Day8_Pandas_Continued

August 4, 2021

Day 8: Working With Data in Pandas

In Day 6, we learned how to open, view, change and save dataframes. Today we are going to do more data manipulation.

Goals for the day:

- Do simple math and string manipulation
- Work with dictionaries and Pandas
- Combine data and work with multiple tables: `merge`, `concatenate`, `append`
- Apply functions to and get stats out of data: `map`, `apply`, `applymap`
- Analyze data using groupby
- Create pivot tables

Functions Learned:

- Overview of the data: `describe()`
- Add a prefix or suffix to column names: `add_prefix()` or `add_suffix()`
- Translate or map values to other values using dictionaries: `map`
- Apply a function on a series or a dataframe: `apply`
- Apply a function to all the cells in a dataframe: `applymap`
- Merge tables from two data sets: `pd.merge`
- Combine dataframes with columns with the same names but no data similarity: `concat`

[1]:
```
##always start by importing your python libraries

#this line will make it so that when we make plots they show up in this notbook
%matplotlib inline
import matplotlib.pylab as plt
import seaborn as sns

#the usual
import pandas as pd
pd.options.mode.chained_assignment = None  # default='warn'
import numpy as np
```

0. Set directory

[2]:
```
#this is the specific directory where the data we want to use is stored
datadirectory = '../data/'

#this is the directory where we want to store the data we finish analyzing
data_out_directory='../output/'
```

8. Basic Math with a dataframe

Remeber the math you learned with numpy, you can do all of that with entire dataframes or specific columns.

[3]:
```
## load in your pokemon dataset but only keep the Name, HP,Attack, Defense␣
 ↪columns
pokemon=pd.read_csv(datadirectory+'Pokemon.csv',␣
 ↪usecols=['Number','Name','HP','Attack','Defense'])
pokemon.head()
```

[3]:
```
   Number                     Name  HP  Attack  Defense
0       1                Bulbasaur  45      49       49
1       2                  Ivysaur  60      62       63
2       3                 Venusaur  80      82       83
3       3  VenusaurMega Venusaur  80     100      123
4       4               Charmander  39      52       43
```

[4]:
```
pokemon.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 800 entries, 0 to 799
Data columns (total 5 columns):
 #   Column   Non-Null Count  Dtype
---  ------   --------------  -----
 0   Number   800 non-null    int64
 1   Name     800 non-null    object
 2   HP       800 non-null    int64
 3   Attack   800 non-null    int64
 4   Defense  800 non-null    int64
dtypes: int64(4), object(1)
memory usage: 31.4+ KB
```

8.1 Simple stats

[5]:
```
# we can also get info on how much data we have by calling .shape
#this returns a tuple with the dimensions of the dataframe
#.shape comes from np.shape(something)

pokemon.shape
```

```
[5]: (800, 5)
```

```
[6]: ### we can run describe and get an overview of the data
     pokemon.describe([.1,.6,.9])
```

```
[6]:             Number          HP      Attack     Defense
     count   800.000000  800.000000  800.000000  800.000000
     mean    362.813750   69.258750   79.001250   73.842500
     std     208.343798   25.534669   32.457366   31.183501
     min       1.000000    1.000000    5.000000    5.000000
     10%      73.900000   40.000000   40.000000   40.000000
     50%     364.500000   65.000000   75.000000   70.000000
     60%     431.400000   71.000000   85.000000   77.000000
     90%     651.100000  100.000000  125.000000  115.000000
     max     721.000000  255.000000  190.000000  230.000000
```

```
[7]: ### mean, then select HP
     ##we can also use numpy, on the entire dataframe np.mean(df)
     pokemon.mean()
```

```
[7]: Number     362.81375
     HP          69.25875
     Attack      79.00125
     Defense     73.84250
     dtype: float64
```

```
[8]: #mean of one column df.mean[column]
     pokemon.mean()
```

```
[8]: Number     362.81375
     HP          69.25875
     Attack      79.00125
     Defense     73.84250
     dtype: float64
```

```
[9]: ##std or np.std(df[column])
     pokemon.std()
```

```
[9]: Number     208.343798
     HP          25.534669
     Attack      32.457366
     Defense     31.183501
     dtype: float64
```

```
[10]: ## get unique values with len and numpy
      ## or len(pokemon.Number.unique())

      print (np.unique(pokemon['Number']))
```

```python
print (len(np.unique(pokemon['Number'])))
```

```
[  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18
  19  20  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36
  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54
  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72
  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
  91  92  93  94  95  96  97  98  99 100 101 102 103 104 105 106 107 108
 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126
 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144
 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162
 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198
 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216
 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234
 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252
 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288
 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306
 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324
 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342
 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360
 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378
 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396
 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414
 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432
 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450
 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468
 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486
 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504
 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522
 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540
 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558
 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576
 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594
 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612
 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630
 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648
 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666
 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684
 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702
 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720
 721]
721
```

8.2 Math with entire rows or columns

[11]:

```
pokemon.head()
```

[11]:

```
   Number                    Name  HP  Attack  Defense
0       1               Bulbasaur  45      49       49
1       2                 Ivysaur  60      62       63
2       3                Venusaur  80      82       83
3       3  VenusaurMega Venusaur  80     100      123
4       4              Charmander  39      52       43
```

