Lecture 24: Review

CS109A Introduction to Data Science Pavlos Protopapas and Natesh Pillai













What is \hat{y}_q at some x_q ?

Find distances to all other points $D(x_q, x_i)$

Find the nearest neighbor, (x_p, y_p)

Predict $\hat{y}_q = y_p$



Simple Prediction Model

Do the same for "all" x's







What is \hat{y}_q at some x_q ?

Find distances to all other points $D(x_q, x_i)$

Find the k-nearest neighbors, x_{q_1}, \dots, x_{q_k}

Predict $\widehat{y_q} = \frac{1}{k} \sum_{i}^{k} y_{q_i}$



Simple Prediction Models





Simple Prediction Models

We can try different k-models on more data









For a given data set





Is this line good?





Maybe this one?





Or this one?





Question: Which line is the best? First calculate the residuals





Again we use MSE as our loss function,

$$L(\beta_0, \beta_1) = \frac{1}{n} \sum_{i=1}^n (y_i - \widehat{y}_i)^2 = \frac{1}{n} \sum_{i=1}^n [y_i - (\beta_1 X + \beta_0)]^2.$$

We choose $\hat{\beta}_1$ and $\hat{\beta}_0$ in order to minimize the predictive errors made by our model, i.e. minimize our loss function.

Then the optimal values for $\hat{\beta}_0$ and $\hat{\beta}_1$ should be:

$$\widehat{\beta}_0, \widehat{\beta}_1 = \underset{\beta_0, \beta_1}{\operatorname{argmin}} L(\beta_0, \beta_1).$$



One way to estimate our coefficients would be to calculate the loss function for every possible $\boldsymbol{\beta}_0$ and $\boldsymbol{\beta}_1$. Then select the betas where the loss function is at the minimum.

E.g. the loss function for different $\boldsymbol{\beta}_1$ values when $\boldsymbol{\beta}_0$ is fixed to be 6:





Take the partial derivatives of *L* with respect to β_0 and β_1 , set to zero, and find the solution to that equation. This procedure will give us explicit formulae for $\hat{\beta}_0$ and $\hat{\beta}_1$:

$$\hat{\beta}_1 = \frac{\sum_i (x_i - \overline{x})(y_i - \overline{y})}{\sum_i (x_i - \overline{x})^2}$$
$$\hat{\beta}_0 = \overline{y} - \hat{\beta}_1 \overline{x}$$

where \bar{y} and \bar{x} are sample means.

The line:

$$\widehat{Y} = \widehat{\beta}_1 X + \widehat{\beta}_0$$

is called the **regression line**.









In our magical realisms, we can now sample multiple times





Another sample





Another sample





And another sample





Repeat this for 100 times





We can now estimate the mean and standard deviation of all the estimates $\hat{\beta}_1.$





Finally we can calculate the confidence intervals, which are the ranges of values such that the true value of is contained in this interval with n percent probability.





How well do we know \hat{f} ?

Below we show all regression lines for a thousand of such bootstrapped samples.

For a given x, we examine the distribution of \hat{f} , and determine the mean and standard deviation.





How well do we know \hat{f} ?

Below we show all regression lines for a thousand of such sub-samples. For each one of those "realizations" we can fit a model and testament the coefficients.





How well do we know \hat{f} ?

For every x, we calculate the mean of the models, \hat{f} (shown with dotted line) and the 95% CI of those models (shaded area).





Confidence in predicting \hat{y}





Confidence in predicting \hat{y}

- for a given *x*, we have a distribution of models
- for each of these the prediction for





Confidence in predicting \hat{y}

- for a given x, we have a distribution of models f(x)
- for each of these f(x), the prediction for $y \sim N(f, \sigma_{\epsilon})$










Using a single validation set to select amongst multiple models can be problematic - **there is the possibility of overfitting to the validation set**.



It is obvious that degree=3 is the correct model but the validation set by chance favors the linear model.



Train-Validation-Test

We introduce a different sub-set, which we called validation and we use it to select the model.





Train-Validation-Test The test set should never be touched for model training or We introduce a different sub-set, which we called validat selection. select the model. Validation Train Test We use this to We use this to We use this to report model train a model select model performance























Error







Bias vs Variance





Bias vs Variance





Bias vs Variance





Linear models: 20 data points per line 2000 simulations

















Poly 10 degree models : 20 data points per line 2000 simulations





Left: 2000 best fit straight lines, each fitted on a different 20 point training set.

Right: Best-fit models using degree 10 polynomial





The idea of regularization revolves around modifying the loss function L; in particular, we add a regularization term that penalizes some specified properties of the model parameters

$$L_{reg}(\beta) = L(\beta) + \lambda R(\beta),$$



Since we wish to discourage extreme values in model parameter, we need to choose a regularization term that penalizes parameter magnitudes. For our loss function, we will again use MSE.

