Do not distribute course material

You may not and may not allow others to reproduce or distribute lecture notes and course materials publicly whether or not a fee is charged.

Topic 3 Model Selection continued

PROF. LINDA SELLIE

Outline

■ Motivating example: What polynomial degree should a model use? How to create a more complex hypothesis □Polynomial transformation □Underfitting and overfitting Understanding where the error comes from, and how to □Understanding error: Bias and variance and noise estimate $E_{\text{out}}[g(\mathbf{x})]$ □Learning curves □validation and model selection If we have many different hypothesis classes ■ Model selection (with limited data) to choose from - how can we choose wisely? And how can we estimate $E_{\text{out}}[g(\mathbf{x})]$? K-fold cross validation ■ Regularization

Outline

■ Motivating example: What polynomial degree should a Yea! How to create a more complex hypothesis □Polynomial transformation Uh oh.... □Underfitting and overfitting Understanding where the error Understanding comes from, and how to □Understanding error: Bias and variand what wrong estimate $E_{\text{out}}[g(\mathbf{x})]$ □Learning curves □validation and model selection If we have many different hypothesis classes ■ Model selection (with li to choose from - how can we choose wisely? Our strategy And how can we estimate $E_{\text{out}}[g(\mathbf{x})]$? K-fold cross validation ■ Regularization

Selecting a model using a validation set

- \Box For each H_i , fit its optimal hypothesis g_i^- using the training set D_{train}
- $\ \Box$ For each g_i^- estimate the out of sample error e_i using $\mathsf{D}_{\mathsf{val}}$
- $lue{}$ Pick the H_i that had the smallest e_i
- ☐ If we have a test set, we can use that to estimate the error of our hypothesis that had the smallest validation error

If we didn't have a large training set:

- We can then train the selected model using all the data D (i.e. use both D_{train} and D_{val}). Let g_{m^*} be the optimal hypothesis found this way.
- \blacksquare If we have a test set, we can use that to estimate the error of g_{m^*}

These could be any models Notation on this slide \mathcal{H}_1 \mathcal{H}_{M} \mathcal{H}_2 g_i^- is the fitted i^{th} model using the Dtrain training examples $\{(\mathbf{x}^{(1)}, \mathbf{y}^{(1)}), ..., (\mathbf{x}^{(N'-K)}, \mathbf{y}^{(N'-K)})\}$ m^* is the model with the smallest validation $g_1^$ $g_M^$ $g_2^$ error g_{m^*} is the fitted D_{val} model *m* * using all {(**x'**⁽¹⁾,y'⁽¹⁾),... e_1 e_{2} ,(x'(K),y'(K))} the examples N = N'-K $(\mathcal{H}_{m^*}, e_{m^*})$ best model Biased estimate $D = \{(x^{(1)}, y^{(1)}), \dots, (x^{(N')}, y^{(N')})\}$ g_{m^*}

What if we don't have enough data for a test set?

Thought experiment

1. If we have enough examples in the validation set, is e is a good estimate of E_out?

- yes, it is unbiased
- it is an optimistic estimate, but relatively good estimate
- no, it is not a good estimate

Two hypothesis h_1, h_2

$$E_{\mathsf{out}}(h_1) = E_{\mathsf{out}}(h_2) = \frac{1}{2}$$

Given the error $e_1,\,e_2$ estimates for the hypothesis where we assume (for this thought experiment) that $e_1,\,e_2$ is uniform on [0,1]

pick
$$h \in \{h_1, h_2\}$$
 where $e = \min(e_1, e_2)$

Thought experiment

Two hypothesis h_1, h_2

$$E_{\mathsf{out}}(h_1) = E_{\mathsf{out}}(h_2) = \frac{1}{2}$$

e_1	e_2	$e = \min\{e_1, e_2\}$
$e_1 > 0.5$	$e_2 > 0.5$	e > 0.5
$e_1 < 0.5$	$e_2 > 0.5$	e < 0.5
$e_1 > 0.5$	$e_2 < 0.5$	e < 0.5
$e_1 < 0.5$	$e_2 < 0.5$	e < 0.5

