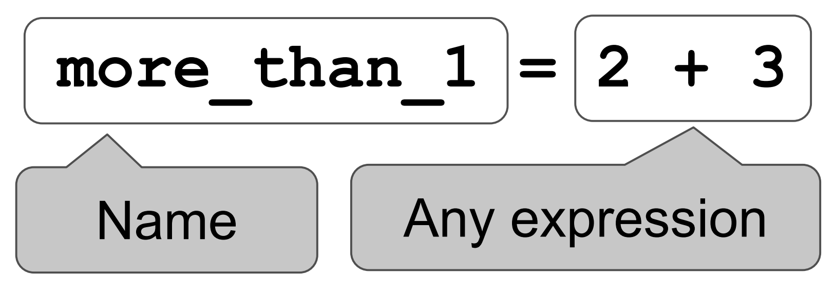
MATH 108 Final Reference Guide

Statements



- Statements don't have a value; they perform an action
- An assignment statement changes the meaning of the name to the left of the = symbol
- The name is bound to a value (not an equation).

Comparisons

- < and > mean what you expect (less than, greater than)
- <= means "less than or equal"; likewise for >=
- == means "equal"; != means "not equal"
- Comparing strings compares their alphabetical order

Arrays - sequences of the same type that can be manipulated
- Arithmetic and comparisons are applied to each element of an array individually
  - `make_array(1,2,3) ** 2 # array([1, 4, 9])`
- Elementwise operations can be done on arrays of the same size
  - `make_array(3,2) * make_array(5,4) # array([15,8])`

Defining a Function

```
def function_name(arg1, arg2, ...):
    # Body can contain anything inside of it
    return # a value (the output of the function call)
```

Defining a Function with no arguments

```
def function_name():
    # Body can contain anything inside of it
    return # a value (the output of the function call)
```

- Functions with no arguments can be called by `function_name()`

For Statements

```
total = 0
for i in np.arange(12):
    total = total + i
```

- The body is executed **for** every item in a sequence
- The body of the statement can have multiple lines
- The body should do something: assign, sample, print, etc.

Conditional Statements

```
if <if expression>:
    <if body>
elif <elif expression 0>:
    <elif body 0>
elif <elif expression 1>:
    <elif body 1>
...
else:
    <else body>
```

Total Variation Distance

Total variation distance is a statistic that represents the difference between two distributions

```
TVD = 0.5*(np.sum(np.abs(dist1-dist2)))
```

