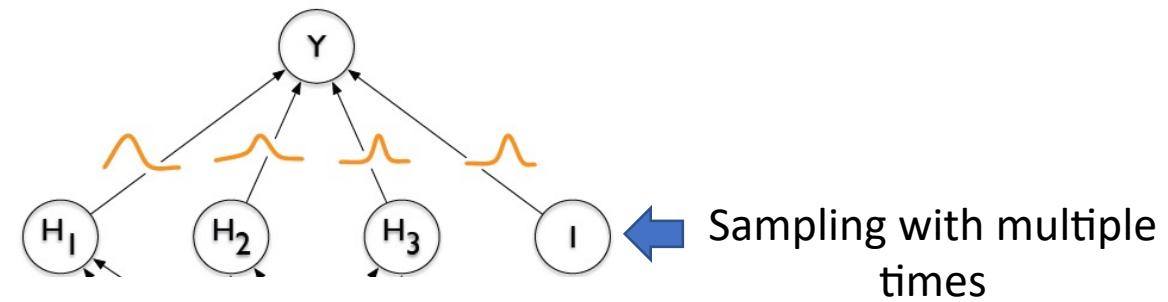
Deterministic Neural Networks (e.g., CNNs, FCNs)



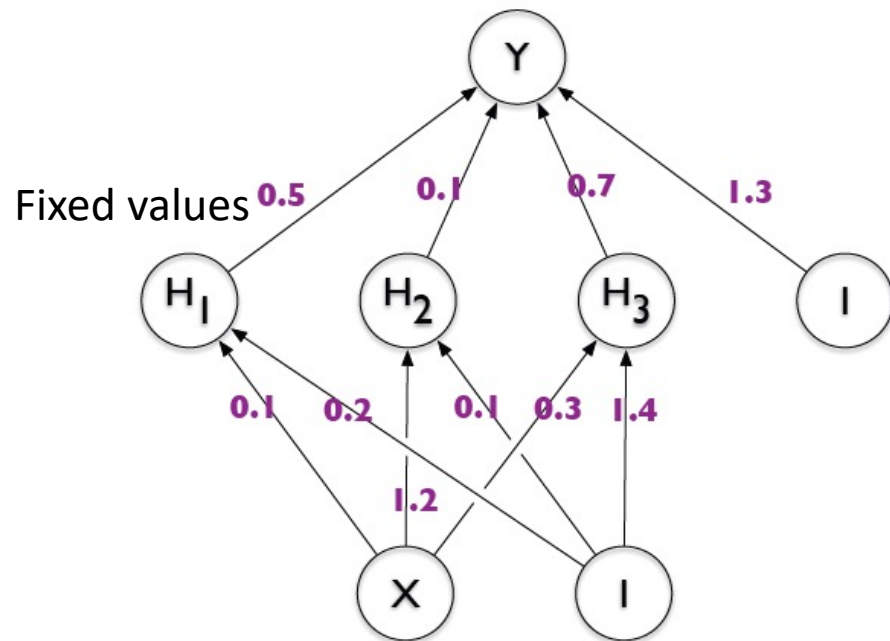
Bayesian Neural Networks



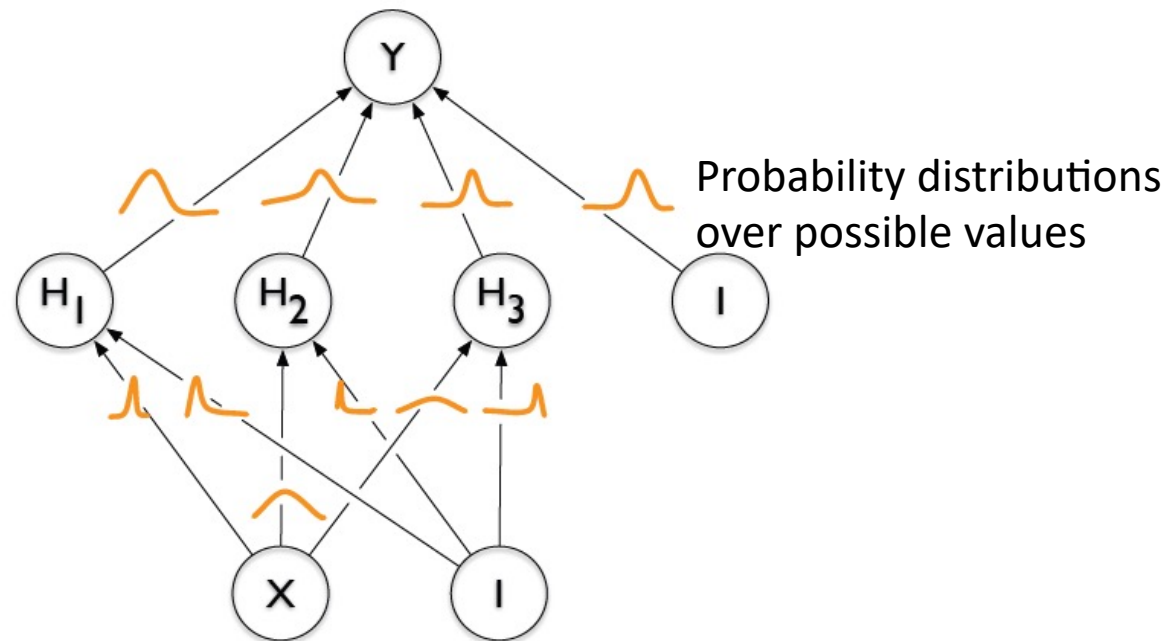
1. Richer representations and predictions from cheap model averaging.