Together our regularized loss function is:

$$\begin{split} L_{LASSO}(\beta) &= \frac{1}{n} \sum_{i=1}^{n} |y_i - \boldsymbol{\beta}^\top \boldsymbol{x}_i|^2 + \lambda \sum_{j=1}^{J} |\beta_j|. \end{split}$$
 Note that $\sum_{j=1}^{J} |\beta_j|$ is the l_1 norm of the vector $\boldsymbol{\beta}$
$$\sum_{j=1}^{J} |\beta_j| = \|\boldsymbol{\beta}\|_1 \end{split}$$



Alternatively, we can choose a regularization term that penalizes the squares of the parameter magnitudes. Then, our regularized loss function is:

$$L_{Ridge}(\beta) = \frac{1}{n} \sum_{i=1}^{n} |y_i - \boldsymbol{\beta}^{\top} \boldsymbol{x}_i|^2 + \lambda \sum_{j=1}^{J} \beta_j^2$$

Note that
$$\sum_{j=1}^{J} |\beta_j|^2$$
 is the l_2 norm of the vector $\boldsymbol{\beta}$

$$\sum_{j=1}^{J} \beta_j^2 = \|\boldsymbol{\beta}\|_2^2$$



Ridge regularization with a **single validation** set





Ridge regularization with **k-fold cross-validation**









Top PCA components capture the most of amount of variation (interesting features) of the data.

Each component is a linear combination of the original predictors - we visualize them as vectors in the feature space.





Transforming our observed data means projecting our dataset onto the space defined by the top *m* PCA components, these components are our new predictors.





An Alternative Interpretation of PCA

- We've seen an interpretation of PCA as finding the directions in the predictor space along which the data varies the most
- An alternative interpretation is that PCA finds a low-dimensional linear surface which is closest to the data points

















A Simple Classification Problem: Binary Response

What could go wrong with this linear regression model?





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Output Should Be Interpretable As Probabilities

Think of a function that would do this for us




Logistic Regression





Probability Mass Function (PMF):

$$P(Y = 1) = p$$
$$P(Y = 0) = 1 - p$$

$$P(Y = y) = p^{y}(1-p)^{(1-y)}$$

where:

$$p = P(Y = 1 | X = x) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 X)}}$$

and therefore p depends on X.

Thus not every p_i is the same for each individual measurement.



The likelihood of a single observation for p given x and y is:

$$L(p_i|Y_i) = P(Y_i = y_i) = p_i^{y_i}(1 - p_i)^{1 - y_i}$$

Given the observations are independent, what is the likelihood function for *p*?

$$L(p|Y) = \prod_{i} P(Y_i = y_i) = \prod_{i} p_i^{y_i} (1 - p_i)^{1 - y_i}$$

$$l(p|Y) = -\log L(p|Y) = -\sum_{i} y_i \log p_i + (1 - y_i) \log(1 - p_i)$$



$$l(p|Y) = -\sum_{i} \left[y_i \log \frac{1}{1 + e^{-(\beta_0 + \beta_1 X_i)}} + (1 - y_i) \log \left(1 - \frac{1}{1 + e^{-(\beta_0 + \beta_1 X_i)}} \right) \right]_i$$

How do we minimize this?

Differentiate, equate to zero and solve for it!

But yikes, does this look messy! It will not necessarily have a closed form solution.

So how do we determine the parameter estimates? Through an iterative approach!



How can we estimate a classifier, based on logistic regression, for the following plot?



 X_1



Earlier we saw the general form of *simple* logistic regression, meaning when there is just one predictor used in the model. What was the model statement (in terms of linear predictors)?

$$\log\left(\frac{P(Y=1)}{1-P(Y=1)}\right) = \beta_0 + \beta_1 X$$

Multiple logistic regression is a generalization to multiple predictors. More specifically we can define a multiple logistic regression model to predict P(Y = 1) as such:

$$\log\left(\frac{P(Y=1)}{1 - P(Y=1)}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_p X_p$$



A penalty factor can then be added to this loss function and results in a new loss function that penalizes large values of the parameters:

$$\underset{\beta_0,\beta_1,\ldots,\beta_p}{\operatorname{argmin}} \left[-\sum_{i=1}^n (y_i \ln(p_i) + (1-y_i) \ln(1-p_i)) + \lambda \sum_{j=1}^p \beta_j^2 \right]$$

The result is just like in linear regression: shrink the parameter estimates towards zero.

In practice, the intercept is usually not part of the penalty factor.

Note: the sklearn package uses a different tuning parameter: instead of λ they use a constant that is essentially $C = \frac{1}{\lambda}$.



The Radio Operator Characteristics (ROC) curve illustrates the trade-off for all possible thresholds ROC Curve for Predicting AHD in a Logistic Regression Model chosen for the two types of error (or correct



classification).

The vertical axis displays the true positive predictive value and the horizontal axis depicts the true negative predictive value.

The overall performance of a classifier, calculated over all possible thresholds, is given by the **area under the ROC curve** (AUC).

An ideal ROC curve will hug the top left corner, so the larger the AUC the better the classifier.



The *k*-NN classifier first identifies the *k* points in the training data that are closest to x_0 , represented by \mathcal{N}_0 . It then estimates the conditional probability for class *j* as the fraction of points in \mathcal{N}_0 whose response values equal *j*:

$$P(Y = j | X = x_0) = \frac{1}{k} \sum_{i \in \mathcal{N}_0} I(y_i = j)$$

Then, the k-NN classifier predicts this new observation, x_0 , to be in the class with largest estimated probability.



