DSC 80 winter 2025 final review

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final logistics

- thursday, 3/20
- 11:30am-2:30pm in SOLIS 104
- see seating chart <u>here</u>
- 180 minutes paper exam
- 2 sheets of hand-written notes (front + back)
- all lectures (first half is midterm redemption)

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HTML and web scraping

HTML tags

element	description
<html></html>	root element: enclose the whole document (indicates this is an html file).
<head></head>	metadata: contains metadata you want to apply across whole document.
<body></body>	document content: contains all visible content of the page.
<div></div>	block-level container: groups a block of content; usually used for layout purposes.
	inline container: used to manipulate a portion of text or elements within a line.
	paragraph: starts on a new line and adds margin before and after the block.
<a>	hyperlink: creates a clickable link
<h1>, <h2>,</h2></h1>	different level headings : gets smaller as you go from h1 h6.
	image: displays images. self-closing (no tag required).

```
<title>Title Text</title>
<h1>h1 text</h1>
<h2>h2 text</h2>
<h3>h3 text</h3>
    First p tag: The giant panda (Ailuropoda melanoleuca), also known as the panda bear or
    simply panda, is a bear species endemic to China. It is characterised by its white coat
    with black patches around the eyes, ears, legs and shoulders.
Second p tag:
    <a href="https://sdzwildlifeexplorers.org/stories/precious-pandas">
        this is a hyperlink to San Diego Zoo's page about pandas
<img src="panda-closeup.jpg" alt="local image" height=200/>
<img src="https://www.telegraph.co.uk/content/dam/news/2016/08/23/</pre>
106598324PandawaveNEWS_trans_NvBQzQNjv4Bqeo_i_u9APj8RuoebjoAHt0k9u7HhRJvuo-ZLenGRumA.jpg?"
alt="remote source" height=200/>
```



h1 text

h2 text

h3 text

First p tag: The giant panda (Ailuropoda melanoleuca), also known as the panda bear or simply panda, is a bear species endemic to China. It is characterised by its white coat with black patches around the eyes, ears, legs and shoulders.

Second p tag: this is a hyperlink to San Diego Zoo's page about pandas





parsing HTML

```
soup = bs4.BeautifulSoup(HTML string)
```

- → parsed document where you can access elements of the HTML
 - soup.find(tag, attrs={})
 finds the first occurrence of a tag (matching the specified attributes)
 - soup.find_all(tag, attrs={})
 finds all occurrences of a tag (matching the specified attributes) as a list
 - soup.find(tag).text: returns only the text that is part of the tag
 - soup.find(tag).attrs: lists all attributes of the tag
 - soup.find(tag).get(attr): returns the value of specified attribute

```
<html>
   <head>
     <title>ZOMBO</title>
  </head>
   <body>
      <h1>Welcome to Zombo.com</h1>
      <div id="greeting">
         <11>
            This is Zombo.com, welcome!
            This is Zombo.com
            Velcome to Zombo.com
            You can do anything at Zombo.com — anything at all!
            The only limit is yourself.
         </div>
      <div id="footnotes" class="faded">
         <h3>Footnotes</h3>

    id="footnotes">

            Please consider <a href="paypal.html">donating!</a>
            </div>
   </body>
</html>
```

Problem 3.2

The page shown above contains five greetings, each one a list item in an unordered list. The first greeting is This is Zombo.com, welcome!, and the last is The only limit is yourself.

Suppose we have parsed the HTML into a BeautifulSoup object stored in the variable named soup.

Which of the following pieces of code will produce a list of BeautifulSoup objects, each one representing a single greeting list item? Mark all which apply.

- soup.find('div').find_all('li')
- soup.find_all('li', id='greeting')
- soup.find('div',
 id='greeting').find_all('li')
- □ soup.find_all('ul/li')

regex and text features

regex functions

- re.findall(pattern, str):returns a list containing all matches
- re.search(pattern, str):
 returns a match object if there is a match anywhere in the string
- re.split(pattern, str):returns a list where the string has been split at each match
- re.sub(pattern, replace, str):replaces all matches with the replace text

