

Data Science With Python

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Contents

Chapter 1

Overview

These are some notes that may be helpful for computational biology analysis that focuses on Python use.

Chapter 2

Python

2.1 General

Here is a general skeleton that can be used to start a python script that takes input.

```
#!/usr/bin/env python

def runArgparse():
    import argparse

    parser = argparse.ArgumentParser()
    parser.add_argument('--indir', '-i', type=str, nargs='*', help='Input directory containing the vcf files')
    parser.add_argument('--loadolddata', '-o', action='store_true', help='Load previously existing data.')

    args = parser.parse_args()
    indir = args.indir
    return indir

if __name__ == '__main__':
    runArgparse()
```

2.2 Numba

Numba speeds up python code without having to switch to a different interpreter, and doesn't require static typing of variables as Cython does. Just calling Numba will increase the speed of a script (except during the compilation which will add some time). But this isn't the best way to take advantage of the speed boost.

Here is an example script that uses jit to invoke Numba.

```
#!/usr/bin/env python

from numba import jit
import numpy as np
import time

def go_slow(x):
```

```

    for i in range(14):
        x *= x

@jit(nopython=True)
def go_fast(x):
    for i in range(14):
        x *= x

# DO NOT REPORT THIS... COMPILATION TIME IS INCLUDED IN THE EXECUTION TIME!
start = time.time()
go_slow(5)
end = time.time()
print("Elapsed slow (with compilation) = %s" % (end - start))
start = time.time()
go_fast(5)
end = time.time()
print("Elapsed fast (with compilation) = %s" % (end - start))

# DO NOT REPORT THIS... COMPILATION TIME IS INCLUDED IN THE EXECUTION TIME!
start = time.time()
go_slow(5)
end = time.time()
print("Elapsed slow (after compilation) = %s" % (end - start))
start = time.time()
go_fast(5)
end = time.time()
print("Elapsed fast (after compilation) = %s" % (end - start))

```

Parallelization can be used to automatically utilize multiple cores.

```

from numba import njit, prange
@njit(parallel=True)
def prange_test(A):
    s = 0
    for i in prange(A.shape[0]):
        s += A[i]
    return s

```

2.3 Cython

Installation

```
conda install -c conda-forge cython
```

Ipython usage

```

%load_ext Cython

%%cython
def f(x):
    return 2 * x

```



```
or

def f(int x):
    return 2 * x

timeit(f(4))
```


Chapter 3

JupyterLab

Here is a simple template that I use that controls a couple useful things when starting a new notebook.

```
import sys
sys.path.append('../util')

%reload_ext autoreload
%autoreload 2

from util import *
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns

sns.set_palette('pastel')
sns.set_style('ticks')
sns.set_context('paper', font_scale=1)
```

It is often convenient to have a notebook automatically refresh the imported libraries so that they can be modified while working on a JupyterLab notebook.

```
%reload_ext autoreload
%autoreload 2
```

To allow directory organization, dependencies can be separated into different directories and imported into a jupyter notebook using the following import statement.

```
import sys
sys.path.append('../util')
```

A table of contents can be created to refer to each of the headers throughout a notebook in html format. The code is below (Obviously needs to be simplified.)

```
<h1>Table of Contents<span class="tocSkip"></span></h1>
<div class="toc">
  <ul class="toc-item">
```



```

        <ul class="toc-item">
          <li><span><a href="#DNMT3A" data-toc-modified-id="DNMT3A-7.0.1"><span class="toc-item-num">
          <li><span><a href="#TET2" data-toc-modified-id="TET2-7.0.2"><span class="toc-item-num">7.0.1
          <li><span><a href="#ASXL1" data-toc-modified-id="ASXL1-7.0.3"><span class="toc-item-num">7.0.3&nb
          <li><span><a href="#TP53" data-toc-modified-id="TP53-7.0.4"><span class="toc-item-num">7.0.4&nb
          <li><span><a href="#Functions-for-calculating-the-expected-number-of-observations-of-a-variant" data
          <li><span><a href="#Maximum-Likelihood-Estimation-for-s" data-toc-modified-id="Maximum-Likelihood-E
            <ul class="toc-item"><li><span><a href="#DNMT3A-variants" data-toc-modified-id="DNMT3A-variants
            <li><span><a href="#TET2-variants" data-toc-modified-id="TET2-variants-9.2"><span class="toc-it
            <li><span><a href="#ASXL1-variants" data-toc-modified-id="ASXL1-variants-9.3"><span class="toc-
            <li><span><a href="#TP53-variants" data-toc-modified-id="TP53-variants-9.4"><span class="toc-it
          </ul>
        </li>
      </ul>
    </div>

