CS181 Assignment 3

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1 Problem 1

a. The probability that all of the M dimensions of $x - y$ are between $-\epsilon$ and ϵ is $\boxed{\rho = (2\epsilon)^M}$.
For each dimension i of χ, the probability that $|x_i - y_i| \leq \epsilon$ is equivalent to

$$P(|x_i - y_i| \leq \epsilon) =$$
$$P(-\epsilon \leq x_i - y_i \leq \epsilon) =$$
$$P(-\epsilon - x_i \leq -y_i \leq \epsilon - x_i) =$$
$$P(\epsilon + x_i \geq y_i \geq x_i - \epsilon) =$$
$$P(x_i - \epsilon \leq y_i \leq \epsilon + x_i)$$

This distribution function is equivalent to $\int_{\epsilon+x_i}^{x_i-\epsilon} f(x)dx$, where $f(x)$ is the PDF of y_i, which we know to have a uniform distribution, so $f(x) = \frac{1}{b-a} = 1$. Thus, we get:

$$\int_{\epsilon+x_i}^{x_i-\epsilon} 1dx =$$
$$\epsilon + x_i - (x_i - \epsilon) = 2\epsilon$$

Because we want to know the probability that all of the M dimensions of $x - y$ are between $-\epsilon$ and ϵ, we simply take $\Pi_{i=1}^{M} P(|x_i - y_i| \leq \epsilon) = (2\epsilon)^M$.

b. The probability of $max_m|x_m - y_m| \leq \epsilon$ is at most ρ because as shown in (a), ρ does not depend on x_i and thus holds for all x_i. In addition, logically, if x is the center point, the average distance from it to any other point y is at most $\frac{1}{2}$ for any one dimension. As x moves farther and farther away from the center, the average distance increases so that it becomes at most 1 in any one dimension. So, if x is not in the center $max_m|x_m - y_m|$ grows and is less likely to be less than ϵ, decreasing that probability so that it is less than ρ.

c. We will show that $||x - y|| \geq max_m|x_m - y_m|$.

$$||x - y|| = \sqrt{\Sigma_{m=1}^{M}(x_m - y_m)^2}$$
$$\sqrt{\Sigma_{m=1}^{M}(x_m - y_m)^2} \geq max_m|x_m - y_m|$$
$$\Sigma_{m=1}^{M}(x_m - y_m)^2 \geq (max_m|x_m - y_m|)^2$$

This is true because the left side of the inequality includes the right side in its sum. $||x - y||$ is the total Euclidean distance between two points whereas $max_m|x_m - y_m|$ is only the distance between one dimension of two points. The left side must be larger.

If x is any point in χ, and y is a point in χ drawn randomly from a uniform distribution on χ, then the probabilty that $||x-y|| \leq \epsilon$ is also at most p because $||x-y||$ is greater than or equal to $max_m|x_m-y_m|$, making it less likely to be less than ϵ and thus giving it a probability lower than ρ of being less than ϵ.

d. Lowerbound on number N of points needed to guarantee that the nearest neighbor of point x will be within a radius ϵ of it is $\boxed{log\delta/log(1-(2\epsilon)^M)}$.
For the nearest neighbor not to be within a radius ϵ, none of the neighbors can be within a radius ϵ.

The probability that any one neighbor is not within a radius ϵ of x is $1-(2\epsilon)^M$, so the probability that all the nighbors are not within a radius ϵ of x is equivalent to $(1-(2\epsilon)^M)^N$, where N is the number of neighbors. So, the probability that at least one neighbor is within a radius ϵ is 1 - that quantity. Since we want to guarantee with probability at least $1-\delta$ that the nearest neighbor will be within a radius ϵ of it, we can solve for a lower bound for N by setting the two equations equal to each other.

$$\begin{gathered}1-\delta = 1-(1-(2\epsilon)^M)^N \\ 1-1+(1-(2\epsilon)^M)^N = \delta \\ (1-(2\epsilon)^M)^N = \delta \\ Nlog(1-(2\epsilon)^M) = log\delta \\ \boxed{N = log\delta/log(1-(2\epsilon)^M)}\end{gathered}$$

e. We can conclude that the effectiveness of the hierarchical agglomerative clustering algorithm in high dimensional spaces is ineffective as the dimension M grows because N would also grow too large and HAC would require too many N points to actually be effective. As M increases, the denominator of the lower bound for N decreases, thus leading to an increase in N overall. In addition, as covered in class, when the size of the dataset gets larger, the probability that two points from different clusters are closer to each other in terms of distance than two points from separate clusters converges to 1/2.

2 Problem 2

a. Given a prior distribution $Pr(\theta)$ and likelihood $Pr(D|\theta)$, the predictive distribution $Pr(x|D)$ for a new datum,

   (a) ML: $Pr(x|D) = Dist(\arg\max_{\theta}(\ln(Pr(D|\theta))))$,
   where $Dist()$ is a distribution applied to the θ we obtain with the given formula.