Character	Description	Example pattern
[]	a set of characters	"[A-Z#]"
•	any single character (except newline)	"heo"
٨	starts with (i.e. check beginning of string)	"^pandas"
\$	ends with (i.e. check end of string)	"pandas\$"
*	zero or more occurrences of the preceding character	"lo*k"
+	one or more occurrences of the preceding character	"lo+k"
?	zero or one occurrence of the preceding character	"colou?r"
{}	specify exactly the number of occurrences	"ap{2}le"
I	"or"; matches either the pattern before or after	"this that"
()	capture / group	"#(tag)"

Character	Description	Example pattern
\b	word break	"\bword"
\d	digits (numbers 0-9)	"\d{4}"
\s	space	"hi\shello"
\w	alphanumeric and "_"	"\w+@\w+.com"
[a-z]	lower case characters from a to z	"[a-h]+"
[^abc]	NOT a, b, or c	"[^a-z]+"

bag of words

 \rightarrow defines a vector space in \mathbb{R}^n number of unique words

e.g. if you have 3 separate strings with 10 total unique words across all of them, you get a bag of words matrix of size 3x10

	text		hello	world	good	morning	happy
0	hello world	0	1	1	0	0	0
1	good morning world	1	0	1	1	1	0
2	happy world	2	0	1	0	0	1

cosine similarity

	hello	world	good	morning	happy
0	1	1	0	0	0
1	0	1	1	1	0
2	0	1	0	0	1

for text 0 and text 1:

$$\cos \theta = \frac{\vec{a} \cdot \vec{b}}{|\vec{a}||\vec{b}|} = \frac{[1,1,0,0,0] \cdot [0,1,1,1,0]}{\sqrt{2}\sqrt{3}} = \frac{1}{\sqrt{6}}$$

TF-IDF

• **term frequency** (tf) of a word **t** in a document **d**:

$$tf(t,d) = \frac{\text{\# of occurrences of } t \text{ in } d}{\text{total } \text{\# of words in } d}$$
 if tf(t,d) is large, then t occurs often in d.

• inverse document frequency (idf) of a word t in a set of documents:

$$idf(t) = log(\frac{total \# of documents}{\# of documents in which t appears})$$

if idf(t) is large, then t does not occur often in the set of documents

TF-IDF $(t,d) = tf(t,d) \cdot idf(t)$

- TF-IDF quantifies how well a word t summarizes document d.
- This value is largest when:
 - both tf(t,d) and idf(t) are large
 - → t occurs often in d but does not occur often in other documents.
 - \rightarrow good summary
- When tf(t,d) is large but idf(t) is small
 - → t occurs often in general; not a good word to summarize d
- When idf(t) is large but tf(t,d) is small
 - → t does not occur often in d or in general; just a random word

Problem 5.3

Chen downloaded 4 independent reviews of a new vacuum cleaner from Amazon (as shown in the 4 sentences below).

```
Sentence 1: 'if i could give this vacuum zero stars i would'
Sentence 2: 'i will not order again this vacuum is garbage'
Sentence 3: 'Love Love Love i love this product'
Sentence 4: 'this little vacuum is so much fun to use i love it'
```

X is the 'Term frequency-Inverse Document Frequency (TF-IDF)' of the word 'vacuum' in sentence 1.

Chen replaces sentence 3 with the following new sentence/review.

```
New Sentence 3: 'Love Love Love i love this vacuum'
```

Y is the 'TF-IDF' of the word 'vacuum' in sentence 1 after the sentence 3 is replaced by the new sentence 3.

Given the above information, which of the following statements is true?

$$\bigcirc X = Y$$

$$\bigcirc$$
 $X>0$ and $Y=0$

$$\bigcirc$$
 $X>0$ and $Y>X$

linear regression

linear regression

Given prediction function:

$$H(\mathbf{x}_i) = w_0 + w_1(x_1) + w_2(x_2) + ... + w_m(x_m)$$

Find the $w_0, w_1, ... w_m$ that minimize:

$$MSE = \frac{1}{n} \sum_{i=1}^{n} (y_i - H(\mathbf{x}_i))^2$$

7	

^	E	
u	5	Using a single value to predict v
•	-	TIGINA A GINAIA VAILIA LA NEGAICI V

$$H = \text{predicted } y = w_0$$

4 3
$$w_0 = mean(y) = 3$$

X =			y =		
fe	eature 1	feature 2		У	Using only one feature of X (column 'feature 1'):
0	2.0	1	0	5	U(m) - prodicted $u - u + u $ (facture 1)
1	1.5	0	1	4	$H(x_i) = \text{predicted } y = w_0 + w_1(\text{feature 1})$
2	1.0	1	2	2	What are the best parameters w_0, w_1
3	0.4	0	3	1	that minimize MSE / RMSE ?