Estimated Probabilities in k-NN Classification







There are 3 major types of missingness to be concerned about:

- Missing Completely at Random (MCAR) the probability of missingness in a variable is the same for all units. Like randomly poking holes in a data set.
- 2. Missing at Random (MAR) the probability of missingness in a variable depends only on available information (in other predictors).
- 3. Missing Not at Random (MNAR) the probability of missingness depends on information that has not been recorded and this information also predicts the missing values.

What are examples of each these 3 types?



There are several different approaches to imputing missing values:

- **1.** Impute the mean or median (quantitative) or most common class (categorical) for all missing values in a variable.
- 2. Create a new variable that is an **indicator of missingness**, and include it in any model to predict the response (also plug in zero or the mean in the actual variable).
- **3.** Hot deck imputation: for each missing entry, randomly select an observed entry in the variable and plug it in.
- 4. Model the imputation: plug in predicted values (\hat{y}) from a model based on the other observed predictors.
- 5. Model the imputation with uncertainty: plug in predicted values plus randomness $(\hat{y} + \epsilon)$ from a model based on the other observed predictors.

What are the advantages and disadvantages of each approach?



Schematic: imputation through modeling

How do we use models to fill in missing data? Using *k*-NN for k = 2?





Imputation through modeling /w uncertainty: an illustration







Python For Data Science Cheat Sheet

Pandas Basics

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Pandas

The Pandas library is built on NumPy and provides easy-to-use data structures and data analysis tools for the Python programming language. pandas 归

Use the following import convention:

>>> import pandas as pd



Asking For Help >>> help(pd.Series.loc)

Selection Also see NumPy Arra Getting >>> s['b'] Get one element -5 >>> df[1:] Get subset of a DataFrame Country Capital Population India New Delhi 1303171035 2 Brazil Brasília 207847528

Selecting, Boolean Indexing & Setting

By Position

>>> df.iloc[[0],[0]]

Dropping

		_
ys	<pre>>>> s.drop(['a', 'c']) >>> df.drop('Country', axis=1) Drop values from rows (axis=0) Drop values from columns(axis=1)</pre>	
	Sort & Rank	
	<pre>>>> df.sort_index() >>> df.sort_values(by='Country') >>> df.rank() Sort by labels along an axis Sort by the values along an axis Assign ranks to entries</pre>	
	Retrieving Series/DataFrame Information	
	Basic Information	
&	>>> df.shape(rows,columns)>>> df.indexDescribe index>>> df.columnsDescribe DataFrame columns>>> df.info()Info on DataFrame>>> df.count()Number of non-NA values	
	Summary	
&	<pre>>>> df.sum() >>> df.cumsum() >>> df.idxmin()/df.max() >>> df.idxmin()/df.idxmax() >>> df.describe() >>> df.mean() >>> df.median()</pre> Sum of values Minimum/Maximum index value Summary statistics Mean of values Median of values	
	Applying Functions	
	<pre>>>> f = lambda x: x*2 >>> df.apply(f) >>> df.applymap(f) Apply function Apply function element-wise</pre>	
	Data Alignment	
	(Internal Data Alianment	
	NA values are introduced in the indices that den't everlap:	
	NA values are introduced in the indices that don't overlap.	
.>1	>>> s + s3	
me	a 10.0	
	b NaN	
	d 7.0	
	Arithmetic Operations with Fill Methods	
_	You can also do the internal data alignment yourself with	
	the help of the fill methods:	
	>>> s.add(s3, fill_value=0)	
	a 10.0 b -5.0	
	c 5.0	
e)	d 7.0 >>> s.sub(s3, fill value=2)	
1	>>> s.div(s3, fill_value=4)	
-	>>> s.mul(s3, fill value=3)	

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Python For Data Science Cheat Sheet NumPv Basics

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NumPv

The NumPy library is the core library for scientific computing in Python. It provides a high-performance multidimensional array object, and tools for working with these arrays.

NumPv

Use the following import convention:

```
>>> import numpy as np
```



>>> c = np.array([((1.5,2,3), (4,5,6)], [(3,2,1), (4,5,6)]],dtype = float)

Initial Placeholders

Create an array of zeros >>> np.zeros((3,4)) Create an array of ones >>> np.ones((2,3,4),dtype=np.int16 >>> d = np.arange(10,25,5) Create an array of evenly spaced values (step value) Create an array of evenly >>> np.linspace(0,2,9) spaced values (number of samples) Create a constant array >>> e = np.full((2,2),7) >>> f = np.eye(2)Create a 2X2 identity matrix Create an array with random values >>> np.random.random((2,2)) >>> np.empty((3,2)) Create an empty array

1/0

Saving & Loading On Disk

>>> np.save('my array', a) >>> np.savez('array.npz', a, b) >>> np.load('my array.npy')

Saving & Loading Text Files

>>> np.loadtxt("myfile.txt") >>> np.genfromtxt("my file.csv", delimiter=',') >>> np.savetxt("myarray.txt", a, delimiter=" ")

