ECE 2372 - Pattern Recognition

Week 8

Model selection:

In statistical learning, a **model** is a mathematical representation of a function such as a

- classifier
- regression function
- density
- clustering

So far, we have one (or more) "free parameters" that are not automatically determined by the learning algorithm. And often, the value chosen for these free parameters has a significant impact on the algorithm's output.

The problem of selecting values for these parameters is called model selection.

Examples:

Method	**Parameter**
• polynomial regression	• polynomial degree d
• ridge regression	• regularization parameter λ
• SVMs	• margin violation cost C kernel parameters C try to separate the data vs being robust to outliers
• neural networks	• regularization parameter λ stopping criteria
• k-nearest neighbors—take one point find its k-nearest neighbors and take a vote	• number of clusters k

We want to figure out automatic ways of setting up these parameters.

- We need to select appropriate values for the free parameters
- All we have is the training data
- why are these parameters here to start with?

- These parameters usually control the balance between **underfitting** and **overfitting**
- Here is a **dilemma**: they were left "free" precisely because we don't want to let the training data influence their selection, as this always leads to overfitting.
  - for example in regression, if we let the training data determine the degree, we will just end up choosing largest degree and end up doing interpolation...

Up until now, we have focused on trying to judge if we are learning via decomposition of the forms

$$\text{true risk} = \text{empirical risk} + \text{excess risk}$$
$$R(h) = \hat{R}(h) + \text{excess risk}$$

We looked at controlling excess risk using VC dimension and regularization. We also looked at:

$$\text{true risk} = \text{bias} + \text{variance}$$

Now we will consider more practical approach: **Validation**.

Almost whole semester we were trying to understand risk, right we said maybe we can break it up into other things that we can kind of control/or analyze...in one way or another...but why didn't we just try a little bit harder to directly estimate what this risk was?

After we select h, why don't we try to estimate

$$R(h) = \mathbb{E}[e(h(X), Y)]$$

directly from data–somehow? Here, "e" is just some function that measure the difference between $h(X)$ and Y. I am being intentionally vague here because we covered both regression and classification–so if we are talking about classification this could be the "probability of error", and it could be the "squared error" if we are talking about regression. This is kind of the reason we introduced Risk at the first place, so we can talk about all these things in one-word.

Okay, no theory here, once we pick h can we somehow estimate its performance?– at least have some prediction what the risk is gonna be...

Validation

Suppose we have this another dataset $(x_1, y_1), ..., (x_k, y_k)$, in addition to our training data

- k additional input-output pairs to our training dataset.

We can use the validation set to form an estimate $\hat{R}_{val}(h)$. A natural way to define this estimate would be:

$$\hat{R}_{val}(h) := \frac{1}{k}\sum_{i=1}^{k} e(h(x_i), y_i)$$

- For classification:

$$\hat{R}_{val}(h) = \frac{1}{k}\sum_{i=1} 1_{h(x_i)\neq y_i}$$

- For regression:

$$\hat{R}_{val}(h) = \frac{1}{k}\sum_{i=1}(h(x_i) - y_i)^2$$
$$\hat{R}_{val}(h) = \frac{1}{k}\sum_{i=1}|h(x_i) - y_i|$$

whatever error function you pick this is easy to estimate

Accuracy of validation

What can we say about the accuracy of $\hat{R}_{val}(h)$?

In the case of classification, $e(h(x_i), y_i) = 1_{h(x_i\neq y_i}(i)$ which is just a Bernoulli random variable

$$\text{Hoeffding}: \ \mathbb{P}[|\hat{R}_{val}(h) - R(h)|] \leq 2e^{-2\epsilon^2 k}$$

decays exponentially fast as k grows – no surprises here. The same story hold for any kind of error metric, the little e function here...More generally, we always have whats the expected value of these RVs – empirical estimates

$$\mathbb{E}[\hat{R}_{val}(h)] = \frac{1}{k}\sum_{i=1}^{k}\mathbb{E}[e(h(x_i), y_i)] = R(h)$$
$$\text{var}[\hat{R}_{val}(h)] = \frac{1}{k^2}\sum_{i=1}^{k}\mathbb{E}var[e(h(x_i), y_i)] = \frac{\sigma^2}{k}$$

so we do it k times, the variance goes down. I am not saying anything sophisticated here, I am just saying if you are trying to estimate something – here you are trying to estimate this mean by taking bunch of things that are randomly distributed as $R(h)$ is its mean, and averaging them, then this is an unbiased estimate of the thing we are trying to get – and the variance of this estimator goes down as you add more samples...