4 3

0.4

1.2

```
lr = LinearRegression()
                                                Training step:
lr.fit(X[['feature 1']],y)
                                                    Linear Regression model takes in X
                                                    matrix with one column 'feature 1'
    LinearRegression 🕛 🥙
                                                    and target y and calculates
                                                    intercept and coefficient that best
LinearRegression()
                                                    minimizes mean square error.
lr.predict(X[['feature 1']])
                                                Prediction:
array([[5.04971591],
                                                    The "trained" model predicts y based
         [3.73579545],
                                                    on the parameters it learned
         [2.421875].
         [0.84517045],
         [2.94744318]])
                                                Best parameters:
print('w0 = ', lr.intercept_[0])
```

print('w0 = ', tr.intercept_[0])
print('w1 = ', tr.coef_[0,0])

w0 = -0.20596590909090902
w1 = 2.627840909090909
• sklearn LinearRegression allows you to access the parameters once model is fitted.

		x be a	5x3 m			
X =				y =		
	x1	x2	хЗ		У	Using all features of X:
0	1	2.0	100	0	5	$H(x_i) = \text{predicted } y = w_0 + w_1(x_1) + w_2(x_2) + w_3(x_3)$
1	0	1.5	120	1	4	
2	1	1.0	200	2	2	What are the best parameters w_0,w_1,w_2,w_3 that minimize MSE $/$ RMSE ?
3	0	0.4	75	3	1	
4	1	1.2	150	4	3	

```
lr = LinearRegression()
                                                   Training step:
lr.fit(X,y)
                                                        Fitting on the entire X matrix
    LinearRegression 🔍 🥙
LinearRegression()
lr.predict(X)
                                                   Prediction:
array([[5.08879116],
                                                        Predicting on entire X matrix
        [3.95837914],
        [2.12624993].
        [1.04162086],
        [2.7849589 ]])
print('w0 = ', lr.intercept_[0]) • • •
                                                   Best parameters:
      0.11037380241869155
                                                        w0 is the intercept
w1 = -0.2846578713156235
                                                        w1, w2, and w3 are the coefficients for
w2 = 2.7418721532904042
                                                        each feature of X.
       -0.0022066907491752833
```

how good is my linear regression model?

$$RMSE = \sqrt{rac{1}{n}\sum_{i=1}^{n}(y_i - H(\mathbf{x}_i))^2} egin{array}{l} ext{Lower} \ o ext{ actual y is close to predicted y on average} \ ext{= good prediction} \end{array}$$

Lower

$$R^2 = rac{ ext{var}(ext{predicted } y ext{ values})}{ ext{var}(ext{actual } y ext{ values})}$$

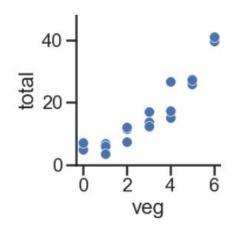
range = (0, 1)

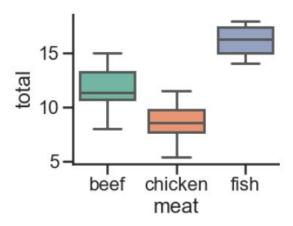
Closer to 1

- → variation in the y is explained by the linear model
- = good linear fit

Every week, Lauren goes to her local grocery store and buys a varying amount of vegetable but always buys exactly one pound of meat (either beef, fish, or chicken). We use a linear regression model to predict her total grocery bill. We've collected a dataset containing the pounds of vegetables bought, the type of meat bought, and the total bill. Below we display the first few rows of the dataset and two plots generated using the entire training set.

veg	meat	total
1	beef	13
3	fish	19
2	beef	16
0	chicken	9





Problem 9.1

Suppose we fit the following linear regression models to predict <code>'total'</code> using the squared loss function. Based on the data and visualizations shown above, for each of the following models H(x), determine whether **each fitted model coefficient** w^* is positive (+), negative (-), or exactly 0. The notation meat=beef refers to the one-hot encoded <code>'meat'</code> column with value 1 if the original value in the <code>'meat'</code> column was <code>'beef'</code> and 0 otherwise. Likewise, meat=chicken and meat=fish are the one-hot encoded <code>'meat'</code> columns for <code>'chicken'</code> and <code>'fish'</code>, respectively.