Given the error e_1 , e_2 estimates for the hypothesis where we assume (for this thought experiment) that e_1 , e_2 is uniform on [0,1]

pick
$$h \in \{h_1, h_2\}$$
 where $e = \min(e_1, e_2)$

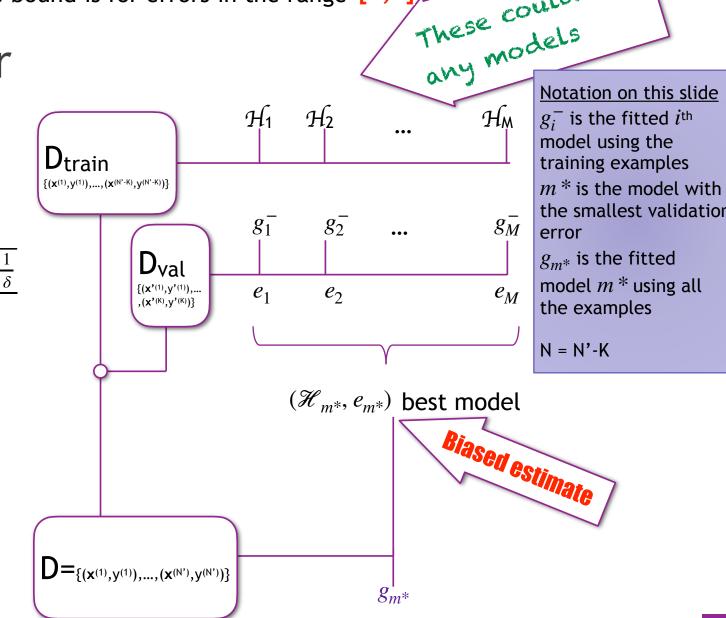
Notice that $E[e] \leq 0.5$

We have an optimistic biased estimate of the error if we estimate

The bound is for errors in the range [0,1]Using validation error to bound out of sample error

If our validation set has K items, then with probability $1 - \delta$

$$E_{\text{out}}(g_{m^*}) \leq^? E_{\text{out}}(g_{m^*}^-) \leq E_{\text{val}}(g_{m^*}^-) + \sqrt{\frac{\ln 2M + \ln \frac{1}{\delta}}{2K}}$$



These could be

Outline

■ Motivating example: What polynomial degree should a Yea! How to create a more complex hypothesis □Polynomial transformation Uh oh.... □Underfitting and overfitting Understanding where the error Understanding comes from, and how to □Understanding error: Bias and variand what wrong estimate $E_{\text{out}}[g(\mathbf{x})]$ □Learning curves □validation and model selection If we have many different hypothesis classes ■Model selection (with limit to choose from - how can we choose wisely? Our strategy ☐ K-fold cross validation And how can we estimate $E_{\text{out}}[g(\mathbf{x})]$? ■ Regularization

Strategies for dealing with a small dataset

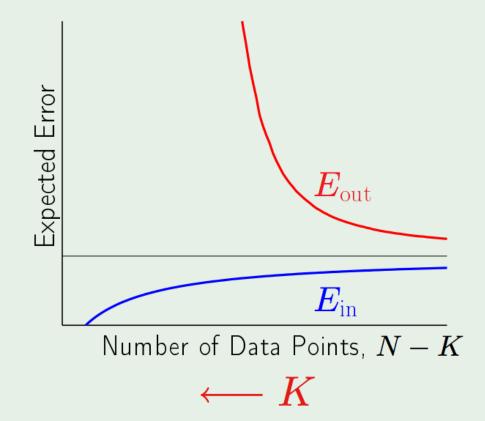
K is taken out of N

Given the data set $\mathcal{D} = (\mathbf{x}^{(1)}, \mathbf{y}^{(1)}), (\mathbf{x}^{(2)}, \mathbf{y}^{(2)}), ..., (\mathbf{x}^{(N)}, \mathbf{y}^{(N)})$

$$\underbrace{K \text{ points}}_{\mathcal{D}_{val}} \rightarrow \text{ validation } \underbrace{N-K \text{ points}}_{\mathcal{D}_{train}} \rightarrow \text{ training}$$

