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Introduction to Pandas

pandas is a Python package providing fast, flexible, and expressive data structures designed to work with *relational* or *labeled* data both. It is a fundamental high-level building block for doing practical, real world data analysis in Python.

pandas is well suited for:

- Tabular data with heterogeneously-typed columns, as in an SQL table or Excel spreadsheet
- Ordered and unordered (not necessarily fixed-frequency) time series data.
- Arbitrary matrix data (homogeneously typed or heterogeneous) with row and column labels
- Any other form of observational / statistical data sets. The data actually need not be labeled at all to be placed into a pandas data structure

Key features:

- Easy handling of **missing data**
- **Size mutability**: columns can be inserted and deleted from DataFrame and higher dimensional objects
- Automatic and explicit **data alignment**: objects can be explicitly aligned to a set of labels, or the data can be aligned automatically

- Powerful, flexible **group by functionality** to perform split-apply-combine operations on data sets
- Intelligent label-based **slicing, fancy indexing, and subsetting** of large data sets
- Intuitive **merging and joining** data sets
- Flexible **reshaping and pivoting** of data sets
- **Hierarchical labeling** of axes
- Robust **IO tools** for loading data from flat files, Excel files, databases, and HDF5
- **Time series functionality**: date range generation and frequency conversion, moving window statistics, moving window linear regressions, date shifting and lagging, etc.

In [1]:

```python
import pandas as pd
import numpy as np
pd.options.mode.chained_assignment = None  # default='warn', Mutes warnings when copying
```

Pandas Data Structures

Series

A **Series** is a single vector of data (like a NumPy 1-d array) with an *index* that labels each element in the vector.

In [2]:

```python
counts = pd.Series([632, 1638, 569, 115])
counts
```

Out[2]:

```
0     632
1    1638
2     569
3     115
dtype: int64
```

If an **index** is not specified, a default sequence of integers is assigned as the index. A NumPy array comprises the values of the `Series`, while the index is a pandas `Index` object.

In [3]:

```python
counts.values
```

Out[3]:

```
array([ 632, 1638,  569,  115])
```

In [4]:

```python
counts.index
```

Out[4]:

```
RangeIndex(start=0, stop=4, step=1)
```

We can assign meaningful labels to the index, if they are available:

In [5]:

```python
bacteria = pd.Series([632, 1638, 569, 115],
    index=['Firmicutes', 'Proteobacteria', 'Actinobacteria', 'Bacteroidetes'])

bacteria
```

Out[5]:

```
Firmicutes         632
Proteobacteria    1638
Actinobacteria     569
Bacteroidetes      115
dtype: int64
```

These labels can be used to refer to the values in the `Series`.

In [6]:

```python
bacteria['Actinobacteria'] #dictionary style
```

Out[6]:
```
569
```

In [7]:
```
bacteria[[name.endswith('bacteria') for name in bacteria.index]]
```

Out[7]:
```
Proteobacteria    1638
Actinobacteria     569
dtype: int64
```

In [8]:
```
[name.endswith('bacteria') for name in bacteria.index] #mask
```

Out[8]:
```
[False, True, True, False]
```

Notice that the indexing operation preserved the association between the values and the corresponding indices.

We can still use **positional indexing** if we wish.

In [9]:
```
bacteria[0]
```

Out[9]:
```
632
```

We can give both the array of values and the index **meaningful labels** themselves:

In [10]:
```
bacteria.name = 'counts'
bacteria.index.name = 'phylum'
bacteria
```

Out[10]:
```
phylum
Firmicutes         632
Proteobacteria    1638
Actinobacteria     569
Bacteroidetes      115
Name: counts, dtype: int64
```

NumPy's math functions and other operations can be applied to Series without losing the data structure.

In [10]:
```
np.log(bacteria)
```

Out[10]:
```
Firmicutes        6.448889
Proteobacteria    7.401231
Actinobacteria    6.343880
Bacteroidetes     4.744932
dtype: float64
```

In [11]:
```
bacteria.apply(np.log)
```

Out[11]:
```
Firmicutes        6.448889
Proteobacteria    7.401231
Actinobacteria    6.343880
Bacteroidetes     4.744932
dtype: float64
```

We can also filter according to the values in the `Series`:

In [13]:
```
bacteria[bacteria>1000]
```

Out[13]:
```
phylum
Proteobacteria    1638
Name: counts, dtype: int64
```

A `Series` can be thought of as an ordered key-value store. In fact, we can create one from a `dict`:

In [14]:

```
bacteria_dict = { 'Firmicutes': 632,
                  'Proteobacteria': 1638,
                  'Actinobacteria': 569,
                  'Bacteroidetes': 115 }
pd.Series(bacteria_dict)
```

Out[14]:

```
Firmicutes         632
Proteobacteria    1638
Actinobacteria     569
Bacteroidetes      115
dtype: int64
```

Notice that the `Series` is created in key-sorted order.

If we pass a custom index to `Series`, it will select the corresponding values from the dict, and treat indices without corrsponding values as missing. Pandas uses the `NaN` (not a number) type for missing values.

In [15]:

```
bacteria2 = pd.Series(bacteria_dict,
                      index=['Cyanobacteria','Firmicutes',
                             'Proteobacteria','Actinobacteria'])
bacteria2
```

Out[15]:

```
Cyanobacteria        NaN
Firmicutes         632.0
Proteobacteria    1638.0
Actinobacteria     569.0
dtype: float64
```

In [16]:

```
bacteria2.isnull()
```

Out[16]:

```
Cyanobacteria      True
Firmicutes        False
Proteobacteria    False
Actinobacteria    False
dtype: bool
```

Critically, the labels are used to **align data** when used in operations with other Series objects:

In [17]:

```
bacteria + bacteria2
```

Out[17]:

```
Actinobacteria    1138.0
Bacteroidetes        NaN
Cyanobacteria        NaN
Firmicutes        1264.0
Proteobacteria    3276.0
dtype: float64
```

Contrast this with NumPy arrays, where arrays of the same length will combine values **element-wise**; adding Series combined values with the same label in the resulting series. Notice also that the missing values were propagated by addition.

DataFrame

Inevitably, we want to be able to store, view and manipulate data that is *multivariate*, where for every index there are multiple fields or columns of data, often of varying data type.

A `DataFrame` is a tabular data structure, encapsulating multiple series like columns in a spreadsheet. Data are stored internally as a 2-dimensional object, but the `DataFrame` allows us to represent and manipulate higher-dimensional data.

In [13]:

```
data = pd.DataFrame({'value':[632, 1638, 569, 115, 433, 1130, 754, 555],
                     'patient':[1, 1, 1, 1, 2, 2, 2, 2],
                     'phylum':['Firmicutes', 'Proteobacteria', 'Actinobacteria',
    'Bacteroidetes', 'Firmicutes', 'Proteobacteria', 'Actinobacteria', 'Bacteroidetes']})
data
```

Out[13]:

	value	patient	phylum
0	632	1	Firmicutes
1	1638	1	Proteobacteria
2	569	1	Actinobacteria
3	115	1	Bacteroidetes
4	433	2	Firmicutes
5	1130	2	Proteobacteria
6	754	2	Actinobacteria
7	555	2	Bacteroidetes

Notice the `DataFrame` is sorted by column name. We can change the order by indexing them in the order we desire:

In [14]:

```
data[['phylum','value','patient']]
```

Out[14]:

	phylum	value	patient
0	Firmicutes	632	1
1	Proteobacteria	1638	1
2	Actinobacteria	569	1
3	Bacteroidetes	115	1
4	Firmicutes	433	2
5	Proteobacteria	1130	2
6	Actinobacteria	754	2
7	Bacteroidetes	555	2

A `DataFrame` has a second index, representing the columns:

In [41]:

```
data.index
```

Out[41]:

```
RangeIndex(start=0, stop=8, step=1)
```

The `dtypes` attribute reveals the data type for each column in our DataFrame.