In either case, this shows us that

$$\hat{R}_{val}(h) = R(h) \pm O(\frac{1}{\sqrt{k}})$$

Thus, we can get as accurate an estimate of $R(h)$ using validation set as long as k is large enough. But **"where is this validation set coming from?"**

Remember h is ultimately something we learned from the training data.

This is completely artificial distinction validation and training set–wiseElf

Validation vs training

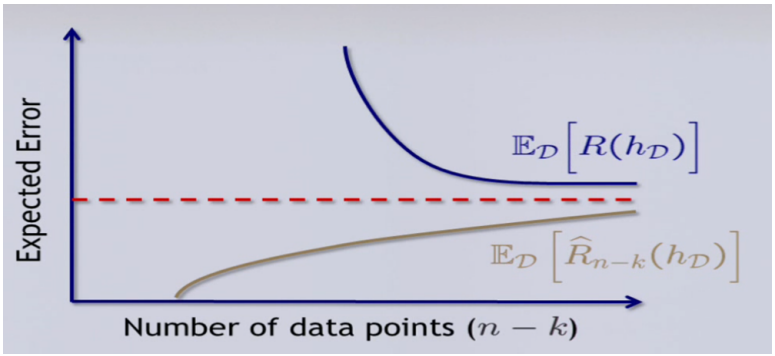
You have to decide and split the data $(x_1, y_1), ..., (x_n, y_n)$ into two sets:

- validation (holdout) set : $(x_1, y_1), ..., (x_k, y_k)$
- training set: $(x_{k+1}, y_{k+1}), ..., (x_n, y_n)$

Validation error is $O(1/\sqrt{k})$:

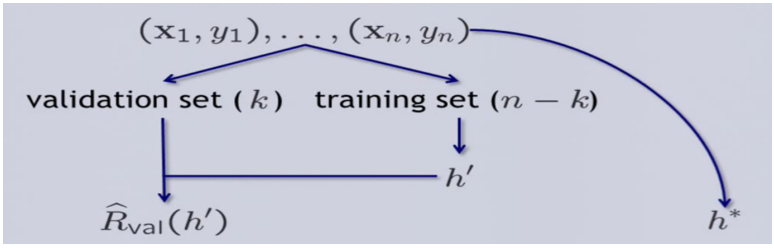
$$\begin{aligned} \text{Small } k &\implies \text{bad estimate} \\ \text{Large } k &\implies \text{accurate estimate, but of what?} \end{aligned}$$

Large k let's us say that we are very confident that we have selected a terrible h.



What if we decide to be greedy?

After using the validation set to estimate the error, re-train on the whole data set. We use



$(x_1, y_1), ..., (x_n, y_n) \implies h^*$:

- training set: $(n-k) \implies h'$
- validation (holdout) set : $k \implies \hat{R}_{val}(h')$

$$\begin{aligned} \text{Small } k &\implies \text{bad estimate of } R(h'), \text{but } R(h') \approx R(h^*) \\ \text{Large } k &\implies \text{good estimate of } R(h'), \text{but } R(h') \gg R(h^*) \end{aligned}$$

$\hat{R}_{val}(h')$ is a rough (independent) estimate of how good of a job h^* is doing!

Rule of thumb: Set $k = n/5 \implies 20\ \%$ of your data

Validation vs testing

We call this "validation", but how is it any different than simply "testing"?

There is a saddle difference! you had this in the first homework, it was a heart disease data (last problem) where you had a test data and training data separate. That might seem like about the same idea, but there is a saddle difference between that and this idea of validation.