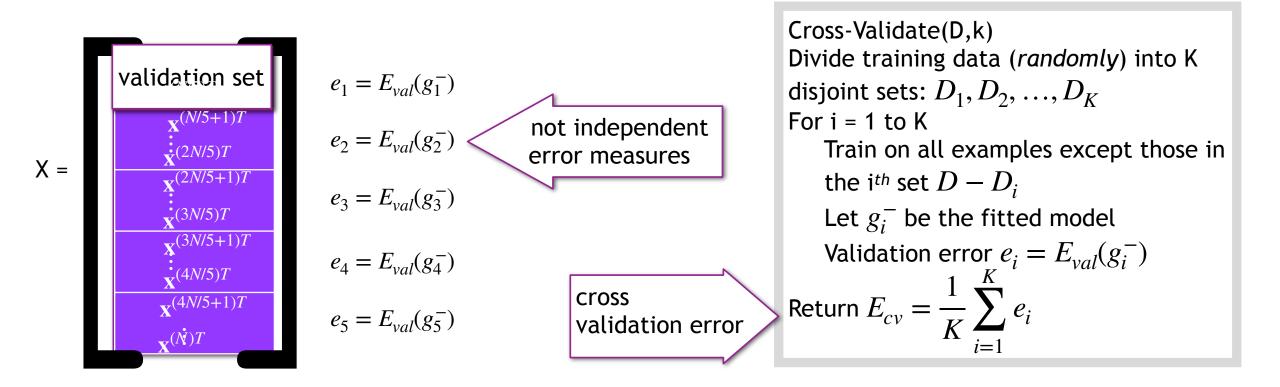
Small $K \implies \mathsf{bad} \; \mathsf{estimate}$

Large $K \implies ?$



Choosing the right model using K-fold cross validation

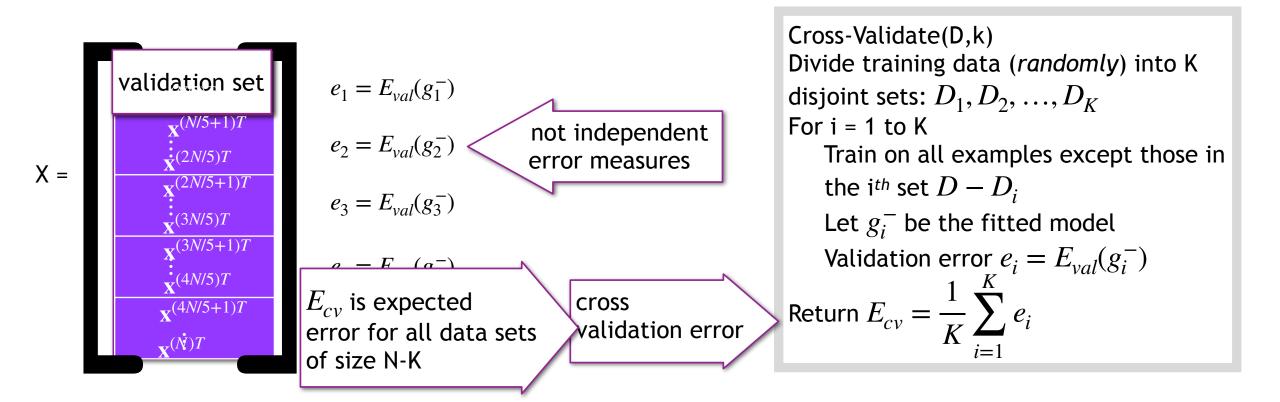
- •If there is not enough data, instead of training and validation sets, divide the data into k sets. Commonly K = 5, K = 6, K = 10, or K = N.
- •Then train on K-1 of the sets and validate on the remaining set. The estimated error will be the average of the errors.



During this process, you computed K different classifiers. After you are done, run the algorithm again on **all** the data

Choosing the right model using K-fold cross validation

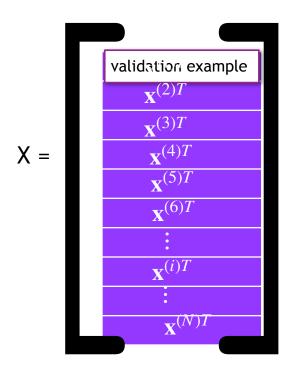
- •If there is not enough data, instead of training and validation sets, divide the data into k sets. Commonly K = 5, K = 6, K = 10, or K = N.
- •Then train on K-1 of the sets and validate on the remaining set. The estimated error will be the average of the errors.



During this process, you computed K different classifiers. After you are done, run the algorithm again on **all** the data

Leave-one-out cross validation

□If there is very little data, let K = N. This will give the best estimate but the running time may be prohibitive. This is called *leave-one-out cross-validation because* 1 example was left out at a time



Only one example in validation set, N-1 examples in the training data

During this process, you computed N different classifiers.