Deterministic Neural Networks (e.g., CNNs, FCNs)



Bayesian Neural Networks



2. Model parameters can be regularized by a prior distribution with less overfitting risk in the context of small data scenarios

$$\theta^* = \arg \min_{\theta} \text{KL}[q(\mathbf{w}|\theta) || P(\mathbf{w}|\mathcal{D})]$$

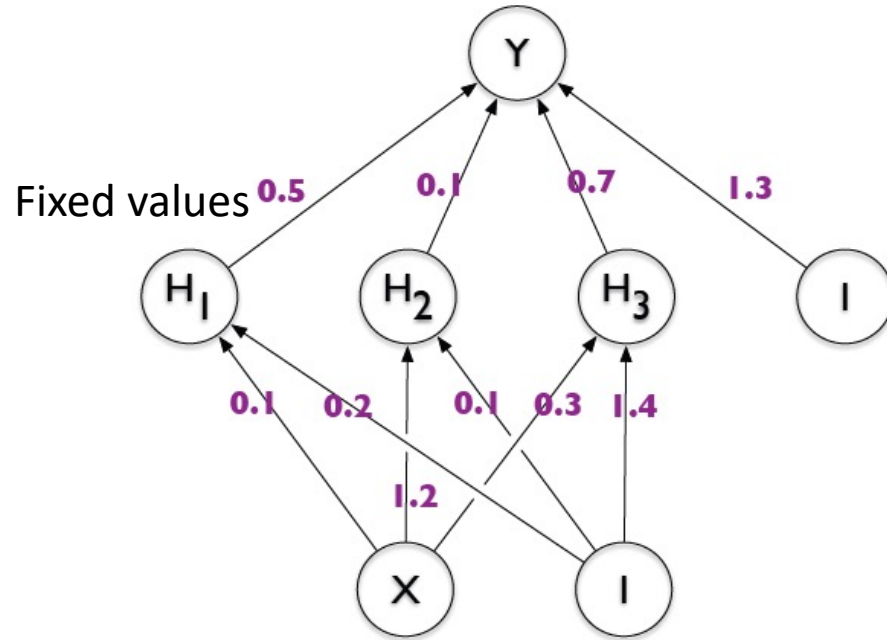
$$= \arg \min_{\theta} \int q(\mathbf{w}|\theta) \log \frac{q(\mathbf{w}|\theta)}{P(\mathbf{w})P(\mathcal{D}|\mathbf{w})} d\mathbf{w}$$

$$= \arg \min_{\theta} \underbrace{\text{KL}[q(\mathbf{w}|\theta) || P(\mathbf{w})]}_{\text{prior-dependent complexity term}} - \underbrace{\mathbb{E}_{q(\mathbf{w}|\theta)} [\log P(\mathcal{D}|\mathbf{w})]}_{\text{Data-dependent Likelihood term}}$$

