Spring 2024 Data C100/C200 Final Reference Sheet

Pandas

grouped.agg(f)

Suppose df is a DataFrame; s is a Series. import pandas as pd

Function	Description		
df.shape	Returns a tuple containing the number of rows and columns, in that order		
df.index	Returns the index (row labels) of df as an Index object		
df[col]	Returns the column labeled col from df as a Series		
df[[col1, col2]]	Returns a DataFrame containing the columns labeled col1 and col2		
s.astype(dtype)	Returns a Series casted to the specified type dtype		
s.loc[rows] / df.loc[rows, co	Returns a Series/DataFrame with rows (and columns) selected by their index values		
s.iloc[rows] / df.iloc[rows,	Returns a Series/DataFrame with rows (and columns) selected by their positions		
s.isnull() / df.isnull()	Returns boolean Series/DataFrame identifying missing values		
s.fillna(value) / df.fillna(v	alue) Returns a Series/DataFrame where missing values are replaced by value		
s.isin(values) / df.isin(valu	Returns a Series/DataFrame of booleans indicating if each element is in values.		
df.drop(labels, axis)	Returns a DataFrame without the rows or columns named labels along axis (either 0 or 1)		
df.rename(index=None, columns	=None) Returns a DataFrame with renamed columns from a dictionary index and/or columns		
df.sort_values(by, ascending=	True) Returns a DataFrame where rows are sorted by the values in columns by		
s.sort_values(ascending=True)	Returns a sorted Series		
s.unique()	Returns a NumPy array of the unique values		
s.value_counts()	Returns the number of times each unique value appears in a Series		
pd.merge(left, right, how='in left_on=col1, right_on=col2)	ner', Returns a DataFrame joining left and right on columns labeled col1 and col2; the join is of type inner		
left.merge(right, left_on=col right_on=col2)	1, Returns a DataFrame joining left and right on columns labeled col1 and col2		
df.pivot_table(values=None, index=None, columns=None, aggfunc='mean', fill_value=No	Returns a DataFrame pivot table where columns are unique values from columns (column name or list), and rows are unique values from index (column name or list); cells are collected values using aggfunc. I values is not provided, cells are collected for each remaining column with multi-level column indexing.		
df.set_index(col)	Returns a DataFrame that uses the values in the column labeled col as the row index		
df.reset_index()	Returns a DataFrame that has row index 0, 1, etc., and adds the current index as a column		
et grouped = df.groupby(by)	where by can be a column label or a list of labels		
Function	Description		
grouped.count()	Return a DataFrame containing the size of each group, excluding missing values		
grouped.size()	Return a Series containing size of each group, including missing values		
<pre>grouped.mean()/.min()/.max()</pre>	Return a Series/DataFrame containing mean/min/max of each group for each column, excluding missing values		
<pre>grouped.first()/.last()</pre>	Return a Series/DataFrame containing first/last of each group for each column		
grouped.filter(f)	Filters or aggregates using the given function f		

Function	Description
s.str.len()	Returns a Series containing length of each string (if Series of strings) or list (if Series of lists)
s.str[a:b]	Returns a Series where each element is a slice of the corresponding string indexed from ${\bf a}$ (inclusive, optional) to ${\bf b}$ (non-inclusive, optional)

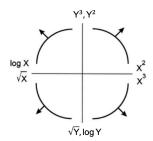
Function	Description		
<pre>s.str.lower()/s.str.upper()</pre>	Returns a Series of lowercase/uppercase versions of each string		
<pre>s.str.replace(pat, repl, regex=False)</pre>	Returns a Series that replaces occurences of substrings matching pat with string repl. When regex=False, pat is treated as a literal string; when regex=True, pat is treated as a RegEx pattern.		
s.str.contains(pat)	Returns a boolean Series indicating if a substring matching the regex pat is contained in each string		
s.str.extract(pat)	Returns a DataFrame of the first subsequence of each string that matches the regex pat. If pat contains one group, then only the substring matching the group is extracted		
s.str.split(pat=" ")	Splits the strings in s at the delimiter pat (defaults to a whitespace). Returns a Series of lists, where each list contains strings of the characters before and after the split.		