Polynomial Features in Scikit-Learn

Generate polynomial transformation of the feature space

"Generate a new feature matrix consisting of all polynomial combinations of the features with degree less than or equal to the specified degree. For example, if an input sample is two dimensional and of the form [a, b], the degree-2 polynomial features are [1, a, b, a², ab, b²]."

Parameters include:
include_bias : boolean
The default is True

"Be aware that the number of features in the output array scales polynomially in the number of features of the input array, and exponentially in the degree. High degrees can cause overfitting."

Example from http://scikit-learn.org/stable/modules/generated/sklearn.preprocessing.PolynomialFeatures.html

```
from sklearn import linear_model
import sklearn.model_selection
```

imin = np.argmin(MSE)

K-Fold Validation in Sklearn

```
regr = linear model.LinearRegression()
nfold = 10
                                                                                   Create a K-fold object
                                                                                                                     Set shuffle to true
kf = sklearn.model selection.KFold(n splits=nfold,shuffle=True)
dval = np.arange(1, nfold) #[1, ..., nfold-1]
                                                                      Select which degree d models to test
                                                                                                                          [1 2 3 4 5 6 7 8 9]
nd = len(dval)
# Loop over the folds
MSEval = np.zeros((nd,nfold)) #create a matrix to hold all the values
                                                                                             "Generate indices to split data into training and test set."
for isplit, Ind in enumerate(kf.split( x )):
                                                                                            Ind holds indices for training and validation sets
    I train, I val = Ind
    X train = X[I train]
    y_train = y[I_train]
                                                                                                         2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, 16, 17, 18,
    X \text{ val} = X[I \text{ val}]
                                                                                                 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36,
                                                                                                 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53,
    y val = y[I val]
                                                                                                 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71,
                                                                                                 72, 73, 74, 77, 78, 79, 80, 81, 83, 84, 85, 86, 88, 89, 92, 93, 94,
                                                                                                 95, 96, 97, 98, 99]), array([ 8, 15, 31, 68, 75, 76, 82, 87, 90, 91]))
   for it, d in enumerate(dval):
                                                                                                If d=1 \mathbf{x}^{(0)} = [0.456]
        # polynomial feature transformation
                                                                                                                                     If d = 2, \mathbf{x}^{(0)} = [0.456]
        poly transformation = PolynomialFeatures(degree=d,include bias=False)
                                                                                               \Phi_1(\mathbf{x}^{(0)}) = [0.456]
                                                                                                                                     \Phi(\mathbf{x}^{(0)})=[0.456 0.208]
       X train d = poly transformation.fit transform(X train)
                                                                                                No change (identity transformation)
       X val d = poly transformation.transform(X val)
        # Fit the training data
                                                                                           MSEval =
        regr.fit(X train d,y train)
                                                                                           [[ 6.77 4.45 7.68 5.44 3. 5.08 4.25 9.32 9.78 5.66]
                                                                                            [ 6.74 4.42 7.66 5.46 3.02 5.09 4.26 11.03 9.87 5.66]
                                                                                            [ 0.16  0.23  0.12  0.11  0.06  0.14  0.2  0.2  0.21  0.06]
        # Measure MSE on test data
                                                                                            [ 0.16  0.23  0.12  0.11  0.05  0.15  0.21  0.19  0.21  0.06]
                                                                                                                                                           0.4 -
        yhat val = regr.predict(X val d)
                                                                                            [ 0.16  0.23  0.12  0.11  0.05  0.15  0.21  0.19  0.21  0.06]
                                                                                            [ 0.17 \quad 0.23 \quad 0.13 \quad 0.11 \quad 0.05 \quad 0.15 \quad 0.23 \quad 0.2 \quad 0.22 \quad 0.06 ]
        MSEval[it,isplit]= np.mean((yhat val-y val)**2)
                                                                                            [ 0.21  0.24  0.13  0.13  0.06  0.15  0.23  0.22  0.22  0.06]
                                                                                            [ 0.21  0.25  0.14  0.12  0.06  0.15  0.23  0.22  0.22  0.06]
                                                                  MSE = [5.99764938, 6.17617688, 0.14325349, 0.14562991, 0.15220936, 0.15745814, 0.16233707, 0.16630905, 0.16562408]
MSE = np.mean(MSEval,axis=1)
```