```


Chapter 4

Visualization

4.1 Color

4.1.1 Colorschemes

Seaborn Themes

```
Pastel: {'Blue': '#a3c6ff', 'Orange': '#f7ab60', 'Green': '#60f7a9', 'Red': '#fc9d94', 'Purple': '#bea3ff',
```

```
Deep: {'Green': '#5baf68'}
```

4.1.2 Controlling Coloration

Not all plots automatically plot with a white background, and when using something dark like jupyterlab or a presentation this can be frustrating. The background color can be set in pyplot like this.

```
fig.patch.set_facecolor('xkcd:mint green')
```

When plotting, samples will not always be colored with the same color, especially when different subsets of samples are included in different plots. Here is a manual workaround to specify the coloration of displayed data. This is a bit cumbersome so there might be a more elegant way of achieving the same outcome.

```
# here is an example where sample order is controlled from a pandas DataFrame
sample_order = all_vars.sort_values(['ID']).drop_duplicates(['Sample']).Sample

# the color order is specified here
# colors should be in the same order as the above sample_order Series, excluding samples with no data
colors = [pastel['Brown'], pastel['Blue'],
          pastel['Orange'], pastel['Purple'],
          pastel['Green'], pastel['Red'],
          ]

plt.figure()
# this is an example of plotting that uses the sample_order and palette to control coloration order
sns.catplot(x='Sample', y='VAF', hue='Gene', jitter=True,
            data=oncogenic[oncogenic.Location == 'Peripheral'],
```

```

        legend=False, order=sample_order, palette=sns.color_palette(colors))

# a colorscheme can be specified if desired
pastel = {'Blue': '#a3c6ff', 'Orange': '#f7ab60',
          'Green': '#60f7a9', 'Red': '#fc9d94',
          'Purple': '#bea3ff', 'Brown': '#d1b485',
          'Pink': '#f7afdf', 'Gray': '#c4c4c4',
          'Yellow': '#ffffaa', 'LBlue': '#baf6ff'}

# this controls the coloration in the legend
import matplotlib.patches as mpatches
egfr = mpatches.Patch(color=pastel['Blue'], label='EGFR')
pik3ca = mpatches.Patch(color=pastel['Orange'], label='PIK3CA')
myc = mpatches.Patch(color=pastel['Green'], label='MYC')

plt.legend(handles=[egfr,pik3ca,myc],
           loc='upper right', bbox_to_anchor=(1.5, 1),
           ncol=1) # no legend overlap

```

4.2 Matplotlib

Plotting a heatmap.

```

import matplotlib.pyplot as plt
import numpy as np
a = np.random.random((16, 16))
plt.imshow(a, cmap='RdBu', interpolation='nearest')
plt.show()

```

Possible heatmap colors are:

Accent, Accent_r, Blues, Blues_r, BrBG, BrBG_r, BuGn, BuGn_r, BuPu, BuPu_r, CMRmap, CMRmap_r, Dark2, Dark2_r, Set1_r, Set2, Set2_r, Set3, Set3_r, Spectral, Spectral_r, Wistia, Wistia_r, YlGn, YlGnBu, YlGnBu_r, YlGn_r, gist_stern, gist_stern_r, gist_yarg, gist_yarg_r, gnuplot, gnuplot2, gnuplot2_r, gnuplot_r, gray, gray_r, twilight, twilight_r, twilight_shifted, twilight_shifted_r, viridis, viridis_r, vlag, vlag_r, winter, winter_r

A simple venn diagram.

```

from matplotlib_venn import venn2
venn2(subsets = (3, 2, 1))