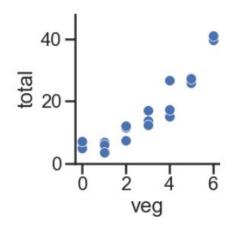
For example, in part (iv), you'll need to provide three answers: one for w_0^* (either positive, negative, or 0), one for w_1^* (either positive, negative, or 0), and one for w_2^* (either positive, negative, or 0).

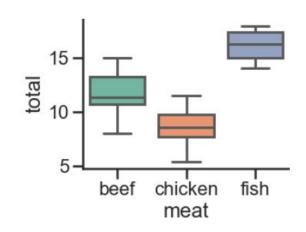
or need more information

i.
$$H(x)=w_0$$

ii. $H(x)=w_0+w_1\cdot ext{veg}$
iii. $H(x)=w_0+w_1\cdot ext{(meat=chicken)}$
iv. $H(x)=w_0+w_1\cdot ext{(meat=beef)}+w_2\cdot ext{(meat=chicken)}$
v. $H(x)=w_0+w_1\cdot ext{(meat=beef)}+w_2\cdot ext{(meat=chicken)}+w_3\cdot ext{(meat=fish)}$

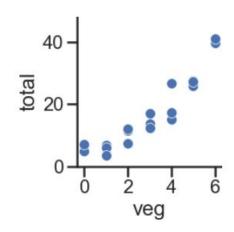
veg	meat	total
1	beef	13
3	fish	19
2	beef	16
0	chicken	9

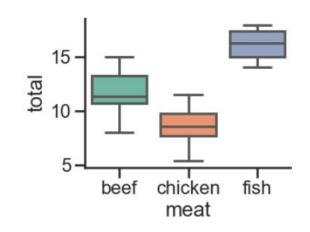




$$H(x)=w_0$$

veg	meat	total
1	beef	13
3	fish	19
2	beef	16
0	chicken	9

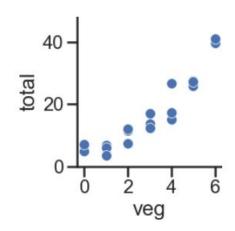


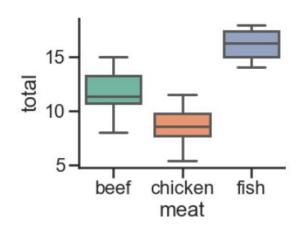


$$H(x) = w_0 + w_1 \cdot \mathrm{veg}$$

w1: positive / negative / 0 / need more information?

veg	meat	total
1	beef	13
3	fish	19
2	beef	16
0	chicken	9

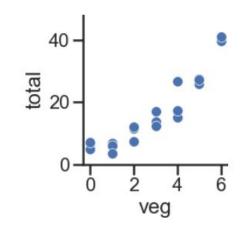


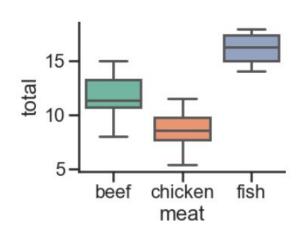


$$H(x) = w_0 + w_1 \cdot (ext{meat=chicken})$$

wl: positive / negative / 0 / need more information?

veg	meat	total
1	beef	13
3	fish	19
2	beef	16
0	chicken	9



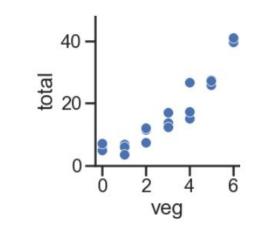


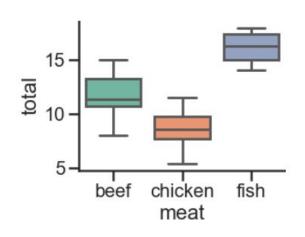
$$H(x) = w_0 + w_1 \cdot (\text{meat=beef}) + w_2 \cdot (\text{meat=chicken})$$

wl: positive / negative / 0 / need more information?

w2: positive / negative / 0 / need more information?