Visualization

Matplotlib: x and y are sequences of values. import matplotlib.pyplot as plt

Function	Description
plt.plot(x, y)	Creates a line plot of x against y
<pre>plt.scatter(x, y)</pre>	Creates a scatter plot of x against y
<pre>plt.hist(x, bins=None)</pre>	Creates a histogram of x; bins can be an integer or a sequence
<pre>plt.bar(x, height)</pre>	Creates a bar plot of categories x and corresponding heights height

Tukey-Mosteller Bulge Diagram.



Seaborn: x and y are column names in a DataFrame data. import seaborn as sns

Function	Description
sns.countplot(data=None, x=None)	Create a barplot of value counts of variable x from data
<pre>sns.histplot(data=None, x=None, stat='count', kde=False) sns.displot(data=None, x=None, kind='hist', rug=False)</pre>	Creates a histogram of x from data, where bin statistics stat is one of 'count', 'frequency', 'probability', 'percent', and 'density'; optionally overlay a kernel density estimator. displot is similar but can optionally overlay a rug plot and/or a KDE plot
sns.rugplot(data=None, x=None)	Adds a rug plot on the x-axis of variable x from data
<pre>sns.boxplot(data=None, x=None, y=None) sns.violinplot(data=None, x=None, y=None)</pre>	Create a boxplot of a numeric feature (e.g., y), optionally factoring by a category (e.g., x), from data. violinplot is similar but also draws a kernel density estimator of the numeric feature
sns.scatterplot(data=None, x=None, y=None)	Create a scatterplot of x versus y from data
<pre>sns.lmplot(data=None, x=None, y=None, fit_reg=True)</pre>	Create a scatterplot of ${\bf x}$ versus ${\bf y}$ from data, and by default overlay a least-squares regression line
<pre>sns.jointplot(data=None, x=None, y=None, kind='scatter')</pre>	Combine a bivariate scatterplot of x versus y from data, with univariate density plots of each variable overlaid on the axes; kind determines the visualization type for the distribution plot, can be scatter, kde or hist

Regular Expressions

Operator	Description	Operator	Description
	Matches any character except \n	*	Matches preceding character/group zero or more times
\	Escapes metacharacters	?	Matches preceding character/group zero or one times
1	Matches expression on either side of expression; has lowest priority of any operator	+	Matches preceding character/group one or more times
\d, \w, \s	Predefined character group of digits (0-9), alphanumerics (a-z, A-Z, 0-9, and underscore), or whitespace, respectively	^, \$	Matches the beginning and end of the line, respectively
\D, \W, \S	Inverse sets of \d, \w, \s, respectively	()	Capturing group used to create a sub-expression
{m}	Matches preceding character/group exactly m times	[]	Character class used to match any of the specified characters or range (e.g. [abcde] is equivalent to [a-e])

Operator	Description	Operator	Description
{m, n}	Matches preceding character/group at least m times and a most n times. If either m or n are omitted, set lower/upper bounds to 0 and ∞ , respectively	t [^]	Invert character class; e.g. [^a-c] matches all characters except a, b, c

Modified lecture example for capture groups:

```
lines = '169.237.46.168 - - [26/Jan/2014:10:47:58 -0800] "GET ... HTTP/1.1"'
re.findall(r'\[\d+\/(\w+)\/\d+:\d+:\d+ .+\]', lines) \# returns ['Jan']
```

Function	Description
re.match(pattern, string)	Returns a match if zero or more characters at beginning of string matches pattern, else None
re.search(pattern, string)	Returns a match if zero or more characters anywhere in string matches pattern, else None
re.findall(pattern, string)	Returns a list of all non-overlapping matches of pattern in string (if none, returns empty list)
re.sub(pattern, repl, string)	Returns string after replacing all occurrences of pattern with repl

Modeling

Concept	Formula	Concept	Formula
Variance, σ_x^2	$\frac{1}{n}\sum_{i=1}^n(x_i-\bar{x})^2$	Correlation ${\it r}$	$r = rac{1}{n} \sum_{i=1}^n rac{x_i - ar{x}}{\sigma_x} rac{y_i - ar{y}}{\sigma_y}$
L_1 loss	$L_1(y,\hat{y}) = \mid y - \hat{y} \mid$	Linear regression estimate $ \text{ of } y$	$\hat{y} = \theta_0 + \theta_1 x$
L_2 loss	$L_2(y,\hat{y}) = (y-\hat{y})^2$	Least squares linear regression	$\hat{ heta}_0 = ar{y} - \hat{ heta}_1 ar{x} \qquad \hat{ heta}_1 = r rac{\sigma_y}{\sigma_x}$