Mainly, the whole reason of doing this validation estimates $\hat{R}_{val}$ is not just to know how well we are doing, but actually to inform our algorithm, helps us make choices as part of the learning – we are going to end up using this validation estimates to help us "how to set λ"...and all that "model selection" choices–fixed parameters in our algorithms.

Typically, $\hat{R}_{val}$ is used to make learning choices.

>> If an estimate of $R(h)$ affects learning, i.e., it impacts which h we choose, than it is no longer a **test** set. It becomes a **validation** set <<

The difference:

- a test set is **unbiased**

  this tells us how well we are doing but the moment that we let that leak back into what classification algorithm we use, or how we're designing our h, then this becomes a validation set and the estimates it produces will be overly optimistic

- a validation set will have (overly) optimistic **bias**

  optimism in general is not bad, but you don't wanna be overly optimistic because then you might think you are doing much better than you actually are (remember the coin tossing experiment?)

Example: Suppose we have 2 hypothesis: $h1, h2$ and that they have equal risk (true risk)

$$R(h_1) = R(h_2) = p$$

Of course, we don't get the observe this risk but, we have some validation data that we calculate validation-error. Next suppose that our error estimates for these two hypothesis, denoted by $\hat{R}_{val}(h_1)$ and $\hat{R}_{val}(h_2)$, are distributed according to

$$\hat{R}_{val}(h_i) \sim U[p - \eta, p + \eta]$$

If this is true for both h, we can use these to help us decide which one of these we should use.

Pick $h \in \{h_1, h_2\}$ that minimizes $\hat{R}_{val}(h)$.

- Then we have a problem, we will pick the one that looks better. But then it is easy to argue the empirical risk of the one you picked-on average is going to be less than p. If it was an unbiased estimate, it would be equal to p, but it is usually less, and in expectation definitely less.

One way to see this: If I have 2 uniform random variables, this expectation will be the minimum of these two uniform random RVs–minimum of 2 uniform RVs is **not** just a uniform random variable over that same range–if you write down the CDF and worked out what it is, you will see.

What is the probability that both $\hat{R}_{val}(h_1), \hat{R}(h_1)$ are bigger than p.

- This is only going to happen 1-quarter of the time

75% percent of the time one-or-both of these will actually be smaller than p. So if 75% percent time you are lower than p, it would be weird that expected value was not less than p. It is easy to argue that $\mathbb{E}[\hat{R}_{val}(h)] < p$ optimistic bias (75% of the time, $min(\hat{R}_{val}(h_1), \hat{R}_{val}(h_2)) < p$).

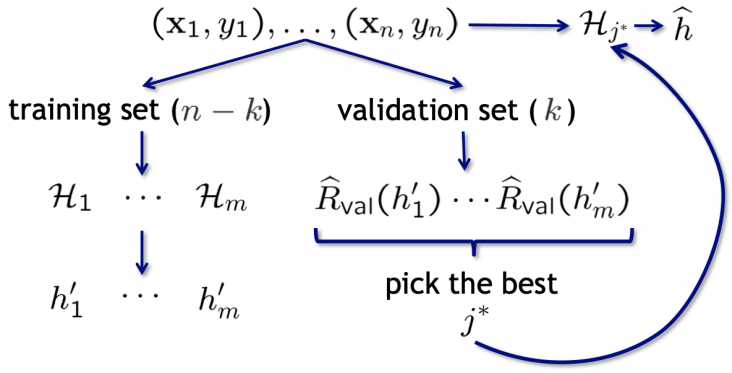
So this is the problem, we are specifically picking h_1 and h_2 based on whether or not they gave us a smaller estimate on our validation error, we are specifically making h depend on "which one of these gives us a smallest value" here, this is gonna become "optimistically biased" estimate of "how well we are performing".

This is all similar idea to what we have been talking about from the beginning of the term, if we look at the data, we could overfit to it! Training error is not super meaningful when we pick our hypothesis with respect to it.

But we could still use it to do model selection.

