

WE tends to be more non-uniform in  
poorly because there is no fixed unit to  
prevent weights from drifting as various  
refracts differ in sample densities

constant

Euclidean distance where  $D_0 = -2\lambda_n(5^\circ)$  is the minimal constant

prevent weights from drifting as various regions differ in sample densities



# Model selection validation for clustering

- Structure can be invalid in two ways: wrong model order and/or inappropriate model type
- Validation methods can be external (comp. with ground truth) or internal
- We want to use convergence guarantees for sums (e.g. law of large numbers) so we convert the log product term to a log sum over exponent
- Every method for valid. introduces a bias

- You may be grossly misled by naively counting the number of params (cf. VC-dim of line)
- General approach: measure quality for diff.  $k$  with some discount (bias complexity penalty) - will move  $k$  to use more bits, params or fit better

- MDL: minimize  $[-\log p(X|A_k) - \log p(A_k)]$   $A_k$ :MLE of  $A$   
 $= [-\log p(X|A_k) + 1/k \cdot \log n]$   $k$ : #params of  $A_k$

- Bayes factor:  $P(X|M_1)/P(X|M_2)$  where  $P(X|M_1) = \int p(X|A_1, M_1) dA_1$ , use Lap. approx.  
 $\log P(X|M_1) = \log P(X|A_1, M_1) - 1/2 \cdot \log n \cdot \log \pi$

- MDL and BF are formally equivalent, consistent

- In modern statistics more d.o.f. we have as we have more data - BF exploits finite dim. param space and grouping data (samples  $n$ ) - classical limit of statistics, we understand it well, but not useful (parametric statistics)
- Then, or well-motivated, they do likelihood based optimization instead of posterior based, which is intrinsically hard

- Gap statistics: find "knee" in costs, it uses max. discrepancy between actual data cost and that of unstructured ref. data (i.e. which cannot be clustered, so-called "null-model"), if the plot is too noisy, the method may fail  
 $gap_k = E_n^*[\log(W_k)] - \log(W_k)$ ,  $D_{ij} = \|x_i - x_j\|^2$   
 $W_k = \sum_{i,j} 1/2n \sum_{i,j} D_{ij} - E_n^*$  is the expected value with sample of size  $n$  from null-model  
 $\hat{k} = \arg \min_k \{gap_k\}$

- In practice approx.  $E_n^*[\log(W_k)]$  by bootstrap-gap stat. works satisfactorily for spherical and well-separated clusters (it assumes compact clusters), a structural bias, it is a point heuristic for k-means-like criteria

- Stability based valid: idea: solutions on two datasets from same source should be similar, stable in both should be same but fluctuations should be different, model mismatch in solution transfer produces unstable clustering solutions - type of classifier has a large influence, has to be selected with care (e.g. path-based clust. data with a nearest centroid classifier)

- Two disjoint sets of equal size: overlap could determine group structure (stat. dependence), algo. should be able to find similar structure in both, cannot find if one is too small and such structure is no longer visible to algo.  
 - Good performance in experimental datasets, but systematic bias towards too simplistic solutions - it is principled but with a deficit: it only tells you how reliable under repeated experimentation the algo. would repeat, but it doesn't take into account the informativeness of solution (disregards the tradeoff) - A tolerable decrease in stability of inferred patterns might be compensated by a substantial increase of their information content

# Stability valid. procedure

1-transfer via prediction: construct classifier  $\phi$  trained on  $(x, y)$  where  $y$  is the clustering solution to  $x$  or  $1 \leq A \leq X$ . we consider labeling  $\phi(x) := (\phi(x_i))_{i=1}^n$  as the extension of the clustering solution  $y$  on dataset  $X$  to data set  $X'$ . These predicted labels can be compared to those generated on the clusters of  $A \leq X$

2-compare solutions: a very natural distance measure for comparing labelings  $\phi(x)$  and  $y$  is Hamming dist. (0-1 loss), this can be treated as the empirical misclassification risk of  $\phi$  with regard to the training set

3-permute solutions: to overcome non-uniqueness we optimally permute solutions to maximize agreement. Hungarian method does this in  $O(n^3)$  by minimum bipartite matching

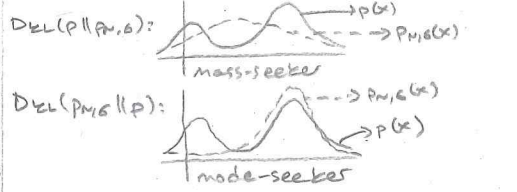
- Dissim.:  $d_{\phi}(\phi(x'), y') = \min_{\pi \in \Pi} \frac{1}{n} \sum_{i=1}^n 1(\pi(\phi(x'_i)) \neq y'_i)$   
 - Stability:  $S(A_k) = E_{x, x'} d_{\phi}(\phi(x'), y')$   
 Smaller the value of the max.  $S(A_k) \in [0, 1]$ , the more stable are the solutions  
 - Calculate relative stability with stability observed by random label guessing:  
 $\bar{S}(A_k) = S(A_k)/S(R_k)$ ,  $R_k$  assigns labels to obj. with prob.  $1/k$