$$R(heta) = rac{1}{n} \sum_{i=1}^n L(y_i, \hat{y_i})$$

Ordinary Least Squares

Multiple Linear Regression Model: $\hat{\mathbb{Y}} = \mathbb{X}\theta$ with design matrix \mathbb{X} , response vector \mathbb{Y} , and predicted vector $\hat{\mathbb{Y}}$. If there are p features plus a bias/intercept, then the vector of parameters $\theta = [\theta_0, \theta_1, \dots, \theta_p]^T \in \mathbb{R}^{p+1}$. The vector of estimates $\hat{\theta}$ is obtained from fitting the model to the sample (X, Y).

Concept	Formula	Concept	Formula
Mean squared error	$R(heta) = rac{1}{n} \mathbb{Y} - \mathbb{X} heta _2^2$	Normal equation	$\mathbb{X}^T\mathbb{X}\hat{\theta} = \mathbb{X}^T\mathbb{Y}$
Least squares estimate, if $\mathbb X$ is full rank	$\hat{\theta} = (\mathbb{X}^T \mathbb{X})^{-1} \mathbb{X}^T \mathbb{Y}$	Residual vector, e	$e=\mathbb{Y}-\hat{\mathbb{Y}}$
		$\begin{array}{l} \mbox{Multiple } R^2 \\ \mbox{(coefficient of } \\ \mbox{determination)} \end{array}$	$R^2 = rac{ ext{variance of fitted values}}{ ext{variance of }y}$
Ridge Regression L2 Regularization	$rac{1}{n} \mathbb{Y}-\mathbb{X} heta _2^2+lpha heta _2^2$	Squared L2 Norm of $ heta \in \mathbb{R}^d$	$ heta _2^2 = \sum_{j=1}^d heta_j^2$
Ridge regression estimate (closed form)	$\hat{ heta}_{ ext{ridge}} = (\mathbb{X}^T \mathbb{X} + n lpha I)^{-1} \mathbb{X}^T \mathbb{Y}$		
LASSO Regression L1 Regularization	$rac{1}{n} \mathbb{Y}-\mathbb{X} heta _2^2+lpha heta _1$	L1 Norm of $ heta \in \mathbb{R}^d$	$ heta _1 = \sum_{j=1}^d heta_j $

Scikit-Learn

Package:	sk1	Learn.	linear	model
Package:	SKI	Learn.	Linear	moaeı

Linear Regression	Logistic Regression	Function(s)	Description
✓	-	LinearRegression(fit_intercept=True)	Returns an ordinary least squares Linear Regression model.
-	✓	LogisticRegression(fit_intercept=True, penalty='12', C=1.0)	Returns an ordinary least squares Linear Regression model. Hyperparameter C is inverse of regularization parameter, $C = 1/\lambda$.
✓	-	LassoCV(), RidgeCV()	Returns a Lasso (L1 Regularization) or Ridge (L2 regularization) linear model, respectively, and picks the best model by cross validation.
✓	✓	model.fit(X, y)	Fits the scikit-learn model to the provided X and y.
✓	✓	model.predict(X)	Returns predictions for the X passed in according to the fitted model.
✓	✓	model.predict_proba(X)	Returns predicted probabilities for the X passed in according to the fitted model. If binary classes, will return probabilities for both class 0 and 1.
✓	✓	model.coef_	Estimated coefficients for the linear model, not including the intercept term.
✓	✓	model.intercept_	Bias/intercept term of the linear model. Set to 0.0 if fit_intercept=False.
Package: sk	learn.model	_selection	
		Function	Description

<pre>train_test_split(*arrays,</pre>	test_size=0.2)	Returns two random subsets of each array passed in, with 0.8 of the array
		in the first subset and 0.2 in the second subset.

Probability

Let X have a discrete probability distribution P(X=x). X has expectation $\mathbb{E}[X] = \sum_x x P(X=x)$ over all possible values x, variance $\mathrm{Var}(X) = \mathbb{E}[(X - \mathbb{E}[X])^2]$, and standard deviation $\mathrm{SD}(X) = \sqrt{\mathrm{Var}(X)}$.