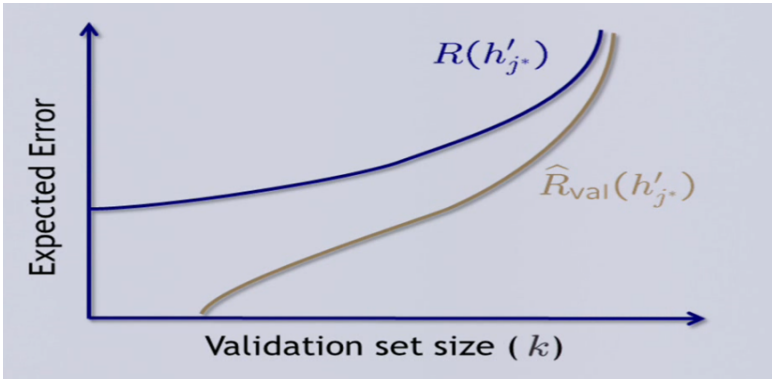
Using validation for model selection

Suppose we have m models: $\mathcal{H}_1, ..., \mathcal{H}_m$



We can't use $\hat{R}_{val}$ to tell how well $\hat{h}$ will perform in practice...biased as we just discussed.."optimistically biased"–usually people just ignore that issue–I know it is not telling me how well h-hat is working, I am just using this to pick one hypothesis..but if you wanna know how well it is actually working and have some unbiased estimate of how well $\hat{h}$is doing, you will need some whole data set separate from all of these...

We select the model $\mathcal{H}_{j^*}$ using validation set. $\hat{R}_{val}(h'_{j*})$ is a biased estimate of $R(h'_{j^*})$ (and $R(h_{j^*})$).



The bias

the curve is going up because as k grows we have smaller amounts of data to work with... We have seen stuff like this before...For m models $\mathcal{H}_1, ..., \mathcal{H}_m$, we use a data set size of k to pick the model that best out of $\{h'_1, ..., h'_m\}$. Back to Hoeffding!

$$R_{val}(h'_{j*}) \leq \hat{R}_{val}(h'_{j*}) + O(\sqrt{\frac{log\ m}{k}})$$

validation error will always going to be a good estimate of the true risk as long as size of validation set is big enough–how big does it need to be?–it needs to be bigger than log of

the number of models we are considering... Or, if the $\mathcal{H}_j$ correspond to a few continuous parameters we can use the VC approach to argue.

So, k, the size of the validation dataset has to be big compared to the m – all of that VC analysis continues to be useful here

if you have fix m, k needs to be bigger than logarithm of that, in order this to be small

$$R_{val}(h'_{j*}) \leq \hat{R}_{val}(h'_{j*}) + O(\sqrt{\frac{\#\text{ of parameters}}{k}})$$

We have now discussed three different kinds of estimates of risk $R(h) : \hat{R}_{train}(h), \hat{R}_{test}(h), \hat{R}_{val}(h)$. These three estimates have different degrees of "contamination" that manifests itself as a (deceptively) optimistic bias. They are all trying to give us an estimate of true risk:

- training set: totally contaminated
- test set: totally clean
- validation set: slightly contaminated

Validation dilemma

We would like to argue

$$\begin{array}{ccc} R(h) \approx R(h') & \approx & \hat{R}_{val}(h') \\ \uparrow & & \uparrow \\ \textbf{small } k & & \textbf{large } k \end{array}$$

All we need to do is to make k simultaneously very small and very large :)

Can we do this? Yes! this is actually rare things you can actually do and not pay a penalty!

Cross-validation

Leave one out: Let's make k small, so let's set $k = 1$!

$$\mathcal{D}_j = (x_1, y_1), ..., \cancel{(x_j, y_j)}, ..., (x_n, y_n)$$

Select a hypothesis h'_j using the data set $\mathcal{D}_j$.