- Del penalizes approximations that misrepresent likely events
- entropy of  $X$  or uncertainty of  $X$  is amount of info. of  $X$  is minimum expected number of questions to guess  $x$
- Forward KL: difference between  $p(x)$  and  $q(x)$  is weighted by  $p(x)$ . During the optimization process then, whenever  $p(x) > 0$ ,  $q(x)$  would be ignored. The difference between  $p(x)$  and  $q(x)$  will be minimized if  $p(x) > 0$ . It is known as zero avoiding, as it is, avoiding  $q(x) > 0$  whenever  $p(x) > 0$

→  $P_{M,6}$  as mass-seeker:  $\arg \min_{P_{M,6}} D_{KL}(P \| P_{M,6})$

- Reverse KL, as we switch the two distr. position in the equation, now  $q(x)$  is the weight. Here, it is better to fit some portion of  $p(x)$  as long as that approx. is good. Consequently reverse KL will try to avoid spreading the approximate. As those properties suggest, this form of KL-div. is known as zero-forcing or it forces  $q(x)$  to be 0 on some areas, even if  $p(x) > 0$

→  $P_{M,6}$  as mode-seeker:  $\arg \min_{P_{M,6}} D_{KL}(P_{M,6} \| P)$



# Model valid by info. theory

Typical set: Asymptotic equipartition property (AEP):  
 $-\frac{1}{n} \log P(X_1, \dots, X_n) \xrightarrow{\text{prob}} H(X)$ , for i.i.d.  $X_1, \dots, X_n \sim P(X)$   
 A typical set  $A_n^\epsilon$  wrt  $P(X)$  is a set of sequences  $(x_1, \dots, x_n) \in X^n$  with prob.  $1 - \epsilon$   
 $2^{-n(H(X) + \epsilon)} \leq P(X_1, \dots, X_n) \leq 2^{-n(H(X) - \epsilon)}$   
 - If  $(x_1, \dots, x_n) \in A_n^\epsilon$  then  $H(X) - \epsilon \leq -\frac{1}{n} \log P(x_1, \dots, x_n) \leq H(X) + \epsilon$   
 $P[A_n^\epsilon] > 1 - \epsilon$  for  $n$  sufficiently large  
 $|A_n^\epsilon| \leq 2^{n(H(X) + \epsilon)}$ , where  $|A_n^\epsilon|$  is the cardinality of the typical set  
 $|A_n^\epsilon| \geq (1 - \epsilon) 2^{n(H(X) - \epsilon)}$  for  $n$  sufficiently large

The typical set  $A_n^\epsilon$  has prob. almost 1, all elements of the typical set are nearly equiprobable, and the number of typical solutions is nearly  $2^{nH}$

Approx. weights  $w_i = C(x_i) \times R_i \rightarrow [0, 1]$ , s.t.  $(C, X, R) \mapsto w(C, X)$   
 weights are non-neg., maximal weight allocated to global minimizer at  $R$  is normalized to one:  
 $w(C, X) = 1$ . Solution with large approx. weights  $w(C, X) \geq 1 - \epsilon$ ,  $\epsilon < 1$  can be accepted as substitutes of the global minimizers. Posterior becomes:  
 $p(C, X) = \frac{w(C, X)}{\sum_C w(C, X)}$  inverse order constraints:  
 $R(C, X) \leq R(C', X) \Leftrightarrow w(C, X) \geq w(C', X)$

Example (unnormalized) weights:  
 - Boltzmann:  $w(C, X) = \exp(-\beta R(C, X))$   
 - Fermi:  $w(C, X) = (1 + \exp(-\beta(R(C, X) - Y)))^{-1}$   
 - Approx:  $w(C, X) = 1$  if  $R(C, X) \leq R(C^*, X) + Y$ , 0 otherwise  
 Normalized Boltzmann weights:  
 $w(C, X) = \exp(-\beta R(C, X))$ ,  $R(C, X) = R(C, X) - R(C^*, X)$   
 $\beta \rightarrow 0$  all weights  $w(C, X) = 1$  ind.-of-costs.  $Z_\beta = \sum_C w(C, X)$  indicates the size of the hypothesis space  
 high  $\beta$  all weights are small compared to  $w(C^*, X)$   
 $Z_\beta$  essentially counts the number of globally optimal  
 Mismatched  $\beta$ :  $Z_\beta$  is the effective number of patterns that approx. fit the dataset  $X$ , where  $\beta$  defines the precision of approx. - noise in measurements  $X$  reduces the resolution and thus coarsens hypo. class  
 weight sum: measures total weight of hypotheses with low costs, delta partition function when we use Boltzmann weights