```

A more complicated venn diagram.

```

from matplotlib import pyplot as plt
import numpy as np
from matplotlib_venn import venn3, venn3_circles
plt.figure(figsize=(4,4))
v = venn3(subsets=(1, 1, 1, 1, 1, 1, 1), set_labels = ('A', 'B', 'C'))
v.get_patch_by_id('100').set_alpha(1.0)
v.get_patch_by_id('100').set_color('white')

```



```

v.get_label_by_id('100').set_text('Unknown')
v.get_label_by_id('A').set_text('Set "A"')
c = venn3_circles(subsets=(1, 1, 1, 1, 1, 1, 1), linestyle='dotted')
c[0].set_lw(1.0)
c[0].set_ls('dotted')
plt.title("Sample Venn diagram")
plt.annotate('Unknown set', xy=v.get_label_by_id('100').get_position() - np.array([0, 0.05]), xytext=(-1, 0.05),
             ha='center', textcoords='offset points', bbox=dict(boxstyle='round,pad=0.5', fc='gray', alpha=0.5),
             arrowprops=dict(arrowstyle='->', connectionstyle='arc3,rad=0.5',color='gray'))
plt.show()

```

An upset plot is a nice alternative to a traditional venn diagram. The project is hosted [here](#), and this is the [documentation](#).

First install the library.

```
pip install upsetplot
```

Here is the code to create the plot.

```

import numpy as np

arrays = [[False,False,False,False,True,True,True,True],
          [False,False,True,True,False,False,True,True],
          [False,True,False,True,False,True,False,True]]
tuples = list(zip(*arrays))

def o(one=False, two=False, three=False):
    if three:
        temp = pd.merge(indels[(indels.Individual==one)], indels[(indels.Individual==two)], how='inner')
        return len(pd.merge(temp, indels[(indels.Individual==three)], how='inner', on=['Loc', 'Var']))
    elif two:
        return len(pd.merge(indels[(indels.Individual==one)], indels[(indels.Individual==two)], how='inner'))
    elif one:
        return len(indels[(indels.Individual==one)])
    else:
        return 0

index = pd.MultiIndex.from_tuples(tuples, names=['Ind 1', 'Ind 2', 'Ind 3'])
s = pd.Series([o(),
               o(3),
               o(2),
               o(2,3),
               o(1),
               o(1,3),
               o(1,2),
               o(1,2,3)], index=index)

from upsetplot import plot as up
up(s)
plt.savefig("../images/indels.svg", format="svg", bbox_inches="tight")

```

Log scales seem to always be a challenge. Here is at least one solution to change ticks to log manually.

```

y_major_ticks = [np.log(100),np.log(200),np.log(300),np.log(400),np.log(500),np.log(600),np.log(700),np
np.log(1000),np.log(2000),np.log(3000),np.log(4000),np.log(5000),np.log(6000),np.log(7000),np.log(8000),np
np.log(10000),np.log(20000),np.log(30000),np.log(40000),np.log(50000),np.log(60000),np.log(70000),np.log(80000),np
np.log(100000),np.log(200000),np.log(300000),np.log(400000),np.log(500000),np.log(600000),np.log(700000),np.log(800000),np
np.log(1000000),np.log(2000000),np.log(3000000),np.log(4000000),np.log(5000000),np.log(6000000),np.log(7000000),np.log(8000000),np
np.log(10000000)]

y_major_tick_labels = ["100","","","","","","","","","","","1000","","","","","","","","","","10,000","\
","","","","","","","","","","100,000","","","","","","","","","","1,000,000","","","","",""]
ax1.set_yticks(y_major_ticks)
ax1.set_yticklabels(y_major_tick_labels, fontsize = axisfont)
ax1.yaxis.set_tick_params(width=scale, color = grey3, length = 6)