veg	meat	total
1	beef	13
3	fish	19
2	beef	16
0	chicken	9





$$H(x) = w_0 + w_1 \cdot (\text{meat=beef}) + w_2 \cdot (\text{meat=chicken}) + w_3 \cdot (\text{meat=fish})$$

w1: positive / negative / 0 / need more information?

w2: positive / negative / 0 / need more information?

w3: positive / negative / 0 / need more information?

feature engineering

feature transformations

One hot encoding:

- turns categorical features into multiple binary features
- # of binary features = number of unique values in the original column

• Standardization:

$$x_i
ightarrow rac{x_i - ar{x}}{\sigma_x}$$

ensures all quantitative features are on the same scale

• Linearization:

apply a non-linear transformation to data to make it linear

• Binarization:

turn quantitative data into 2 groups (1s and 0s) based on a threshold

Discretization

turn quantitative data into percentiles or quantiles

One-Hot-Encoding

	meat				
0	Beef		([[1.,	0	0.1.
1	Chicken	<pre>ohe = OneHotEncoder()</pre>			0.],
2	Chicken	<pre>ohe.fit(df) ohe.transform(df)</pre>		1000000	0.],
3	Fish			- 50	1.], 0.],
4	Beef		1.	A00-000	1.]])
5	Fish			-	

Standardization

	х1	x2	х3
0	1	2.0	100
1	0	1.5	120
2	1	1.0	200
3	0	0.4	75
4	1	1.2	150

```
scaler = StandardScaler()
scaler.fit(X)
scaler.transform(X).round(2)

[ 0.82,  1.47, -0.67],
[-1.22,  0.53, -0.21],
[ 0.82, -0.41,  1.64],
[-1.22, -1.55, -1.25],
[ 0.82, -0.04,  0.49]]
```

Multicollinearity

- Occurs when we have redundant features or features that are highly correlated with each other
 - → makes coefficients of the regression model uninterpretable
 - → **does not** impact the model's prediction though!

instead of this:

do this:

classification

decision trees

```
x0 x1 y
```

```
dt.fit(data[['x0', 'x1']], data['y'])
sklearn.tree.plot_tree(dt)
plt.show()
                       x[1] <= 2.5
                    entropy = 0.918
                       samples = 6
                      value = [4, 2]
                   liue v
                                    <del>т ат</del>5е
             x[0] <= 0.5
                                entropy = 0.0
           entropy = 0.722
                                samples = 1
             samples = 5
                                value = [0, 1]
            value = [4, 1]
                      entropy = 0.0
  entropy = 0.0
   samples = 1
                       samples = 4
  value = [0, 1]
                      value = [4, 0]
```

dt = DecisionTreeClassifier(criterion='entropy')

decision trees

pros:

- Fast training and prediction.
- Ignores irrelevant features (will not choose a bad split).
- Not affected by different scales of data.

cons:

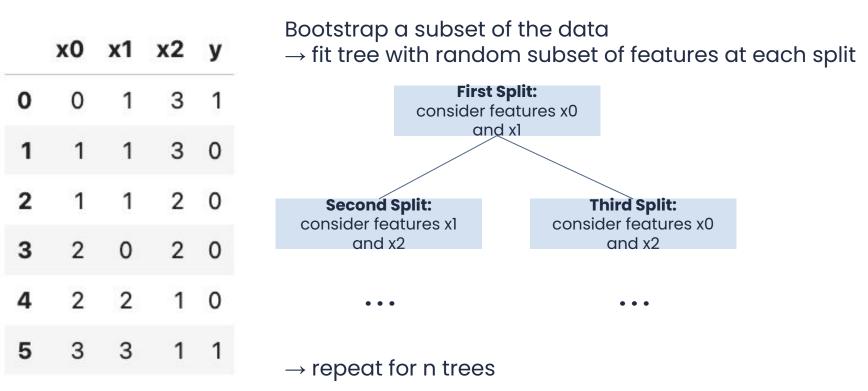
- Complete tree almost always overfits to the training data (high variance).
- Not the best at predicting on unseen data.

random forest

- addresses the challenges of decision trees by introducing randomness.
- uses a random subset of features (also bootstrap by default).
- also able to find feature importance.

random forest

fits multiple trees, each with a random subset of features.