Equivalence transformations: idea is shifting posterior Assume transformation  $T$  s.t.  
 $\forall x, x' \in \mathcal{X}, \|P(C|T(x)) - P(C|T(x'))\|_1 > 0$  invertible  
 implies  $\|T\| \leq |C|$  for discrete hypo. spaces  
 $\sum_{T \in \mathcal{T}} P(C|T(x)) \in [\frac{|T|}{|C|} (1 - p), \frac{|T|}{|C|}]$   $p$  measures inhomogeneity of transformation

To  $C(X) = C(T(x)) \rightarrow$  equivalence of algorithm examples: permutation for graph clustering, rotation for SVD, translation for mean estimation, scaling for linear regression, permutation and scaling for sparse linear regression

# Communication scenario

Sender and receiver both receive an instance  $x'$  from problem generator, calculate  $P(C|x')$  and agree on a set of  $m$  randomly drawn transforms  $T = \{T_1, \dots, T_m\}$  with  $P(C) = \mathbb{E}[T]$ . Here posteriors  $P(C|T_j, x')$  play the role of codewords in Shannon's random coding theory.

Sender selects a transformation  $T_j$  as message and sends it to the problem generator. PG generates new instance  $x'' \sim P(x)$  and applies  $T_j$ , which yields  $\tilde{x} = T_j \circ x''$ . PG sends  $\tilde{x}$  to receiver without revealing other  $T$ s or  $x'$ . So receiver loses both the knowledge of  $T$ s and suffers from the stochastic variability of  $x$ . Then receiver calculates the expected posterior  $P(C|\tilde{x})$  and decodes the message  $\hat{T}$ :  
 $\hat{T} \in \arg \max_{T \in \mathcal{T}} E_{x'} P(C|T(x')) P(C|\tilde{x})$

We introduce kernel function to be used in decoding:  
 $k_{T_j T_k}(x', x'') = \mathbb{E}_{C \sim P(C|T_j, x')} P(C|T_k, x'')$   
 $= \sum_{C \in \mathcal{C}} P(C|T_j, x') P(C|T_k, x'') \in [0, 1]$

Posterior agreement kernel for  $T_j = T_k$ :

$k(x', x'') = \sum_{C \in \mathcal{C}} P(C|x') P(C|x'')$  measures the similarity of  $x'$  and  $x''$  that is induced by the posterior distribution of width  $\beta$  - essentially, the posterior specifies a sampling procedure how to choose hypotheses  $C$  that are highly likely, given data  $x$

$Z_q = Z(x^{(q)}) = \sum_{C \in \mathcal{C}} \exp(-\beta R(C, x^{(q)}))$ ,  $q = 1, 2$

$Z_{12} = Z(x^{(1)}, x^{(2)}) = \sum_{C \in \mathcal{C}} \exp(-\beta(R(C, x^{(1)}) + R(C, x^{(2)})))$

$\hat{T} \in \arg \max_{T \in \mathcal{T}} \sum_{C \in \mathcal{C}} \exp(-\beta(R(C, T(x^{(1)})) + R(C, T(x^{(2)}))))$

variational error rate:  $P \leq I_B(T, \hat{T}) = \frac{1}{n} \log \left( \frac{Z_1 Z_2}{Z_{12}} \right)$

approx. capacity:  $CAP(T, \hat{T}) = \max_P I_B(T, \hat{T})$

WASC application: randomly split  $x$  into  $x^{(1)}$  and  $x^{(2)}$ , for each candidate cost function  $R(C, x)$  ER compute mutual info and max. it wrt  $\beta$  then select  $R$  that achieves highest capacity at the best resolution  $\beta^*$   
 $I_B(T, \hat{T}) = \frac{1}{n} \left( \log \frac{Z_1 Z_2}{Z_{12}} + \log \frac{|C^{(2)}|}{Z_2} - \log \frac{|C^{(2)}|}{Z_{12}} \right)$

$\{T_j\}$ : cod. of set of possible transformations

$P(\hat{T} \neq T_j) = P(\max_{T_j \neq \hat{T}} k_{T_j T_{\hat{T}}}(x', x'') \geq k_{T_j T_{\hat{T}}}(x', x''))$

(union)  $\leq \sum_{T_j \neq \hat{T}} P(k_{T_j T_{\hat{T}}}(x', x'') \geq k_{T_j T_{\hat{T}}}(x', x''))$   
 $= \sum_{T_j \neq \hat{T}} E_{x', x''} [P(k_{T_j T_{\hat{T}}}(x', x'') \geq k_{T_j T_{\hat{T}}}(x', x''))]$

(Markov)  $\leq \sum_{T_j \neq \hat{T}} E_{x', x''} \frac{E_{T_j} k_{T_j T_{\hat{T}}}(x', x'')}{k(x', x'')}$