[12]:

```
### make a total column by adding each column
pokemon['total2']=pokemon['Name']+pokemon['Attack']
pokemon.head()
#you will encounter an error, this is because when adding columns they must have␣
 ↪the same data type
```

```
---------------------------------------------------------------------------
TypeError                                 Traceback (most recent call last)
~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/ops/array_ops.py in␣
 ↪_na_arithmetic_op(left, right, op, is_cmp)
    141     try:
--> 142         result = expressions.evaluate(op, left, right)
    143     except TypeError:

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/computation/expressions.p␣
 ↪in evaluate(op, a, b, use_numexpr)
    234             # error: "None" not callable
--> 235             return _evaluate(op, op_str, a, b)  # type: ignore[misc]
    236     return _evaluate_standard(op, op_str, a, b)

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/computation/expressions.p␣
 ↪in _evaluate_numexpr(op, op_str, a, b)
    119     if result is None:
--> 120         result = _evaluate_standard(op, op_str, a, b)
    121

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/computation/expressions.p␣
 ↪in _evaluate_standard(op, op_str, a, b)
     68     with np.errstate(all="ignore"):
---> 69         return op(a, b)
     70

TypeError: can only concatenate str (not "int") to str

During handling of the above exception, another exception occurred:

TypeError                                 Traceback (most recent call last)
```

```
<ipython-input-12-1e8b7a36f184> in <module>
      1 ### make a total column by adding each column
----> 2 pokemon['total2']=pokemon['Name']+pokemon['Attack']
      3 pokemon.head()
      4 #you will encounter an error, this is because when adding columns they␣
 ↪must have the same data type

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/ops/common.py in␣
 ↪new_method(self, other)
     63         other = item_from_zerodim(other)
     64
---> 65         return method(self, other)
     66
     67     return new_method

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/arraylike.py in␣
 ↪__add__(self, other)
     87     @unpack_zerodim_and_defer("__add__")
     88     def __add__(self, other):
---> 89         return self._arith_method(other, operator.add)
     90
     91     @unpack_zerodim_and_defer("__radd__")

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/series.py in␣
 ↪_arith_method(self, other, op)
   4996         lvalues = extract_array(self, extract_numpy=True)
   4997         rvalues = extract_array(other, extract_numpy=True)
-> 4998         result = ops.arithmetic_op(lvalues, rvalues, op)
   4999
   5000         return self._construct_result(result, name=res_name)

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/ops/array_ops.py in␣
 ↪arithmetic_op(left, right, op)
    187     else:
    188         with np.errstate(all="ignore"):
--> 189             res_values = _na_arithmetic_op(lvalues, rvalues, op)
    190
    191     return res_values

~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/ops/array_ops.py in␣
 ↪_na_arithmetic_op(left, right, op, is_cmp)
    147             #  will handle complex numbers incorrectly, see GH#32047
    148             raise
--> 149         result = _masked_arith_op(left, right, op)
    150
    151     if is_cmp and (is_scalar(result) or result is NotImplemented):
```

```
~/opt/anaconda3/lib/python3.8/site-packages/pandas/core/ops/array_ops.py in␣
 ↪_masked_arith_op(x, y, op)
     89         if mask.any():
     90             with np.errstate(all="ignore"):
---> 91                 result[mask] = op(xrav[mask], yrav[mask])
     92 
     93     else:

TypeError: can only concatenate str (not "int") to str
```

[13]:
```
### make a total column by adding each column
## both of the columns are numeric so this works
pokemon['total']=pokemon['HP']+pokemon['Attack']
pokemon.head()
```

[13]:
```
   Number                   Name  HP  Attack  Defense  total
0       1              Bulbasaur  45      49       49     94
1       2                Ivysaur  60      62       63    122
2       3               Venusaur  80      82       83    162
3       3  VenusaurMega Venusaur  80     100      123    180
4       4             Charmander  39      52       43     91
```

[14]:
```
## delete total to not complicate things
del pokemon['total']
```

[15]:
```
pokemon.head()
```

[15]:
```
   Number                   Name  HP  Attack  Defense
0       1              Bulbasaur  45      49       49
1       2                Ivysaur  60      62       63
2       3               Venusaur  80      82       83
3       3  VenusaurMega Venusaur  80     100      123
4       4             Charmander  39      52       43
```

[16]:
```
# let's add a column with the total across, axis=1 means columns
pokemon.loc[:,"Total_across"] = pokemon.sum(axis=1)
pokemon.head(5)
```

[16]:
```
   Number                   Name  HP  Attack  Defense  Total_across
0       1              Bulbasaur  45      49       49           144
1       2                Ivysaur  60      62       63           187
2       3               Venusaur  80      82       83           248
3       3  VenusaurMega Venusaur  80     100      123           306
4       4             Charmander  39      52       43           138
```

[17]:
```
#let's add a row with the total down each column
## if we don't specify axis then pandas will do rows automatically
```

```
pokemon.loc["Total_down",:] = pokemon.sum()
pokemon.tail(5)
```

[17]:

```
              Number                                                Name  \
796            719.0                                   DiancieMega Diancie
797            720.0                                  HoopaHoopa Confined
798            720.0                                   HoopaHoopa Unbound
799            721.0                                            Volcanion
Total_down  290251.0  BulbasaurIvysaurVenusaurVenusaurMega VenusaurC...

                 HP   Attack  Defense  Total_across
796            50.0    160.0    110.0        1039.0
797            80.0    110.0     60.0         970.0
798            80.0    160.0     60.0        1020.0
799            80.0    110.0    120.0        1031.0
Total_down  55407.0  63201.0  59074.0      467933.0
```

[18]:

```
## to select specif rows and columns we can combine math and .iloc or loc
pokemon['total_iloc']=pokemon.iloc[:,[3,4]].sum(axis=1)
pokemon.head()
```

[18]:

```
   Number                   Name    HP  Attack  Defense  Total_across  \
0     1.0              Bulbasaur  45.0    49.0     49.0         144.0
1     2.0                Ivysaur  60.0    62.0     63.0         187.0
2     3.0               Venusaur  80.0    82.0     83.0         248.0
3     3.0  VenusaurMega Venusaur  80.0   100.0    123.0         306.0
4     4.0             Charmander  39.0    52.0     43.0         138.0

   total_iloc
0        98.0
1       125.0
2       165.0
3       223.0
4        95.0
```

[19]:

```
#let's remove the new column so it doesn't confuse us later
pokemon.drop(columns=['Total_across','total_iloc'],inplace=True)
pokemon.head()
```