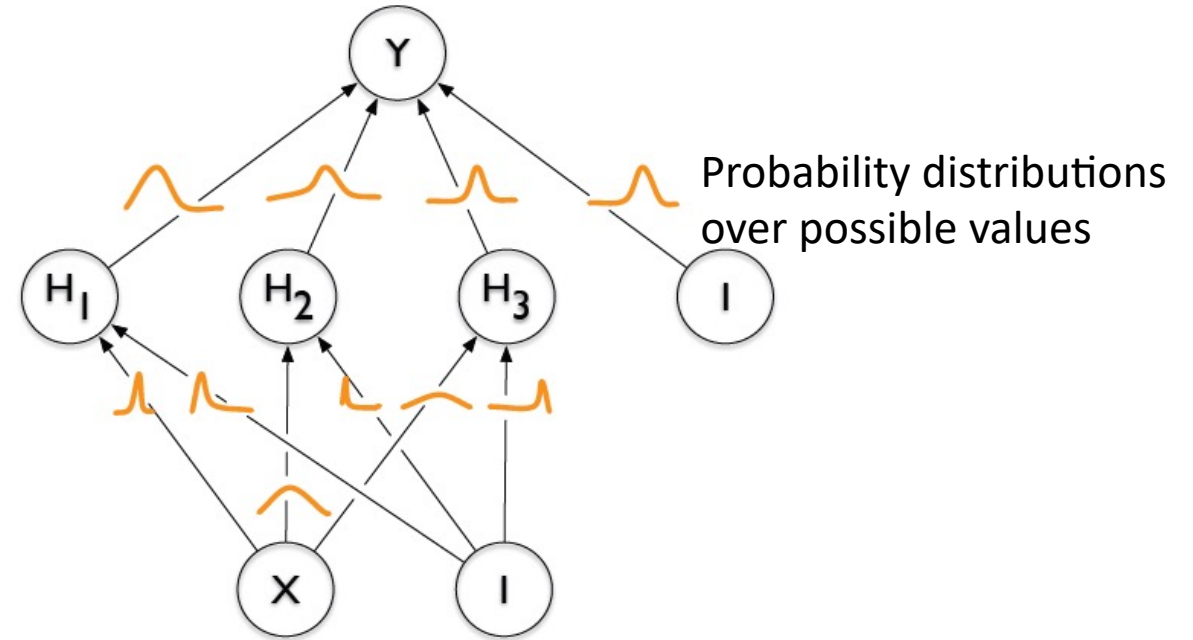
prior-dependent
complexity term

Data-dependent
Likelihood term

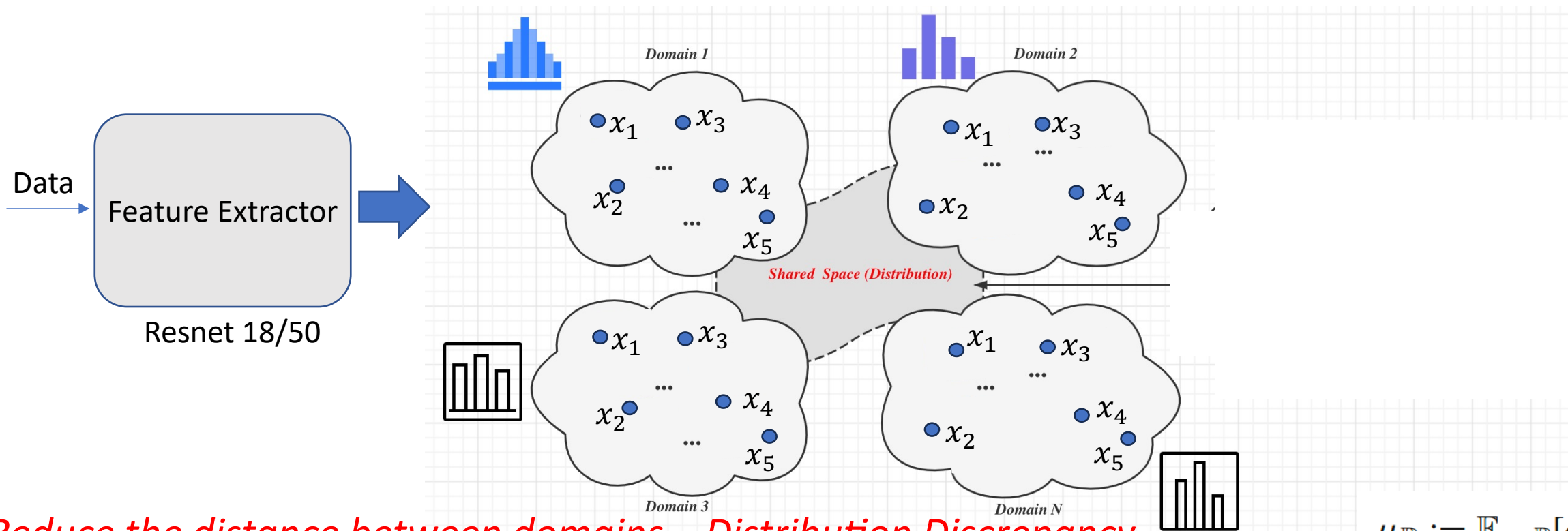
Deterministic Neural Networks (e.g., CNNs, FCNs)



Bayesian Neural Networks

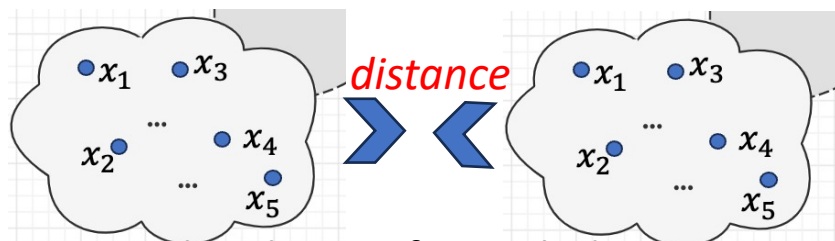


1. Richer representations and predictions from cheap model averaging.
2. Less overfitting risk in the context of small data scenarios



Reduce the distance between domains – Distribution Discrepancy

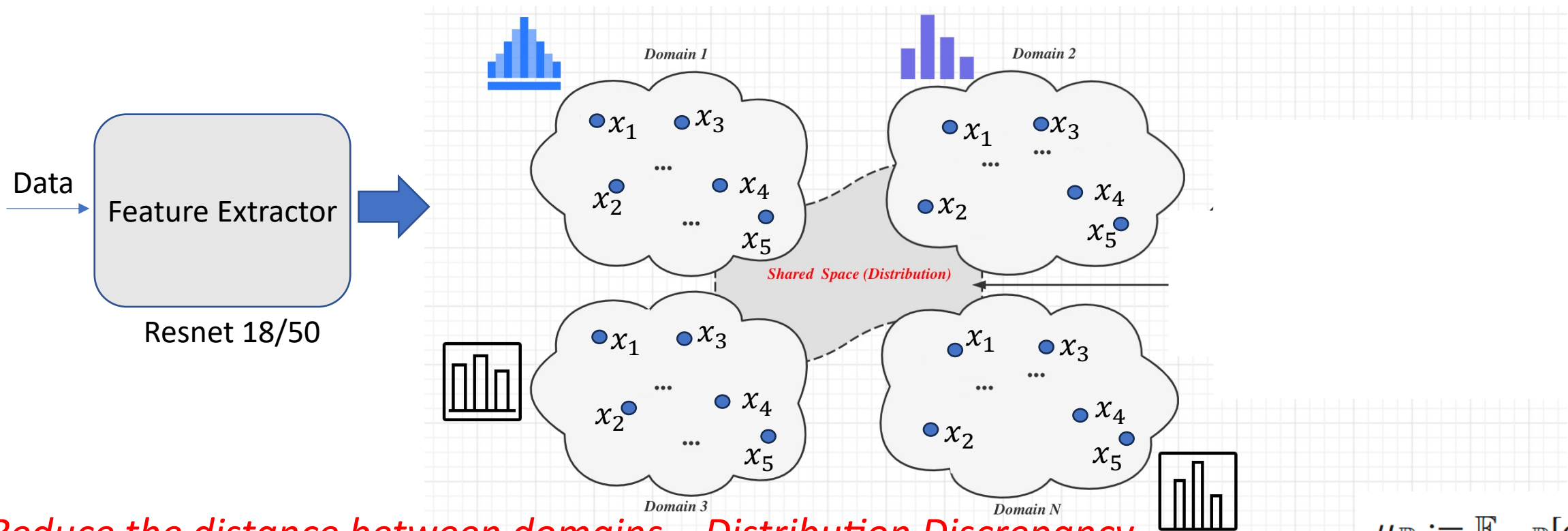
$$\mu_{\mathbb{P}} := \mathbb{E}_{\mathbf{z} \sim \mathbb{P}}[\phi(\mathbf{z})]$$