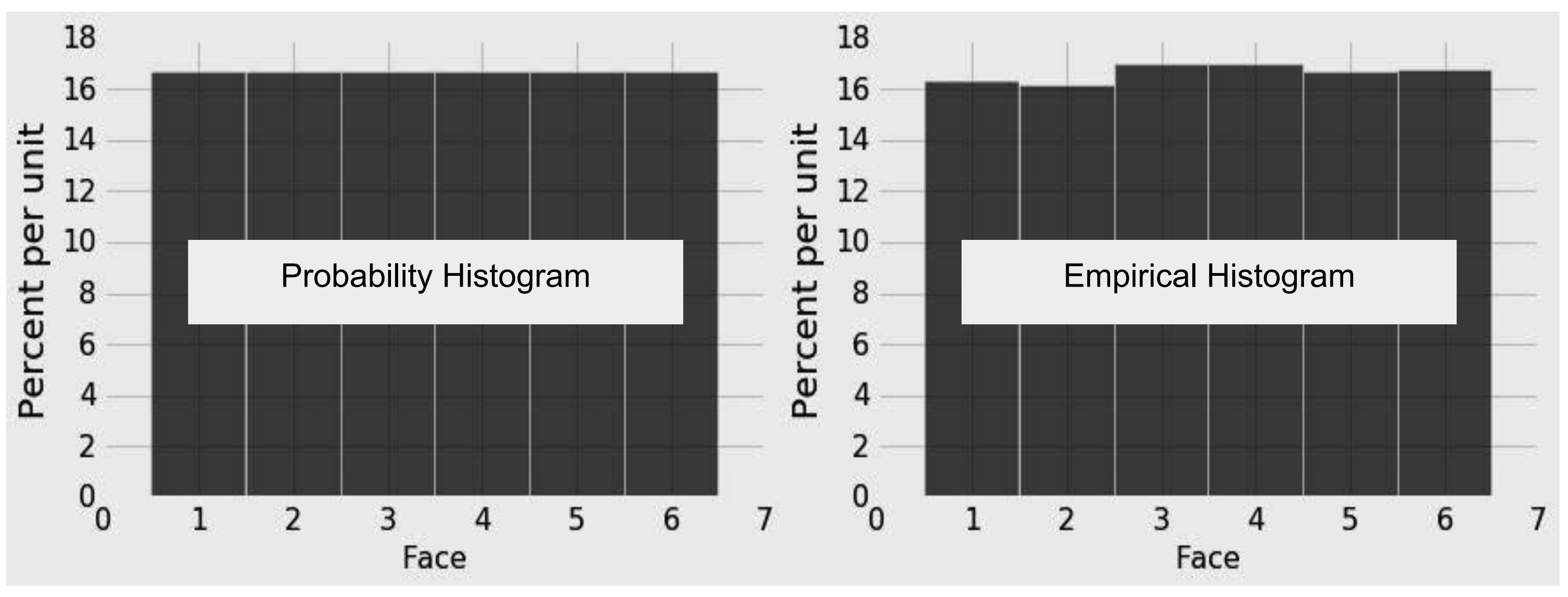
Operations: addition `2+3=5`; subtraction `4-2=2`; division `9/2=4.5` multiplication `2*3=6`; division remainder `11%3=2`; exponentiation `2**3=8`

Data Types: string `"hello"`; **boolean** `True, False`; **int** `1, -5`; **float** `- 2.3, -52.52, 7.9, 8.0`

`Table.where` predicates: Any of these predicates can be negated by adding "not_" in front of them, e.g. `are.not_equal_to(x)`
- `are.equal_to(x) # val == x`
- `are.above(x) # val > x`
- `are.above_or_equal_to(x) # val >= x`
- `are.below(x) # val < x`
- `are.between(x, y) # x <= val < y`
- `are.containing(s) # contains the string s`

A **histogram** has a few defining properties:
- The bins are continuous (though some might be empty) and are drawn to scale
- The **area** of each bar is equal to the percent of entries in the bin
- The total area is 100%

- The histogram on the left represents the theoretical probabilities in the distribution of the face that appears on one roll of a fair die
- The histogram on the right represents the observed distribution of the faces after rolling the die many times
- If we keep rolling, the right hand histogram is likely to look more like the one on the left



Calculating Probabilities

Complement Rule: P(event does not happen) = 1 - P(event happens)

Multiplication Rule: P(two events both happen) =
P(one happens) * P(the other happens, given that the first happened)

Addition Rule: If an event can happen in ONLY one of two ways:
P(event happens) =
P(first way it can happen) + P(second way it can happen)

Bayes' Rule: P(event A happened given event B happened) =
P(both event A and event B happened) / P(event B happened)

For Bayes' rule, if the probabilities are displayed on a tree diagram, the denominator is the chance of the branches in which B happens, and the numerator is the chance of the branches in which both A and B happen.

Simulating a Statistic:

- Create an empty array in which to collect the simulated values
- For each repetition of the process
  - Simulate one value of the statistic
  - Append this value to the collection array
- At the end, all simulated values will be in the collection array

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- **P-Value**: The chance, **under the null hypothesis**, that the test statistic comes out equal to the one in the sample, or more in the direction of the alternative:
  - If the p-value is small and the null is true, something very unlikely has happened.
  - Conclude that the data support the alternative hypothesis more than they support the null.