[19]:

```
   Number                   Name    HP  Attack  Defense
0     1.0              Bulbasaur  45.0    49.0     49.0
1     2.0                Ivysaur  60.0    62.0     63.0
2     3.0               Venusaur  80.0    82.0     83.0
3     3.0  VenusaurMega Venusaur  80.0   100.0    123.0
4     4.0             Charmander  39.0    52.0     43.0
```

Skill Check

Print the mean and standard deviation of the 'Attack' for only the first 5 rows of the dataframe

[20]:

```
### Your work here

###mean



###std
```

Answer

[21]:

```
### use iloc to select the rows and column you want then call mean and std
print (pokemon.iloc[0:6,[3]].mean())
print (pokemon.iloc[0:6,[3]].std())
```

```
Attack    68.166667
dtype: float64
Attack    19.43622
dtype: float64
```

9. Math discaimer

If you want to do full on calculation with dataframes then use numpy. Pandas is best suited for analyzing dataframes with some categorical column. You can create functions to analyze your df and there are some cool tricks that I will mention below but again if you want to do mathematical analyses on your tables then numpy is your go to.

10. String manipulation with columns

We are going to use one of my old datasets to better understand the power of pandas and string manipulations

[22]:

```
### let's open up a genetics dataset
gene_info=pd.read_csv(datadirectory+'contig_information.csv')
## info to see count
gene_info.info()
gene_info.head()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 17034 entries, 0 to 17033
Data columns (total 4 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   CAMNT_ID           17034 non-null  object
 1   WGCNA_Module_Num   17034 non-null  int64
 2   RAIN_diel_Results  17034 non-null  bool
```

```
 3   KEGG_Annotations   11231 non-null  object
dtypes: bool(1), int64(1), object(2)
memory usage: 416.0+ KB
```

[22]:
```
           CAMNT_ID  WGCNA_Module_Num  RAIN_diel_Results  \
0  CAMNT_0024302971                 7              False
1  CAMNT_0024014877                 4              False
2  CAMNT_0024014645                 9               True
3  CAMNT_0023937169                 9               True
4  CAMNT_0024335527                 9               True

                               KEGG_Annotations
0        00910 Nitrogen metabolism [PATH:ko00910]
1  00030 Pentose phosphate pathway [PATH:ko00030]
2  00190 Oxidative phosphorylation [PATH:ko00190]
3  00190 Oxidative phosphorylation [PATH:ko00190]
4  00190 Oxidative phosphorylation [PATH:ko00190]
```

[23]:
```
### let's drop the rows without values since I can't do anything with them
gene_info_clean=gene_info.dropna()
gene_info_clean.info()
gene_info_clean.head()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 11231 entries, 0 to 11881
Data columns (total 4 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   CAMNT_ID           11231 non-null  object
 1   WGCNA_Module_Num   11231 non-null  int64
 2   RAIN_diel_Results  11231 non-null  bool
 3   KEGG_Annotations   11231 non-null  object
dtypes: bool(1), int64(1), object(2)
memory usage: 361.9+ KB
```

[23]:
```
           CAMNT_ID  WGCNA_Module_Num  RAIN_diel_Results  \
0  CAMNT_0024302971                 7              False
1  CAMNT_0024014877                 4              False
2  CAMNT_0024014645                 9               True
3  CAMNT_0023937169                 9               True
4  CAMNT_0024335527                 9               True

                               KEGG_Annotations
0        00910 Nitrogen metabolism [PATH:ko00910]
1  00030 Pentose phosphate pathway [PATH:ko00030]
2  00190 Oxidative phosphorylation [PATH:ko00190]
3  00190 Oxidative phosphorylation [PATH:ko00190]
4  00190 Oxidative phosphorylation [PATH:ko00190]
```

A challenge that I often have in my data is messy names annotation names

-Let's clean up the Kegg annotations so I only have the actual annotation

```
[24]: #partition my string based on the delimter, in this case the space
gene_info_clean['KEGG_clean']=[i.partition(' ') for i in␣
 ↪gene_info_clean['KEGG_Annotations']].copy()
gene_info_clean.head()
```

```
[24]:            CAMNT_ID  WGCNA_Module_Num  RAIN_diel_Results  \
0  CAMNT_0024302971                 7              False
1  CAMNT_0024014877                 4              False
2  CAMNT_0024014645                 9               True
3  CAMNT_0023937169                 9               True
4  CAMNT_0024335527                 9               True

                             KEGG_Annotations  \
0        00910 Nitrogen metabolism [PATH:ko00910]
1  00030 Pentose phosphate pathway [PATH:ko00030]
2  00190 Oxidative phosphorylation [PATH:ko00190]
3  00190 Oxidative phosphorylation [PATH:ko00190]
4  00190 Oxidative phosphorylation [PATH:ko00190]

                                     KEGG_clean
0     (00910,  , Nitrogen metabolism [PATH:ko00910])
1  (00030,  , Pentose phosphate pathway [PATH:ko0...
2  (00190,  , Oxidative phosphorylation [PATH:ko0...
3  (00190,  , Oxidative phosphorylation [PATH:ko0...
4  (00190,  , Oxidative phosphorylation [PATH:ko0...
```

```
[25]: # then I select the values I want from the list
gene_info_clean['KEGG_clean1']=[i.partition(' ')[2] for i in␣
 ↪gene_info_clean['KEGG_Annotations']].copy()
gene_info_clean.head()
```

```
[25]:            CAMNT_ID  WGCNA_Module_Num  RAIN_diel_Results  \
0  CAMNT_0024302971                 7              False
1  CAMNT_0024014877                 4              False
2  CAMNT_0024014645                 9               True
3  CAMNT_0023937169                 9               True
4  CAMNT_0024335527                 9               True

                             KEGG_Annotations  \
0        00910 Nitrogen metabolism [PATH:ko00910]
1  00030 Pentose phosphate pathway [PATH:ko00030]
2  00190 Oxidative phosphorylation [PATH:ko00190]
3  00190 Oxidative phosphorylation [PATH:ko00190]
4  00190 Oxidative phosphorylation [PATH:ko00190]
```

```
                                       KEGG_clean  \
0     (00910,   , Nitrogen metabolism [PATH:ko00910])
1  (00030,   , Pentose phosphate pathway [PATH:ko0...
2  (00190,   , Oxidative phosphorylation [PATH:ko0...
3  (00190,   , Oxidative phosphorylation [PATH:ko0...
4  (00190,   , Oxidative phosphorylation [PATH:ko0...

                              KEGG_clean1
0        Nitrogen metabolism [PATH:ko00910]
1  Pentose phosphate pathway [PATH:ko00030]
2  Oxidative phosphorylation [PATH:ko00190]
3  Oxidative phosphorylation [PATH:ko00190]
4  Oxidative phosphorylation [PATH:ko00190]
```