As a distribution for each domain

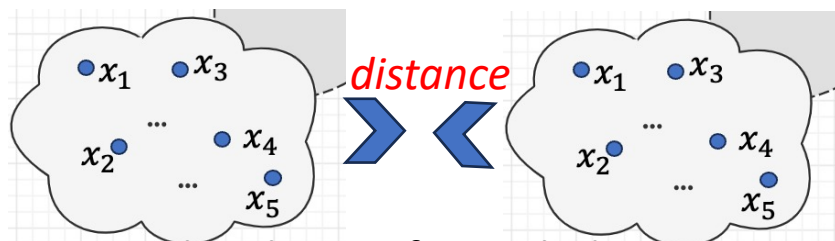
$$\text{MMD}(\mathbb{P}_l, \mathbb{P}_t)^2 = \left\| \frac{1}{n_l} \sum_{i=1}^{n_l} \phi(\mathbf{z}_{l_i}) - \frac{1}{n_t} \sum_{j=1}^{n_t} \phi(\mathbf{z}_{t_j}) \right\|_{\mathcal{H}}^2$$

The probability measure can be mapped into a reproducing kernel Hilbert space (RKHS) as an element



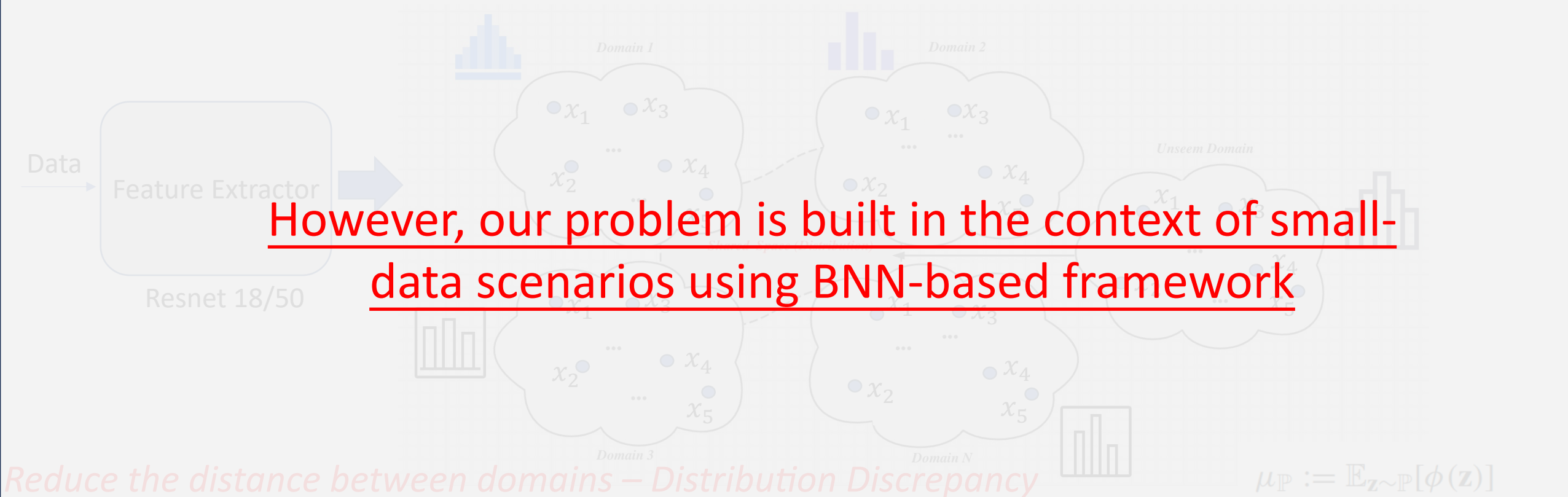
Reduce the distance between domains – Distribution Discrepancy

$$\mu_{\mathbb{P}} := \mathbb{E}_{\mathbf{z} \sim \mathbb{P}}[\phi(\mathbf{z})]$$



$$\text{MMD}(\mathbb{P}_l, \mathbb{P}_t)^2 = \left\| \frac{1}{n_l} \sum_{i=1}^{n_l} \phi(\mathbf{z}_{l_i}) - \frac{1}{n_t} \sum_{j=1}^{n_t} \phi(\mathbf{z}_{t_j}) \right\|_{\mathcal{H}}^2$$

The probability measure can be mapped into a reproducing kernel Hilbert space (RKHS) as an element



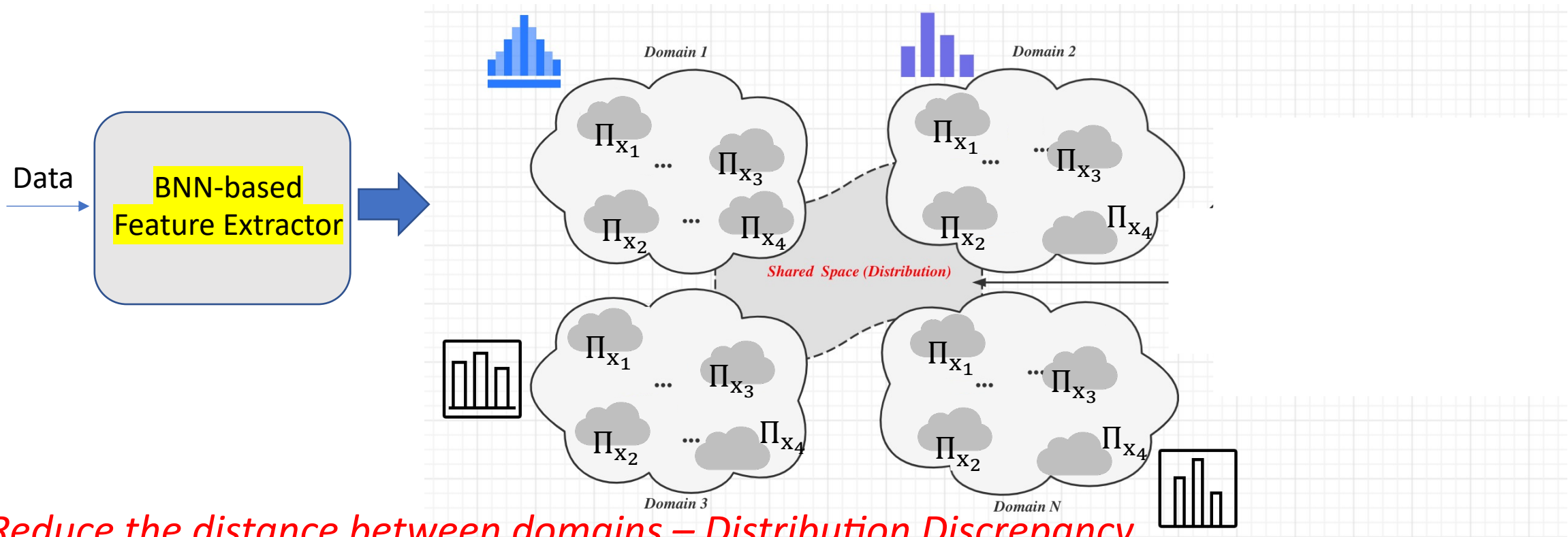
$$\mu_{\mathbb{P}} := \mathbb{E}_{\mathbf{z} \sim \mathbb{P}}[\phi(\mathbf{z})]$$