```

4.3 Seaborn

Here is a general bar plot that includes some commonly used parameters.

```

# fits my 22 inch monitor
plt.figure(figsize=(19.17,11.98))
# order controls the display order of the samples
sns.catplot(x="Sample", y="Somatic", kind="bar", data=var_counts, order=labels);
# keeps x-axis labels, but eliminates the tick mark
plt.tick_params(labelbottom=True, bottom=False)
# trim off the x-axis
sns.despine(offset=10, trim=True, bottom=True)
# labels
plt.title('')
plt.ylabel('', fontsize=8)
plt.xlabel('', fontsize=8)
# manual control of xlabels
labels = ['Indiv_1-a','Indiv_2','Indiv_3','Indiv_1-b']
# control xtick order
plt.xticks(range(len(labels)), labels, rotation=45)
# control the number of x-ticks
plt.locator_params(axis='x', nbins=10)
# legend positioning
plt.legend(loc='upper right')
# log scale
plt.gca().set_yscale('log')
# this is better if neg values are needed
plt.gca().set_yscale('symlog')
# fit plot to display
plt.tight_layout()
plt.show()
# save figure with tight_layout
plt.savefig("test.svg", format="svg", bbox_inches="tight", dpi=1000)

```

Significance information can be added by including p-values and label bars using the following code.

```

x1, x2 = 0, 1 # columns to annotate on the plot
y2, y1 = 20, 15 # placement of the line and how far down the vertical legs go

```

```
plt.plot([x1,x1, x2, x2], [y1, y2, y2, y1], linewidth=1, color='k') # stats line
plt.text((x1+x2)*.5, y2+2, "p=0.09", ha='center', va='bottom', fontsize=8) # p-value or sig
```

4.4 Statistics

This is a two-sided T-test for the null hypothesis that two populations have the same means. It is important to note that it assumes the population variances are the same, so this must be changed if the assumption is incorrect.

```
# ttest_ind(a, b, axis=0, equal_var=True, nan_policy='propagate')
from scipy.stats import ttest_ind
ttest_ind(df[df['sample'] == 'one']['means'], df[df['sample'] == 'two']['means'])
```

4.5 Various Plot Styles

This displays each individual datapoint overlayed on a boxplot

```
ax = sns.boxplot(x='day', y='total_bill', data=tips)
ax = sns.swarmplot(x='day', y='total_bill', data=tips, color='.25')
```


Chapter 5

Biology

5.1 General

Some helpful commands for genetic sequence.

```
from string import ascii_uppercase # python 3
from string import upper, lower # python 2
upper('tcga')
lower('TCGA')
title('tcga') # capitalize the first letter
```

5.2 Biopython

Reverse complement of sequence

```
from Bio.Seq import Seq
str(Seq(i).reverse_complement())
```

5.3 UCSC Genome Browser

Get sequence from UCSC genome browser

```
from subprocess import check_output, STDOUT
temp = check_output('wget -q0- http://genome.ucsc.edu/cgi-bin/das/hg19/dna?segment=%s:%s,%s' % (vcfObj.chrom, vcfObj.start, vcfObj.end), stderr=STDOUT, shell=True)
```

5.4 Ref Genome

Get sequence from reference genome

```
from subprocess import check_output, STDOUT
temp = check_output('samtools faidx %s %s:%s-%s' % (ref, vcfObj.chrom, low, high), stderr=STDOUT, shell=True)
```

```
finalSeq = ''
for line in temp.decode('UTF-8').split('\n'):
for line in temp.decode('UTF-8').split('\n'): # this is only necessary in python 3 to convert binary to
    if '>' not in line:
        finalSeq += line

finalSeq = finalSeq.upper()
```

5.5 Personal Information

```
# parse vcf file with parseline
if '#' not in line and 'chr' in line: # skip the info
# vcf handling
from parseline import VCFObj
# or
from util import VCFObj
vcfObj = VCFObj(vcfLine)
# available attributes: ao, dp, af, wt, var, chrom, location
```

Chapter 6

Data I/O

6.1 Reading Data Files

Opening .gz files

```
import gzip
for line in gzip.open('myFile.gz'):
    print line
```

6.2 Pickles

Writing data in pickle format

```
import pickle
p = open('principle.pkl', 'wb')
pickle.dump(principleData, p)
p.close()
```

Reading data in pickle format

```
import pickle
p = open('principle.pkl', 'rb')
principleData = pickle.load(p)
p.close()
```