Data Types

- >>> np.int64 >>> np.float32 >>> np.complex >>> np.bool >>> np.object >>> np.string >>> np.unicode
- Signed 64-bit integer types Standard double-precision floating point Complex numbers represented by 128 floats Boolean type storing TRUE and FALSE values Python object type Fixed-length string type Fixed-length unicode type

Inspecting Your Array	/		
<pre>>>> a.shape >>> len(a) >>> b.ndim >>> e.size >>> b.dtype >>> b.dtype.name >>> b.astype(int)</pre>	Array dimensions Length of array Number of array dimensions Number of array elements Data type of array elements Name of data type Convert an array to a different type		
Asking For Help			
>>> np.info(np.ndarray.dtyp	e)		
Array Mathematics			
Arithmetic Operations			
Varianneele operations			
>>> $g = a - b$ array([[-0.5, 0, . 0,].	Subtraction		
<pre>[-3., -3., -3.]]) >>> np.subtract(a,b) >>> b + a array([[2.5, 4., 6.], [5., 7., 9.]]) >>> np.add(b,a) >>> a / b array([[0.66666667, 1. [0.25 , 0.4 >>> np.divide(a,b) >>> a * b array([[1.5, 4., 9.] [4., 10., 18.] >>> np.sqr(b) >>> np.sqr(b) >>> np.sin(a) >>> np.log(a) >>> e.dot(f) array([[7., 7.], [7., 7.]])</pre>	Subtraction Addition Addition Division Division Multiplication Square root Print sines of an array Element-wise cosine Element-wise natural logarithm Dot product		
Comparison			
Comparison			
>>> a == b array([[False, True, True]	Element-wise comparison		
<pre>[False, False, False] >>> a < 2 array([True, False, False], >>> np.array egual(a, b)</pre>), dtype=bool) dtype=bool) Arrav-wise comparison		
2 · · · · · · · · · · · · · · · · · · ·			

Aggregate Functions

>>	a.sum()
>>	a.min()
>>	b.max(axis=0)
>>	b.cumsum(axis=1)
>>	a.mean()
>>	b.median()
>>	a.corrcoef()
>>	np.std(b)

Copying Arrays

>>> h = a.view()>>> np.copy(a) >>> h = a.copy()

Sorting Arrays

>>> a.sort() >>> c.sort(axis=0) Create a view of the array with the same data Create a copy of the array Create a deep copy of the array

Sort the elements of an array's axis

Array-wise minimum value

Correlation coefficient

Standard deviation

Maximum value of an array row

Cumulative sum of the elements

Array-wise sum

Mean

Sort an array

Median

Subsetting, Slicing, Indexing Also see Lists Subsetting 1 2 3 Select the element at the 2nd index >>> a[2] 1.5 2 3 Select the element at row 0 column 2 >>> b[1,2] 4 5 6 (equivalent to b[1] [2]) 6.0 Slicing >>> a[0:21 Select items at index 0 and 1 1 2 3 array([1, 2]) 3 >>> b[0:2,1] Select items at rows 0 and 1 in column 1 array([2., 5.]) 4 5 6 Select all items at row o >>> b[:1] 4 5 6 array([[1.5, 2., 3.]]) (equivalent to b[0:1, :]) Same as [1, :, :] >>> c[1,...] array([[[3., 2., 1.], [4., 5., 6.]]]) >>> a[::-1] array([3, 2, 1]) Reversed array a **Boolean Indexing** >>> a[a<2] Select elements from a less than 2 1 2 3 array([1]) Fancy Indexing >>> b[[1, 0, 1, 0], [0, 1, 2, 0]] Select elements (1,0), (0,1), (1,2) and (0,0) array([4., 2., 6., 1.5]) >>> b[[1, 0, 1, 0]][:,[0,1,2,0]] Select a subset of the matrix's rows and columns array([[4.,5.,6.,4.], 1.5,2.,3.,1.5]; 4. 5. 6. 4. **Array Manipulation**

Transposing Array >>> i = np.transpose(b) >>> i.T

Changing Array Shape >>> b.ravel() >>> g.reshape(3,-2)

Adding/Removing Elements >>> h.resize((2,6)) >>> np.append(h,q) >>> np.insert(a, 1, 5) >>> np.delete(a,[1])

Combining Arrays

>>> np.concatenate((a,d),axis=0) array([1, 2, 3, 10, 15, 20]) >>> np.vstack((a,b)) array([[1. , 2. , 3.], [1.5, 2. , 3.], [4. , 5. , 6.]]) >>> np.r_[e,f] >>> np.hstack((e,f)) array([[7., 7., 1., 0.], [7., 7., 0., 1.]]) >>> np.column stack((a,d)) array([[1, 10], [2, 15], [3, 20]]) >>> np.c_[a,d]

Splitting Arrays

>>> np.hsplit(a,3) [array([1]), array([2]), array([3])] >>> np.vsplit(c,2) [array([[[1.5, 2., 1.], [4., 5., 6.]]]), array([[[3., 2., 3.], [4., 5., 6.]]])]