• • •

classifier evaluation

	Predicted Negative	Predicted Positive
Actually Negative	TN 🔽	FP X
Actually Positive	FN 🗙	TP 🔽

$$ext{accuracy} = rac{TP + TN}{TP + FP + FN + TN}$$

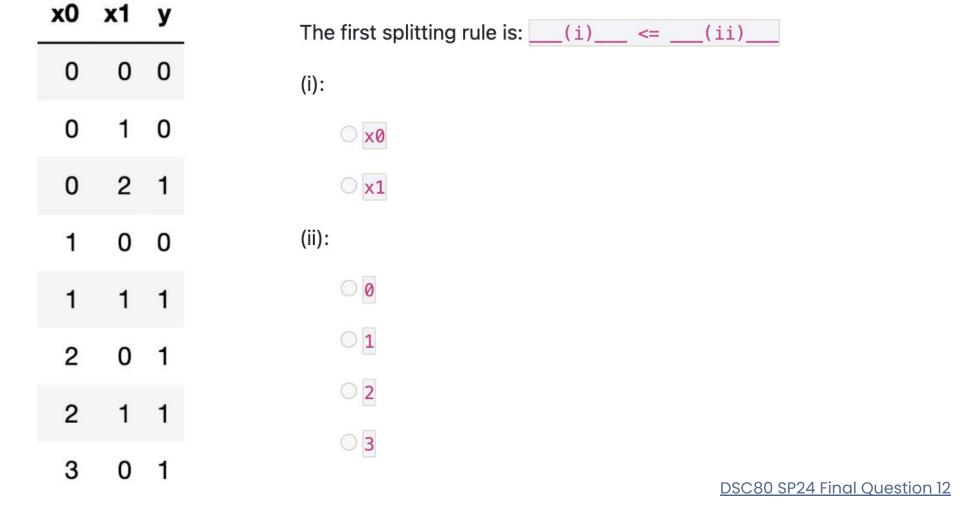
$$ext{recall} = rac{TP}{TP + FN} \qquad ext{precision} = rac{TP}{TP + FP}$$

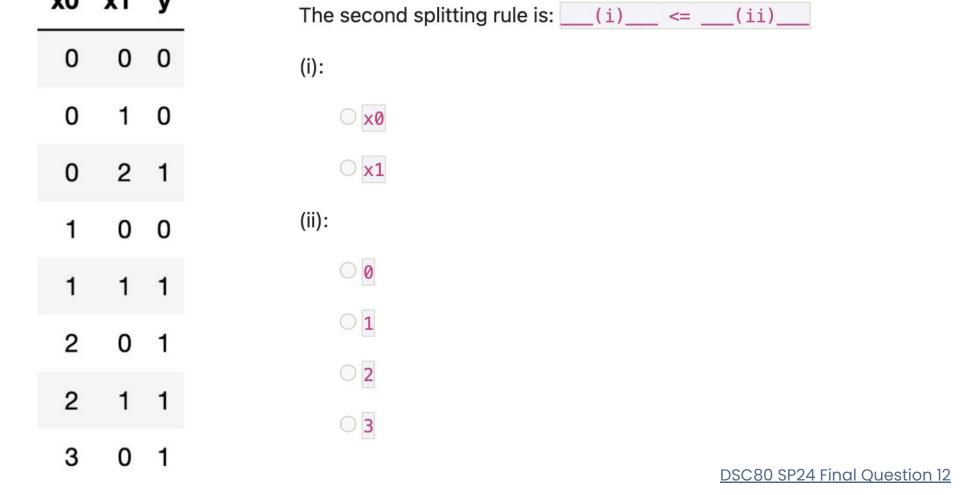
Problem 12

Suppose you fit a decision tree to the training set below, using the features x_0 and x_1 to predict the outcome y.