Validation error $\hat{R}_{val}(h'_j) = e(h'_j(x_j), y_j) := e_j$

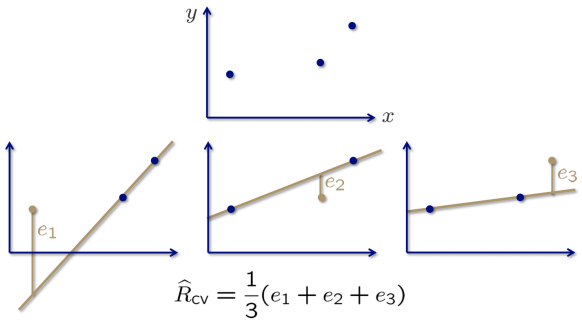
We set k to be too small, so this is a terrible estimate

Repeat this for all possible choices of j and average! Go through his process n times by leaving each one of these our one time.

$$\hat{R}_{CV} = \frac{1}{n}\sum_{i=1}^{n} e_j$$

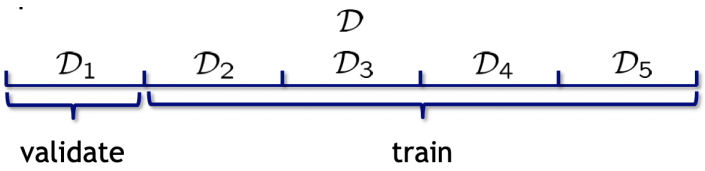
this is called the **leave one our cross validation estimate**

Example: Suppose we are fitting a line to 3 data points.



The downside here is if you have a lot of points, this becomes computationally demanding. Because you have to train your classifier that many times. Then let's leave more out!

k-fold cross validation: Train k times on $n - \frac{n}{k}$ points each.



5-fold

Common choices are $k = 5, 10$. This is one of the work-horses of practical machine learning. there is always parameters, and you don't know how to fit them, this is the principal and robust way to do it.

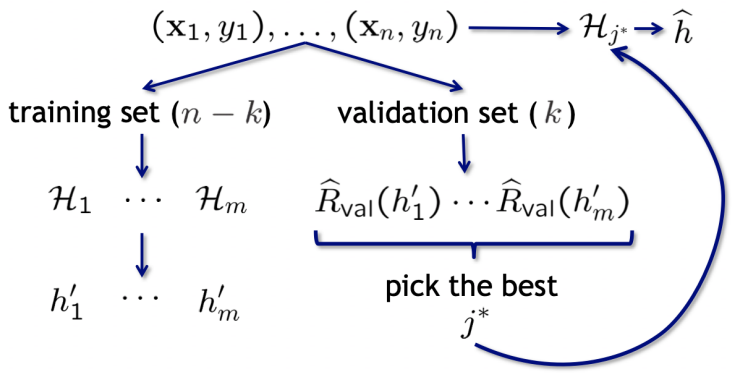
(Notice k changed meaning in the last part. Next: bootstrap ...)

Recap:

We have talked about model selection dilemma:

- we need to select appropriate values for the free parameters
- these free parameters usually control the balance between underfitting and overfitting

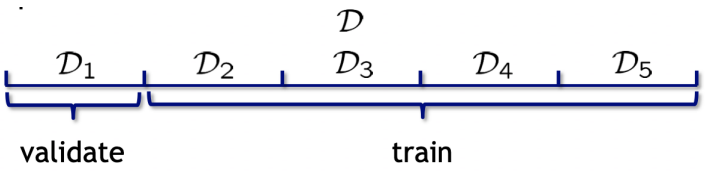
- but all we have training data to select parameters
- they were left "free" precisely because we don't want to let the training data influence their selection, as this almost always leads to overfitting.
- **Using validation for model selection**: Suppose we have m models $\mathcal{H}_1, ..., \mathcal{H}_m$:
  - Take the training data (n samples)
  - Split it up into two pieces:
    * training set: $n - k$ samples
    * validation (holdout) set: k samples
    * train m models using the $n - k$ samples : $h'_1, ..., h'_m$.
    * using k samples validation set, get an estimate of risk: $\hat{R}_{val}(h'_1), ..., \hat{R}_{val}(h'_m)$
    * pick the model that gives the best result, lowest $\hat{R}_{val}(h'_{j^*}) \implies j^*$.
    * after picking the model h_{j^*}, re-train this on the entire data set (n-samples) to output $\hat{h}$.