Stack arrays vertically (row-wise) Stack arrays vertically (row-wise) Stack arrays horizontally (column-wise)

Create stacked column-wise arrays

Permute array dimensions

Permute array dimensions

Append items to an array

Delete items from an array

Insert items in an array

Concatenate arrays

Reshape, but don't change data

Return a new array with shape (2.6)

Flatten the array

Create stacked column-wise arrays

Split the array horizontally at the 3rd index Split the array vertically at the 2nd index

(C)

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Python For Data Science Cheat Sheet

SciPy - Linear Algebra

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SciPv

The SciPy library is one of the core packages for SSCiPv scientific computing that provides mathematical algorithms and convenience functions built on the NumPy extension of Python.

Interacting With NumPv

>>> import numpy as np >>> a = np.array([1,2,3]) >>> b = np.array([(1+5j,2j,3j), (4j,5j,6j)]) >>> c = np.array([(1.5,2,3), (4,5,6)], [(3,2,1), (4,5,6)]))

Index Tricks

>>> np.mgrid[0:5,0:5] >>> np.ogrid[0:2,0:2] >>> np.r [3,[0]*5,-1:1:10j] >>> np.c [b,c]

Shape Manipulation

>>> np.transpose(b)

Create a dense meshqrid Create an open meshqrid Stack arrays vertically (row-wise) Create stacked column-wise arrays Permute array dimensions

Create a polynomial object

Return the real part of the array elements

Cast object to a data type

Return the imaginary part of the array elements

Return a real array if complex parts close to o

>>> b.flatten() Flatten the array Stack arrays horizontally (column-wise) >>> np.hstack((b,c)) >>> np.vstack((a,b)) Stack arrays vertically (row-wise) >>> np.hsplit(c,2) Split the array horizontally at the 2nd index >>> np.vpslit(d,2) Split the array vertically at the 2nd index

Polynomials

>>> from numpy import polyld >>> p = poly1d([3, 4, 5])

Vectorizing Functions

>>> def myfunc(a): if a < 0: return a*2 else: return a/2 >>> np.vectorize(mvfunc) Vectorize functions

Type Handling

>>> np.real(b) >>> np.imag(b) >>> np.real if close (c,tol=1000) >>> np.cast['f'](np.pi)

Other Useful Functions

>>>	<pre>np.angle(b,deg=True) g = np.linspace(0,np.pi,num=5)</pre>	Return the angle of the complex argument Create an array of evenly spaced values
>>>	g [3:] += np.pi	(number of samples)
>>>	np.unwrap(g)	Unwrap
>>>	np.logspace(0,10,3)	Create an array of evenly spaced values (log scale)
>>>	<pre>np.select([c<4],[c*2])</pre>	Return values from a list of arrays depending on conditions
>>>	misc.factorial(a)	Factorial
>>>	misc.comb(10,3,exact=True)	Combine N things taken at k time
>>>	misc.central diff weights(3)	Weights for Np-point central derivative
>>>	misc.derivative(myfunc,1.0)	Find the n-th derivative of a function at a point

Linear Algebra

>>> from scipy import linalg, sparse

Creating Matrices

>>> A = np.matrix(np.random.random((2,2))) >>> B = np.asmatrix(b) >>> C = np.mat(np.random.random((10,5)))

Inverse

Inverse

Trace

Tranpose matrix

Frobenius norm

Matrix rank

Determinant

equation

(SVD)

Conjugate transposition

L1 norm (max column sum)

L inf norm (max row sum)

Solver for dense matrices

Solver for dense matrices

(least-squares solver)

Least-squares solution to linear matrix

Compute the pseudo-inverse of a matrix

Compute the pseudo-inverse of a matrix

>>> D = np.mat([[3,4], [5,6]])

Basic Matrix Routines

Inverse >>> A.I

>>> linalg.inv(A) Transposition

>>> A.T >>> A.H

Trace >>> np.trace(A)

Norm

Also see NumPy

>>> linalg.norm(A) >>> linalg.norm(A,1) >>> linalg.norm(A,np.inf)

Rank >>> np.linalg.matrix rank(C)

Determinant >>> linalg.det(A)

Solving linear problems >>> linalg.solve(A,b)

>>> E = np.mat(a).T >>> linalg.lstsq(F,E)

Generalized inverse

>>> linalg.pinv(C)

>>> linalg.pinv2(C)

Creating Sparse Matrices

Create a 2X2 identity matrix >>> F = np.eye(3, k=1)>>> G = np.mat(np.identity(2) Create a 2x2 identity matrix >>> C[C > 0.5] = 0>>> H = sparse.csr matrix(C) Compressed Sparse Row matrix >>> I = sparse.csc matrix(D) Compressed Sparse Column matrix Dictionary Of Keys matrix >>> J = sparse.dok matrix(A) >>> E.todense() Sparse matrix to full matrix >>> sparse.isspmatrix csc(A) Identify sparse matrix Sparse Matrix Routines Inverse Inverse >>> sparse.linalg.inv(I)

Norm >>> sparse.linalg.norm(I)

Solving linear problems >>> sparse.linalg.spsolve(H,I)

Sparse Matrix Functions

>>> sparse.linalg.expm(I)