The selected model order is 3

```
from sklearn import linear_model
import sklearn.model_selection
```

imin = np.argmin(MSE)

K-Fold Validation in Sklearn

```
regr = linear model.LinearRegression()
nfold = 10
                                                                                   Create a K-fold object
                                                                                                                     Set shuffle to true
kf = sklearn.model selection.KFold(n splits=nfold,shuffle=True)
dval = np.arange(1, nfold) #[1, ..., nfold-1]
                                                                       Select which degree d models to test
                                                                                                                           [1 2 3 4 5 6 7 8 9]
nd = len(dval)
# Loop over the folds
MSEval = np.zeros((nd,nfold)) #create a matrix to hold all the values
                                                                                             "Generate indices to split data into training and test set."
for isplit, Ind in enumerate(kf.split( x )):
                                                                                             Ind holds indices for training and validation sets
     I train, I val = Ind
    X train = X[I train]
    y_train = y[I_train]
                                                                                                         2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, 16, 17, 18,
    X \text{ val} = X[I \text{ val}]
                                                                                                 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36,
                                                                                                 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53,
    y val = y[I val]
                                                                                                 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71,
                                                                                                 72, 73, 74, 77, 78, 79, 80, 81, 83, 84, 85, 86, 88, 89, 92, 93, 94,
                                                                                                 95, 96, 97, 98, 99]), array([ 8, 15, 31, 68, 75, 76, 82, 87, 90, 91]))
   for it, d in enumerate(dval):
        # polynomial feature transformation
                                                                                               If d = 3, \mathbf{x}^{(0)} = [0.456]
                                                                                                                                             If d = 4, \mathbf{x}^{(0)} = [0.456]
        poly transformation = PolynomialFeatures(degree=d,include bias=False)
                                                                                               \Phi_3(\mathbf{x}^{(0)})=[0.456 0.208 0.095]
                                                                                                                                             \Phi_{A}(\mathbf{x}^{(0)})=[0.456\ 0.208\ 0.095\ 0.043]
       X train d = poly transformation.fit transform(X train)
       X val d = poly transformation.transform(X val)
        # Fit the training data
                                                                                           MSEval =
        regr.fit(X train d,y train)
                                                                                           [[ 6.77 4.45 7.68 5.44 3. 5.08 4.25 9.32 9.78 5.66]
                                                                                            [ 6.74 4.42 7.66 5.46 3.02 5.09 4.26 11.03 9.87 5.66]
                                                                                            [ 0.16  0.23  0.12  0.11  0.06  0.14  0.2  0.2  0.21  0.06]
        # Measure MSE on test data
                                                                                            [ 0.16  0.23  0.12  0.11  0.05  0.15  0.21  0.19  0.21  0.06]
                                                                                                                                                            0.4 -
        yhat val = regr.predict(X val d)
                                                                                            [ 0.16  0.23  0.12  0.11  0.05  0.15  0.21  0.19  0.21  0.06]
        MSEval[it,isplit] = np.mean((yhat val-y val)**2)
                                                                                            [ 0.17 \quad 0.23 \quad 0.13 \quad 0.11 \quad 0.05 \quad 0.15 \quad 0.23 \quad 0.2 \quad 0.22 \quad 0.06 ]
                                                                                            [ 0.21  0.24  0.13  0.13  0.06  0.15  0.23  0.22  0.22  0.06]
                                                                                            [ 0.21  0.25  0.14  0.12  0.06  0.15  0.23  0.22  0.22  0.06]
                                                                  MSE = [5.99764938, 6.17617688, 0.14325349, 0.14562991, 0.15220936, 0.15745814, 0.16233707, 0.16630905, 0.16562408]
MSE = np.mean(MSEval,axis=1)
```

The selected model order is 3

Extra Slides

You are not responsible for the following material

Validation estimate

$$E_{\text{out}}(g_{m^*}) \le^? E_{\text{out}}(g_{m^*}^-) \le E_{\text{val}}(g_{m^*}^-) + O(\sqrt{\frac{\ln M}{K}})$$

Dval used to choose the best model in

$$\{\mathcal{H}_1,\mathcal{H}_2,...,\mathcal{H}_M\}$$

Can we use E_{m^*} to bound the error of $g_{m^*}^-$?