- Even if the null is true, your random sample might indicate the alternative, just by chance
- The **cutoff** for P is the chance that your test makes the wrong conclusion when the null hypothesis is true
- Using a small cutoff limits the probability of this kind of error

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A/B test for comparing two samples
- **Example**: Among babies born at some hospital, is there an association between birth weight and whether the mother smokes?
- **Null hypothesis**: The distribution of birth weights is the same for babies with smoking mothers and non-smoking mothers.
- **Inferential Idea:** If maternal smoking and birth weight were not associated, then we could simulate new samples by replacing each baby's birth weight by a randomly picked value from among all the birth weights.
- **Simulating the test statistic under the null:**
  - Permute (shuffle) the outcome column many times. Each time:
    - Create a shuffled table that pairs each individual with a random outcome.
    - Compute a sampled test statistic that compares the two groups, such as the difference in mean birth weights.

The 80th percentile is the value in a set that is at least as large as 80% of the elements in the set

For `s = [1, 7, 3, 9, 5]`, `percentile(80, s)` is 7

The 80th percentile is ordered element 4: `(80/100) * 5`

For a percentile that does not exactly correspond to an element, take the next greater element instead

`percentile(10, s)` is 1 `percentile(20, s)` is 1
`percentile(21, s)` is 3 `percentile(40, s)` is 3

- `minimize` must take in a function whose arguments are numerical, and returns an array of those numerical arguments
- If the function `rmse(a, b)` returns the root mean squared error of estimation using the line "estimate = $ax + b$",
  - then `minimize(rmse)` returns array [a_0, b_0]
  - a_0 is the slope and b_0 the intercept of the line that minimizes the rmse among lines with arbitrary slope a and arbitrary intercept b (that is, among all lines)

Population (fixed) → Sample (random) → Statistic (random)

A 95% **Confidence Interval** is an interval constructed so that it will contain the true population parameter for approximately 95% of samples

For a particular sample, the generated interval either contains the true parameter or it doesn't; the process works 95% of the time

Bootstrap: When we wish we could sample again from the population, instead sample from the *original large random sample the same number of times as there are data-points in the sample*

Using a confidence interval to test a hypothesis about a numerical parameter:
- Null hypothesis: **Population parameter = *x***
- Alternative hypothesis: **Population parameter ≠ *x***
- Cutoff for P-value: *p*%
- Method:
  - Construct a (100-*p*)% confidence interval for the population parameter
  - If *x* is not in the interval, reject the null
  - If *x* is in the interval, fail to reject the null

The Central Limit Theorem (CLT)

If the sample is large, and drawn at random with replacement,

Then, *regardless of the distribution of the population,*

the probability distribution of the sample average (or sample sum) is roughly bell-shaped
- Fix a large sample size
- Draw all possible random samples of that size
- Compute the mean of each sample
- You'll end up with a lot of means
- The distribution of those is the *probability distribution of the sample mean*
- It's roughly normal, centered at the population mean
- The SD of this distribution is the (population SD) /√sample size

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Choosing sample size so that the 95% confidence interval is small
- CLT says the distribution of a sample proportion is roughly normal, centered at the true population proportion
- **95% confidence interval:**
  - Sample proportion ± 2 SDs of the sample proportion
- **CI Width** = 4 SDs of the sample proportion

  = 4 x (SD of 0/1 population)/√sample size
- The SD of a 0/1 population is less than or equal to 0.5

Expression	Description
`percentile(n, arr)`	Returns the n-th percentile of array `arr`
`np.std(arr)`	Return the standard deviation of an array `arr` of numbers
`minimize(fn)`	Return an array of arguments that minimize the function `fn`
`tbl1.append(tbl2)` `tbl1.append(row)`	Append a row or all rows of `tbl2`, mutating `tbl1`. Appended object and `tbl1` must have identical columns.
`table.rows`	All rows of a table; used in `for row in table.rows:`
`table.row(i)`	Return the row of a table at index *i*
`row.item(j)`	Returns item `j` from some row

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Mean (or average): Balance point of the histogram