We also talked about more complicated ideas like **"cross-validation"**. Try a different split each time and repeat the whole process (the one depicted in the figure) again, and finally average all of the empirical estimates $\hat{R}_{val}$.

- Leave one out: Train n times on $n - 1$ points each. This is ideal, but computationally demanding
- $k - fold$ cross validation: Train k times on $n - \frac{n}{k}$ points each

Notation clarification: in here k is the number of folds $k' = \frac{n}{k}$ is the size of the validation set. Iterate over all 5 choices of validation set, and average.



5-fold

Remarks:

- For $k-fold$ cross validation, the estimate depends on the particular choice of partition.
- It is common to form several estimates based on different partitions and then average them
- One thing to keep in mind: when using $k-fold$ cross validation for classification, you should ensure that each of the sets $\mathcal{D}_j$ contain training data from each class in the same proportion as in the full data set

In practice, cross-validation is a common choice to pick these free parameters in an automatic way. But there are other strategies. I want to mention just one of them here briefly because it can be useful when you have smaller datasets.

The bootstrap:

- What else can you do when your training set is really small?
- You really need as much training data as possible to get reasonable result
- Fix $B \geq 1$
- For $b = 1, ..., B$ let $\mathcal{D}_b$ be a subset of size n obtained by sampling with replacement from the full data set $\mathcal{D}$.

  Example: $n = 5$

$$\mathcal{D}_1 = (x_4, y_4), (x_3, y_3), (x_5, y_5), (x_4, y_4), (x_1, y_1)$$
$$\mathcal{D}_2 = (x_1, y_1), (x_2, y_2), (x_5, y_5), (x_5, y_5), (x_2, y_2)$$
$$\vdots$$

- Define $h_b :=$ model learned base on the data $\mathcal{D}_b$
- And define $\mathcal{D}_b^c := \mathcal{D} \backslash \mathcal{D}_b$
  - In the example this could of been for $\mathcal{D}_1$, (x_2, y_2)
  - for $\mathcal{D}_1$, (x_3, y_3) and (x_4, y_4)

- Set $e_b = \frac{1}{|\mathcal{D}_b^c|} \sum_{(x_i,y_i)\in\mathcal{D}_b^c} 1_{\{h_b(x_i)\neq y_i\}}$

The **bootstrap error estimate** is given by

$$\hat{R}_B := \frac{1}{B}\sum_{b=1}^{B} e_b$$

Typically, in practice, B must be large, several hundred (say $B \approx 200$) (or more if you can afford it) for the estimate to be accurate. It is very computationally demanding, but also you can get nice confidence intervals in addition to $\hat{R}_B$.

- The bootstrap error estimate $\hat{R}_B$ tends to be **pessimistic**, so it is common to combine the training and bootstrap error estimates.
  - A common choice is the **"0.632 bootstrap estimate"**. This is really it's name and these weights are actually derived from theory (not a rule of thumb, even though it looks totally like one). And I am sure you can find $5k+$ papers on bootstrap error estimates...

$$0.632\ \hat{R}_B + 0.368\ \hat{R}_{train}$$

- The "balanced" bootstrap chooses $\mathcal{D}_1, ..., \mathcal{D}_B$ such that each input-output pair appears exactly B times.

Linear Methods for Supervised Learning In terms of linear techniques, so far, we have talked about:

- LDA
- Logistic Regression
- Naive Bayes
- PLA
- Maximum margin hyperplanes
- Soft-margin hyperplanes
- Least squares regression
- Ridge regression

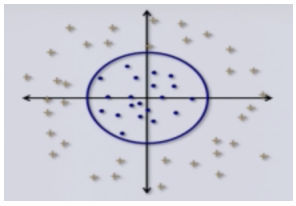
Sometimes linear methods (in both regression and classification) just don't work. One way to create "nonlinear estimators" or classifiers is to first transform the data via a nonlinear feature map $\phi : \mathbb{R}^d \to \mathbb{R}^p$.