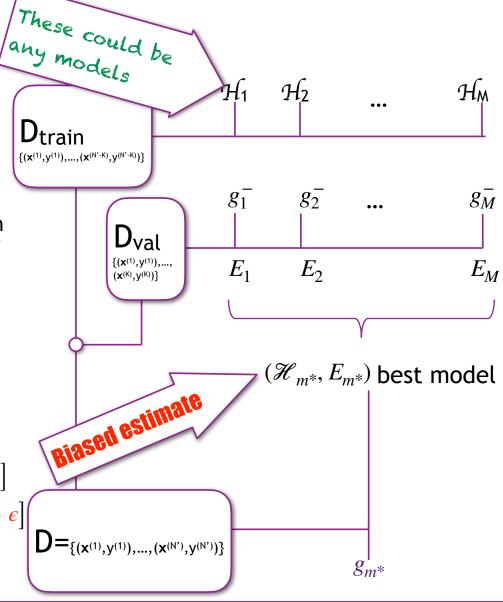
Hoeffding inequality (stated without proof) for any sample size K, where each random variable is bounded in [a,b] the probability that a average value, v, of the random variables will deviate from its average μ by more that ε is:

$$P[|v - \mu| > \epsilon] \le 2e^{-2\epsilon^2 K/(b-a)^2}$$
 for any $\epsilon > 0$

Union bound $P[B_1 \text{ or } B_2 \text{ or } \cdots \text{ or } B_M] \leq P[B_1] + P[B_1] + \cdots + P[B_M]$

Using the *Hoeffding inequality*, union bound and M choices (and targets in range [0,1]) we get:

$$\begin{split} &P\left[|E_1 - E_{\mathsf{Out}}(g_1^-)| > \epsilon \ \text{ or } |E_2 - E_{\mathsf{Out}}(g_2^-)| > \epsilon \ \text{ or } \cdots \ \text{ or } |E_M - E_{\mathsf{Out}}(g_M^-)| > \epsilon\right] \\ &< P\left[|E_1 - E_{\mathsf{Out}}(g_1^-)| > \epsilon\right] + P\left[|E_2 - E_{\mathsf{Out}}(g_2^-)| > \epsilon\right] + \cdots + P\left[|E_M - E_{\mathsf{Out}}(g_M^-)| > \epsilon\right] \\ &\leq M2e^{-2\epsilon^2I/(b-a)^2} = \delta \text{ for any } \epsilon > 0 \end{split}$$



Approach taken from pages 19-24 in Learning from Data

The bound is for errors in the range [a,b]

Validation estimate

The bound is for targets in the range [0, 1]

$$E_{\text{out}}(g_{m^*}) \le^? E_{\text{out}}(g_{m^*}^-) \le E_{\text{val}}(g_{m^*}^-) + O(\sqrt{\frac{\ln M}{K}})$$

$$P\left[|E_1 - E_{\text{Out}}(g_1^-)| > \epsilon \text{ or } |E_2 - E_{\text{Out}}(g_2^-)| > \epsilon \text{ or } \cdots \text{ or } |E_M - E_{\text{Out}}(g_M^-)| > \epsilon\right]$$

$$< P\left[|E_1 - E_{\mathsf{out}}(g_1^-)| > \epsilon\right] + P\left[|E_2 - E_{\mathsf{out}}(g_2^-)| > \epsilon\right] + \dots + P\left[|E_M - E_{\mathsf{out}}(g_M^-)| > \epsilon\right]$$

$$\leq M2e^{-2\epsilon^2K} = \delta$$
 for any $\epsilon > 0$

How can this help us determine a good estimate?