- `int64` is numeric integer values
- `object` strings (letters and numbers)
- `float64` floating-point values

In [16]:

```
data.dtypes
```

Out[16]:

```
value        int64
patient      int64
```

```
phylum      object
dtype: object
```

If we wish to access columns, we can do so either by dict-like indexing or by attribute:

In [17]:
```
data['patient']
```

Out[17]:
```
0     1
1     1
2     1
3     1
4     2
5     2
6     2
7     2
Name: patient, dtype: int64
```

In [27]:
```
x = data.value
a= 1
```

```
/Applications/PyCharm.app/Contents/plugins/python/helpers/pydev/_pydevd_bundle/pydevd_ut
ils.py:606: FutureWarning: iteritems is deprecated and will be removed in a future versi
on. Use .items instead.
  for item in s.iteritems():
/Applications/PyCharm.app/Contents/plugins/python/helpers/pydev/_pydevd_bundle/pydevd_ut
ils.py:606: FutureWarning: iteritems is deprecated and will be removed in a future versi
on. Use .items instead.
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on. Use .items instead.
  for item in s.iteritems():
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ils.py:606: FutureWarning: iteritems is deprecated and will be removed in a future versi
on. Use .items instead.
  for item in s.iteritems():
/Applications/PyCharm.app/Contents/plugins/python/helpers/pydev/_pydevd_bundle/pydevd_ut
ils.py:606: FutureWarning: iteritems is deprecated and will be removed in a future versi
on. Use .items instead.
  for item in s.iteritems():
---------------------------------------------------------------------------
KeyboardInterrupt                         Traceback (most recent call last)
Cell In[27], line 2
      1 x = data.value
----> 2 a= 1

Cell In[27], line 2
      1 x = data.value
----> 2 a= 1

File _pydevd_bundle/pydevd_cython_darwin_39_64.pyx:1179, in _pydevd_bundle.pydevd_cython
_darwin_39_64.SafeCallWrapper.__call__()

File _pydevd_bundle/pydevd_cython_darwin_39_64.pyx:620, in _pydevd_bundle.pydevd_cython_
darwin_39_64.PyDBFrame.trace_dispatch()

File _pydevd_bundle/pydevd_cython_darwin_39_64.pyx:929, in _pydevd_bundle.pydevd_cython_
darwin_39_64.PyDBFrame.trace_dispatch()

File _pydevd_bundle/pydevd_cython_darwin_39_64.pyx:920, in _pydevd_bundle.pydevd_cython_
darwin_39_64.PyDBFrame.trace_dispatch()
```

```
File _pydevd_bundle/pydevd_cython_darwin_39_64.pyx:317, in _pydevd_bundle.pydevd_cython_
darwin_39_64.PyDBFrame.do_wait_suspend()

File /Applications/PyCharm.app/Contents/plugins/python/helpers/pydev/pydevd.py:1160, in
PyDB.do_wait_suspend(self, thread, frame, event, arg, send_suspend_message, is_unhandled
_exception)
   1157         from_this_thread.append(frame_id)
   1159 with self._threads_suspended_single_notification.notify_thread_suspended(thread_
id, stop_reason):
-> 1160     self._do_wait_suspend(thread, frame, event, arg, suspend_type, from_this_thr
ead)

File /Applications/PyCharm.app/Contents/plugins/python/helpers/pydev/pydevd.py:1175, in
PyDB._do_wait_suspend(self, thread, frame, event, arg, suspend_type, from_this_thread)
   1172             self._call_mpl_hook()
   1174         self.process_internal_commands()
-> 1175         time.sleep(0.01)
   1177 self.cancel_async_evaluation(get_current_thread_id(thread), str(id(frame)))
   1179 # process any stepping instructions

KeyboardInterrupt:
```

In [29]:

```python
x = data[['value']]
a = 1
```

In [30]:

```python
type(data[['value']])
```

Out[30]:

```
pandas.core.frame.DataFrame
```

In [31]:

```python
type(data.value)
```

Out[31]:

```
pandas.core.series.Series
```

Notice this is different than with `Series`, where dict-like indexing retrieved a particular element (row).

If we want access to a row in a `DataFrame`, we index its `loc` attribute.

In [27]:

```python
data.loc[3]
```

Out[27]:

```
value                 115
patient                 1
phylum      Bacteroidetes
Name: 3, dtype: object
```

Exercise 1

Find the size of the first dimension of `data`.

In [28]:

```python
data.shape[0]
```

Out[28]:

```
8
```

An alternative way of initializing a `DataFrame` is with a list of dicts:

In [29]:

```python
data = pd.DataFrame([{'patient': 1, 'phylum': 'Firmicutes', 'value': 632},
                    {'patient': 1, 'phylum': 'Proteobacteria', 'value': 1638},
                    {'patient': 1, 'phylum': 'Actinobacteria', 'value': 569},
                    {'patient': 1, 'phylum': 'Bacteroidetes', 'value': 115},
                    {'patient': 2, 'phylum': 'Firmicutes', 'value': 433},
                    {'patient': 2, 'phylum': 'Proteobacteria', 'value': 1130},
                    {'patient': 2, 'phylum': 'Actinobacteria', 'value': 754},
                    {'patient': 2, 'phylum': 'Bacteroidetes', 'value': 555}])
data
```

Out[29]:

	patient	phylum	value
0	1	Firmicutes	632
1	1	Proteobacteria	1638
2	1	Actinobacteria	569
3	1	Bacteroidetes	115
4	2	Firmicutes	433
5	2	Proteobacteria	1130
6	2	Actinobacteria	754
7	2	Bacteroidetes	555

It's important to note that the `Series` returned when a `DataFrame` is indexed is merely a **view** on the `DataFrame`, and not a copy of the data itself. So you must be cautious when manipulating this data:

In [30]:

```
vals = data.value
vals
```

Out[30]:

```
0     632
1    1638
2     569
3     115
4     433
5    1130
6     754
7     555
Name: value, dtype: int64
```

In [31]:

```
vals[5] = 0
data.value
```

Out[31]:

```
0     632
1    1638
2     569
3     115
4     433
5       0
6     754
7     555
Name: value, dtype: int64
```

If we plan on modifying an extracted Series, its a good idea to make a copy.

In [32]:

```
vals = data.value.copy()
vals[5] = 1000
data.value
```

Out[32]:

```
0     632
1    1638
2     569
3     115
4     433
5       0
6     754
```

```
7      555
Name: value, dtype: int64
```

We can create or modify columns by assignment:

In [33]:

```
data.value[[3,4,6]] = [14, 21, 5]
data
```

Out[33]:

	patient	phylum	value
0	1	Firmicutes	632
1	1	Proteobacteria	1638
2	1	Actinobacteria	569
3	1	Bacteroidetes	14
4	2	Firmicutes	21
5	2	Proteobacteria	0
6	2	Actinobacteria	5
7	2	Bacteroidetes	555

In [34]:

```
data['year'] = 2013
data
```

Out[34]:

	patient	phylum	value	year
0	1	Firmicutes	632	2013
1	1	Proteobacteria	1638	2013
2	1	Actinobacteria	569	2013
3	1	Bacteroidetes	14	2013
4	2	Firmicutes	21	2013
5	2	Proteobacteria	0	2013
6	2	Actinobacteria	5	2013
7	2	Bacteroidetes	555	2013

But note we cannot use the attribute indexing method to add a new column:

In [35]:

```
data.treatment = 1
data
```

Out[35]:

	patient	phylum	value	year
0	1	Firmicutes	632	2013
1	1	Proteobacteria	1638	2013
2	1	Actinobacteria	569	2013
3	1	Bacteroidetes	14	2013
4	2	Firmicutes	21	2013
5	2	Proteobacteria	0	2013
6	2	Actinobacteria	5	2013
7	2	Bacteroidetes	555	2013

In [36]:

```
data.treatment
```

Out[36]:

```
1
```

In [32]:

```
data[[name.endswith('bacteria') for name in data.phylum] and data.value>1000]
data[data['phylum'].apply(lambda x: x.endswith('bacteria')) & data['value'].apply(lambda
```

Out[32]:

	value	patient	phylum
1	1638	1	Proteobacteria
5	1130	2	Proteobacteria

Exercise 2

From the `data` table above, return all rows for which the phylum name ends in "bacteria" and the value is greater than 1000.

In [33]:

```
data[data['phylum'].apply(lambda x: x.endswith('bacteria')) & data['value'].apply(lambda
```

Out[33]:

	value	patient	phylum
1	1638	1	Proteobacteria
5	1130	2	Proteobacteria

Specifying a `Series` as a new column causes its values to be added according to the `DataFrame` 's index:

In [35]:

```
treatment = pd.Series([0]*4 + [1]*2)
treatment
```

Out[35]:

```
0    0
1    0
2    0
3    0
4    1
5    1
dtype: int64
```

In [36]:

```
data['treatment'] = treatment
data
```

Out[36]:

	value	patient	phylum	treatment
0	632	1	Firmicutes	0.0
1	1638	1	Proteobacteria	0.0
2	569	1	Actinobacteria	0.0
3	115	1	Bacteroidetes	0.0
4	433	2	Firmicutes	1.0
5	1130	2	Proteobacteria	1.0
6	754	2	Actinobacteria	NaN
7	555	2	Bacteroidetes	NaN

We can use the `drop` method to remove rows or columns, which by **default drops rows**. We can be explicit by using the `axis` argument:

In [37]:

```python
data_nomonth = data.drop('treatment', axis=1)
data_nomonth
```

Out[37]:

	value	patient	phylum
0	632	1	Firmicutes
1	1638	1	Proteobacteria
2	569	1	Actinobacteria
3	115	1	Bacteroidetes
4	433	2	Firmicutes
5	1130	2	Proteobacteria
6	754	2	Actinobacteria
7	555	2	Bacteroidetes

In [38]:

```python
data_nomonth.drop(0)
```

Out[38]:

	value	patient	phylum
1	1638	1	Proteobacteria
2	569	1	Actinobacteria
3	115	1	Bacteroidetes
4	433	2	Firmicutes
5	1130	2	Proteobacteria
6	754	2	Actinobacteria
7	555	2	Bacteroidetes

The dtype is automatically chosen to be as general as needed to accommodate all the columns.

In [39]:

```python
df = pd.DataFrame({'foo': [1,2,3], 'bar':[0.4, -1.0, 4.5]})
df.values
```

Out[39]:

```
array([[ 1. ,  0.4],
       [ 2. , -1. ],
       [ 3. ,  4.5]])
```

In [40]:

```python
df.values.dtype
```

Out[40]:

```
dtype('float64')
```

`Index` objects are **immutable**:

In [44]:

```python
#data.index[0] = 15 #that doesn't work
```

This is so that `Index` objects can be shared between data structures without fear that they will be changed.