Standard deviation (SD) =

root	mean	square of	deviations from	average
5	4	3	2	1

Measures roughly how far off the values are from average

Most values are within the range "average ± *z* SDs"

- *z* measures "how many SDs above average"
- If *z* is negative, the value is below average
- *z* is a value in **standard units**
- Chebyshev: At most $1/z^2$ are z or more SDs from the mean
- Almost all standard unit values are in the range (-5, 5)
- Convert a value to standard units: (value - average) / SD
- *z* * SD + average is the original value

Percent in Range	All Distributions	Normal Distribution
average ± 1 SD	at least 0%	about 68%
average ± 2 SDs	at least 75%	about 95%
average ± 3 SDs	at least 88.888...%	about 99.73%

Correlation Coefficient (*r*) =

average of	product of	x in standard units	and	y in standard units

Measures how clustered the scatter is around a straight line

- $-1 \le r \le 1$; r = 1 (or -1) if the scatter is a perfect straight line
- *r* is a pure number, with no units

Regression for y and x in standard units: $y_{predicted,su} = r * x_{su}$

The regression line minimizes the root mean square error among all lines used to predict y from x.
The slope and intercept found by linear regression are unique.
Fitted value: height of the regression line at some x: a*x + b
Residual: difference between y and regression line height at x

$$y_{predicted} = slope * x + intercept$$

$$\text{slope of the regression line} = r \cdot \frac{\text{SD of } y}{\text{SD of } x}$$

$$\text{intercept of the regression line} = \text{mean of } y - \text{slope} * \text{mean of } x$$

Properties of fitted values, residuals, and the correlation r:

- mean of fitted values = mean of y
- SD of fitted values = |r| * (SD of y)
- mean of residuals = 0
- SD of residuals = $\sqrt{1 - r^2}$ * (SD of y)

The following functions were defined in lecture, but will **not** be available for use during the final exam. If you would like to use one of the functions, you must define it yourself.

- `standard_units`
- `correlation`
- `slope`
- `intercept`
- `fitted_values`
- `residuals`
- `prediction_at`

- **Regression Model**: y is a linear function of x + normal "noise"
- The errors are randomly sampled from a normal distribution that has mean 0
- Under this model, residual plot looks like a formless cloud

Prediction Intervals (assuming the regression model)

- Creating an interval of predictions of the true value of *y* based on a specified value of *x*
- Steps for creating an approximate 95% prediction interval:
  - Bootstrap your original sample
  - Calculate the slope and intercept of the regression line based on the new sample
  - Calculate slope * x + intercept, for the given *x*
  - Repeat the above steps many times and keep track of all of your fitted values
  - Create the prediction interval by taking the middle 95% of all the fitted values

Distance between two points

- Two numerical attributes *x* and *y*: $D = \sqrt{(x_0 - x_1)^2 + (y_0 - y_1)^2}$.
- Three numerical attributes *x, y,* and *z:*

$$D = \sqrt{(x_0 - x_1)^2 + (y_0 - y_1)^2 + (z_0 - z_1)^2}$$

***k*-Nearest Neighbors Classifier**

Choose *k* to be odd. To find the *k* nearest neighbors of an example:

- Find the distance between the example and each example in the training set
- Augment the training data table with a column containing all the distances
- Sort the augmented table in increasing order of the distances
- Take the top *k* rows of the sorted table

To classify an example into one of two classes:

- Find its *k* nearest neighbors
- Take a majority vote of the *k* nearest neighbors to see which of the two classes appears more often
- Assign the example the class that wins the majority vote

Accuracy of a classifier: The proportion of examples in the data set that are classified correctly

Table Functions and Methods

In the examples in the left column, np refers to the NumPy module, as usual. Everything else is a function, a method, an example of an argument to a function or method, or an example of an object we might call the method on. For example, tbl refers to a table, array refers to an array, and num refers to a number. array.item(0) is an example call for the method item, and in that example, array is the name previously given to some array.