   (b) MAP: $Pr(x|D) = Dist(\arg\max_{\theta}(\ln(P(D|\theta)P(\theta))))$,
   where $Dist()$ is a distribution applied to the θ we obtain with the given formula.

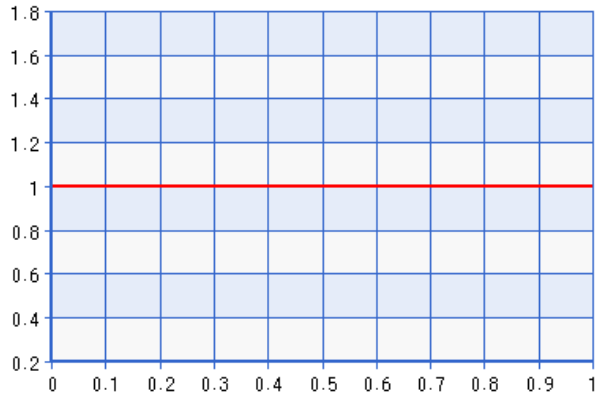
   (c) FB: $Pr(x|D) = \int p(x|\theta)P(\theta|D)d\theta$

b. MAP can be considered "more Bayesian" than ML because it takes into account the distribution of θ instead of assuming same weight or uniformity.

c. One advantage the MAP method enjoys over the ML method is that it accounts for the more likely distribution, as opposed to simply assuming uniformity, as with ML. FB, on the other hand, maintains a probability distribution is maintained over the set of all parameter values possible. However, because the normalizing factor contains an integration over all parameter values, it can be difficult to compute. This means that it also unnecessarily takes into account the less likely, meaning that FB is less practical than MAP to calculate. Therefore, MAP sits in the "sweet spot" of taking more into account in terms of distribution than ML but less excessively than FB.

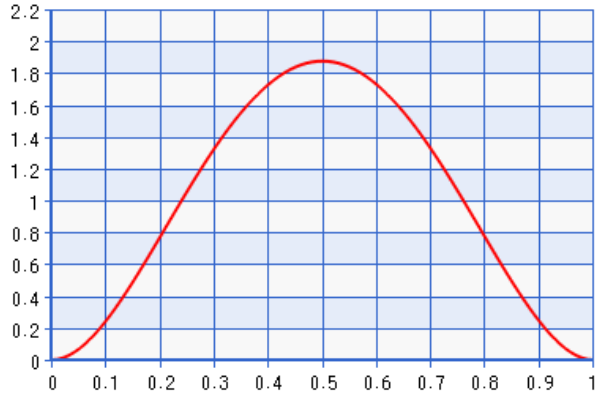
d. Soccer team example based on different Beta distributions as priors for the probability of a win,

   - Beta(1,1)

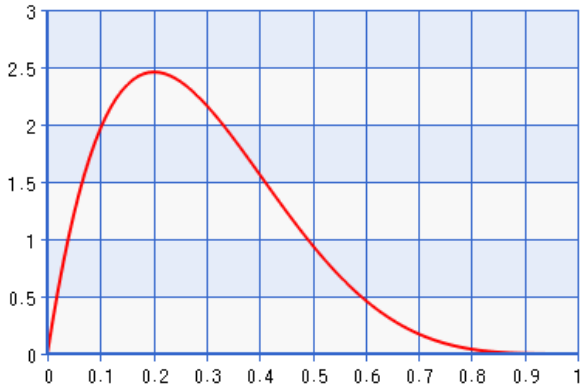


The Beta(1,1) distribution is equated with the Uniform(1,1) distribution.

- Beta(3,3)



- Beta(2,5)



e. The Beta distribution is the conjugate prior of the Bernoulli.

f. Under the ML approach

3 Problem 3

a. The K -means clustering objective is to minimize the sum of squared distances between prototype and data.

b. PCA relates to K-means

4 Problem 4

a. K-means clustering algorithm

b. HAC algorithm

(a) Comparing clusters formed using *min* distance metric against clusters formed using *max* distance metric

i. Table showing number of instances in each cluster

Metric	C1	C2	C3	C4
min	1	1	73	25
max	7	21	46	26

ii. Scatterplot of the instances in 3-dimensions

It seems that the *min* distance metric produced ?? clusters compared to the *max* metric... This makes sense given the definition of the metrics because...

(b) Comparing clusters formed using *mean* distance metric against clusters formed using *centroid* distance metric

i. Table showing number of instances in each cluster

Metric	C1	C2	C3	C4
mean	1	1	46	152
cent	1	5	147	47

ii. Scatterplot of the instances in 3-dimensions

It seems that the *mean* distance metric produced ?? clusters compared to the *cent* metric... This makes sense given the definition of the metrics because...

c. Autoclass clustering algorithm