Notes	Property of Expectation	Property of Variance
\boldsymbol{X} is a random variable.	$\mathbb{E}[X] = \sum_x x P(X=x)$	$\operatorname{Var}(X) = \mathbb{E}[(X - \mathbb{E}[X])^2] = E[X^2] - (E[X])^2$
X is a random variable, $a,b\in\mathbb{R}$ are scalars.	$\mathbb{E}[aX+b] = a\mathbb{E}[X] + b$	$\mathrm{Var}(aX+b)=a^2\mathrm{Var}(X)$
X,Y are random variables.	$\mathbb{E}[X+Y] = \mathbb{E}[X] + \mathbb{E}[Y]$	$\operatorname{Var}(X+Y) = \operatorname{Var}(X) + \operatorname{Var}(Y) + 2\operatorname{Cov}(X,Y)$
X is a Bernoulli random variable that takes on value 1 with probability p and 0 otherwise.	$\mathbb{E}[X] = p$	$\mathrm{Var}(X) = p(1-p)$

Parameter Estimation and Gradient Descent

Parameter Estimation

Suppose for each individual with fixed input x, we observe a random response $Y = g(x) + \epsilon$, where g is the true relationship and ϵ is random noise with zero mean and variance σ^2 .

For a new individual with fixed input x, define our random prediction $\hat{Y}(x)$ based on a model fit to our observed sample (\mathbb{X},\mathbb{Y}) . The model risk is the mean squared prediction error between Y and $\hat{Y}(x)$: $\mathbb{E}[(Y-\hat{Y}(x))^2] = \sigma^2 + \left(\mathbb{E}[\hat{Y}(x)] - g(x)\right)^2 + \mathrm{Var}(\hat{Y}(x))$.

Suppose that input x has p features and the true relationship g is linear with parameter $\theta \in \mathbb{R}^{p+1}$. Then $Y = f_{\theta}(x) = \theta_0 + \sum_{j=1}^p \theta_j x_j + \epsilon$ and $\hat{Y} = f_{\hat{\theta}}(x)$ for an estimate $\hat{\theta}$ fit to the observed sample (\mathbb{X}, \mathbb{Y}) .

Gradient Descent

Let $L(\theta, \mathbb{X}, \mathbb{Y})$ be an objective function to minimize over θ , with some optimal $\hat{\theta}$. Suppose $\theta^{(0)}$ is some starting estimate at t=0, and $\theta^{(t)}$ is the estimate at step t. Then for a learning rate α , the gradient update step to compute $\theta^{(t+1)}$ is

$$\theta^{(t+1)} = \theta^{(t)} - \alpha \nabla_{\theta} L(\theta^{(t)}, \mathbb{X}, \mathbb{Y})$$

where $\nabla_{\theta}L(\theta^{(t)}, \mathbb{X}, \mathbb{Y})$ is the partial derivative/gradient of L with respect to θ , evaluated at $\theta^{(t)}$.

SQL

SQL syntax:

```
SELECT [DISTINCT]
    {* | expr [[AS] c_alias]
        {,expr [[AS] c_alias] ...}}
FROM tableref {, tableref}
[[INNER | LEFT ] JOIN table_name
        ON qualification_list]
[WHERE search_condition]
[GROUP BY colname {,colname...}]
[HAVING search_condition]
[ORDER BY column_list]
[LIMIT number]
[OFFSET number of rows];
```

Syntax	Description
SELECT column_expression_list	List is comma-separated. Column expressions may include aggregation functions (MAX, FIRST, COUNT, AVG, etc). AS renames columns. DISTINCT selects only unique rows.
FROM s INNER JOIN t ON cond	Inner join tables s and t using cond to filter rows; the INNER keyword is optional.
FROM s LEFT JOIN t ON cond	Left outer join of tables s and t using cond to filter rows.
FROM s, t	Cross join of tables s and t: all pairs of a row from s and a row from t
WHERE a IN cons_list	Select rows for which the value in column a is among the values in a cons_list.
ORDER BY RANDOM LIMIT n	Draw a simple random sample of n rows.
ORDER BY a, b DESC	Order by column ${\bf a}$ (ascending by default) , then ${\bf b}$ (descending).
CASE WHEN pred THEN cons ELSE alt END	Evaluates to cons if pred is true and alt otherwise. Multiple WHEN/THEN pairs can be included, and ELSE is optional.
WHERE s.a LIKE 'p'	Matches each entry in the column ${\sf a}$ of table ${\sf s}$ to the text pattern ${\sf p}$. The wildcard ${\sf \$}$ matches at least zero characters.
LIMIT number	Keep only the first number rows in the return result.
OFFSET number	Skip the first number rows in the return result.