In [45]:

```python
bacteria2.index = bacteria.index
```

In [46]:

```python
bacteria2
```

Out[46]:

```
phylum
Firmicutes              NaN
Proteobacteria        632.0
Actinobacteria       1638.0
Bacteroidetes         569.0
dtype: float64
```

Importing data

A key, but often under-appreciated, step in data analysis is importing the data that we wish to analyze. Though it is easy to load basic data structures into Python using built-in tools or those provided by packages like NumPy, it is non-trivial to import structured data well, and to easily convert this input into a robust data structure:

```
genes = np.loadtxt("genes.csv", delimiter=",", dtype=[('gene', '|S10'),
('value', '<f4')])
```

Pandas provides a convenient set of functions for importing tabular data from a number of formats directly into a `DataFrame` object. These functions include a slew of options to perform type inference, indexing, parsing, iterating and cleaning automatically as data are imported.

Let's start with some more bacteria data, stored in csv format.

In [43]:

```
!head Data/microbiome.csv
```

```
Taxon,Patient,Group,Tissue,Stool
Firmicutes,1,0,136,4182
Firmicutes,2,1,1174,703
Firmicutes,3,0,408,3946
Firmicutes,4,1,831,8605
Firmicutes,5,0,693,50
Firmicutes,6,1,718,717
Firmicutes,7,0,173,33
Firmicutes,8,1,228,80
Firmicutes,9,0,162,3196
```

This table can be read into a DataFrame using `read_csv`:

In [46]:

```
mb = pd.read_csv("Data/microbiome.csv", sep=',')
mb.head()
```

Out[46]:

	Taxon	Patient	Group	Tissue	Stool
0	Firmicutes	1	0	136	4182
1	Firmicutes	2	1	1174	703
2	Firmicutes	3	0	408	3946
3	Firmicutes	4	1	831	8605
4	Firmicutes	5	0	693	50

Notice that `read_csv` automatically considered the first row in the file to be a header row.

We can override default behavior by customizing some the arguments, like `header`, `names` or `index_col`.

In [49]:
```
pd.read_csv("Data/microbiome.csv", header=None).head()
```

Out[49]:

	0	1	2	3	4
0	Taxon	Patient	Group	Tissue	Stool
1	Firmicutes	1	0	136	4182
2	Firmicutes	2	1	1174	703
3	Firmicutes	3	0	408	3946
4	Firmicutes	4	1	831	8605

`read_csv` is just a convenience function for `read_table`, since csv is such a common format:

In [50]:
```
mb = pd.read_csv("Data/microbiome.csv", sep=',')
```

The `sep` argument can be customized as needed to accomodate arbitrary separators. For example, we can use a regular expression to define a variable amount of whitespace, which is unfortunately very common in some data formats:

```
sep='\s+'
```

For a more useful index, we can specify the first two columns, which together provide a unique index to the data.

In [51]:
```
mb = pd.read_csv("Data/microbiome.csv", index_col=['Patient','Taxon'])
mb.head()
```

Out[51]:

		Group	Tissue	Stool
Patient	**Taxon**			
1	**Firmicutes**	0	136	4182
2	**Firmicutes**	1	1174	703
3	**Firmicutes**	0	408	3946
4	**Firmicutes**	1	831	8605
5	**Firmicutes**	0	693	50

This is called a *hierarchical* index, which we will revisit later in the section.

If we have sections of data that we do not wish to import (for example, known bad data), we can populate the `skiprows` argument:

In [52]:
```
pd.read_csv("Data/microbiome.csv", skiprows=[3,4,6]).head()
```

Out[52]:

	Taxon	Patient	Group	Tissue	Stool
0	Firmicutes	1	0	136	4182
1	Firmicutes	2	1	1174	703
2	Firmicutes	5	0	693	50
3	Firmicutes	7	0	173	33
4	Firmicutes	8	1	228	80

If we only want to import a small number of rows from, say, a very large data file we can use `nrows`:

In [53]:

```
pd.read_csv("Data/microbiome.csv", nrows=4)
```

Out[53]:

	Taxon	Patient	Group	Tissue	Stool
0	Firmicutes	1	0	136	4182
1	Firmicutes	2	1	1174	703
2	Firmicutes	3	0	408	3946
3	Firmicutes	4	1	831	8605

Missing Values

Most real-world data is incomplete, with values missing due to incomplete observation, data entry or transcription error, or other reasons. Pandas will automatically recognize and parse common missing data indicators, including `NA` and `NULL`.

In [45]:

```
!head -n 10 Data/microbiome_missing.csv
```

```
Taxon,Patient,Tissue,Stool
Firmicutes,1,632,305
Firmicutes,2,136,4182
Firmicutes,3,,703
Firmicutes,4,408,3946
Firmicutes,5,831,8605
Firmicutes,6,693,50
Firmicutes,7,718,717
Firmicutes,8,173,33
Firmicutes,9,228,NA
```

In [55]:

```
pd.read_csv("Data/microbiome_missing.csv").head(10)
```

Out[55]:

	Taxon	Patient	Tissue	Stool
0	Firmicutes	1	632	305.0
1	Firmicutes	2	136	4182.0
2	Firmicutes	3	NaN	703.0
3	Firmicutes	4	408	3946.0
4	Firmicutes	5	831	8605.0
5	Firmicutes	6	693	50.0
6	Firmicutes	7	718	717.0
7	Firmicutes	8	173	33.0
8	Firmicutes	9	228	NaN
9	Firmicutes	10	162	3196.0

Above, Pandas recognized `NA` and an empty field as missing data.

In [56]:

```
pd.isnull(pd.read_csv("Data/microbiome_missing.csv")).head(10)
```

Out[56]:

	Taxon	Patient	Tissue	Stool
0	False	False	False	False

1	False	False	False	False
2	False	False	True	False
3	False	False	False	False
4	False	False	False	False
5	False	False	False	False
6	False	False	False	False
7	False	False	False	False
8	False	False	False	True
9	False	False	False	False

Unfortunately, there will sometimes be inconsistencies in the conventions for missing data. In this example, there is a question mark "?" and a large negative number where there should have been a positive integer. We can specify additional symbols with the `na_values` argument:

In [57]:

```
pd.read_csv("Data/microbiome_missing.csv", na_values=['?', -99999]).head(10)
```

Out[57]:

	Taxon	Patient	Tissue	Stool
0	Firmicutes	1	632.0	305.0
1	Firmicutes	2	136.0	4182.0
2	Firmicutes	3	NaN	703.0
3	Firmicutes	4	408.0	3946.0
4	Firmicutes	5	831.0	8605.0
5	Firmicutes	6	693.0	50.0
6	Firmicutes	7	718.0	717.0
7	Firmicutes	8	173.0	33.0
8	Firmicutes	9	228.0	NaN
9	Firmicutes	10	162.0	3196.0

These can be specified on a column-wise basis using an appropriate dict as the argument for `na_values`.

Microsoft Excel

Since so much financial and scientific data ends up in Excel spreadsheets (regrettably), Pandas' ability to directly import Excel spreadsheets is valuable. This support is contingent on having one or two dependencies (depending on what version of Excel file is being imported) installed: `xlrd` and `openpyxl` (these may be installed with either `pip` or `easy_install`).

The `read_excel` convenience function in pandas imports a specific sheet from an Excel file

In [58]:

```
mb = pd.read_excel('Data/microbiome_MID2.xls', sheet_name='Sheet 1', header=None)
mb.head()
```

Out[58]:

	0	1
0	Archaea "Crenarchaeota" Thermoprotei Acidiloba...	2

1	Archaea "Crenarchaeota" Thermoprotei Acididoba...	14
2	Archaea "Crenarchaeota" Thermoprotei Desulfuro...	23
3	Archaea "Crenarchaeota" Thermoprotei Desulfuro...	1
4	Archaea "Crenarchaeota" Thermoprotei Desulfuro...	2

There are several other data formats that can be imported into Python and converted into `DataFrames`, with the help of buitl-in or third-party libraries. These include JSON, XML, HDF5, relational and non-relational databases, and various web APIs. These are beyond the scope of this tutorial, but are covered in Python for Data Analysis.

Indexing and Selection

This section introduces the new user to the key functionality of Pandas that is required to use the software effectively.

For some variety, we will leave our digestive tract bacteria behind and employ some baseball data.