Name	**Description**	**Input**	**Output**
Table()	Create an empty table, usually to extend with data (Ch 6)	None	An empty **Table**
Table().read_table(filename)	Create a table from a data file (Ch 6)	**string**: the name of the file	**Table** with the contents of the data file

tbl.with_columns(name, values)
tbl.with_columns(n1, v1, n2, v2,...)
	A table with an additional or replaced column or columns. name is a string for the name of a column, values is an array (Ch 6)	1. **string**: the name of the new column;
		2. **array**: the values in that column
			Table: a copy of the original Table with the new columns added

tbl.column(column_name_or_index)	The values of a column (an array) (Ch 6)	**string** or **int**: the column name or index	**array**: the values in that column
tbl.num_rows	Compute the number of rows in a table (Ch 6)	None	**int**: the number of rows in the table
tbl.num_columns	Compute the number of columns in a table (Ch 6)	None	**int**: the number of columns in the table
tbl.labels	Lists the column labels in a table (Ch 6)	None	**array**: the names of each column (as strings) in the table
tbl.select(col1, col2, ...)	Create a copy of a table with only some of the columns. Each column is the column name or index. (Ch 6)	**string** *or* **int**: column name(s) or index(es)	**Table** with the selected columns
tbl.drop(col1, col2, ...)	Create a copy of a table without some of the columns. Each column is the column name or index. (Ch 6)	**string** *or* **int**: column name(s) or index(es)	**Table** without the selected columns
tbl.relabeled(old_label, new_label)	Creates a new table, changing the column name specified by the old label to the new label, and leaves the original table unchanged. (Ch 6)	1. **string**: the old column name 2. **string**: the new column name	**Table**: a new Table
tbl.show(n)	Display n rows of a table. If no argument is specified, defaults to displaying the entire table. (Ch 6.1)	(Optional) **int**: number of rows you want to display	None: displays a table with n rows
tbl.sort(column_name_or_index)	Create a copy of a table sorted by the values in a column. Defaults to ascending order unless descending = True is included. (Ch 6.1)	1. **string** *or* **int**: column index or name 2. (Optional) descending=True	**Table**: a copy of the original with the column sorted
tbl.where(column, predicate)	Create a copy of a table with only the rows that match some *predicate*. See Table.where predicates below. (Ch 6.2)	1. **string** *or* **int**: column name or index 2. are.(...) predicate	**Table**: a copy of the original table with only the rows that match the predicate
tbl.take(row_indices)	A table with only the rows at the given indices. row_indices is either an array of indices or an integer corresponding to one index. (Ch 6.2)	**array** of ints: the indices of the rows to be included in the Table OR **int**: the index of the row to be included	**Table**: a copy of the original table with only the rows at the given indices

tbl.exclude(row_indices)	A table without the rows at the given indices. row_indices is either an array of indices or an integer corresponding to one index.	**array** of ints: the indices of the rows to be excluded from the Table OR **int**: the index of the row to be excluded	**Table**: a copy of the original table without the rows at the given indices
tbl.scatter(x_column, y_column)	Draws a scatter plot consisting of one point for each row of the table. Note that x_column and y_column must be strings specifying column names. Include optional argument fit_line=True if you want to draw a line of best fit for each set of points. (Ch 7)	1. **string**: name of the column on the x-axis 2. **string**: name of the column on the y-axis 3. (Optional) fit_line=True	None: draws a scatter plot

tbl.plot(x_column, y_column)
tbl.plot(x_column)
	Draw a line graph consisting of one point for each row of the table. If you only specify one column, it will plot the rest of the columns on the y-axis as different colored lines. (Ch 7)	1. **string**: name of the column on the x-axis
		2. **string**: name of the column on the y-axis
			None: draws a line graph

tbl.barh(categories)
tbl.barh(categories, values)
	Displays a bar chart with bars for each category in a column, with height proportional to the corresponding frequency. values argument unnecessary if table has only a column of categories and a column of values. (Ch 7.1)	1. **string**: name of the column with categories
		2. (Optional) **string**: the name of the column with values for corresponding categories
			None: draws a bar chart