Principal Component Analysis (PCA)

The i-th Principal Component of the matrix X is defined as the i-th column of V defined by Singular Value Decomposition (SVD).

 $X = USV^T$ is the SVD of X if U and V^T are matrices with orthonormal columns and S is a diagonal matrix. The diagonal entries of S, $[s_1, \ldots, s_r, 0, \ldots, 0]$, are known as singular values of X, where $s_i > s_j$ for i < j and $r = \operatorname{rank}(X)$.

Define the design matrix $X \in \mathbb{R}^{n \times p}$. Define the total variance of X as the sum of individual variances of the p features. The amount of variance captured by the i-th principal component is equivalent to s_i^2/n , where n is the number of datapoints.

Syntax	Description

np.linalg.svd(X, full_matrices = True)

SVD of X with shape (M, N) that returns u, s, vt, where s is a 1D array of X's singular values. If full_matrices=True, u and vt have shapes (M, M) and (N, N) respectively; otherwise shapes are (M, K) and (K, N), respectively, where $K = \min(M, N)$.

Classification and Logistic Regression

Confusion Matrix

Columns are the predicted values \hat{y} and rows are the actual classes y.

	$\hat{y} = 0$	$\hat{y}=1$
y = 0	True negative (TN)	False Positive (FP)
y = 1	False negative (FN)	True Positive (TP)

Classification Performance

Suppose you predict n datapoints.

Metric	Formula	Other Names
Accuracy	$^{\frac{TP+TN}{n}}$	
Precision	$\frac{TP}{TP+FP}$	
Recall/TPR	$\frac{TP}{TP+FN}$	True Positive Rate, Sensitivity
FPR	$\frac{FP}{FP+TN}$	False Positive Rate, Specificity

An ROC curve visualizes TPR vs. FPR for different thresholds T.

Logistic Regression Model: For input feature vector x, $\hat{P}_{\theta}(Y=1|x) = \sigma(x^T\theta)$, where $\sigma(z) = 1/(1+e^{-z})$. The estimate $\hat{\theta}$ is the parameter θ that minimizes the average cross-entropy loss on training data. For a single datapoint, define cross-entropy loss as $-[y\log(p)+(1-y)\log(1-p)]$, where p is the probability that the response is 1.

Logistic Regression Classifier: For a given input x and trained logistic regression model with parameter θ , compute $p = \hat{P}(Y = 1|x) = \sigma(x^T\theta)$. Predict response \hat{y} with classification threshold T as follows:

$$\hat{y} = \operatorname{classify}(x) = egin{cases} 1 & p \geq T \\ 0 & \operatorname{otherwise} \end{cases}$$

Clustering

K-Means Clustering: Pick an arbitrary k, and randomly place k "centers", each a different color. Then repeat until convergence:

- 1. Color points according to the closest center (defined as squared distance).
- 2. Move center for each color to center of points with that color.

To evaluate a K-Means clustering, we minimize a loss function. Two common ones are:

- Inertia: the sum of squared distances from each datapoint to its center. It is defined as $\sum_{i=1}^{N} (x_i C_k)^2$, where N is the total number of datapoints, x_i represents datapoint i, and C_k is x_i 's closest center.
- **Distortion**: the weighted sum of squared distances from each data point to its center. It is defined as $\sum_{k=1}^K \frac{1}{n} \sum_{i=1}^n (x_{k,i} C_k)^2$, where K represents the total number of clusters. For each cluster k, we sum the squared distances from each datapoint $x_{k,i}$ to it's center C_k and divide it by the total number of datapoints in that cluster, denoted as n. We add up these weighted sums to obtain the final value.

Agglomerative Clustering: Assign each datapoint to its own cluster. Then, recursively merge pairs of clusters together until there are k clusters remaining.

A datapoint's **silhouette score** S is defined as $S = (B - A)/\max(A, B)$, where A is the mean distance to other points in its cluster, and B is the mean distance to points in its closest cluster.