[26]:

```python
#step 1, let's remove the last part of the name
gene_info_clean['KEGG_clean']=[i.split('[')[0] for i in␣
 ↪gene_info_clean['KEGG_clean1']]
gene_info_clean.head()
```

[26]:

```
          CAMNT_ID  WGCNA_Module_Num  RAIN_diel_Results  \
0  CAMNT_0024302971                 7              False
1  CAMNT_0024014877                 4              False
2  CAMNT_0024014645                 9               True
3  CAMNT_0023937169                 9               True
4  CAMNT_0024335527                 9               True

                               KEGG_Annotations                 KEGG_clean  \
0        00910 Nitrogen metabolism [PATH:ko00910]        Nitrogen metabolism
1  00030 Pentose phosphate pathway [PATH:ko00030]  Pentose phosphate pathway
2  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation
3  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation
4  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation

                              KEGG_clean1
0        Nitrogen metabolism [PATH:ko00910]
1  Pentose phosphate pathway [PATH:ko00030]
2  Oxidative phosphorylation [PATH:ko00190]
3  Oxidative phosphorylation [PATH:ko00190]
4  Oxidative phosphorylation [PATH:ko00190]
```

When cleaning up strings it is really usuful to know all the tricks there are. Here is one website I use for my string tricks.

Let's open up another dataset I need to work with

[27]:

```python
###read the contig data
gene_counts=pd.read_csv(datadirectory+'contig_counts.csv')
```

```
gene_counts.head()
```

[27]:

```
                CAMNT  sm001  sm002  sm003  sm004  sm005  sm008  sm009  sm010  \
0  CAMNT_0023928115    214    376    204    347    411    237    262    198   
1  CAMNT_0023928149     56     40     28     37     27    112     76     50   
2  CAMNT_0023928253     30     45     11     38     38     28     16     29   
3  CAMNT_0023928285     12     12     11     11     15     13      3     13   
4  CAMNT_0023928443    210    215    216    266    338    286    225    231   

   sm011  ...  sm013  sm016  sm017  sm018  sm019  sm020  sm024  sm025  sm026  \
0    199  ...    411    394    299    277    251    411    288    221    256   
1     26  ...     27    169     76     45     35     27     61     73     66   
2     23  ...     38     15      9     31     16     38     21     28     11   
3      9  ...     15      7      8      7     23     15     16     11      6   
4    174  ...    338    523    897    316    246    338    243    263    235   

   sm027  
0    230  
1     29  
2     10  
3     11  
4    134  

[5 rows x 21 columns]
```

[28]:

```
### read in my data_dictionary
data_dict=pd.read_csv(datadirectory+'time_dict.csv')
data_dict
```

[28]:

```
      TD Sample Sample2  Hours  Dark    R  R2            times
0   10pm  SM001   sm001      0     0   R1   1  2015-07-26 2200
1    2am  SM002   sm002      4     1   R2   2  2015-07-27 0200
2    6am  SM003   sm003      8     2   R3   3  2015-07-27 0600
3   10am  SM004   sm004     12     3   R4   4  2015-07-27 1000
4    2pm  SM005   sm005     16     4   R5   5  2015-07-27 1400
5    6pm  SM008   sm008     20     5   R6   6  2015-07-27 1800
6   10pm  SM009   sm009     24     6   R7   7  2015-07-27 2200
7    2am  SM010   sm010     28     7   R8   8  2015-07-28 0200
8    6am  SM011   sm011     32     8   R9   9  2015-07-28 0600
9   10am  SM012   sm012     36     9  R10  10  2015-07-28 1000
10   2pm  SM013   sm013     40    10  R11  11  2015-07-28 1400
11   6pm  SM016   sm016     44    11  R12  12  2015-07-28 1800
12  10pm  SM017   sm017     48    12  R13  13  2015-07-28 2200
13   2am  SM018   sm018     52    13  R14  14  2015-07-29 0200
14   6am  SM019   sm019     56    14  R15  15  2015-07-29 0600
15  10am  SM020   sm020     60    15  R16  16  2015-07-29 1000
16   2pm  SM021   sm021     64    16  R17  17  2015-07-29 1400
```

```
17   6pm  SM024   sm024     68    17  R18  18  2015-07-29 1800
18  10pm  SM025   sm025     72    18  R19  19  2015-07-29 2200
19   2am  SM026   sm026     76    19  R20  20  2015-07-30 0200
20   6am  SM027   sm027     80    20  R21  21  2015-07-30 0600
```

[29]:
```
## make_dict
sample2_Hours_dict=dict(zip(data_dict.iloc[:,2],data_dict.iloc[:,3]))
sample2_Hours_dict
```