As a distribution for each domain

$$\text{MMD}(\mathbb{P}_l, \mathbb{P}_t)^2 = \left\| \frac{1}{n_l} \sum_{i=1}^{n_l} \phi(\mathbf{z}_{l_i}) - \frac{1}{n_t} \sum_{j=1}^{n_t} \phi(\mathbf{z}_{t_j}) \right\|_{\mathcal{H}}^2$$

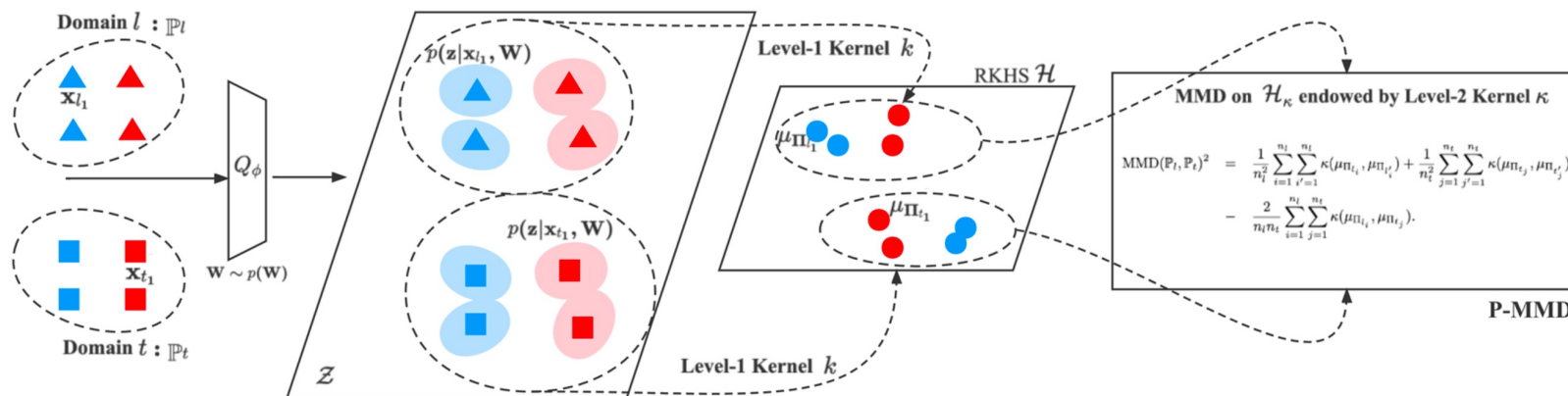
The probability measure can be mapped into a reproducing kernel Hilbert space (RKHS) as an element



As a **distribution over distributions** for each domain

$$\mathbb{P}_l = \{\Pi_{l_1}, \dots, \Pi_{l_{n_l}}\}$$

No previous works explore such distribution distance



Introduce a level-1 kernel κ and a level-2 kernel K

$$K(\Pi_{l_i}, \Pi_{t_j}) = \kappa(\mu_{\Pi_{l_i}}, \mu_{\Pi_{t_j}}) = \langle \psi(\mu_{\Pi_{l_i}}), \psi(\mu_{\Pi_{t_j}}) \rangle_{\mathcal{H}_\kappa}$$

Direct extension

$$\text{MMD}(\mathbb{P}_l, \mathbb{P}_t)^2 = \left\| \frac{1}{n_l} \sum_{i=1}^{n_l} \phi(\mathbf{z}_{l_i}) - \frac{1}{n_t} \sum_{j=1}^{n_t} \phi(\mathbf{z}_{t_j}) \right\|_{\mathcal{H}}^2$$

$$\text{P-MMD}(\mathbb{P}_l, \mathbb{P}_t)^2 = \left\| \frac{1}{n_l} \sum_{i=1}^{n_l} \psi(\mu_{\Pi_{l_i}}) - \frac{1}{n_t} \sum_{j=1}^{n_t} \psi(\mu_{\Pi_{t_j}}) \right\|_{\mathcal{H}_\kappa}^2$$

$$= \frac{1}{n_l^2} \sum_{i=1}^{n_l} \sum_{i'=1}^{n_l} K(\Pi_{l_i}, \Pi_{l_{i'}}) + \frac{1}{n_t^2} \sum_{j=1}^{n_t} \sum_{j'=1}^{n_t} K(\Pi_{t_j}, \Pi_{t_{j'}})$$

$$- \frac{2}{n_l n_t} \sum_{i=1}^{n_l} \sum_{j=1}^{n_t} K(\Pi_{l_i}, \Pi_{t_j}).$$