In [59]:

```
baseball = pd.read_csv("Data/baseball.csv", index_col='id')
baseball.head()
```

Out[59]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	so	ibb	hbp	sh
id																			
88641	womacto01	2006	2	CHN	NL	19	50	6	14	1	...	2.0	1.0	1.0	4	4.0	0.0	0.0	3.0
88643	schilcu01	2006	1	BOS	AL	31	2	0	1	0	...	0.0	0.0	0.0	0	1.0	0.0	0.0	0.0
88645	myersmi01	2006	1	NYA	AL	62	0	0	0	0	...	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0
88649	helliri01	2006	1	MIL	NL	20	3	0	0	0	...	0.0	0.0	0.0	0	2.0	0.0	0.0	0.0
88650	johnsra05	2006	1	NYA	AL	33	6	0	1	0	...	0.0	0.0	0.0	0	4.0	0.0	0.0	0.0

5 rows × 22 columns

Notice that we specified the `id` column as the index, since it appears to be a unique identifier. We could try to create a unique index ourselves by combining `player` and `year`:

In [60]:

```
baseball.index.is_unique
```

Out[60]:

```
True
```

In [61]:

```
player_id = baseball.player + baseball.year.astype(str)
baseball_newind = baseball.copy()
baseball_newind.index = player_id
baseball_newind.head()
```

Out[61]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	so	ibb
womacto012006	womacto01	2006	2	CHN	NL	19	50	6	14	1	...	2.0	1.0	1.0	4	4.0	0.0
schilcu012006	schilcu01	2006	1	BOS	AL	31	2	0	1	0	...	0.0	0.0	0.0	0	1.0	0.0
myersmi012006	myersmi01	2006	1	NYA	AL	62	0	0	0	0	...	0.0	0.0	0.0	0	0.0	0.0
helliri012006	helliri01	2006	1	MIL	NL	20	3	0	0	0	...	0.0	0.0	0.0	0	2.0	0.0
johnsra052006	johnsra05	2006	1	NYA	AL	33	6	0	1	0	...	0.0	0.0	0.0	0	4.0	0.0

5 rows × 22 columns

This looks okay, but let's check:

```
In [62]: baseball_newind.index.is_unique
```

```
Out[62]: False
```

So, indices need not be unique. Our choice is not unique because some players change teams within years.

The most important consequence of a non-unique index is that indexing by label will return multiple values for some labels:

```
In [63]: baseball_newind.loc['wickmbo012007']
```

Out[63]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	so	ibb	hb
wickmbo012007	wickmbo01	2007	2	ARI	NL	8	0	0	0	0	...	0.0	0.0	0.0	0	0.0	0.0	0
wickmbo012007	wickmbo01	2007	1	ATL	NL	47	0	0	0	0	...	0.0	0.0	0.0	0	0.0	0.0	0

2 rows × 22 columns

We will learn more about indexing below.

We can create a truly unique index by combining `player`, `team` and `year`:

```
In [64]: player_unique = baseball.player + baseball.team + baseball.year.astype(str)
         baseball_newind = baseball.copy()
         baseball_newind.index = player_unique
         baseball_newind.head()
```

Out[64]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	so	i
womacto01CHN2006	womacto01	2006	2	CHN	NL	19	50	6	14	1	...	2.0	1.0	1.0	4	4.0	0
schilcu01BOS2006	schilcu01	2006	1	BOS	AL	31	2	0	1	0	...	0.0	0.0	0.0	0	1.0	0
myersmi01NYA2006	myersmi01	2006	1	NYA	AL	62	0	0	0	0	...	0.0	0.0	0.0	0	0.0	0
helliri01MIL2006	helliri01	2006	1	MIL	NL	20	3	0	0	0	...	0.0	0.0	0.0	0	2.0	0
johnsra05NYA2006	johnsra05	2006	1	NYA	AL	33	6	0	1	0	...	0.0	0.0	0.0	0	4.0	0

5 rows × 22 columns

```
In [65]: baseball_newind.index.is_unique
```

```
Out[65]: True
```

We can create meaningful indices more easily using a hierarchical index; for now, we will stick with the numeric `id` field as our index.

Exercise 3

Build another unique index without using the same columns as `player_unique`.

In [66]:

```
player_unique = baseball.team + baseball.year.astype(str) + baseball.player
player_unique.is_unique
```

Out[66]:

```
True
```

Indexing works analogously to indexing in NumPy arrays, except we can use the labels in the `Index` object to extract values in addition to arrays of integers.

In [67]:

```
# Numpy-style indexing
baseball_newind[:3]
```

Out[67]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	so	il
womacto01CHN2006	womacto01	2006	2	CHN	NL	19	50	6	14	1	...	2.0	1.0	1.0	4	4.0	(
schilcu01BOS2006	schilcu01	2006	1	BOS	AL	31	2	0	1	0	...	0.0	0.0	0.0	0	1.0	(
myersmi01NYA2006	myersmi01	2006	1	NYA	AL	62	0	0	0	0	...	0.0	0.0	0.0	0	0.0	(

3 rows × 22 columns

We can also slice with data labels, since they have an intrinsic order within the Index:

In [68]:

```
baseball_newind['womacto01CHN2006':'gonzalu01ARI2006']
```

Out[68]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb
womacto01CHN2006	womacto01	2006	2	CHN	NL	19	50	6	14	1	...	2.0	1.0	1.0	4
schilcu01BOS2006	schilcu01	2006	1	BOS	AL	31	2	0	1	0	...	0.0	0.0	0.0	0
myersmi01NYA2006	myersmi01	2006	1	NYA	AL	62	0	0	0	0	...	0.0	0.0	0.0	0
helliri01MIL2006	helliri01	2006	1	MIL	NL	20	3	0	0	0	...	0.0	0.0	0.0	0
johnsra05NYA2006	johnsra05	2006	1	NYA	AL	33	6	0	1	0	...	0.0	0.0	0.0	0
finlest01SFN2006	finlest01	2006	1	SFN	NL	139	426	66	105	21	...	40.0	7.0	0.0	46
gonzalu01ARI2006	gonzalu01	2006	1	ARI	NL	153	586	93	159	52	...	73.0	0.0	1.0	69

7 rows × 22 columns

In [69]:

```
baseball_newind['womacto01CHN2006':'gonzalu01ARI2006'] = 5
baseball_newind.head(10)
```

Out[69]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	so	ib
womacto01CHN2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
schilcu01BOS2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
myersmi01NYA2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
helliri01MIL2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
johnsra05NYA2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
finlest01SFN2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
gonzalu01ARI2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5	5.0	5
seleaa01LAN2006	seleaa01	2006	1	LAN	NL	28	26	2	5	1	...	0.0	0.0	0.0	1	7.0	0
francju01ATL2007	francju01	2007	2	ATL	NL	15	40	1	10	3	...	8.0	0.0	0.0	4	10.0	1

francju01NYN2007	francju01	2007	1	NYN	NL	40	50	7	10	0	...	8.0	2.0	1.0	10	13.0	0

10 rows × 22 columns

For a more concise (and readable) syntax, we can use the new `query` method to perform selection on a `DataFrame`. Instead of having to type the fully-specified column, we can simply pass a string that describes what to select. The query above is then simply:

In [70]:
```
baseball_newind.query('ab > 500')
```

Out[70]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	
vizquom01SFN2007	vizquom01	2007	1	SFN	NL	145	513	54	126	18	...	51.0	14.0	6.0	44	
thomafr04TOR2007	thomafr04	2007	1	TOR	AL	155	531	63	147	30	...	95.0	0.0	0.0	81	
rodriiv01DET2007	rodriiv01	2007	1	DET	AL	129	502	50	141	31	...	63.0	2.0	2.0	9	
griffke02CIN2007	griffke02	2007	1	CIN	NL	144	528	78	146	24	...	93.0	6.0	1.0	85	
delgaca01NYN2007	delgaca01	2007	1	NYN	NL	139	538	71	139	30	...	87.0	4.0	0.0	52	1
biggicr01HOU2007	biggicr01	2007	1	HOU	NL	141	517	68	130	31	...	50.0	4.0	3.0	23	1

6 rows × 22 columns

The `DataFrame.index` and `DataFrame.columns` are placed in the query namespace by default. If you want to refer to a variable in the current namespace, you can prefix the variable with `@`:

In [71]:
```
min_ab = 500
```

In [72]:
```
baseball_newind.query('ab > @min_ab')
```

Out[72]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb	
vizquom01SFN2007	vizquom01	2007	1	SFN	NL	145	513	54	126	18	...	51.0	14.0	6.0	44	
thomafr04TOR2007	thomafr04	2007	1	TOR	AL	155	531	63	147	30	...	95.0	0.0	0.0	81	
rodriiv01DET2007	rodriiv01	2007	1	DET	AL	129	502	50	141	31	...	63.0	2.0	2.0	9	
griffke02CIN2007	griffke02	2007	1	CIN	NL	144	528	78	146	24	...	93.0	6.0	1.0	85	
delgaca01NYN2007	delgaca01	2007	1	NYN	NL	139	538	71	139	30	...	87.0	4.0	0.0	52	1
biggicr01HOU2007	biggicr01	2007	1	HOU	NL	141	517	68	130	31	...	50.0	4.0	3.0	23	1

6 rows × 22 columns

The indexing field `loc` allows us to select subsets of rows and columns in an intuitive way:

In [73]:
```
baseball_newind.loc['gonzalu01ARI2006', ['h','X2b', 'X3b', 'hr']]
```

Out[73]:
```
h      5
X2b    5
X3b    5
hr     5
Name: gonzalu01ARI2006, dtype: object
```

In [74]:
```
baseball_newind.loc[:'myersmi01NYA2006', 'hr']
```

Out[74]:
```
womacto01CHN2006     5
schilcu01BOS2006     5
```

```
myersmi01NYA2006    5
Name: hr, dtype: int64
```

In addition to using `loc` to select rows and columns by **label**, pandas also allows indexing by **position** using the `iloc` attribute.