[29]:
```
{'sm001': 0,
 'sm002': 4,
 'sm003': 8,
 'sm004': 12,
 'sm005': 16,
 'sm008': 20,
 'sm009': 24,
 'sm010': 28,
 'sm011': 32,
 'sm012': 36,
 'sm013': 40,
 'sm016': 44,
 'sm017': 48,
 'sm018': 52,
 'sm019': 56,
 'sm020': 60,
 'sm021': 64,
 'sm024': 68,
 'sm025': 72,
 'sm026': 76,
 'sm027': 80}
```

[30]:
```
### let's rename the columns in gene_counts
gene_counts.set_index('CAMNT',inplace=True)
gene_counts.rename(columns=sample2_Hours_dict,inplace=True)
gene_counts.reset_index(inplace=True)
gene_counts.head()
```

[30]:
```
             CAMNT    0    4    8   12   16   20   24   28   32  ...   40  \
0  CAMNT_0023928115  214  376  204  347  411  237  262  198  199  ...  411
1  CAMNT_0023928149   56   40   28   37   27  112   76   50   26  ...   27
2  CAMNT_0023928253   30   45   11   38   38   28   16   29   23  ...   38
3  CAMNT_0023928285   12   12   11   11   15   13    3   13    9  ...   15
4  CAMNT_0023928443  210  215  216  266  338  286  225  231  174  ...  338

    44   48   52   56   60   68   72   76   80
0  394  299  277  251  411  288  221  256  230
1  169   76   45   35   27   61   73   66   29
```

```
2   15    9   31   16   38   21   28   11   10
3    7    8    7   23   15   16   11    6   11
4  523  897  316  246  338  243  263  235  134

[5 rows x 21 columns]
```

Skill check

Make a new variable called 'my_new_genes_df' that hold the gene_count table, but this time I want the columns to have the numbers in the 'Dark' column as column labels. Hint: you need to make a new dictionary first.

[31]:

```
##### your code

###make new dictionary

###make new df with new column names
```

Answer

[32]:

```
## make new dictionary
hour_dark_dict=dict(zip(data_dict.Hours,data_dict.Dark))

#make new table, we don't need inplace=True since we are making a new variable
my_new_genes_df=gene_counts.rename(columns=hour_dark_dict)
my_new_genes_df.head()
```

[32]:

```
              CAMNT    0    1    2    3    4    5    6    7    8  ...   10  \
0  CAMNT_0023928115  214  376  204  347  411  237  262  198  199  ...  411
1  CAMNT_0023928149   56   40   28   37   27  112   76   50   26  ...   27
2  CAMNT_0023928253   30   45   11   38   38   28   16   29   23  ...   38
3  CAMNT_0023928285   12   12   11   11   15   13    3   13    9  ...   15
4  CAMNT_0023928443  210  215  216  266  338  286  225  231  174  ...  338

    11   12   13   14   15   17   18   19   20
0  394  299  277  251  411  288  221  256  230
1  169   76   45   35   27   61   73   66   29
2   15    9   31   16   38   21   28   11   10
3    7    8    7   23   15   16   11    6   11
4  523  897  316  246  338  243  263  235  134

[5 rows x 21 columns]
```

10.1 Pro-tip: String manipulation with column names

[33]:

```
## let use the pokemon data for this

pokemon_full=pd.read_csv(datadirectory+'Pokemon.csv')
pokemon_full.head()
```

[33]:

```
   Number                   Name Type 1  Type 2  Total  HP  Attack  Defense  \
0       1              Bulbasaur  Grass  Poison    318  45      49       49
1       2                Ivysaur  Grass  Poison    405  60      62       63
2       3               Venusaur  Grass  Poison    525  80      82       83
3       3  VenusaurMega Venusaur  Grass  Poison    625  80     100      123
4       4             Charmander   Fire     NaN    309  39      52       43

   Sp. Atk  Sp. Def  Speed  Generation  Legendary
0       65       65     45           1      False
1       80       80     60           1      False
2      100      100     80           1      False
3      122      120     80           1      False
4       60       50     65           1      False
```

[34]:

```
## let's add a prefix to the column names
pokemon_full=pokemon_full.add_prefix('{}_'.format("x"))
pokemon_full.head()
```

[34]:

```
   x_Number                 x_Name x_Type 1 x_Type 2  x_Total  x_HP  x_Attack  \
0         1              Bulbasaur   Grass   Poison      318    45        49
1         2                Ivysaur   Grass   Poison      405    60        62
2         3               Venusaur   Grass   Poison      525    80        82
3         3   VenusaurMega Venusaur   Grass   Poison      625    80       100
4         4             Charmander    Fire      NaN      309    39        52

   x_Defense  x_Sp. Atk  x_Sp. Def  x_Speed  x_Generation  x_Legendary
0        49         65         65       45             1        False
1        63         80         80       60             1        False
2        83        100        100       80             1        False
3       123        122        120       80             1        False
4        43         60         50       65             1        False
```

[35]:

```
## let's add a suffix to the column names
pokemon_full=pokemon_full.add_suffix('_{}'.format("y"))
pokemon_full.head()
```

[35]:

```
   x_Number_y               x_Name_y x_Type 1_y x_Type 2_y  x_Total_y  x_HP_y  \
0           1              Bulbasaur      Grass     Poison        318      45
1           2                Ivysaur      Grass     Poison        405      60
2           3               Venusaur      Grass     Poison        525      80
3           3   VenusaurMega Venusaur      Grass     Poison        625      80
```

```
4           4             Charmander       Fire        NaN        309      39

   x_Attack_y  x_Defense_y  x_Sp. Atk_y  x_Sp. Def_y  x_Speed_y  \
0          49           49           65           65         45
1          62           63           80           80         60
2          82           83          100          100         80
3         100          123          122          120         80
4          52           43           60           50         65

   x_Generation_y  x_Legendary_y
0               1          False
1               1          False
2               1          False
3               1          False
4               1          False
```

[36]:

```
##let's change the symbol in all the column names
pokemon_full.columns=pokemon_full.columns.str.replace('_','/')
pokemon_full.head()
```