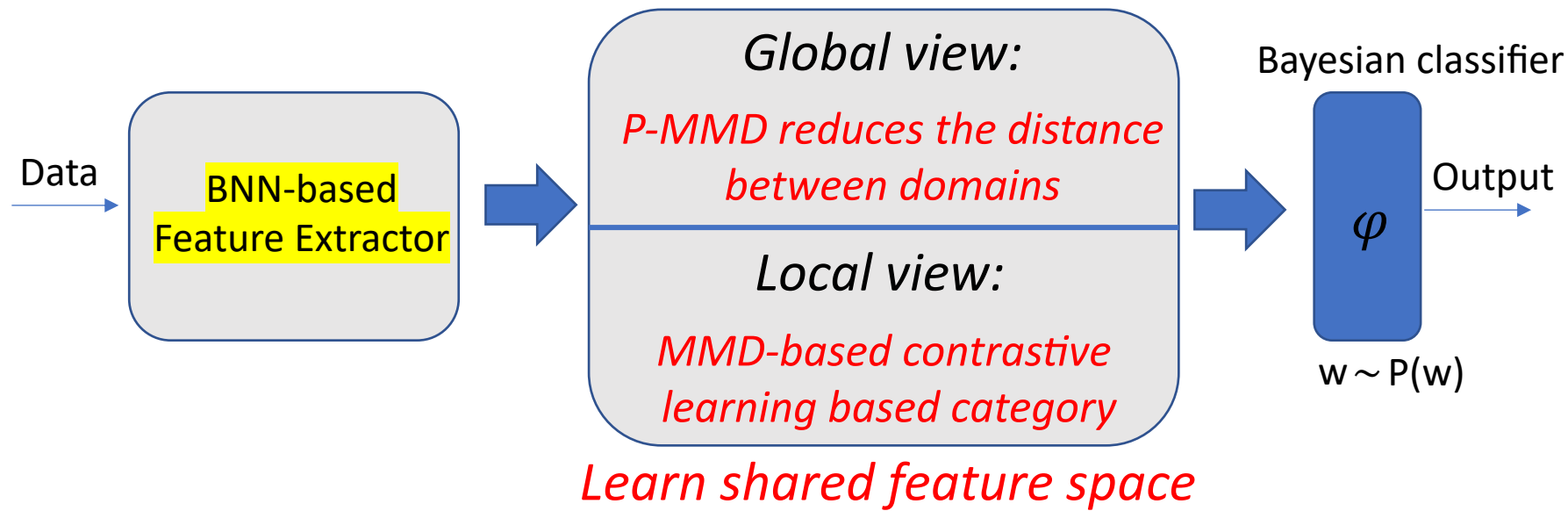
$$\begin{aligned} K(\Pi_{l_i}, \Pi_{t_j}) &= \kappa(\mu_{\Pi_{l_i}}, \mu_{\Pi_{t_j}}) = \exp\left(-\frac{\lambda}{2} \|\mu_{\Pi_{l_i}} - \mu_{\Pi_{t_j}}\|_{\mathcal{H}_\kappa}^2\right) \\ &= \exp\left(-\frac{\lambda}{2} (\langle \mu_{\Pi_{l_i}}, \mu_{\Pi_{l_i}} \rangle_{\mathcal{H}_\kappa} - 2\langle \mu_{\Pi_{l_i}}, \mu_{\Pi_{t_j}} \rangle_{\mathcal{H}_\kappa} + \langle \mu_{\Pi_{t_j}}, \mu_{\Pi_{t_j}} \rangle_{\mathcal{H}_\kappa})\right) \\ &= \exp\left(-\frac{\lambda}{2} \left(\frac{1}{m_l^2} \sum_{i=1}^{m_l} \sum_{i'=1}^{m_l} k(\mathbf{z}_{l_i}, \mathbf{z}_{l_{i'}}) - \frac{2}{m_l m_t} \sum_{i=1}^{m_l} \sum_{j=1}^{m_t} k(\mathbf{z}_{l_i}, \mathbf{z}_{t_j}) + \frac{1}{m_t^2} \sum_{j=1}^{m_t} \sum_{j'=1}^{m_t} k(\mathbf{z}_{t_j}, \mathbf{z}_{t_{j'}})\right)\right) \end{aligned}$$

Unbiased estimation

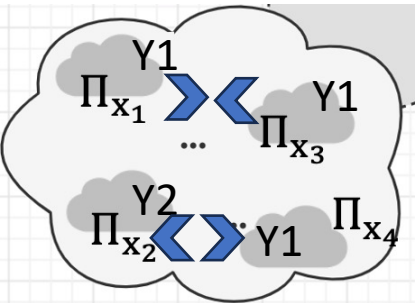
Reduce computation complexity from $O(n^2) \Rightarrow O(n)$

$$\text{P-MMD}(\mathbb{P}_l, \mathbb{P}_t)^2 \approx \frac{2}{n_l} \sum_{i=1}^{n_l} [K(\Pi_{l_{2i}}, \Pi_{l'_{2i+1}}) + K(\Pi_{l_{2i}}, \Pi_{l'_{2i+1}}) - K(\Pi_{l_{2i}}, \Pi_{l_{2i+1}}) - K(\Pi_{l_{2i+1}}, \Pi_{l_{2i}})] + \dots$$

DG with Small Data



Local view:



$$\mathcal{L}_{local}^{pos} = \frac{1}{2} \left\| \frac{1}{T} \sum_{i=1}^T \phi \left(M_{\Theta}(\mathbf{z}_{n_i}) \right) - \frac{1}{T} \sum_{j=1}^T \phi \left(M_{\Theta}(\mathbf{z}_{q_j}) \right) \right\|_{\mathcal{H}}^2, \text{ Same category}$$

$$\begin{aligned} \mathcal{L}_{local}^{neg} = & \frac{1}{2} \max[0, \xi - \text{MMD}(\Pi_n, \Pi_q)^2] = \frac{1}{2} \max[0, \xi \\ & - \left\| \frac{1}{T} \sum_{i=1}^T \phi \left(M_{\Theta}(\mathbf{z}_{n_i}) \right) - \frac{1}{T} \sum_{j=1}^T \phi \left(M_{\Theta}(\mathbf{z}_{q_j}) \right) \right\|_{\mathcal{H}}^2], \text{ Different category} \end{aligned}$$

