Summer 2023 Data C100 Final Reference Sheet

Pandas

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

Function	Description
`pd.read_csv(filepath, delimiter)`	Loads the data file at `filepath` into a DataFrame with column fields separated by `delimiter` (`','`, `'\t'`)
`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.loc[rows] / df.loc[rows, cols]`	Returns a Series/DataFrame with rows (and columns) selected by their index values.
`s.iloc[rows] / df.iloc[rows, cols]`	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(value)`	Returns a Series/DataFrame where missing values are replaced by `value`
`s.isin(values) / df.isin(values)`	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, sorted in descending order of count.
`pd.merge(left, right, how='inner', on='a')`	Returns a DataFrame joining `left` and `right` on the column labeled `a`; the join is of type `inner`
`left.merge(right, left_on=col1, right_on=col2)`	Returns a DataFrame joining `left` and `right` on columns labeled `col1` and `col2`.
`df.pivot_table(index, columns, values=None, aggfunc='mean')`	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`. If `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.
`df.sample(n=1, replace=False)`	Returns `n` randomly sampled rows from `df`. By default, sampling is performed without replacement.

Let `grouped = df.groupby(by)` where `by` can be a column label or a list of labels.

Function	Description
`grouped.count()`	Return a Series containing the size of each group, excluding missing values
`grouped.size()`	Return a Series containing size of each group, including missing values
`grouped.mean()/.min()/.max()`	Return a Series/DataFrame containing mean/min/max of each group for each column, excluding missing values
`grouped.filter(f)` `grouped.agg(f)`	Filters or aggregates using the given function `f`

Text Wrangling and Regular Expressions

Pandas `str` methods

Function	Description
`s.str.len()`	Returns a Series containing length of each string
`s.str[a:b]`	Returns a Series where each element is a slice of the corresponding string indexed from `a` (inclusive, optional) to `b` (non-inclusive, optional)
`s.str.lower()`/`s.str.upper()`	Returns a Series of lowercase/uppercase versions of each string
`s.str.replace(pat, repl)`	Returns a Series that replaces occurences of substrings matching the regex `pat` with string `repl`
`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 Series of the first subsequence of each string that matches the regex `pat`. If `pat` contains capturing group(s), outputs a DataFrame with one column for each group.
`s.str.split(pat)`	Splits the strings in `s` at the delimiter `pat`. Returns a Series of lists, where each list contains strings of the characters before and after the split.

Regex patterns

Operator	Description	Operator	Description
`.`	Matches any character except `\n`	`*`	Matches preceding character/group zero or more times
`\`	Escapes metacharacters	`+`	Matches preceding character/group one or more times
`|`	Matches expression on either side of expression; has lowest priority of any operator	`^`	Matches the beginning of the string
`\d`, `\w`, `\s`	Predefined character group of digits (0-9), alphanumerics (a-z, A-Z, 0-9, and underscore), or whitespace, respectively	`$`	Matches the end of the string
`\D`, `\W`, `\S`	Inverse sets of `\d`, `\w`, `\s`, respectively	`( )`	Capturing group or 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]`)
`{m, n}`	Matches preceding character/group at least `m` times and at most `n` times. If either `m` or `n` are omitted, set lower/upper bounds to 0 and ∞, respectively	`[^ ]`	Invert character class; e.g. `[^a-c]` matches all characters except `a`, `b`, `c`

Python `re` methods

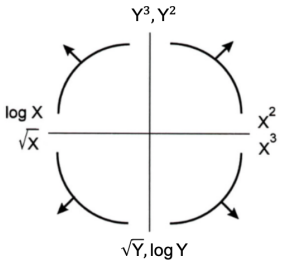
Function	Description
`re.match(pattern, string)`	Returns all matching characters if zero or more characters at beginning of `string` matches `pattern`, else None
`re.search(pattern, string)`	Returns all matching characters if zero or more characters anywhere in `string` matches `pattern`, else None
`re.findall(pattern,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

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
`plt.scatter(x, y)`	Creates a scatter plot of x against y
`plt.hist(x, bins=None)`	Creates a histogram of x; `bins` can be an integer or a sequence
`plt.bar(x, height)`	Creates a bar plot of categories x and corresponding heights `height`

Tukey-Mosteller Bulge Diagram.