So, we can query rows and columns by absolute position, rather than by name:

In [75]:
```
baseball_newind.iloc[:5, 5:8]
```

Out[75]:

	g	ab	r
womacto01CHN2006	5	5	5
schilcu01BOS2006	5	5	5
myersmi01NYA2006	5	5	5
helliri01MIL2006	5	5	5
johnsra05NYA2006	5	5	5

Exercise 4

You can use the `isin` method query a DataFrame based upon a list of values as follows:

```
data['phylum'].isin(['Firmicutes', 'Bacteroidetes'])
```

Use `isin` on `baseball` to find all players that played for the Los Angeles Dodgers (LAN) or the San Francisco Giants (SFN). How many records contain these values?

In [76]:
```
len(baseball[baseball.team.isin(['LAN', 'SFN'])])
```

Out[76]:
```
15
```

Hierarchical indexing

In the baseball example, it was necessary to combine 3 fields to obtain a unique index that was not simply an integer value. A more elegant way to have done this would be to create a hierarchical index from the three fields.

In [77]:
```
baseball_h = baseball.set_index(['year', 'team', 'player'])
baseball_h.head(10)
```

Out[77]:

			stint	lg	g	ab	r	h	X2b	X3b	hr	rbi	sb	cs	bb	so	ibb	hbp
year	**team**	**player**																
2006	**CHN**	**womacto01**	2	NL	19	50	6	14	1	0	1	2.0	1.0	1.0	4	4.0	0.0	0.0
	BOS	**schilcu01**	1	AL	31	2	0	1	0	0	0	0.0	0.0	0.0	0	1.0	0.0	0.0
	NYA	**myersmi01**	1	AL	62	0	0	0	0	0	0	0.0	0.0	0.0	0	0.0	0.0	0.0
	MIL	**helliri01**	1	NL	20	3	0	0	0	0	0	0.0	0.0	0.0	0	2.0	0.0	0.0
	NYA	**johnsra05**	1	AL	33	6	0	1	0	0	0	0.0	0.0	0.0	0	4.0	0.0	0.0
	SFN	**finlest01**	1	NL	139	426	66	105	21	12	6	40.0	7.0	0.0	46	55.0	2.0	2.0

	ARI	gonzalu01	1	NL	153	586	93	159	52	2	15	73.0	0.0	1.0	69	58.0	10.0	7.0
	LAN	seleaa01	1	NL	28	26	2	5	1	0	0	0.0	0.0	0.0	1	7.0	0.0	0.0
2007	ATL	francju01	2	NL	15	40	1	10	3	0	0	8.0	0.0	0.0	4	10.0	1.0	0.0
	NYN	francju01	1	NL	40	50	7	10	0	0	1	8.0	2.0	1.0	10	13.0	0.0	0.0

In [78]:

```
baseball_h.index.is_unique
```

Out[78]:

```
True
```

Try using this hierarchical index to retrieve Julio Franco (`francju01`), who played for the Atlanta Braves (`ATL`) in 2007:

In [79]:

```
baseball_h.loc[(2007, 'ATL', 'francju01')]
```

Out[79]:

```
stint        2
lg          NL
g           15
ab          40
r            1
h           10
X2b          3
X3b          0
hr           0
rbi        8.0
sb         0.0
cs         0.0
bb           4
so        10.0
ibb        1.0
hbp        0.0
sh         0.0
sf         1.0
gidp       1.0
Name: (2007, ATL, francju01), dtype: object
```

Recall earlier we imported some microbiome data using two index columns. This created a 2-level hierarchical index:

In [80]:

```
mb = pd.read_csv("Data/microbiome.csv", index_col=['Taxon','Patient'])
```

In [81]:

```
mb.head(10)
```

Out[81]:

		Group	Tissue	Stool
Taxon	**Patient**			
Firmicutes	**1**	0	136	4182
	2	1	1174	703
	3	0	408	3946
	4	1	831	8605
	5	0	693	50
	6	1	718	717
	7	0	173	33
	8	1	228	80
	9	0	162	3196

10	1	372	32

With a hierachical index, we can select subsets of the data based on a *partial* index:

In [82]:

```
mb.loc['Proteobacteria']
```

Out[82]:

	Group	Tissue	Stool
Patient			
1	0	2469	1821
2	1	839	661
3	0	4414	18
4	1	12044	83
5	0	2310	12
6	1	3053	547
7	0	395	2174
8	1	2651	767
9	0	1195	76
10	1	6857	795
11	0	483	666
12	1	2950	3994
13	0	1541	816
14	1	1307	53

Hierarchical indices can be created on either or **both axes**. Here is a trivial example:

In [83]:

```
frame = pd.DataFrame(np.arange(12).reshape(( 4, 3)),
                     index =[['a', 'a', 'b', 'b'], [1, 2, 1, 2]],
                     columns =[['Ohio', 'Ohio', 'Colorado'], ['Green', 'Red', 'Green']])

frame
```

Out[83]:

		Ohio		Colorado
		Green	**Red**	**Green**
a	**1**	0	1	2
	2	3	4	5
b	**1**	6	7	8
	2	9	10	11

If you want to get fancy, both the row and column indices themselves can be given names:

In [84]:

```
frame.index.names = ['key1', 'key2']
frame.columns.names = ['state', 'color']
frame
```

Out[84]:

	state	**Ohio**		**Colorado**
	color	**Green**	**Red**	**Green**

key1	key2			
a	1	0	1	2
	2	3	4	5
b	1	6	7	8
	2	9	10	11

Additionally, the order of the set of indices in a hierarchical `MultiIndex` can be changed by swapping them pairwise:

In [85]:

```
frame.columns = frame.columns.swaplevel('state', 'color')
frame
```

Out[85]:

	color	Green	Red	Green
	state	Ohio	Ohio	Colorado
key1	key2			
a	1	0	1	2
	2	3	4	5
b	1	6	7	8
	2	9	10	11

Operations

`DataFrame` and `Series` objects allow for several operations to take place either on a single object, or between two or more objects.

For example, we can perform arithmetic on the elements of two objects, such as combining baseball statistics across years. First, let's (artificially) construct two Series, consisting of home runs hit in years 2006 and 2007, respectively:

In [86]:

```
hr2006 = baseball.loc[baseball.year==2006, 'hr']
hr2006.index = baseball.player[baseball.year==2006]

hr2007 = baseball.loc[baseball.year==2007, 'hr']
hr2007.index = baseball.player[baseball.year==2007]
```

In [87]:

```
hr2007.head(10)
```

Out[87]:

```
player
francju01      0
francju01      1
zaungr01      10
witasja01      0
williwo02      1
wickmbo01      0
wickmbo01      0
whitero02      4
whiteri01      0
wellsda01      0
Name: hr, dtype: int64
```

Now, let's add them together, in hopes of getting 2-year home run totals:

In [88]:

```
hr_total = hr2006 + hr2007
hr_total.head(20)
```

Out[88]:

```
player
alomasa02    NaN
aloumo01     NaN
ausmubr01    NaN
benitar01    NaN
benitar01    NaN
biggicr01    NaN
bondsba01    NaN
cirilje01    NaN
cirilje01    NaN
claytro01    NaN
claytro01    NaN
clemero02    NaN
coninje01    NaN
coninje01    NaN
cormirh01    NaN
delgaca01    NaN
easleda01    NaN
edmonji01    NaN
embreal01    NaN
finlest01    7.0
Name: hr, dtype: float64
```

Pandas' data alignment places `NaN` values for labels that do not overlap in the two Series. In fact, there are only 6 players that occur in both years.

In [89]:

```
hr_total[hr_total.notnull()]
```

Out[89]:

```
player
finlest01     7.0
gonzalu01    30.0
johnsra05     0.0
myersmi01     0.0
schilcu01     0.0
seleaa01      0.0
Name: hr, dtype: float64
```

While we do want the operation to honor the data labels in this way, we probably do not want the missing values to be filled with `NaN`. We can use the `add` method to calculate player home run totals by using the `fill_value` argument to insert a zero for home runs where labels do not overlap:

In [90]:

```
hr2007.add(hr2006, fill_value=0).head(20)
```

Out[90]:

```
player
alomasa02     0.0
aloumo01     13.0
ausmubr01     3.0
benitar01     0.0
benitar01     0.0
biggicr01    10.0
bondsba01    28.0
cirilje01     0.0
cirilje01     2.0
claytro01     0.0
claytro01     1.0
clemero02     0.0
coninje01     0.0
coninje01     6.0
cormirh01     0.0
delgaca01    24.0
easleda01    10.0
```

```
edmonji01    12.0
embreal01     0.0
finlest01     7.0
Name: hr, dtype: float64
```

Operations can also be **broadcast** between rows or columns.

For example, if we subtract the maximum number of home runs hit from the `hr` column, we get how many fewer than the maximum were hit by each player:

In [91]:

```
(baseball.hr - baseball.hr.max()).head(20)
```

Out[91]:

```
id
88641   -34
88643   -35
88645   -35
88649   -35
88650   -35
88652   -29
88653   -20
88662   -35
89177   -35
89178   -34
89330   -25
89333   -35
89334   -34
89335   -35
89336   -35
89337   -31
89338   -35
89339   -35
89340   -35
89341   -35
Name: hr, dtype: int64
```

Sorting

Pandas objects include methods for re-ordering data.