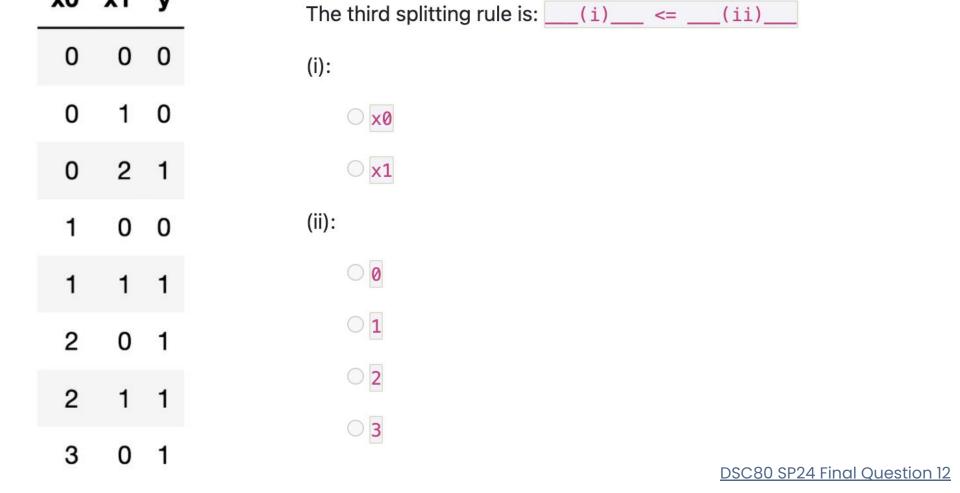
x0	х1	у
0	0	0
0	1	0
0	2	1
1	0	0
1	1	1
2	0	1
2	1	1
3	0	1

Write the first four splitting rules that are created by the decision tree when fitting this training set (using weighted entropy). Assume that the tree is constructed in a depth-first order. If two candidate splits have the same weighted entropy, choose the one that splits on $\times 0$.