Table 2 Domain generalization results on skin lesion classification

| Method | DMF | D7P | MSK | PH2 | SON | UDA | Average |
|--------------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|---------------|
| DeepAll | 0.2492 ±0.0127 | 0.5680±0.0181 | 0.6674±0.0083 | 0.8000±0.0167 | 0.8613±0.0296 | 0.6264±0.0312 | 0.6287 |
| MASF (Dou et al., 2019) | 0.2692±0.0146 | 0.5678±0.0361 | 0.6815±0.0122 | 0.7833±0.0101 | 0.9204±0.0227 | 0.6538±0.0196 | 0.6460 |
| LDDG (Li et al., 2020) | 0.2793±0.0244 | 0.6007±0.0187 | 0.6967±0.0211 | 0.8167±0.0209 | 0.9272±0.0117 | 0.6978±0.0182 | 0.6697 |
| KDDG (Wang et al., 2021) | 0.3189±0.0256 | 0.5829±0.0212 | 0.7014±0.0178 | 0.9021±0.0314 | 0.9398±0.0213 | 0.6882±0.0139 | 0.6889 |
| SWAD (Cha et al., 2021) | 0.3582 ±0.0234 | 0.5491 ±0.0231 | 0.6842 ±0.0156 | 0.9167 ±0.0121 | 0.9824 ±0.0012 | 0.7240 ±0.0251 | 0.7024 |
| BDIL (Xiao et al., 2021) | 0.2985±0.0452 | 0.6204 ±0.0212 | 0.7059±0.0145 | 0.8967±0.0096 | <u>0.9860</u> ±0.0198 | 0.7219±0.0284 | 0.7049 |
| DNA (Chu et al., 2022) | 0.3532 ±0.0133 | 0.5581 ±0.0178 | <u>0.7120</u> ±0.0194 | <u>0.9333</u> ±0.0045 | 0.9851 ±0.0032 | 0.7314 ±0.0141 | 0.7122 |
| DSU (Li et al., 2022) | 0.3830 ±0.0267 | 0.5739 ±0.0147 | 0.6935 ±0.0165 | 0.8833 ±0.0231 | 0.9841 ±0.0098 | 0.7201 ±0.0121 | 0.7063 |
| MIRO (Cha et al., 2022) | 0.3432 ±0.0092 | 0.5863 ±0.0113 | 0.6919 ±0.0101 | 0.9300±0.0021 | 0.9659 ±0.0292 | <u>0.7328</u> ±0.0233 | 0.7084 |
| Ours (in this paper) | <u>0.3781</u> ±0.0136 | <u>0.6120</u> ±0.0115 | 0.7276 ±0.0201 | 0.9416 ±0.0103 | 0.9889 ±0.0041 | 0.7486 ±0.0123 | 0.7328 |

Each column denotes a cross-domain task. For example, in the second column, we use DMF dataset as the target domain and the remaining datasets as the source domains. The best and second-best performance on each target domain are bolded and underlined, respectively. Note that all baseline methods adopt the SWAD method (Cha et al., 2021) for weight averaging. The baseline in the sixth row, namely SWAD, denotes the ERM training strategy with the SWAD method

Table 3 Domain generalization results on gray matter segmentation task. For the DSC, CC, TPR, and JI, the higher the better. For the ASD, the lower the better. Note that all baseline methods adopt the SWAD method (Cha et al., 2021) for weight averaging. The baseline, namely SWAD, denotes the ERM training strategy with the SWAD method.

| (a) MASF | | | | | | | (b) KDDG | | | | | | |
|----------|--------|---------------|--------------|---------------|---------------|--------|----------|--------|---------------|--------------|---------------|--------|---------------|
| source | target | DSC | CC | JI | TPR | ASD | source | target | DSC | CC | JI | TPR | ASD |
| 2,3,4 | 1 | 0.8502 | 64.22 | 0.7415 | 0.8903 | 0.2274 | 2,3,4 | 1 | <u>0.8745</u> | <u>70.75</u> | <u>0.7795</u> | 0.8949 | 0.0539 |
| 1,3,4 | 2 | 0.8115 | 53.04 | 0.6844 | 0.8161 | 0.0826 | 1,3,4 | 2 | 0.8229 | 56.71 | 0.6997 | 0.8226 | 0.0490 |
| 1,2,4 | 3 | 0.5285 | -99.3 | 0.3665 | 0.5155 | 1.8554 | 1,2,4 | 3 | 0.5676 | -63.1 | 0.3866 | 0.5904 | <u>1.2805</u> |
| 1,2,3 | 4 | 0.8938 | 76.14 | 0.8083 | <u>0.8991</u> | 0.0366 | 1,2,3 | 4 | 0.8894 | 75.06 | 0.8011 | 0.9222 | 0.0377 |
| Average | | 0.7710 | 23.52 | 0.6502 | 0.7803 | 0.5505 | Average | | 0.7886 | 34.86 | 0.6667 | 0.8075 | 0.3553 |

| (c) LDDG | | | | | | | (d) SWAD | | | | | | |
|----------|--------|--------|-------|---------------|---------------|---------------|----------|--------|--------|--------------|--------|--------|---------------|
| source | target | DSC | CC | JI | TPR | ASD | source | target | DSC | CC | JI | TPR | ASD |
| 2,3,4 | 1 | 0.8708 | 69.29 | 0.7753 | 0.8978 | 0.0411 | 2,3,4 | 1 | 0.8726 | 70.23 | 0.7702 | 0.8995 | 0.0502 |
| 1,3,4 | 2 | 0.8364 | 60.58 | 0.7199 | <u>0.8485</u> | 0.0416 | 1,3,4 | 2 | 0.8378 | 60.71 | 0.7230 | 0.8176 | 0.0424 |
| 1,2,4 | 3 | 0.5543 | -71.6 | <u>0.3889</u> | <u>0.5923</u> | 1.5187 | 1,2,4 | 3 | 0.5388 | -99.0 | 0.3789 | 0.5083 | 1.4789 |
| 1,2,3 | 4 | 0.8910 | 75.46 | 0.8039 | 0.8844 | 0.0289 | 1,2,3 | 4 | 0.8903 | <u>75.89</u> | 0.8026 | 0.8859 | <u>0.0302</u> |
| Average | | 0.7881 | 33.43 | 0.6720 | 0.8058 | 0.4076 | Average | | 0.7849 | 26.96 | 0.6687 | 0.7778 | 0.4002 |