In [92]:

```
baseball_newind.sort_index().head()
```

Out[92]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb
alomasa02NYN2007	alomasa02	2007	1	NYN	NL	8	22	1	3	1	...	0.0	0.0	0.0	0
aloumo01NYN2007	aloumo01	2007	1	NYN	NL	87	328	51	112	19	...	49.0	3.0	0.0	27
ausmubr01HOU2007	ausmubr01	2007	1	HOU	NL	117	349	38	82	16	...	25.0	6.0	1.0	37
benitar01FLO2007	benitar01	2007	2	FLO	NL	34	0	0	0	0	...	0.0	0.0	0.0	0
benitar01SFN2007	benitar01	2007	1	SFN	NL	19	0	0	0	0	...	0.0	0.0	0.0	0

5 rows × 22 columns

In [93]:

```
baseball_newind.sort_index(ascending=False).head()
```

Out[93]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	rbi	sb	cs	bb
zaungr01TOR2007	zaungr01	2007	1	TOR	AL	110	331	43	80	24	...	52.0	0.0	0.0	51
womacto01CHN2006	5	5	5	5	5	5	5	5	5	5	...	5.0	5.0	5.0	5

witasja01TBA2007	witasja01	2007	1	TBA	AL	3	0	0	0	0	...	0.0	0.0	0.0	0	0
williwo02HOU2007	williwo02	2007	1	HOU	NL	33	59	3	6	0	...	2.0	0.0	0.0	0	2
wickmbo01ATL2007	wickmbo01	2007	1	ATL	NL	47	0	0	0	0	...	0.0	0.0	0.0	0	0

5 rows × 22 columns

Try sorting the **columns** instead of the rows, in ascending order:

In [94]:
```
baseball_newind.sort_index(axis=1).head()
```

Out[94]:

	X2b	X3b	ab	bb	cs	g	gidp	h	hbp	hr	...	player	r	rbi	sb	sf	sh	so
womacto01CHN2006	5	5	5	5	5.0	5	5.0	5	5.0	5	...	5	5	5.0	5.0	5.0	5.0	5.0
schilcu01BOS2006	5	5	5	5	5.0	5	5.0	5	5.0	5	...	5	5	5.0	5.0	5.0	5.0	5.0
myersmi01NYA2006	5	5	5	5	5.0	5	5.0	5	5.0	5	...	5	5	5.0	5.0	5.0	5.0	5.0
helliri01MIL2006	5	5	5	5	5.0	5	5.0	5	5.0	5	...	5	5	5.0	5.0	5.0	5.0	5.0
johnsra05NYA2006	5	5	5	5	5.0	5	5.0	5	5.0	5	...	5	5	5.0	5.0	5.0	5.0	5.0

5 rows × 22 columns

We can also use `sort_values` to sort a `Series` by value, rather than by label.

In [95]:
```
baseball.hr.sort_values(ascending=False).head(10)
```

Out[95]:
```
id
89360    35
89462    30
89521    28
89361    26
89378    25
89489    24
89374    21
89371    21
89396    20
89439    20
Name: hr, dtype: int64
```

For a `DataFrame`, we can sort according to the values of one or more columns using the `by` argument of `sort_values`:

In [96]:
```
baseball[['player','sb','cs']].sort_values(ascending=[False,True],
                                           by=['sb', 'cs']).head(10)
```

Out[96]:

	player	sb	cs
id			
89378	sheffga01	22.0	5.0
89430	loftoke01	21.0	4.0
89347	vizquom01	14.0	6.0
89463	greensh01	11.0	1.0
88652	finlest01	7.0	0.0
89462	griffke02	6.0	1.0
89530	ausmubr01	6.0	1.0

89466	gonzalu01	6.0	2.0
89521	bondsba01	5.0	0.0
89438	kleskry01	5.0	1.0

Exercise 5

Calculate **on base percentage** for each player, and return the ordered series of estimates.

$$obp = \frac{h + bb + hbp}{ab + bb + hbp + sf}$$

In [97]:
```
baseball['obp']=baseball.apply(lambda p: (p.h+p.bb+p.hbp)/(p.ab+p.bb+p.hbp+p.sf) if (p.a
```

Missing data

The occurence of missing data is so prevalent that it pays to use tools like Pandas, which seamlessly integrates missing data handling so that it can be dealt with easily, and in the manner required by the analysis at hand.

Missing data are represented in `Series` and `DataFrame` objects by the `NaN` floating point value. However, `None` is also treated as missing, since it is commonly used as such in other contexts (*e.g.* NumPy).

In [98]:
```
foo = pd.Series([np.nan, -3, None, 'foobar'])
foo
```

Out[98]:
```
0        NaN
1         -3
2       None
3     foobar
dtype: object
```

In [99]:
```
foo.isnull()
```

Out[99]:
```
0     True
1    False
2     True
3    False
dtype: bool
```

Missing values may be dropped or indexed out:

In [100…
```
foo.dropna()
```

Out[100]:
```
1         -3
3     foobar
dtype: object
```

In [101…
```
foo[foo.notnull()]
```

Out[101]:
```
1         -3
3     foobar
dtype: object
```

By default, `dropna` drops entire rows in which one or more values are missing.

In [102…

```
data.dropna()
```

Out[102]:

	patient	phylum	value	year	treatment
0	1	Firmicutes	632	2013	0.0
1	1	Proteobacteria	1638	2013	0.0
2	1	Actinobacteria	569	2013	0.0
3	1	Bacteroidetes	14	2013	0.0
4	2	Firmicutes	21	2013	1.0
5	2	Proteobacteria	0	2013	1.0

This can be overridden by passing the `how='all'` argument, which only drops a row when every field is a missing value.

In [103…

```
data.dropna(how='all')
```

Out[103]:

	patient	phylum	value	year	treatment
0	1	Firmicutes	632	2013	0.0
1	1	Proteobacteria	1638	2013	0.0
2	1	Actinobacteria	569	2013	0.0
3	1	Bacteroidetes	14	2013	0.0
4	2	Firmicutes	21	2013	1.0
5	2	Proteobacteria	0	2013	1.0
6	2	Actinobacteria	5	2013	NaN
7	2	Bacteroidetes	555	2013	NaN

Rather than omitting missing data from an analysis, in some cases it may be suitable to fill the missing value in, either with a default value (such as zero) or a value that is either imputed or carried forward/backward from similar data points. We can do this programmatically in Pandas with the `fillna` argument.

In [104…

```
bacteria2.fillna(0)
```

Out[104]:

```
phylum
Firmicutes           0.0
Proteobacteria     632.0
Actinobacteria    1638.0
Bacteroidetes      569.0
dtype: float64
```

In [105…

```
data.fillna({'year': 2013, 'treatment':2})
```

Out[105]:

	patient	phylum	value	year	treatment
0	1	Firmicutes	632	2013	0.0
1	1	Proteobacteria	1638	2013	0.0
2	1	Actinobacteria	569	2013	0.0
3	1	Bacteroidetes	14	2013	0.0
4	2	Firmicutes	21	2013	1.0

5	2	Proteobacteria	0	2013	1.0
6	2	Actinobacteria	5	2013	2.0
7	2	Bacteroidetes	555	2013	2.0

Notice that `fillna` by default returns a new object with the desired filling behavior, rather than changing the `Series` or `DataFrame` **in place**.

We can alter values in-place using `inplace=True`.

In [106…

```
data['treatment'].fillna(2, inplace=True)
data
```

Out[106]:

	patient	phylum	value	year	treatment
0	1	Firmicutes	632	2013	0.0
1	1	Proteobacteria	1638	2013	0.0
2	1	Actinobacteria	569	2013	0.0
3	1	Bacteroidetes	14	2013	0.0
4	2	Firmicutes	21	2013	1.0
5	2	Proteobacteria	0	2013	1.0
6	2	Actinobacteria	5	2013	2.0
7	2	Bacteroidetes	555	2013	2.0

Missing values can also be interpolated, using any one of a variety of methods:

In [107…

```
bacteria2.fillna(method='bfill')
```

Out[107]:

```
phylum
Firmicutes         632.0
Proteobacteria     632.0
Actinobacteria    1638.0
Bacteroidetes      569.0
dtype: float64
```

Data summarization

We often wish to summarize data in `Series` or `DataFrame` objects, so that they can more easily be understood or compared with similar data. The NumPy package contains several functions that are useful here, but several summarization or reduction methods are built into Pandas data structures.