[36]:

```
   x/Number/y               x/Name/y x/Type 1/y x/Type 2/y  x/Total/y  x/HP/y  \
0           1              Bulbasaur      Grass     Poison        318      45
1           2                Ivysaur      Grass     Poison        405      60
2           3               Venusaur      Grass     Poison        525      80
3           3  VenusaurMega Venusaur      Grass     Poison        625      80
4           4             Charmander       Fire        NaN        309      39

   x/Attack/y  x/Defense/y  x/Sp. Atk/y  x/Sp. Def/y  x/Speed/y  \
0          49           49           65           65         45
1          62           63           80           80         60
2          82           83          100          100         80
3         100          123          122          120         80
4          52           43           60           50         65

   x/Generation/y  x/Legendary/y
0               1          False
1               1          False
2               1          False
3               1          False
4               1          False
```

Any string manipulation you can do on a list, you can do on a str column. More info here link text

11. Map, Apply, Applymap — Skip during class–But please review

You can make dictionaries by combining the infor in two columns.

```
[37]: ## open the dataset again
      pokemon_full2=pd.read_csv(datadirectory+'Pokemon.csv')
```

11.1 map

map is a series method, works on columns, allows us to translate or map values to other values using dictionaries

```
[38]: #let's pretend our data doesn't already have type and make a column with type␣
       ↪based on the name

      pokemon_full2['Legend_bool']=pokemon_full2['Legendary'].map({False:0,True:1})
      pokemon_full2.head()
```

```
[38]:    Number                   Name Type 1  Type 2  Total  HP  Attack  Defense  \
      0       1              Bulbasaur  Grass  Poison    318  45      49       49
      1       2                Ivysaur  Grass  Poison    405  60      62       63
      2       3               Venusaur  Grass  Poison    525  80      82       83
      3       3  VenusaurMega Venusaur  Grass  Poison    625  80     100      123
      4       4             Charmander   Fire     NaN    309  39      52       43

         Sp. Atk  Sp. Def  Speed  Generation  Legendary  Legend_bool
      0       65       65     45           1      False            0
      1       80       80     60           1      False            0
      2      100      100     80           1      False            0
      3      122      120     80           1      False            0
      4       60       50     65           1      False            0
```

11.2 apply

apply is both a series and a dataframe method, we can use it to apply a function on a series or a dataframe

```
[39]: ## pass apply to a str series
      pokemon_full2['name_length']=pokemon_full2['Name'].apply(len)
      pokemon_full2.head()
```

```
[39]:    Number                   Name Type 1  Type 2  Total  HP  Attack  Defense  \
      0       1              Bulbasaur  Grass  Poison    318  45      49       49
      1       2                Ivysaur  Grass  Poison    405  60      62       63
      2       3               Venusaur  Grass  Poison    525  80      82       83
      3       3  VenusaurMega Venusaur  Grass  Poison    625  80     100      123
      4       4             Charmander   Fire     NaN    309  39      52       43

         Sp. Atk  Sp. Def  Speed  Generation  Legendary  Legend_bool  name_length
      0       65       65     45           1      False            0            9
      1       80       80     60           1      False            0            7
      2      100      100     80           1      False            0            8
```

```
3       122       120      80             1      False             0            21
4        60        50      65             1      False             0            10
```

```
[40]: ## pass apply to a numerical series
      #let's make a bad column for our example
      pokemon_full2['total_bad']=pokemon_full2['Total']+0.7
      #let's fix it uring np.round
      pokemon_full2['total_rounded']=pokemon_full2['total_bad'].apply(np.around)
      pokemon_full2.head()
      ## you can pass any function to apply
```

```
[40]:    Number                   Name Type 1  Type 2  Total  HP  Attack  Defense  \
      0       1              Bulbasaur  Grass  Poison    318  45      49       49
      1       2                Ivysaur  Grass  Poison    405  60      62       63
      2       3               Venusaur  Grass  Poison    525  80      82       83
      3       3  VenusaurMega Venusaur  Grass  Poison    625  80     100      123
      4       4             Charmander   Fire     NaN    309  39      52       43

         Sp. Atk  Sp. Def  Speed  Generation  Legendary  Legend_bool  name_length  \
      0       65       65     45           1      False            0            9
      1       80       80     60           1      False            0            7
      2      100      100     80           1      False            0            8
      3      122      120     80           1      False            0           21
      4       60       50     65           1      False            0           10

         total_bad  total_rounded
      0      318.7          319.0
      1      405.7          406.0
      2      525.7          526.0
      3      625.7          626.0
      4      309.7          310.0
```

```
[41]: ### let's use apply on the dataframe

      #this will run the function in apply, (in this case max), along the specified␣
       ↪axis (in this case rows) and
      #give us the max value for each column we selected
      pokemon_full2.loc[:,'Total':'Defense'].apply(max,axis=0)
```

```
[41]: Total      780
      HP         255
      Attack     190
      Defense    230
      dtype: int64
```

11.3 applymap

applymap applies a function to all the elements in a dataframe, (all the cells)

[42]:

```
def check_data_type(some_cell):
    if type(some_cell)==str:
        return 'chicken'
    else:
        return 'beef'

check_data_type('Y')
```