tbl.hist(column, unit, bins, group)	Generates a histogram of the numerical values in a column. unit and bins are optional arguments, used to label the axes and group the values into intervals (bins), respectively. Bins have the form [a, b), where a is included in the bin and b is not. (Ch 7.2)	1. **string**: name of the column with categories 2. (Optional) **string**: units of x-axis 3. (Optional) **array** of ints/floats denoting bin boundaries 4. (Optional) **string**: name of categorical column to draw separate overlaid histograms for	None: draws a histogram

tbl.bin(column_name_or_index)
tbl.bin(column_name_or_index, bins)
	Groups values into intervals, known as bins. Results in a two-column table that contains the number of rows in each bin. The first column lists the left endpoints of the bins, except in the last row. If the bins argument isn't used, default is to produce 10 equally wide bins between the min and max values of the data. (Ch 7.2)	1. **string** *or* **int**: column name(s) or index(es)
		2. (Optional) **array** of ints/floats denoting bin boundaries or an **int** of the number of bins you want
			Table: a new tables

tbl.apply(function)
tbl.apply(function, col1, col2, ...)
	Returns an array of values resulting from applying a function to each item in a column. (Ch 8.1)	1. **function**: function to apply to column
		2. (Optional) **string**: name of the column to apply function to (if you have multiple columns, the respective column's values will be passed as the corresponding argument to the function), and if there is no argument, your function will be applied to every row object in tbl
			array: contains an element for each value in the original column after applying the function to it

tbl.group(column_or_columns, func)	Group rows by unique values or combinations of values in a column(s). Multiple columns must be entered in array or list form. Other values aggregated by count (default) or optional argument func. (Ch 8.2)	1. **string** or **array of strings**: column(s) on which to group 2. (Optional) **function**: function to aggregate values in cells (defaults to count)	**Table**: a new Table

tbl.pivot(col1, col2, values, collect)
tbl.pivot(col1, col2)
	A pivot table where each unique value in col1 has its own column and each unique value in col2 has its own row. Count or aggregate values from a third column, collect with some function. Default values and collect return counts in cells. (Ch 8.3)	1. **string**: name of column whose unique values will make up columns of pivot table
		2. **string**: name of column whose unique values will make up rows of pivot table
		3. (Optional) **string**: name of column that describes the values of cell
		4. (Optional) **function**: how the values are collected, e.g. sum or np.mean
			Table: a new Table

tblA.join(colA, tblB, colB)
tblA.join(colA, tblB)
	Generate a table with the columns of tblA and tblB, containing rows for all values of a column that appear in both tables. Default colB is colA. colA and colB must be strings specifying column names. (Ch 8.4)	1. **string**: name of a column in tblA with values to join on
		2. **Table**: other Table
		3. (Optional) **string**: if column names are different between Tables, the name of the shared column in tblB
			Table: a new Table

tbl.sample(n)
tbl.sample(n, with_replacement)
	A new table where n rows are randomly sampled from the original table; by default, n=tbl.num_rows. Default is with replacement. For sampling without replacement, use argument with_replacement=False. For a non-uniform sample, provide a third argument weights=distribution where distribution is an array or list containing the probability of each row. (Ch 10)	1. **int**: sample size
		2. (Optional) with_replacement=False
			Table: a new Table with n rows

tbl.row(row_index)	Accesses the row of a table by taking the index of the row as its argument. Note that rows are in general not arrays, as their elements can be of different types. However, you can use .item to access a particular element of a row using row.item(label). (Ch 17.3)	**int**: row index	**Row object** with the values of the row and labels of the corresponding columns
tbl.rows	Can use to access all of the rows of a table.	None	**Rows object** made up of all rows as individual row objects