After applying ϕ, we can then try applying a linear method to transformed data $\phi(x_1), ..., \phi(x_n)$. We actually talked about couple of examples of this already. For example, in the case of regression, our model becomes, $f(x) = \beta^T \phi(x) + \beta_0$ where $\beta \in \mathbb{R}^p$. Fitting linear models to nonlinear features...

Example: Suppose $d = 1$ but $f(x)$ is a cubic polynomial, how do we find a least squares estimate of f from training data?

$$\phi_k(x) = x^k \implies A = \begin{bmatrix} 1 & x_1 & x_1^2 & x_1^3 \\ 1 & x_2 & x_2^2 & x_2^3 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & x_n & x_n^2 & x_n^3 \end{bmatrix}$$

And we have talked about classification long time ago too...Pictured data set is not linearly separable but can be in a higher dimension with a transform:



$$\Phi(x) = \begin{bmatrix} 1 \\ x(1) \\ x(2) \\ x(1)x(2) \\ x(1)^2 \\ x(2)^2 \end{bmatrix}$$

This dataset is linearly separable after applying such transformation with w=$[-1, 0, 0, 1, 1]^T$

Potential Problems with nonlinear feature maps

Suppose we transform our data via

$$x = \begin{bmatrix} x(1) \\ \vdots \\ x(d) \end{bmatrix} \xrightarrow{\phi} \Phi(x) = \begin{bmatrix} \Phi^{(1)}(x) \\ \vdots \\ \Phi^{(p)}(x) \end{bmatrix}$$

where typically $p \gg d$. The challenges that could arise:

- If $p \gtrapprox n$, then this can lead to an ill-conditioned problem
  - can be mitigated via regularization
  - in addition, when p is very large, this can cause an increase in computational burden
    - (e.g., inverting $p \times p$ matrix)

The "kernel trick"

Shortly, do the mapping without the cost.

There is a clever way to get around this computational challenge by exploiting two facts:

- Many ML algorithms only involve the data through inner products.
- For many interesting feature maps ϕ, the function

  $$k(x, x') := \langle \phi(x), \phi'(x) \rangle$$

  has a simple, closed form expression that can be evaluated **without explicitly calculating** $\phi(x)$ and $\phi'(x)$.

Example: Quadratic kernel $k(u, v) = (u^T v)^2$

Suppose $d = 2$ and try to think backwards: "what was the feature map that this kernel is computing an inner product for?"

$$\begin{aligned} k(\mathrm{u},\mathrm{v}) &= (\mathrm{u}^T \mathrm{v})^2 \\ &= \left([u(1)u(2)] \begin{bmatrix} v(1) \\ v(2) \end{bmatrix} \right)^2 \\ &= (u(1)v(1) + u(2)v(2))^2 \\ &= u(1)^2 v(1)^2 + 2u(1)u(2)v(1)v(2) + u(2)^2 v(2)^2 \\ &= \langle \phi(\mathrm{u}), \phi(\mathrm{v}) \rangle \end{aligned}$$

$$\phi(\mathrm{u}) = \begin{bmatrix} u(1)^2 \\ \sqrt{2}u(1)u(2) \\ u(2)^2 \end{bmatrix}$$

Now suppose d is arbitrary, and

$$\begin{aligned} k(\mathrm{u},\mathrm{v}) &= (\mathrm{u}^T \mathrm{v})^2 \\ &= \left(\sum_{i=1}^{d} u(i)v(i) \right)^2 \\ &= \left(\sum_{i=1}^{d} u(i)v(i) \right) \left(\sum_{j=1}^{d} u(j)v(j) \right) \\ &= \sum_{i=1}^{d} \sum_{j=1}^{d} u(i)v(i)u(j)v(j) \end{aligned}$$

What is the feature mapping in this case? And what is the dimension p of the corresponding feature space?

$$\sum_{i=1}^{d}\sum_{j=1}^{d} u(i)v(i)u(j)v(j) \stackrel{?}{=} \langle \phi(\mathrm{u}), \phi(\mathrm{v}) \rangle$$

$$\phi(\mathrm{u}) = \Big[u(1)^2, ..., u(d)^2, ..., \sqrt{2}u(1)u(2), ..., \sqrt{2}u(d-1)u(d) \Big]^T$$

$\therefore p = d + \frac{d(d-1)}{2}$

So we can do this for quadratic. what happens if we have cubic kernel?