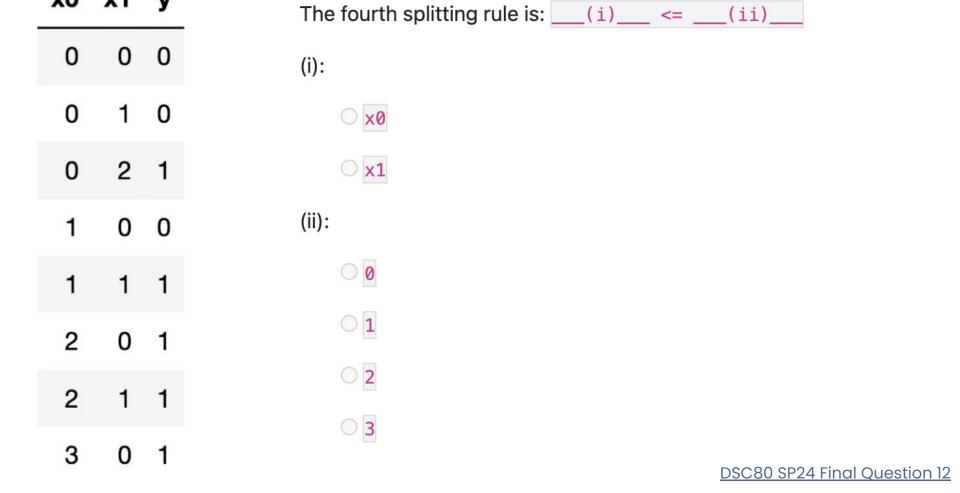




x0 x1 y



x0 x1 y



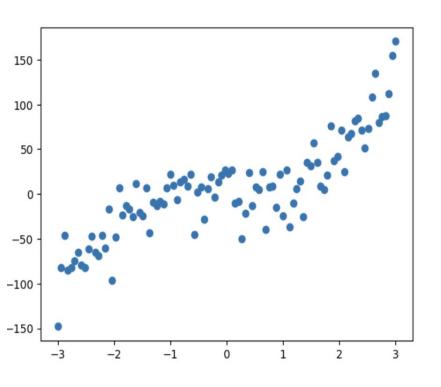
x0 x1 y

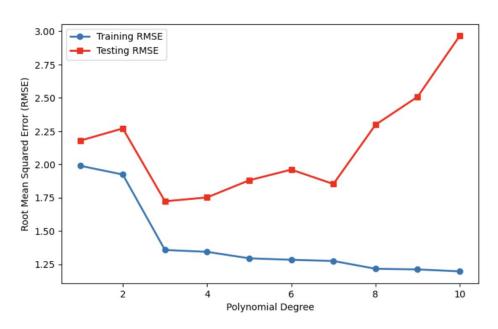
model tuning

Bias vs. Variance

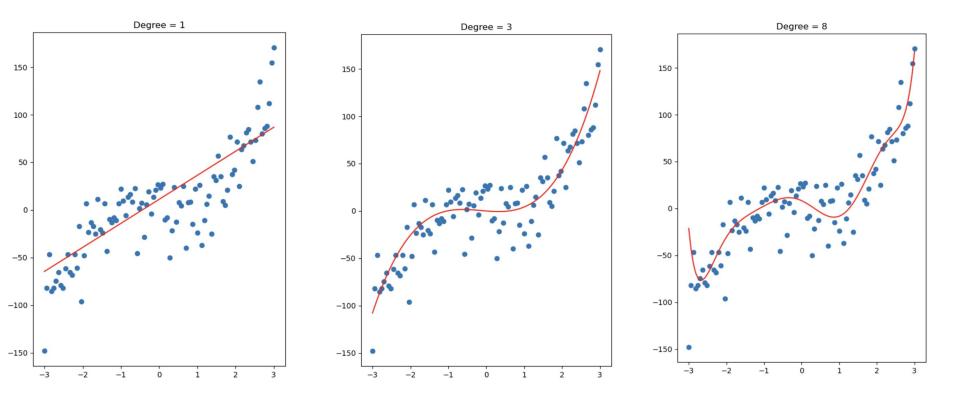
- Bias: the expected deviation between a predicted value and the actual value
 - low bias = good model
 - high bias = underfitting; the model fails to capture the complexity of the relationship between the features and the response variable.
- Variance: how much does the prediction vary on different datasets
 - low variance = good model
 - high variance = overfitting; the model is too complicated and is fitting too much of the noise in the training set

in the case of polynomial regression





in the case of polynomial regression



examples of hyperparameters:

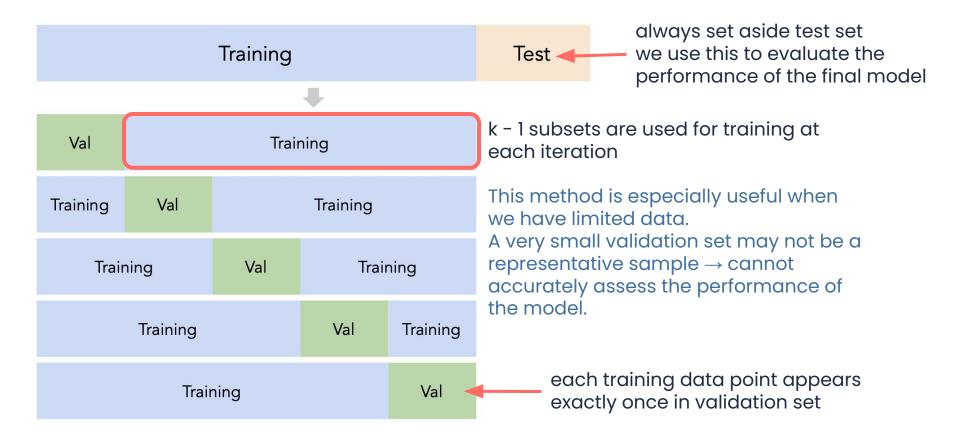
Decision trees

- max tree depth
 determines when to stop splitting; smaller = less overfitting
- min_samples_split
 determines the minimum number of samples required in an internal node; larger = less overfitting
- criterion
 'gini', 'entropy' etc.; different functions to measure quality of split

Random forest

- all the hyperparameters for decision trees also apply
- n_estimators
 how many trees to fit; more trees = less variance but more costly
- max_features
 how many features to consider at each split

k-fold cross-validation



Suppose we write the following code:

```
hyperparameters = {
    'n_estimators': [10, 100, 1000], # number of trees per forest
    'max_depth': [None, 100, 10] # max depth of each tree
}
grids = GridSearchCV(
    RandomForestClassifier(), param_grid=hyperparameters,
    cv=3, # 3-fold cross-validation
)
grids.fit(X_train, y_train)
```

1. How many random forests are fit in total?

Answer the following questions with a single number.

- 2. How many decision trees are fit in total?
- 3. How many times in total is the first point in X_train used to train a decision tree?

```
hyperparameters = {
    'n_estimators': [10, 100, 1000], # number of trees per forest
    'max_depth': [None, 100, 10] # max depth of each tree
}
```

Grid search with k = 3.

1. How many random forests are fit in total?

1. How many decision trees are fit in total?

2. How many times in total is the first point in X_train used to train a decision tree?

good luck on the final!

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