Chapter 7

Pandas

7.1 File I/O

Read a csv file into a DataFrame.

```
pd.read_csv(filepath)
```

Write a DataFrame to a file.

```
x.to_csv(path_or_buf='outputDir', sep='\n', header=False, index=False)
```

7.2 Data Structure Creation

Create a DataFrame.

```
frame = pd.DataFrame(np.random.randn(4,3), columns=list('bde'), index=['Utah','Ohio','Texas','Oregon'])
```

A DataFrame can conveniently be created from a dictionary.

```
import pandas as pd
data = {'AAA' : [4,5,6,7], 'BBB' : [10,20,30,40], 'CCC' : [100,50,-30,-50]}
df2 = pd.DataFrame(data=data, index=[1,2,3,4]) #Note index starts at 1.
df2
```

```
##      AAA  BBB  CCC
## 1      4   10  100
## 2      5   20   50
## 3      6   30  -30
## 4      7   40  -50
```

7.3 Selection

Is data within a DataFrame found within a dictionary or list? (Instead of a dictionary a series can be used and maybe another DataFrame)

```
import pandas as pd
df = pd.DataFrame({'A': [1, 2, 3], 'B': ['a', 'b', 'f']})
df.isin([1, 3, 12, 'a'])
```

```
##      A      B
## 0   True   True
## 1  False  False
## 2   True  False
```

```
df[df.isin([1, 3, 12, 'a'])]
```

```
##      A      B
## 0  1.0     a
## 1  NaN    NaN
## 2  3.0    NaN
```

Data within a DataFrame can be selected based on position within the DataFrame.

```
import pandas as pd
df2.iloc[1:3]
```

```
##      AAA  BBB  CCC
## 2     5   20   50
## 3     6   30  -30
```

Data within a DataFrame can be selected based on position within the DataFrame.

```
import pandas as pd
df2.loc[1:3]
```

```
##      AAA  BBB  CCC
## 1     4   10  100
## 2     5   20   50
## 3     6   30  -30
```

The opposite of matching data can be selected with the inverse operator.

```
df[~((df.AAA <= 6) & (df.index.isin([0,2,4])))]
```

7.4 Splitting

Concatenate two DataFrames together without dropping any values or renaming indices.

```
left = pd.concat([left, left])
```

Concatenate two DataFrames together without dropping values, but renaming index.

```
left = pd.concat([left, left], ignore_index=True)
```

Count the number of each unique value in a specified column.

```
left['key1'].value_counts()
left.key1.value_counts()
```

Value counts can also be calculated as percentages so that raw counts as percent makeup can be compared.

```
left['key1'].value_counts(normalize=True) * 100
```

Two DataFrames can be merged such that only the data containing matching keys is retained.

```
result = pd.merge(left, right, how='inner', on=['key1', 'key2'])
```

This DataFrame merge will retain all of the data in the right DataFrame.

```
result = pd.merge(left, right, how='right', on=['key1', 'key2'])
```

Filter by multiple columns.

```
df[(df.one == 1) & (df.two == 2)]
```

Filter by multiple columns but only return certain values.

```
# this just returns the data in column AAA
df = pd.DataFrame({'AAA' : [4,5,6,7], 'BBB' : [10,20,30,40], 'CCC' : [100,50,-30,-50]})
newseries = df.loc[(df['BBB'] < 25) & (df['CCC'] >= -40), 'AAA']
```

Filtering by values and using assignment will modify the original DataFrame.

```
df.loc[(df['BBB'] > 25) | (df['CCC'] >= 75), 'AAA'] = 0.1
```

Select multiple values from a particular column, where Letter is the column header.

```
df[df.Letter.isin(['a', 'b'])]
```

Use itertools to find combinations of data within a column of two DataFrames.

```
itertools.product(df1['a'], df2['a'])
```

Add data to a particular cell within a DataFrame.

```
df.loc[index, column]=num
```

Make a copy of a DataFrame.

```
df.copy(deep=True)
```

Iterate through a DataFrame.

```
for i in df.itertuples():
    pass
```

Change order of columns.

```
x = x.reindex(columns=['header', 'seq', 'plus', 'qual'])
```