Seaborn: x and y are keyword arguments assigned to string 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`
`sns.histplot(data=None, x=None, stat='count', kde=False)` `sns.displot(data=None, x=None, stat='count', rug=False, kde=True)`	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.
`sns.boxplot(data=None, x=None, y=None)` `sns.violinplot(data=None, x=None, y=None)`	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`
`sns.lmplot(data=None, x=None, y=None, fit_reg=True)`	Create a scatterplot of x versus y from `data`, and by default overlay a least-squares regression line
`sns.jointplot(data=None, x=None, y=None, kind)`	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`
`sns.kdeplot(data=None, x=None)`	Create a kernel density estimate (KDE) of the distribution of x from `data`

Modeling

Concept	Formula	Concept	Formula
Variance, σ_x^2	$\frac{1}{n}\sum_{i=1}^{n}(x_i-\bar{x})^2$	Correlation r	$r=\frac{1}{n}\sum_{i=1}^{n}\frac{x_i-\bar{x}}{\sigma_x}\frac{y_i-\bar{y}}{\sigma_y}$
L_1 loss	$L_1(y,\hat{y})=\mid y-\hat{y}\mid$	Linear regression estimate 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	$\hat{\theta}_0=\bar{y}-\hat{\theta}_1\bar{x}$ $\quad$ $\hat{\theta}_1=r\frac{\sigma_y}{\sigma_x}$
Empirical risk with loss L	$R(\theta)=\frac{1}{n}\sum_{i=1}^{n}L(y_i,\hat{y}_i)$		

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 $\theta = [\theta_0, \theta_1, \ldots, \theta_p]^T \in \mathbb{R}^{p+1}$. The vector of estimates $\hat{\theta}$ is obtained from fitting the model to the sample $(\mathbb{X}, \mathbb{Y})$.

Concept	Formula	Concept	Formula
Mean squared error	$R(\theta) = \frac{1}{n}\|\|\mathbb{Y} - \mathbb{X}\theta\|\|_2^2$	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	$e = \mathbb{Y} - \hat{\mathbb{Y}}$
		Multiple R^2 (coefficient of determination)	$R^2 = \frac{\text{variance of fitted values}}{\text{variance of } y}$

Regularization

Concept	Formula	Concept	Formula
Ridge Regression L2 Regularization	$\frac{1}{n}\|\|\mathbb{Y} - \mathbb{X}\theta\|\|_2^2 + \lambda\|\|\theta\|\|_2^2$	Squared L2 Norm of $\theta \in \mathbb{R}^p$	$\|\|\theta\|\|_2^2 = \sum_{j=1}^p \theta_j^2$
Ridge regression estimate (closed form)	$\hat{\theta}_{\text{ridge}} = (\mathbb{X}^T\mathbb{X} + n\lambda I)^{-1}\mathbb{X}^T\mathbb{Y}$		
LASSO Regression L1 Regularization	$\frac{1}{n}\|\|\mathbb{Y} - \mathbb{X}\theta\|\|_2^2 + \lambda\|\|\theta\|\|_1$	L1 Norm of $\theta \in \mathbb{R}^p$	$\|\|\theta\|\|_1 = \sum_{j=1}^p \|\theta_j\|$

Gradient Descent

Let L be an objective function to minimize with respect to θ; assume that some optimal parameter vector $\hat{\theta}$ exists. 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:

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

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

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:

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

Scikit-Learn

Package: `sklearn.linear_model`

Linear Regression	Logistic Regression	Class/Function(s)	Description
✓	-	`LinearRegression(fit_intercept=True)`	Returns an ordinary least squares Linear Regression model.
-	✓	`LogisticRegression( fit_intercept=True, penalty='l2', C=1.0)`	Returns an ordinary least squares Linear Regression model. Hyperparameter C is inverse of regularization parameter, C = 1/λ.
✓	-	`Lasso()`, `Ridge()`	Returns a Lasso (L1 Regularization) or Ridge (L2 regularization) linear model, respectively.
✓	✓	`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 `X` passed in according to the fitted `model`. If binary classes, returns probabilities for both classes 0 and 1.
✓	✓	`model.coef_`	Estimated coefficients for the linear model, not including the intercept.
✓	✓	`model.intercept_`	Bias/intercept term of the linear model. Set to 0.0 if `fit_intercept=False`.

Package: `sklearn.model_selection`

Function	Description
`train_test_split(*arrays, 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 $\mathbb{E}[X] = \sum_x xP(X = x)$ over all possible values x, variance $\text{Var}(X) = \mathbb{E}[(X - \mathbb{E}[X])^2]$, and standard deviation $\text{SD}(X) = \sqrt{\text{Var}(X)}$.

The covariance of two random variables X and Y is $\mathbb{E}[(X - \mathbb{E}[X])(Y - \mathbb{E}[Y])]$. If X and Y are independent, then $\text{Cov}(X, Y) = 0$.

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

Central Limit Theorem

Let $(X_1, \ldots, X_n)$ be a sample of independent and identically distributed random variables drawn from a population with mean μ and standard deviation σ. The sample mean $\overline{X}_n = \sum_{i=1}^{n} X_i$ is normally distributed, where $\mathbb{E}[\overline{X}_n] = \mu$ and $\text{SD}(\overline{X}_n) = \sigma/\sqrt{n}$.

Model Risk

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 $\hat{Y}(x)$: $\mathbb{E}[(Y - \hat{Y}(x))^2] = \sigma^2 + \left(\mathbb{E}[\hat{Y}(x)] - g(x)\right)^2 + \text{Var}(\hat{Y}(x))$.

SQL

```
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`, `SUM`, `COUNT`, `AVG`, etc). `AS` renames columns. `DISTINCT` selects only unique rows.

`WHERE a IN cons_list`
`WHERE a IS NOT val`
`WHERE a LIKE 'p'`
	• Select rows for which the value in column `a` is among the values in a `cons_list`.
	• Selects rows for which the value in column `a` is not equal to `val` (of any data type).
	• Matches each entry in the column `a` to the text pattern `p`. The wildcard `%` matches at least zero characters. `_` matches exactly one character.

`ORDER BY RANDOM() LIMIT n`	Draw a simple random sample of `n` rows.
`ORDER BY a, b DESC`	Order by column `a` (ascending by default) , then `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.
`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 $U\Sigma$ defined by Singular Value Decomposition (SVD).

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

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)`.

Decision Trees

Suppose you have a **decision tree** classifier for k classes. For each node, define the probability for class $C \in \{1, \ldots, k\}$ as $p_C = d_C/d$, where d_C is the number of datapoints in class C (of the total d in the node). The entropy of the node (in bits) is defined as $S = -\sum_C p_C \log_2 p_C$, and the weighted entropy of the split is the average entropy of child nodes weighted by the number of datapoints in each.
Decision tree generation algorithm: all of the data starts in the root node. Repeat until every node is either pure or unsplittable.

- Pick the best feature x and best split value β to maximize the change in weighted entropy.
- Split data into two nodes, one where $x < \beta$, and one where $x \geq \beta$

A node that only has samples from one class is called a "pure" node. A node that has overlapping datapoints from different classes and thus cannot be split is called "unsplittable."

A **random forest** is a collection of many decision trees fit to variations of the same training data (e.g. bootstrapped samples, also called bagging). It is an ensemble method.