In [108…

```
baseball.sum()
```

Out[108]:

```
player    womacto01schilcu01myersmi01helliri01johnsra05f...
year                                                 200692
stint                                                   113
team      CHNBOSNYAMILNYASFNARILANATLNYNTORTBAHOUARIATLM...
lg        NLALALNLALNLNLNLNLNLALALNLNLNLALNLNLNLNLALALNL...
g                                                      5238
ab                                                    13654
r                                                      1869
h                                                      3582
X2b                                                     739
X3b                                                      55
```

```
hr                                                         437
rbi                                                     1847.0
sb                                                       138.0
cs                                                        46.0
bb                                                        1549
so                                                      2408.0
ibb                                                      177.0
hbp                                                      112.0
sh                                                       138.0
sf                                                       120.0
gidp                                                     354.0
obp                                                  20.751829
dtype: object
```

Clearly, `sum` is more meaningful for some columns than others. For methods like `mean` for which application to string variables is not just meaningless, but impossible, these columns are **automatically exculded**:

In [109…

```
baseball.mean(numeric_only=True)
```

Out[109]:

```
year     2006.920000
stint       1.130000
g          52.380000
ab        136.540000
r          18.690000
h          35.820000
X2b         7.390000
X3b         0.550000
hr          4.370000
rbi        18.470000
sb          1.380000
cs          0.460000
bb         15.490000
so         24.080000
ibb         1.770000
hbp         1.120000
sh          1.380000
sf          1.200000
gidp        3.540000
obp         0.207518
dtype: float64
```

The important difference between NumPy's functions and Pandas' methods is that the latter have built-in support for handling missing data.

In [110…

```
bacteria2
```

Out[110]:

```
phylum
Firmicutes           NaN
Proteobacteria     632.0
Actinobacteria    1638.0
Bacteroidetes      569.0
dtype: float64
```

In [111…

```
bacteria2.mean()
```

Out[111]:

```
946.3333333333334
```

Sometimes we may not want to ignore missing values, and allow the `nan` to propagate.

In [112…

```
bacteria2.mean(skipna=False)
```

Out[112]:

```
nan
```

Passing `axis=1` will summarize over rows instead of columns, which only makes sense in certain situations.

In [113…

```
extra_bases = baseball[['X2b','X3b','hr']].sum(axis=1)
extra_bases.sort_values(ascending=False).head(20)
```

Out[113]:

```
id
88653    69
89439    57
89361    56
89462    55
89396    54
89360    54
89489    54
89371    50
89378    46
89374    46
89389    45
89523    44
89521    42
89463    41
89466    40
88652    39
89438    36
89330    35
89533    33
89481    29
dtype: int64
```

A useful summarization that gives a quick snapshot of multiple statistics for a `Series` or `DataFrame` is `describe`:

In [114…

```
baseball.describe()
```

Out[114]:

	year	stint	g	ab	r	h	X2b	X3b
count	100.00000	100.000000	100.000000	100.000000	100.00000	100.000000	100.000000	100.000000
mean	2006.92000	1.130000	52.380000	136.540000	18.69000	35.820000	7.390000	0.550000
std	0.27266	0.337998	48.031299	181.936853	27.77496	50.221807	11.117277	1.445124
min	2006.00000	1.000000	1.000000	0.000000	0.00000	0.000000	0.000000	0.000000
25%	2007.00000	1.000000	9.500000	2.000000	0.00000	0.000000	0.000000	0.000000
50%	2007.00000	1.000000	33.000000	40.500000	2.00000	8.000000	1.000000	0.000000
75%	2007.00000	1.000000	83.250000	243.750000	33.25000	62.750000	11.750000	1.000000
max	2007.00000	2.000000	155.000000	586.000000	107.00000	159.000000	52.000000	12.000000

`describe` can detect non-numeric data and sometimes yield useful information about it.

In [115…

```
baseball.player.describe()
```

Out[115]:

```
count           100
unique           82
top       wellsda01
freq              2
Name: player, dtype: object
```

We can also calculate summary statistics *across* multiple columns, for example, correlation and covariance.

$$cov(x,y) = \sum_i (x_i - \bar{x})(y_i - \bar{y})$$

```
In [116…  baseball.hr.cov(baseball.X2b)
```

```
Out[116]: 69.07646464646454
```

$$corr(x,y) = \frac{cov(x,y)}{(n-1)s_x s_y} = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2 \sum_i (y_i - \bar{y})^2}}$$

```
In [117…  baseball.hr.corr(baseball.X2b)
```

```
Out[117]: 0.7790615182539742
```

```
In [118…  baseball.ab.corr(baseball.h)
```

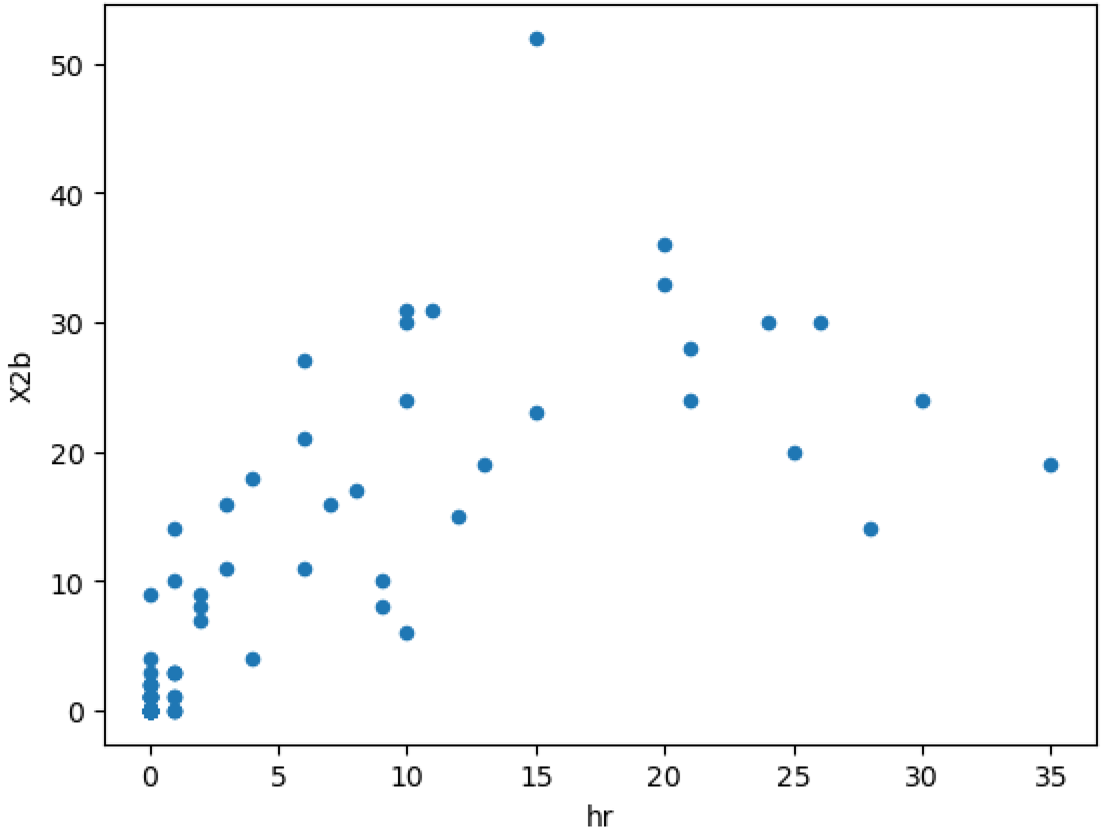
```
Out[118]: 0.9942174036272377
```

Plotting

Sometimes the correlation between two attributes is obvious when we plot them in the 2-d space. Also other kinds of plots (e.g., histograms) help us understand whether our data follows a particular law (e.g., a power law). Thus, it is crucial, not only to know how to select the appropriate slice of our dataset, but also how to properly visualize it.

```
In [119…  baseball.plot.scatter(x='hr', y='X2b')
```

```
Out[119]: <Axes: xlabel='hr', ylabel='X2b'>
```