Make a DataFrame from a dictionary

```
d = {'col1': [1, 2], 'col2': [3, 4]}
x = pd.DataFrame(d)
```

Sample from a DataFrame.

```
df.sample(frac=1)
df.sample(n=20, axis=1)
```

Append to a DataFrame.

```
df=df.append(newdf, ignore_index=True) # without ignore_index, the original indices will be used
```

Remove duplicates

```
x = x[~x.index.duplicated(keep='first')] # most ideal method

data = pd.DataFrame({'k1': ['one', 'two']*3+['two'], 'k2': [1,1,2,3,3,4,4]})
data.duplicated() # identify duplicate data
data['k1'].duplicated()
data['k1'].drop_duplicates()
data.drop_duplicates(['k1']) # this does the same thing as the previous line
data.drop_duplicates(['k1', 'k2'], keep='last') # drops unique found in k1 and k2 and keeps the last ind
```

Check if string is within strings in a given column

```
x[x['strLoc'].str.contains(region)]
```

7.5 Relabeling

Rename a column or group of columns can be done by passing a dictionary of the changes.

```
df = df.rename(columns={'a': 'b', 'c': 'd'})
```

7.6 Sorting and Arranging

The data in a DataFrame can be sorted in numeric or lexicographic order. The following code sorts the values within the columns a and b.

```
df.sort_values(['a','b'], ascending=False)
```

Set a column as the new index

```
x.set_index(['uniques'])
```

7.7 Editing Data

Drop columns from a DataFrame.

```
import numpy as np
df = pd.DataFrame(np.arange(12).reshape(3,4),
                  columns=['A', 'B', 'C', 'D'])
print(df)

df = df.drop(columns=['B', 'C']) # may not work in python 2
df = df.drop(['B', 'C'], axis=1) # this works in python 2
print(df)
```

Changing the datatype of a column of data can be done by just changing column type.

```
df.Age = df.Age.astype(str)
```

Replace values.

```
data = pd.Series([1., -999., 2., -999., -1000., 3.])
data.replace(-999, np.nan)
```

7.7.1 Replace values

New data can be set within a DataFrame one subset at a time in a way that will avoid the SettingWithCopyWarning.

```
import pandas as pd
df = pd.DataFrame({'Trait':['Seed_Shape','Seed_Shape','Flower_Color','Flower_Color'],
                  'Phenotype':['Round','Wrinkled','Purple','White']})
df.loc[df.Trait == 'Seed_Shape', 'Affected_Part'] = 'Seed'
df.loc[df.Trait == 'Flower_Color', 'Affected_Part'] = 'Flower'
print(df)
```

```
##          Trait Phenotype Affected_Part
## 0   Seed_Shape    Round           Seed
## 1   Seed_Shape  Wrinkled           Seed
## 2  Flower_Color   Purple          Flower
## 3  Flower_Color    White          Flower
```

There is a more simple alternative to the above method but it may result in the `SettingWithCopyWarning`.

```
df = df.replace('pork', 'bacon')
```

7.8 Combining Data Structures

The following merges `df` and `df2` using `inner` to get the intersection on the `Sample` column, where indexes are ignored if the merging is performed on a column as in the following example. The other possible merging strategies are: `left`: use only keys from left frame, similar to a SQL left outer join; preserve key order. `right`: use only keys from right frame, similar to a SQL right outer join; preserve key order. `outer`: use union of keys from both frames, similar to a SQL full outer join; sort keys lexicographically. `inner`: use intersection of keys from both frames, similar to a SQL inner join; preserve the order of the left keys.

```
df = pd.merge(df, df2, how='inner', on=['Sample'])
```

Appending to a `DataFrame` attaches a `DataFrame` after another one.

```
df = pd.DataFrame([[1, 2], [3, 4]], columns=list('AB'))
df2 = pd.DataFrame([[5, 6], [7, 8]], columns=list('AB'))
df.append(df2)
```

7.9 Summarizing

The mean of column values can be calculated where each of the columns is grouped by the data in a specified column.

```
temp[['Sample', 'VAF', 'Var_Count']].groupby('Sample').mean()
```