Sparse matrix exponential

Solver for sparse matrices

Norm

Asking For Help >>> help(scipy.linalg.diagsvd) >>> np.info(np.matrix)

Ad	dition
>>>	np.add(A,D)
Sul	otraction
>>>	np.subtract(A,D)
Div	vision

>>> np.divide(A,D) Multiplication >>> A @ D

Matrix Functions

>>> np.multiply(D,A) >>> np.dot(A,D) >>> np.vdot(A,D) >>> np.inner(A,D) >>> np.outer(A,D) >>> np.tensordot(A,D) >>> np.kron(A,D)

Exponential Functions

>>> linalg.expm(A) >>> linalq.expm2(A) >>> linalg.expm3(D)

Logarithm Function >>> linalg.logm(A)

Trigonometric Functions >>> linalg.sinm(D) >>> linalg.cosm(D) >>> linalg.tanm(A)

Hyperbolic Trigonometric Functions >>> linalg.sinhm(D) >>> linalg.coshm(D) >>> linalq.tanhm(A)

Matrix Sign Function >>> np.signm(A)

Matrix Square Root >>> linalg.sqrtm(A)

Arbitrary Functions >>> linalq.funm(A, lambda x: x*x)

Decompositions

Eigenvalues and Eigenvectors Solve ordinary or generalized >>> la, v = linalq.eiq(A)eigenvalue problem for square matrix >>> 11, 12 = la Unpack eigenvalues >>> v[:,0] First eigenvector >>> v[:,1] Second eigenvector >>> linalq.eiqvals(A) Unpack eigenvalues Singular Value Decomposition >>> U,s,Vh = linalq.svd(B) Singular Value Decomposition (SVD) >>> M,N = B.shape >>> Sig = linalg.diagsvd(s,M,N) Construct sigma matrix in SVD LU Decomposition LU Decomposition >>> P,L,U = linalg.lu(C)

Sparse Matrix Decompositions

>>> la, v = sparse.linalg.eigs(F,1) Eigenvalues and eigenvectors >>> sparse.linalg.svds(H, 2) SVD

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Addition

Division

(Python 3)

Multiplication

Vector dot product

Tensor dot product Kronecker product

Matrix exponential

Matrix logarithm

Matrix exponential (Taylor Series)

Matrix exponential (eigenvalue

Dot product

Inner product

Outer product

decomposition)