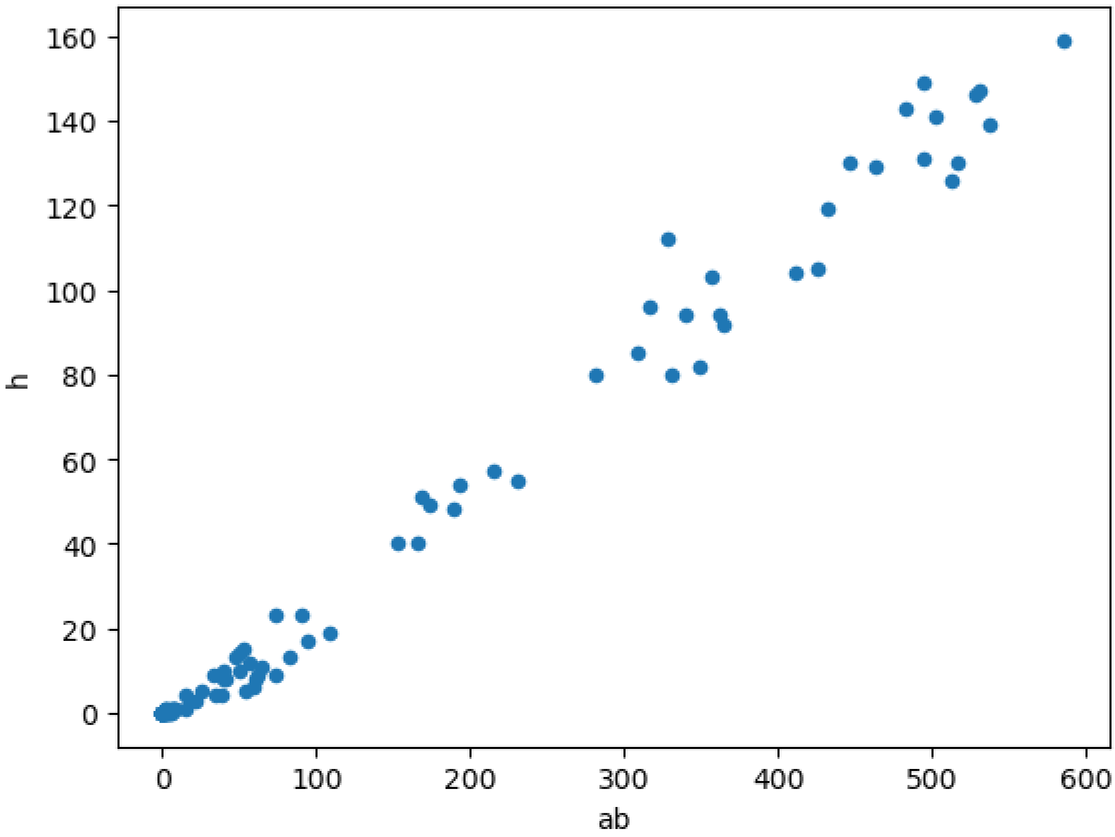


In [120…

```
baseball.plot.scatter(x='ab', y='h')
```

Out[120]:

```
<Axes: xlabel='ab', ylabel='h'>
```



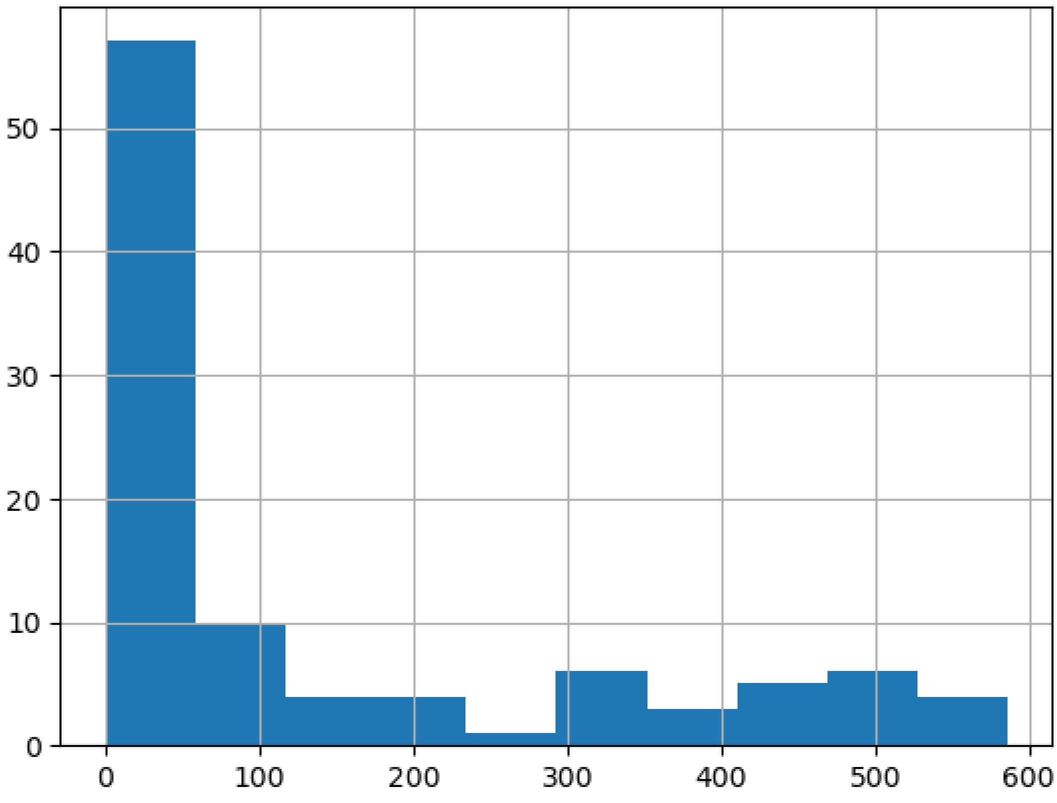
Do you understand which of the above has better correlation?

In [121…

```
baseball['ab'].hist()
```

Out[121]:

```
<Axes: >
```

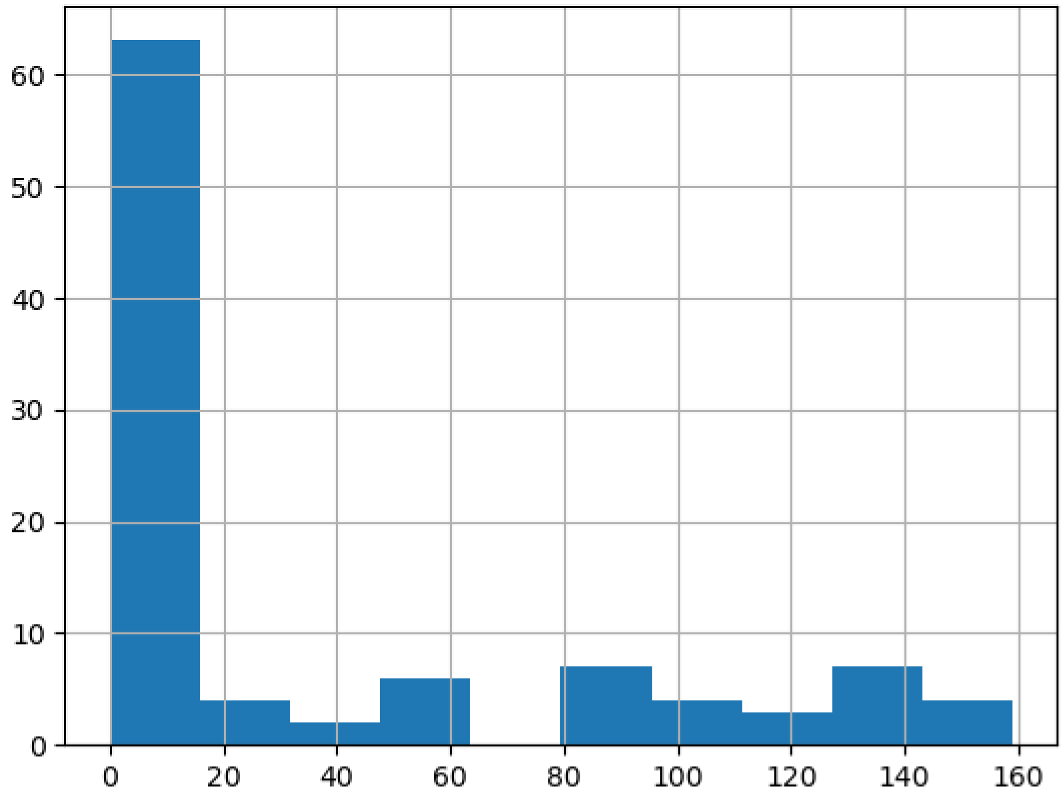


In [122…

```
baseball['h'].hist()
```

Out[122]:

```
<Axes: >
```



What do you observe in the distributions of the two attributes? Is it safe to say that they correlate based on the last two plots? Why we need also the scatterplots?

Writing Data to Files

As well as being able to read several data input formats, Pandas can also export data to a variety of storage formats. We will bring your attention to just a couple of these.

In [123…

```
mb.to_csv("mb.csv")
```

The `to_csv` method writes a `DataFrame` to a comma-separated values (csv) file. You can specify custom delimiters (via `sep` argument), how missing values are written (via `na_rep` argument), whether the index is writen (via `index` argument), whether the header is included (via `header` argument), among other options.

An efficient way of storing data to disk is in **binary format**. Pandas supports this using Python's built-in pickle serialization.

In [124…

```
baseball.to_pickle("baseball_pickle")
```

The complement to `to_pickle` is the `read_pickle` function, which restores the pickle to a `DataFrame` or `Series` :

In [125…

```
pd.read_pickle("baseball_pickle").head()
```

Out[125]:

	player	year	stint	team	lg	g	ab	r	h	X2b	...	sb	cs	bb	so	ibb	hbp	sh	sf
id																			

88641	womacto01	2006	2	CHN	NL	19	50	6	14	1	...	1.0	1.0	4	4.0	0.0	0.0	3.0	0.0
88643	schilcu01	2006	1	BOS	AL	31	2	0	1	0	...	0.0	0.0	0	1.0	0.0	0.0	0.0	0.0
88645	myersmi01	2006	1	NYA	AL	62	0	0	0	0	...	0.0	0.0	0	0.0	0.0	0.0	0.0	0.0
88649	helliri01	2006	1	MIL	NL	20	3	0	0	0	...	0.0	0.0	0	2.0	0.0	0.0	0.0	0.0
88650	johnsra05	2006	1	NYA	AL	33	6	0	1	0	...	0.0	0.0	0	4.0	0.0	0.0	0.0	0.0

5 rows × 23 columns

As Wes warns in his book [1], it is recommended that binary storage of data via pickle only be used as a temporary storage format, in situations where speed is relevant. This is because there is no guarantee that the pickle format will not change with future versions of Python.

References

[1] Python for Data Analysis Wes McKinney