7.10 Arithmetic and Row/Column-wise Analysis

Sometimes it is helpful to analyze the value in a particular cell in a conditional manner depending on it's value and then set the result of this analysis to a corresponding cell in a new column. Here is an example where the VAF of a variant is conditionally analyzed.

```
def LOH(x):
    if x > 0.75: return 1 - x
    elif x <= 0.75 and x > 0.25: return abs(0.5 - x)
    else: return 0
all_vars['LOH'] = all_vars.VAF.transform(LOH)
max_loh = all_vars.groupby('Sample').LOH.max().reset_index().rename(columns={'LOH': 'Max_LOH'})
all_vars = pd.merge(all_vars, max_loh, how='inner', on=['Sample'])
```

Broadcasting arithmetic is an efficient method of calculating across an entire `DataFrame`.

```
frame = pd.DataFrame(np.arange(12.).reshape((4,3)), columns=list('bde'), index=['Utah', 'Ohio', 'Texas', 'California'])
series = frame.iloc[0]
frame - series
# the subtraction function could also be used
# frame.sub(series, axis='columns')
```

Apply a function to each row or column.

```
f = lambda x: x.max() - x.min()
frame.apply(f, axis='index')
```

Add two sets of data together, and use fill_value to avoid replacing any missing data with NaN.

```
x = pd.DataFrame([1,2,3], columns=list('0'))
y = pd.DataFrame([1,2,3], columns=list('1'))
x = x.add(y, fill_value=0)
```

Take the mean or std across specified columns and append as a new column. Below the DataFrame has columns 1-7 that will be used in computing the mean or std and this new data will be appended in a new column labeled 'Mean' or 'Std'.

```
x['Mean']=x[[1,2,3,4,5,6,7]].mean(axis=1)
x['Std']=x[[1,2,3,4,5,6,7]].std(axis=1)
```


Chapter 8

Git

8.1 Setup

8.1.1 Git Setup

The username and email needs to be added after git is installed.

```
git config --global user.name "me"  
git config --global user.email "me@gmail.com"
```

After this information has been set, it can be checked.

```
git config --list
```

8.1.2 Repository Initiation

To setup a repository, create a folder with an initial file like a README and then initiate it.

```
git init  
git status
```

8.1.3 Mirror on Online Repository

Create a repository on a repository like github, gitlab, bitbucket, or sourceforge. Then the local git repository can be synched with the online repository.

```
git remote add origin url-of-online-repository-here  
git push -u origin master
```

Of course the repository could just be setup first and then cloned.

```
git clone url-of-online-repository-here
```

8.2 Manipulating Commits

8.2.1 Repository Status

The commit history of a repository can be displayed in verbose form and in summarized form.

```
git log
git log --oneline
```

8.2.2 File Checkout

To restore a previous version of a file it can be checked out by first identifying the version to be used using the log history and then restoring the desired file.

```
git log --oneline
git checkout <commit number> file.txt
```

8.2.3 Resetting a Repository

To discard the effect of the previous operation on a file.

```
git reset HEAD file.txt
```

The previous version of the a file can then be restored.

```
git checkout -- file.txt
```

Chapter 9

VIM

9.1 Formatting

Automatic newlines are inserted by default; this behavior can be overridden with the following.

```
:set wrap  
:set textwidth=0 wrapmargin=0
```

9.2 Spellcheck

To setup spellchecking first setup a personal dictionary file.

```
# make a directory for personal dictionary  
mkdir -p ~/.vim/spell/
```

Then refer to the dictionary file within VIM, and enable spellchecking.

```
# set personal dictionary  
:set spellfile=~/.vim/spell/en.utf-8.add  
# turn spellcheck on  
:set spell
```

Get spellcheck commands.

```
:help spell
```

Add a word to personal dictionary.

```
zg
```

Move to next and previous misspelled word.

```
]s  
[s
```

Get suggestions for misspelled word.