Matrix sine

Matrix cosine

Matrix tangent

Hypberbolic matrix sine

Matrix sign function

Matrix square root

Hyperbolic matrix cosine

Evaluate matrix function

Hyperbolic matrix tangent

Subtraction

Multiplication operator

Python For Data Science Cheat Sheet	Plot Anatomy & Workflow				
Matplotlib	Plot Anatom	ıy Workflow			
Ivia upio Linteractively at www.DataCamp.com	Axes/Subplot The basic steps to creating plots with matplotlib are: The basic steps to creating plots with matplotlib.pyplot as plot Save plot 6 Show plot Step 1 Step 1 Step 1 Step 2 Step 2 Step 3 Step 4 Step 3 S				
Matplotlib					ave plot O Show plot
Matplotlib is a Python 2D plotting library which produces publication-quality figures in a variety of hardcopy formats and interactive environments across platforms.	<pre>Figure Figure Figu</pre>				ith=3) Step 3, 4
1 Prepare The Data Also see Lists & NumPy			>>> pit.sr	iow() Step o	
1D Data	(4) Cust	omize Plot			
>>> import numpy as np	Colors, Color	r Bars & Color Maps	Mathtext		
>>> $y = np.cos(x)$ >>> $z = np. sin(x)$	>>> plt.plot(x, x, x, x**2, x, x**3)		>>> plt.title(r'\$sigma_i=15\$', fontsize=20)		
2D Data or Images	>>> ax.plot	(x, y, c='k') (x, y, c='k') (x)	Limits, Legends	& Layouts	
<pre>>>> data = 2 * np.random.random((10, 10)) >>> data2 = 3 * np.random.random((10, 10)) >>> Y, X = np.mgrid[-3:3:100j, -3:3:100j] >>> U = -1 - X**2 + Y >>> V = 1 + X - Y**2</pre>	<pre>>>> fig. colorBar(im, oftentation="horizontal") >>> im = ax.imshow(img,</pre>		Limits & Autoscaling >>> ax.margins(x=0.0,y=0.1) >>> ax.set('equal') >>> ax.set(xlim=[0,10.5],ylim=[-1.5,1.5]) >>> ax.set_xlim(0,10.5)		Add padding to a plot Set the aspect ratio of the plot to 1 Set limits for x-and y-axis Set limits for x-axis
<pre>>>> from matplotlib.cbook import get_sample_data >>> img = np.load(get_sample_data('axes_grid/blvariate_normal.npy'))</pre>	<pre>>>> ax.scatter(x,y,marker=".") >>> ax.plot(x,y,marker="0")</pre>		<pre>>> ax.set(title='An Example Axes',</pre>		Set a title and x-and y-axis labels
2) Create Plot	Linestyles		<pre>ylabel='Y-Axis', xlabel='X-Axis') >>> ax.legend(loc='best') Ticks</pre>		No overlapping plot elements
>>> import matplotlib.pyplot as plt Figure	<pre>>>> plt.plot(x,y,ls='solid') >>> plt.plot(x,y,ls='') >>> plt.plot(x,y,'',x**2,y**2,'') >>> plt.setp(lines,color='r',linewidth=4.0)</pre>		<pre>>>> ax.xaxis.set(ticks=range(1,5),</pre>		Manually set x-ticks Make y-ticks longer and go in and out
<pre>>>> fig = plt.figure() >>> fig2 = plt.figure(figsize=plt.figaspect(2.0)) </pre>	Text & Annotations		Subplot Spacing		Adjust the spacing between subplots
All plotting is done with respect to an Axes. In most cases, a subplot will fit your needs. A subplot is an axes on a grid system.	<pre>>>> ax.text(1,</pre>		hspace=0.3, hspace=0.3, left=0.125, right=0.9,		rajuse the spacing between subplots
<pre>>>> fig.add_axes() >>> ax1 = fig.add_subplot(221) # row-col-num >>> ax3 = fig.add_subplot(212)</pre>	xy=(8, 0), xycoords='data', xytext=(10.5, 0), textcoords='data'.		<pre>>>> fig.tight_layout()</pre> Fit subplot(s) in to t Axis Spines		Fit subplot(s) in to the figure area
<pre>>>> fig3, axes = plt.subplots(nrows=2,ncols=2) >>> fig4, axes2 = plt.subplots(ncols=3)</pre>	arrowprops=dict(arrowstyle="->", connectionstyle="arc3"),)		>>> axl.spines['top'].set_visible(False) >>> axl.spines['bottom'].set_position(('outward',10)) Move the bottom axis line outward		
3) Plotting Routines				5) Save Plot	
1D Data	Vector Fields		Save figures		
<pre>>>> fig, ax = plt.subplots() >>> lines = ax.plot(x,y) >>> ax.scatter(x,y) >>> axes[0,0].bar([1,2,3],[3,4,5])</pre> Draw unconnected points, scaled of Plot vertical rectangles (constant w	<pre>connecting them or colored vidth) theight) >>> axes[0,1].arrow(0,0,0.5,0.5) >>> axes[1,1].quiver(y,z) >>> axes[0,1].streamplot(X,Y,U,V) Plot a 2D Plot</pre>		<pre>row to the axes field of arrows field of arrows field of arrows >>> plt.savefig('foo.png') >>> plt.savefig('foo.png', transparent=True)</pre>		ansparent=True)
<pre>>>> axes[1,0].barh([0.5,1,2.5],[0,1,2]) Plot horiontal rectangles (constant >>> axes[1,1].axhline(0.45) Draw a horizontal line across axes</pre>			6) Show Plot		
<pre>>>> axes[0,1].axvline(0.65) >>> ax.fill(x,y,color='blue') Draw a vertical line across axes Draw filled polygons</pre>		>>> ax1.hist(y) Plot a histogram >>> ax3.boxplot(y) Make a box and whisker p	whisker plot >>> plt.show()		
>>> ax.fill_between (x, y, color='yellow') Fill between y-values and o	>>> ax3.violinplot(z) Make a violin plot			Close & Clear	
<pre>>>> fig, ax = plt.subplots() >>> im = ax.imshow(img, cmap='gist earth',</pre> Colormapped or RCB a	rrays	>>> axes2[0].pcolor(data2) Pseudocolor pl >>> axes2[0].pcolormesh(data) Pseudocolor pl	ot of 2D array ot of 2D array	>>> plt.cla() Ch >>> plt.clf() Ch >>> plt.clse() Ch	ear an axis ear the entire figure ose a window
<pre>interpolation='nearest', vmin=-2,</pre>	>>> cs = pic.contour(x,x,U) Plot cont >>> axes2[2].contourf(data1) Plot fillec >>> axes2[2] = ax.clabel(Cs) Labelac		ours r plot	DataCar	np
vmax=2)				Learn Python for Data Scie	nce Interactively





SIMPLE DECISION TREE





Although **regression** models with linear boundaries are intuitive to interpret, it's harder to interpret non-linear decision boundaries.

Trees:

- 1. Allow for complex decision boundaries
- 2. Are easy to interpret



Each comparison and branching represents splitting a region in the feature space on <u>a single feature</u>.

The prediction is based on the most common class

(or mean value).





Considerations

- 1. Splitting Criterion. e.g.,
 - Gini Index
 - misclassification error
 - Entropy
- 2. Stopping Criterion. e.g.,
 - Minimum MSE
 - Uniformity of the data samples' labels
 - Size of tree, such as maximum depth
 - The "gain" converges





Shallow trees have: high bias and low variance

Deep trees have: low bias and high variance

Simple decision trees often:

- Overfit
- Underperform when compared to other classification and regression methods



BAGGING



Bootstrap = generate data via sampling w/ replacement

Aggregating = return the average (regression) or majority class (classification)















Bagging (regression)

The resulting tree is the average of all tree (estimators).