| (e) DSU | | | | | | | (f) Ours | | | | | | |
|---------|--------|--------|-------|--------|---------------|--------|----------|--------|---------------|--------------|---------------|---------------|---------------|
| source | target | DSC | CC | JI | TPR | ASD | source | target | DSC | CC | JI | TPR | ASD |
| 2,3,4 | 1 | 0.8739 | 70.32 | 0.7794 | <u>0.9210</u> | 0.0793 | 2,3,4 | 1 | 0.8786 | 71.57 | 0.7873 | 0.9293 | <u>0.0422</u> |
| 1,3,4 | 2 | 0.8474 | 63.58 | 0.7367 | 0.8502 | 0.0494 | 1,3,4 | 2 | 0.8485 | 63.78 | 0.7389 | 0.8401 | 0.0401 |
| 1,2,4 | 3 | 0.5574 | -70.4 | 0.3923 | 0.6097 | 1.5049 | 1,2,4 | 3 | <u>0.5634</u> | <u>-68.0</u> | 0.3992 | 0.6103 | 1.2239 |
| 1,2,3 | 4 | 0.8897 | 75.10 | 0.8018 | 0.9225 | 0.0415 | 1,2,3 | 4 | <u>0.8921</u> | 75.69 | <u>0.8058</u> | 0.9245 | 0.0362 |
| Average | | 0.7921 | 34.65 | 0.6775 | 0.8225 | 0.4362 | Average | | 0.7957 | 35.76 | 0.6828 | 0.8260 | 0.3356 |

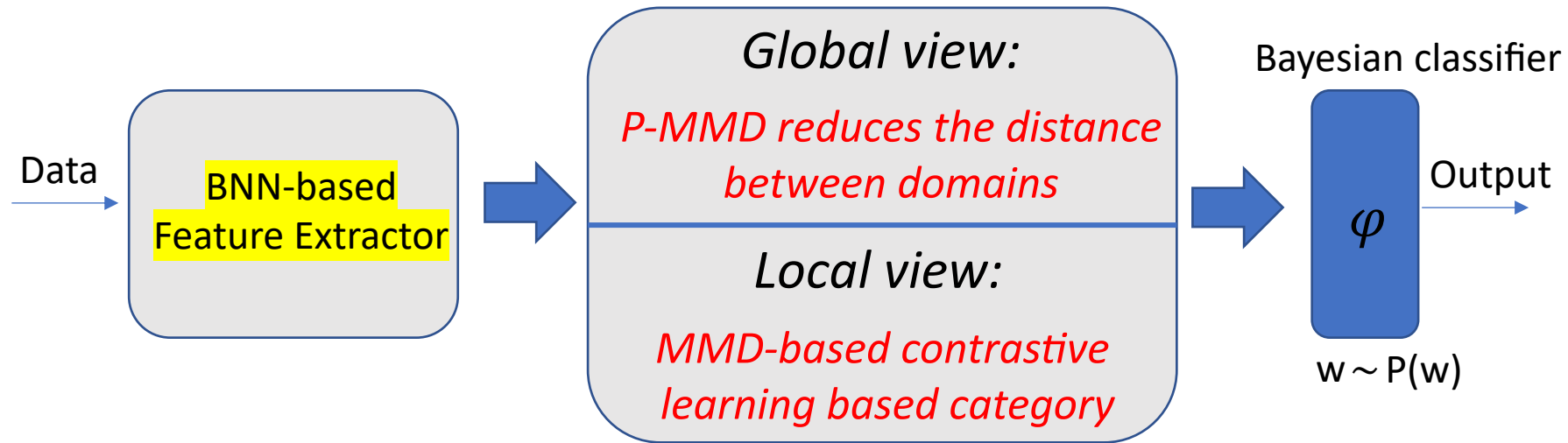
Table 5 Domain generalization results on MSK dataset by randomly picking same proportion of samples from each source domain

| Proportion (%) | BDIL | DNA | Ours |
|----------------------------|----------------|----------------|-----------------------|
| 100 | 0.7059± 0.0284 | 0.7121± 0.0141 | 0.7276 ±0.0123 |
| 80 | 0.6625±0.0920 | 0.6591±0.0022 | 0.6975 ±0.0036 |
| 60 | 0.6468±0.0106 | 0.6149±0.0112 | 0.6641 ±0.0114 |
| 40 | 0.6491±0.0171 | 0.6065±0.0111 | 0.6579 ±0.0057 |
| Average (80,60,40) ↑ | 0.6528 | 0.6268 | 0.6732 |
| Average Attenuation Rate ↓ | 7.67% | 11.98% | 7.37% |

A smaller proportion (< 40%) is unavailable because equal batch sizes cannot be maintained in PH2 dataset

Table 6 Domain generalization results on MSK dataset by randomly picking same number of samples from each class in each domain

| Number of sample | BDIL | DNA | Ours |
|----------------------------|-----------------|-----------------|------------------------|
| 40 | 0.5897 ± 0.0029 | 0.5412 ± 0.0143 | 0.6368 ± 0.0074 |
| 30 | 0.5762 ± 0.0101 | 0.5132 ± 0.0229 | 0.6138 ± 0.0291 |
| 20 | 0.5573 ± 0.0011 | 0.5048 ± 0.0087 | 0.6037 ± 0.0121 |
| Average (40,30,20) ↑ | 0.5744 | 0.5196 | 0.6183 |
| Average attenuation rate ↓ | 5.49% | 6.72% | 5.19% |



SDDG:

1. BNN is more adaptive to small-data scenarios.

Thanks !

2. A new extension of MMD is proposed to compute the distribution distance between distributions over distributions.

3. A more generalized model can be learned by DG in the context of small data