Example: Cubic kernel $k(u, v) = (u^T v)^3$

In $\mathbb{R}^2$, we can work this out, it is not that much worse, but boring...

$$\begin{aligned} k(\mathrm{u,v}) &= \big(u(1)v(1) + u(2)v(2) + u(3)v(3) \big)^3 && (1) \\ &= u(1)^3 v(1)^3 + 3u(1)^2 u(2) v(1)^2 v(2) + 3u(1)u(2)^2 v(1) v(2)^2 + u(2)^3 v(2)^3 && (2) \\ &= \sum_{i=0}^{3} \binom{3}{i} u(1)^{3-i} u(2)^i \cdot v(1)^{3-i} v(2)^i && (3) \end{aligned}$$

$$\phi(\mathrm{u}) = \Big[u(1)^3, \sqrt{3}u(1)^2 u(2), \sqrt{3}u(1)u(2)^2, u(2)^3 \Big]^T$$

and we could do this in d dimensions if we felt like it...But it is probably okay, if we don't...

So let me state what happens in general,

Polynomial Kernels:

$$\begin{aligned} k(\mathrm{u,v}) &= (\mathrm{u}^T \mathrm{v})^m \\ &= \sum_{\substack{\text{partitions} \\ j_1, ..., j_d}} \binom{m}{j_1, ..., j_d} u(1)^{j_1} v(1)^{j_1} \cdots u(d)^{j_d} v(d)^{j_d} \end{aligned}$$

$$\phi(\mathrm{u}) = \left[..., \sqrt{\tbinom{m}{j_1, ..., j_d}} u(1)^{j_1} \cdots u(d)^{j_d}, ... \right]^T$$

In English, all possible monomials of degree m.

This is one example of a kernel. There are lots of different kernels we could use. The general kind of kernel we will use in this class is called **inner product kernel**.

Definition: A inner product kernel is a mapping

$$k : \mathbb{R}^d \times \mathbb{R}^d \to \mathbb{R}$$

for which there exists an inner product space $\mathcal{F}$ and a mapping $\phi : \mathbb{R}^d \to \mathcal{F}$ such that

$$k(u, v) = \langle \phi(\mathrm{u}), \phi(\mathrm{v}) \rangle_{\mathcal{F}}$$

for all $u, v \in \mathbb{R}^d$.

Given a function $k(u, v)$, how can we tell when it is an inner product kernel?

- Mercer's theorem
- Positive semidefinite property

Positive semidefinite kernels

We say that $k(u, v)$ is a positive semidefinite kernel

- if k is symmetric.
- for all n and all $x_1, ..., x_n \in \mathbb{R}^d$, the **Gram matrix K** is defined by

  $$K(i, j) = k(x_i, x_j)$$

  is positive semidefinite, i.e., $x^T K x \geq 0$ for all x.

Theorem: k is an inner product kernel iff k is a positive semidefinite kernel.

Examples:

- Homogeneous polynomial kernel

  $$k(u, v) = (u^T v)^m \qquad m = 1, 2, 3, ...$$

- Inhomogeneous polynomial kernel

  $$k(u, v) = (u^T v + c)^m \qquad m = 1, 2, 3, ... \quad c > 0$$

  ϕ maps to the set of all monomials of degree $\leq m$.

- Gaussian/Radial basis function (RBF) kernel:

  $$k(u, v) = (2\pi\sigma^2)^{-d/2} \exp\left(-\frac{\|u - v\|^2}{2\sigma^2}\right)$$

  You can just do (it doesn't matter if it is a PDF or not):

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

  One can show that k is a positive semidefinite kernel. but what is $\mathcal{F}$?

  - $\mathcal{F}$ is **infinite dimensional**!