$$M2e^{-2e^{2}K} = \delta$$

$$e^{-2e^{2}K} = \delta/(2M)$$

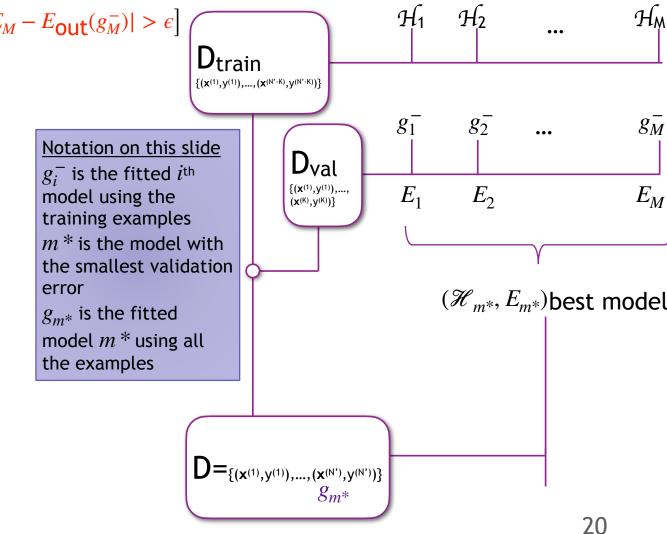
$$-2e^{2}K = \log(\delta/(2M))$$

$$e^{2} = -\frac{1}{2K}\log(\delta/(2M))$$

$$\epsilon = \sqrt{-\frac{1}{2K}\log(\delta/(2M))} = \sqrt{\frac{1}{2K}\log(2M/\delta)}$$

With probability $1 - \delta$ we know that

$$E_{\text{out}}(g_{m^*}^{-}) \le E_{\text{val}}(g_{m^*}^{-}) + O\left(\sqrt{\frac{\ln 2M + \ln \frac{1}{\delta}}{2K}}\right)$$
is $E_{\text{val}}(g_{m^*}^{-}) + O\left(\sqrt{\frac{\ln M}{K}}\right)$



Example:

Suppose we fit 3 different models $g_1^ g_2^ g_3^-$ using our training data $\{(\mathbf{x}^{(1)}, \mathbf{y}^{(1)}), ..., (\mathbf{x}^{(N-K)}, \mathbf{y}^{(N-K)})\}, \mathbf{y}^{(i)} \in \{0,1\}$

For each of our fitted model, we estimated our out of sample error, $E_{out}(g_i^-)$, using a validation set $E_{val}(g_i^-)$

For each fitted model, we can calculate the probability it's estimate is wrong by more than ϵ using the the Hoeffding inequality: $p[|E_{out}(g_i^-) - E_{val}(g_i^-)| > \epsilon] \le 2e^{-2\epsilon^2 K}$ for i = 1,...,3

What is the probability of <u>any</u> of our 3 estimates is wrong by more than ϵ ?

$$\mathsf{p} \big(|E_{\mathsf{out}}(g_1^-) - E_{\mathsf{val}}(g_1^-)| > \epsilon \text{ or } |E_{\mathsf{out}}(g_2^-) - E_{\mathsf{val}}(g_2^-)| > \epsilon \text{ or } |E_{\mathsf{out}}(g_3^-) - E_{\mathsf{val}}(g_3^-)| > \epsilon \big)$$

We can get an upper bound of this probability using the *union bound*:

$$\begin{split} &\mathsf{p} \big(\; |E_{\mathsf{out}}(g_1^-) - E_{\mathsf{val}}(g_1^-)| > \epsilon \; \mathsf{or} \; |E_{\mathsf{out}}(g_2^-) - E_{\mathsf{val}}(g_2^-)| > \epsilon \; \mathsf{or} \; |E_{\mathsf{out}}(g_3^-) - E_{\mathsf{val}}(g_3^-)| > \epsilon \; \big) \\ &\leq \mathsf{p} \big(|E_{\mathsf{out}}(g_1^-) - E_{\mathsf{val}}(g_1^-)| > \epsilon \big) + \mathsf{p} \big(|E_{\mathsf{out}}(g_2^-) - E_{\mathsf{val}}(g_2^-)| > \epsilon \big) + \mathsf{p} \big(|E_{\mathsf{out}}(g_3^-) - E_{\mathsf{val}}(g_3^-)| > \epsilon \big) \\ &< 3 \cdot 2e^{-2\epsilon^2 K} \end{split}$$

If we set $\delta = 3 \cdot 2e^{-2\epsilon^2 K}$ then with probability $1 - \delta$ all 3 of our estimates $E_{val}(g_i^-)$ are within ϵ of their out of sample error $E_{\text{out}}(g_i^-)$.

We can rewrite
$$\delta = 3 \cdot 2e^{-2\epsilon^2 K}$$
 as $\epsilon = \sqrt{\frac{1}{2K} \log \frac{3 \cdot 2}{\delta}}$