String Methods

Name	**Description**
str.split(separator)	Splits the string (str) into a list based on the separator that is passed in
str.join(array)	Combines each element of array into one string, with str being in-between each element
str.replace(old_string, new_string)	Replaces each occurrence of old_string in str with the value of new_string (Ch 4.2.1)

Array Functions and Methods

Name	**Chapter**	**Description**
max(array)	3.3	Returns the maximum value of an array
min(array)	3.3	Returns the minimum value of an array
sum(array)	3.3	Returns the sum of the values in an array
abs(num), np.abs(array)	3.3	Takes the absolute value of a number or each number in an array

round(num), np.round(array)
round(num, decimals), np.round(array, decimals)
	3.3	Rounds a number or an array of numbers to the nearest integer. If decimals (integer) is included, rounds to that many digits. If decimals is negative, remove that many digits of precision.

len(array), len(string)	3.3	Returns the length (number of elements) of an array. If a string (str) is passed in instead, returns the number of characters in the string.
make_array(val1, val2, ...)	5	Makes a numpy array with the values passed in

np.average(array)
np.mean(array)
	5.1	Returns the mean value of an array

np.std(array)	14.2	Returns the standard deviation of an array
np.diff(array)	5.1	Returns a new array of size len(arr)-1 with elements equal to the difference between adjacent elements; val_2 - val_1, val_3 - val_2, etc.
np.sqrt(array)	5.1	Returns an array with the square root of each element

np.arange(start, stop, step)
np.arange(start, stop)
np.arange(stop)
	5.2	An array of numbers starting with start, going up in increments of step, and going up to but excluding stop. When start and/or step are left out, default values are used in their place. Default step is 1; default start is 0.

array.item(index)	5.3	Returns the i-th item in an array (remember Python indices start at 0!)

np.random.choice(array, n)
np.random.choice(array)
	9	Picks one (by default) or some number (n) of items from array at random with replacement.

np.count_nonzero(array)	9	Returns the number of non-zero (or True) elements in an array.
np.append(array, item)	9.2	Returns a copy of the input array with item appended to the end.
percentile(percentile, array)	13.1	Returns the corresponding percentile of an array.

Table Filtering Predicates

Any of these predicates can be negated by adding not_ in front of them, e.g. are.not_equal_to(Z) or are.not_containing(S).

Predicate	Description
are.equal_to(Z)	Equal to Z
are.not_equal_to(Z)	Not equal to Z
are.above(x)	Greater than x
are.above_or_equal_to(x)	Greater than or equal to x
are.below(x)	Less than x
are.below_or_equal_to(x)	Less than or equal to x
are.between(x, y)	Greater than or equal to x and less than y
are.between_or_equal_to(x, y)	Greater than or equal to x, and less than or equal to y
are.strictly_between(x, y)	Greater than x and less than y
are.contained_in(A)	Is a substring of A (if A is a string) or an element of A (if A is a list/array)
are.containing(S)	Contains the string S

Miscellaneous Functions

These are functions in the datascience library that are used in the course that don't fall into any of the categories above. You can also read more about all functions in the datascience library on the datascience documentation.

Name	Description	Intput	Output
sample_proportions(sample_size, model_proportions)	sample_size should be an integer, model_proportions an array of probabilities that sum up to 1. The function samples sample_size objects from the distribution specified by model_proportions. It returns an array with the same size as model_proportions. Each item in the array corresponds to the proportion of times it was sampled out of the sample_size times. (Ch 11.1)	1. **int**: sample size 2. **array**: an array of proportions that should sum to 1	**array**: each item corresponds to the proportion of times that corresponding item was sampled from model_proportions in sample_size draws, should sum to 1
minimize(function)	Returns an array of values such that if each value in the array was passed into function as arguments, it would minimize the output value of function. (Ch 15.4)	**function**: name of a function that will be minimized	**array**: An array in which each element corresponds to an argument that minimizes the output of the function. Values in the array are listed based on the order they are passed into the function; the first element in the array is also going to be the first value passed into the function.