[42]:

```
'chicken'
```

[43]:

```
pokemon_full2.applymap(check_data_type)
```

[43]:

```
    Number     Name   Type 1   Type 2 Total    HP Attack Defense Sp. Atk  \
0     beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
1     beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
2     beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
3     beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
4     beef  chicken  chicken     beef  beef  beef   beef    beef    beef
..     ...      ...      ...      ...   ...   ...    ...     ...     ...
795   beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
796   beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
797   beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
798   beef  chicken  chicken  chicken  beef  beef   beef    beef    beef
799   beef  chicken  chicken  chicken  beef  beef   beef    beef    beef

    Sp. Def Speed Generation Legendary Legend_bool name_length total_bad  \
0      beef  beef       beef      beef        beef        beef      beef
1      beef  beef       beef      beef        beef        beef      beef
2      beef  beef       beef      beef        beef        beef      beef
3      beef  beef       beef      beef        beef        beef      beef
4      beef  beef       beef      beef        beef        beef      beef
..      ...   ...        ...       ...         ...         ...       ...
795    beef  beef       beef      beef        beef        beef      beef
796    beef  beef       beef      beef        beef        beef      beef
797    beef  beef       beef      beef        beef        beef      beef
798    beef  beef       beef      beef        beef        beef      beef
799    beef  beef       beef      beef        beef        beef      beef

    total_rounded
0            beef
1            beef
2            beef
3            beef
4            beef
..            ...
795          beef
796          beef
```

```
797          beef
798          beef
799          beef

[800 rows x 17 columns]
```

12. Working with multiple tables

12.1 Merge

Imagine working with multiple datasets and having to combine tables. Let's merge table 1 and 2. Merge requires that our dataframes have a column that is the same. More details on merge here.

[44]:
```
#pd.merge(left,right,on,how)
contig_full=pd.
↪merge(gene_info_clean,gene_counts,left_on='CAMNT_ID',right_on='CAMNT',how='outer')
print (contig_full.shape)
contig_full.head()
```

```
(17031, 27)
```

[44]:
```
           CAMNT_ID  WGCNA_Module_Num RAIN_diel_Results  \
0  CAMNT_0024302971               7.0             False
1  CAMNT_0024014877               4.0             False
2  CAMNT_0024014877               4.0             False
3  CAMNT_0024014877               4.0             False
4  CAMNT_0024014877               4.0             False

                                   KEGG_Annotations  \
0          00910 Nitrogen metabolism [PATH:ko00910]
1     00030 Pentose phosphate pathway [PATH:ko00030]
2  00710 Carbon fixation in photosynthetic organi...
3    01051 Biosynthesis of ansamycins [PATH:ko01051]
4             01200 Carbon metabolism [PATH:ko01200]

                                KEGG_clean  \
0                     Nitrogen metabolism
1                Pentose phosphate pathway
2  Carbon fixation in photosynthetic organisms
3               Biosynthesis of ansamycins
4                        Carbon metabolism

                                     KEGG_clean1             CAMNT   0  \
0           Nitrogen metabolism [PATH:ko00910]  CAMNT_0024302971  19
1      Pentose phosphate pathway [PATH:ko00030]  CAMNT_0024014877  26
2  Carbon fixation in photosynthetic organisms [P...  CAMNT_0024014877  26
3         Biosynthesis of ansamycins [PATH:ko01051]  CAMNT_0024014877  26
4                 Carbon metabolism [PATH:ko01200]  CAMNT_0024014877  26
```

```
    4   8  ...  40  44  48  52  56  60  68  72  76  80
0  36  14  ...  14  34  23  15  11  14  10  20  14  13
1  48  46  ...  35  30  10  26  42  35  34  45  19  26
2  48  46  ...  35  30  10  26  42  35  34  45  19  26
3  48  46  ...  35  30  10  26  42  35  34  45  19  26
4  48  46  ...  35  30  10  26  42  35  34  45  19  26

[5 rows x 27 columns]
```

Convinently, our dataframes had the ‘Name’ column but you can imagine the case where Name might be the index, not a column. Sure, I can reset the index to have the same name, but that’s too much work.

[45]:

```
#let's chage the CAMNT column in the gene_info and try again
print(gene_info_clean.columns)
gene_info_clean.rename(columns={'CAMNT_ID':'CAMNT'},inplace=True)
print(gene_info_clean.columns)
```

```
Index(['CAMNT_ID', 'WGCNA_Module_Num', 'RAIN_diel_Results', 'KEGG_Annotations',
       'KEGG_clean', 'KEGG_clean1'],
      dtype='object')
Index(['CAMNT', 'WGCNA_Module_Num', 'RAIN_diel_Results', 'KEGG_Annotations',
       'KEGG_clean', 'KEGG_clean1'],
      dtype='object')
```

[46]:

```
# let's try out merge again
contig_full=pd.merge(gene_info_clean,gene_counts,on='CAMNT',how='outer')
print (contig_full.shape)
contig_full.head()
```

```
(17031, 26)
```

[46]:

```
              CAMNT  WGCNA_Module_Num RAIN_diel_Results  \
0  CAMNT_0024302971               7.0             False
1  CAMNT_0024014877               4.0             False
2  CAMNT_0024014877               4.0             False
3  CAMNT_0024014877               4.0             False
4  CAMNT_0024014877               4.0             False

                                    KEGG_Annotations  \
0            00910 Nitrogen metabolism [PATH:ko00910]
1      00030 Pentose phosphate pathway [PATH:ko00030]
2  00710 Carbon fixation in photosynthetic organi...
3     01051 Biosynthesis of ansamycins [PATH:ko01051]
4              01200 Carbon metabolism [PATH:ko01200]

                                     KEGG_clean   \
0                           Nitrogen metabolism
```

```
1                   Pentose phosphate pathway
2 Carbon fixation in photosynthetic organisms
3                  Biosynthesis of ansamycins
4                           Carbon metabolism

                                        KEGG_clean1   0   4   8  12  ...  40  \
0                Nitrogen metabolism [PATH:ko00910]  19  36  14  34  ...  14
1          Pentose phosphate pathway [PATH:ko00030]  26  48  46  40  ...  35
2 Carbon fixation in photosynthetic organisms [P...  26  48  46  40  ...  35
3         Biosynthesis of ansamycins [PATH:ko01051]  26  48  46  40  ...  35
4                  Carbon metabolism [PATH:ko01200]  26  48  46  40  ...  35

   44  48  52  56  60  68  72  76  80
0  34  23  15  11  14  10  20  14  13
1  30  10  26  42  35  34  45  19  26
2  30  10  26  42  35  34  45  19  26
3  30  10  26  42  35  34  45  19  26
4  30  10  26  42  35  34  45  19  26

[5 rows x 26 columns]
```