z=

Chapter 10

Bioinformatics Resources

10.1 Cancer Datasets

- The Cancer Cell Line Encyclopedia has a wealth of information from a large number of cancer cell lines.
- Project score has a number of genetic screens that may be useful in identifying pathways that are critical to cancer growth and survival
- cbiportal has information about codon changes in cancer but does not seem to have any sequence data
- dbGAP has info on genotypes and phenotypes, whatever the fuck that means
 - Here is the page with instructions on how to get dbGAP access
- TCGA
 - This page has the instructions on how to get TCGA access
- COSMIC
 - Cosmic has a project called the Cancer Gene Census in which they are trying to catalog all mutations that have been implicated in playing a causal role in cancer
 - They also have implemented convenient ways of directly downloading information and files from the database in python using the files hosted here.
- Mastermind from genomeron parsed all the articles on pubmed in order to find any and all information for each possible mutation
- GTEx has RNA-Seq, Exome Seq, WGseq, SNP arrays, gene expression arrays and more for cancer and non-cancer?

10.2 Alzheimer's

- The Alzheimers sequencing project is gathering data to understand late onset alzheimer's

10.3 Genome Resources

- Jax has a human to mouse gene matching list that provides gene location matching between human and mouse
- UCSC genome browser has an API for programmatic access

10.4 Genomic Datasets

- AllOfUs is sequencing and collecting other health data on a million individuals
- Color Genomics is one of three companies that will be doing the sequencing and testing for AllOfUs
- 1000 genomes
- 100,000 genomes

10.5 Computing Tools

- AWS looks like it has some healthcare and life sciences resources

10.6 Microbiome Datasets

- The Human Microbiome Project Data Portal from Michael Snyder's group has longitudinal 'omics data that includes diseased and healthy timepoints.
- Michael Snyder's iPOP Personal 'Omics Profiling has some interesting microbiome data specifically targeted to understanding diabetes.

10.7 eQTL/RNASeq and other Tools

- Here are a good number of general tools to check out
- Here is a good python eQTL analysis
- genenetwork2 has a great deal of data and eQTL mapping tools

10.8 Other Data Resources

- The Earth Microbiome Project already has data available, and is trying to sequence all non-eukaryotic life on earth
 - They have detailed information about the project in their PNAS paper from 2018
- Information is Beautiful has some interesting datasets

Chapter 11

Golang

11.1 Installation

Installation of linuxbrew

```
sh -c "$(curl -fsSL https://raw.githubusercontent.com/Linuxbrew/install/master/install.sh)"  
# Add to path  
test -d ~/.linuxbrew && eval "$(~/.linuxbrew/bin/brew shellenv)  
test -d /home/linuxbrew/.linuxbrew && eval "$(/home/linuxbrew/.linuxbrew/bin/brew shellenv)  
test -r ~/.bash_profile && echo "eval \"\${$(brew --prefix)/bin/brew shellenv}\"" >>~/.bash_profile  
echo "eval \"\${$(brew --prefix)/bin/brew shellenv}\"" >>~/.profile  
# debian/ubuntu dependencies  
sudo apt-get install build-essential curl file git
```

LinuxBrew golang installation

```
brew install go
```

The GO PATH should then be checked; it should typically exist at ~/go but it can be checked like this

```
echo $GOPATH
```

11.2 Updating

```
brew install dep  
brew upgrade dep  
brew cask install spotify
```

11.3 Sample Program

Create a file called hello.go

```
package main
```

```
import "fmt"
```

```
func main() {
    fmt.Printf("hello, world\n")
}
```

The program can just be run with
`go run main.go`

Then compile the program
`go build`

Importing multiple things can be done on one line separated by a semicolon
`import ("fmt"; "math")`

11.4 Type conversion

Convert int to float64

```
var i int = 5
j := float64(i)
```

int to string

```
s := strconv.Itoa(97) // s == "97"
```

int64 to string

```
var n int64 = 97
s := strconv.FormatInt(n, 10) // s == "97" (decimal) in base 10
```

string to int

```
s := "97"
if n, err := strconv.Atoi(s); err == nil {
    fmt.Println(n+1)
} else {
    fmt.Println(s, "is not an integer.")
}
```

string to int64

```
s := "97"
n, err := strconv.ParseInt(s, 10, 64)
if err == nil {
    fmt.Printf("%d of type %T", n, n)
}
```

int to int64