For each bootstrap, we build a decision tree. The results is a combination (majority) of the predictions from all trees.





BENEFITS

- More expressive
- Helps prevent overfitting
- Decreases variance (less sensitive to different data)

ISSUES

• interpretability ("majority")

solution: variable importance via the avg

Gini/MSE for each feature

• can still underfit or overfit

solution: validation via <u>out-of-bag error</u>

• Trees tend to be **highly correlated**

(split the same at the beginning)

solution: random forests



RANDOM FORESTS



Random Forest is a modified form of bagging that creates ensembles of <u>independent</u> decision trees.

To de-correlate the trees, we:

- 1. train each tree on a **separate bootstrap sample** of the full training set (same as in bagging)
- 2. for each tree, at each split, we **randomly** select a set of J' predictors from the full set of predictors.

From amongst the J' predictors, we select the optimal predictor and the optimal corresponding threshold for the split.


SPECIFY

- Number of trees (n_estimators)
- Number of predictors (max_features)

CONSIDERATIONS

- Be careful w/ the # of predictors. If you select a small %, you'll have an ensemble of weak models
- A lot of hyperparameters. Vary all of them together.



BOOSTING



Question: Could we address the shortcomings of single decision trees models in some other way?

For example, rather than performing variance reduction on complex trees, can we decrease the bias of simple trees - make them more expressive?

Can we learn from our mistakes?

A solution to this problem, making an expressive model from simple trees, is another class of ensemble methods called *boosting*.



The key intuition behind boosting is that one can take an ensemble of simple models $\{T_h\}_{h \in H}$ and additively combine them into a single, more complex model.

Each model T_h might be a poor fit for the data, but a linear combination of the ensemble:

$$T = \sum_{h} \lambda_{h} T_{H}$$

can be expressive/flexible.



Gradient boosting is a method for iteratively building a complex regression model T by adding simple models.

Each new simple model added to the ensemble compensates for the weaknesses of the current ensemble.



1. Fit a simple model $T^{(0)}$ on the training data

 $\{(x_1, y_1), \dots, (x_N, y_N)\}$

Set $T \leftarrow T^{(0)}$.

Compute the residuals $\{r_1, \ldots, r_N\}$ for T.

2. Fit a simple model, $T^{(1)}$, to the current **residuals**, i.e. train using

 $\{(x_1, r_1), \dots, (x_N, r_N)\}$

3. Set $T \leftarrow T + \lambda T^{(1)}$

4. Compute residuals, set $r_n \leftarrow r_n - \lambda T^i(x_n)$, n = 1, ..., N

5. Repeat steps 2-4 until **stopping** condition met. where λ is a constant called the **learning rate**.







































THE PROBLEM OF UNFAIR BIAS

ML algorithms exhibit biases, and these biases often seem unfair

Examples:

- Amazon hiring
- PredPol predictive policing
- Skin-cancer detection





HOW DOES BIAS ARISE?





ASK QUESTIONS



- Is a proprietary ML algorithm an ethical solution to the problem? Is this a decision for which the decision procedure should be transparent?
- Is it fair for this outcome to depend on this label?



ASK QUESTIONS



- Is the training dataset representative of the group on which the algorithm will be deployed?
- Do the training data reflect any unfair biases that will be reproduced by the algorithm?
- Is it fair for this outcome to depend on these predictors, given that such biases will be reproduced?



ASK QUESTIONS



- Is the algorithm being deployed in a group that was adequately represented in the training data?
- What do users of the algorithm need to know to use it appropriately?













I DON'T TRUST LINEAR REGRESSIONS WHEN IT'S HARDER TO GUESS THE DIRECTION OF THE CORRELATION FROM THE SCATTER PLOT THAN TO FIND NEW CONSTELLATIONS ON IT.





I finally remember what Zoom meetings remind me of.





GETTINGVALUESFROMPANDAS



If a binary tree wore pants would he wear them





. Pillai

Courses Related to Data Science

- CS 109B: Advanced Topics in Data Science
 - https://harvard-iacs.github.io/2021-CS109B/
- CS 171: Visualizations
- CS 181/281: Machine Learning
- CS 182: Artificial Intelligence (AI)
- CS 205: Distributive Computing
- Stat 110/210: Probability Theory
- Stat 111/211: Statistical Inference
- Stat 139: Linear Models
- Stat 149: Generalized Linear Models
- Stat 195: Statistical Machine Learning

This list is not exhaustive!



<u>Kaggle enterprise executive summary report</u>

Kaggle surveyed its community of data enthusiasts to share trends within a quickly growing field.

Based on responses from 20,036 Kaggle members, they've created a report focused on the 13% (2,675 respondents) who are currently employed as data scientists.



Key findings: Gender

GENDER IDENTITY OF DATA SCIENTISTS





Key findings: Age

AGE RANGES OF DATA SCIENTISTS





Key findings: Nationalities





Key findings: Education





Key findings: Salary



SALARY DISTRIBUTION FOR US-BASED DATA SCIENTISTS



Key findings: Salary by Country







Key findings: Methods and Algorithms







Key findings: ML Frameworks

MACHINE LEARNING FRAMEWORK USAGE





Thank You!