Merge more than two dataframes

[47]:

```
## let use the pokemon data for this

pokemon_full=pd.read_csv(datadirectory+'Pokemon.csv')
pokemon_full.head()
```

[47]:

```
   Number                   Name Type 1  Type 2  Total  HP  Attack  Defense  \
0       1              Bulbasaur  Grass  Poison    318  45      49       49
1       2                Ivysaur  Grass  Poison    405  60      62       63
2       3               Venusaur  Grass  Poison    525  80      82       83
3       3  VenusaurMega Venusaur  Grass  Poison    625  80     100      123
4       4             Charmander   Fire     NaN    309  39      52       43

   Sp. Atk  Sp. Def  Speed  Generation  Legendary
0       65       65     45           1      False
1       80       80     60           1      False
2      100      100     80           1      False
3      122      120     80           1      False
4       60       50     65           1      False
```

At some point I'm going to have more than 2 tables that I need to combine and so there has to be a better way to merge than doing two at a time. There is this is a little advanced but I'm sharing with you because it will save you time.

[48]:

```
## let's make three tables that all have one column in common that we will use␣
 ↪to join our tables
table1=pokemon_full[['Name','Total','HP']].copy()
table2=pokemon_full[['Name','Attack','Defense']].copy()
table3=pokemon_full[['Name','Generation','Legendary']].copy()
```

[49]:

```
#import this cool library that allows you to reduce dataframes to list and␣
 ↪combine them
# again this is advanced but it will save you time
from functools import reduce

# create a list of the tables yoou want to combine
my_dataframes=[table1, table2, table3]

#make a variable that will hold the new combined dataframe
#reduce(lambda df_left,df_right: pd.merge(df_left,df_right), on=[on what column␣
 ↪to mege], the list of the columns to merge)
combined_frame=reduce(lambda df_left,df_right: pd.merge(df_left, df_right,␣
 ↪on=['Name']), my_dataframes)

combined_frame.head()
```

[49]:

```
                    Name  Total  HP  Attack  Defense  Generation  Legendary
0              Bulbasaur    318  45      49       49           1      False
1                Ivysaur    405  60      62       63           1      False
2               Venusaur    525  80      82       83           1      False
3  VenusaurMega Venusaur    625  80     100      123           1      False
4             Charmander    309  39      52       43           1      False
```

12.2 Concatenate

Concatenate allows you to combine dataframes that have columns with the same names but no data similarity.

[50]:

```
## let's make tabl4 be a subset of table 1 that only has the top3 rows,
##and table5 will have the next 3 rows of table 1, so that both table 4 and 4␣
 ↪have the same columns but no values in common

table4=table1.loc[0:3,]
print (table4.head())
table5=table1.loc[4:6,]
print (table5.head())
```

```
                    Name  Total  HP
0              Bulbasaur    318  45
1                Ivysaur    405  60
2               Venusaur    525  80
3  VenusaurMega Venusaur    625  80
```

```
         Name  Total  HP
4  Charmander    309  39
5  Charmeleon    405  58
6   Charizard    534  78
```

[51]:
```
## lets concat our tables so that all the rows are in one place
my_tables45=[table4,table5]

table4n5=pd.concat(my_tables45,axis=0)
table4n5
```

[51]:
```
                    Name  Total  HP
0              Bulbasaur    318  45
1                Ivysaur    405  60
2               Venusaur    525  80
3  VenusaurMega Venusaur    625  80
4             Charmander    309  39
5             Charmeleon    405  58
6              Charizard    534  78
```

[52]:
```
## let's go back to tables 1,2,3 and remove name the concat them together
mytables123=[table1.drop(['Name'],axis=1),table2.drop(['Name'],axis=1),table3.
 ↪drop(['Name'],axis=1)]

tables_all=pd.concat(mytables123,axis=1)
tables_all
```

[52]:
```
     Total  HP  Attack  Defense  Generation  Legendary
0      318  45      49       49           1      False
1      405  60      62       63           1      False
2      525  80      82       83           1      False
3      625  80     100      123           1      False
4      309  39      52       43           1      False
..     ...  ..     ...      ...         ...        ...
795    600  50     100      150           6       True
796    700  50     160      110           6       True
797    600  80     110       60           6       True
798    680  80     160       60           6       True
799    600  80     110      120           6       True

[800 rows x 6 columns]
```

12.3 Append

we can also append dataframes to a dataframe as long as the columns are the same

[53]:
```
## make a variable for an empty frame
hold_wanted=pd.DataFrame()
```

```
#make a list of the pokemon numbers you want
pokemon_numbers=[1,4,150]

###quick function to make a a new df from the data
def make_df(num):
  data_out=pokemon.loc[pokemon['Number']==num]
  return data_out

#make a for loop that makes a df for each pokemon in the list you make
# then append each new df to the empty df
for i in pokemon_numbers:
  a=make_df(i)
  hold_wanted=hold_wanted.append(a)

#print the df that is not populated
hold_wanted
```

[53]:

```
     Number                   Name     HP  Attack  Defense
0       1.0              Bulbasaur   45.0    49.0     49.0
4       4.0             Charmander   39.0    52.0     43.0
162   150.0                 Mewtwo  106.0   110.0     90.0
163   150.0  MewtwoMega Mewtwo X  106.0   190.0    100.0
164   150.0  MewtwoMega Mewtwo Y  106.0   150.0     70.0
```

12.4 Pro-tip: glob —Skip in class —-

glob allows you to read in all the files in a directory and append them together without having to read in each file

[54]:

```
#import the glob library
from glob import glob
```

[55]:

```
## tell glob to read all the files in the directory that match the names␣
 ↪specified and
##store all the names in one variable
pokemon_subset=glob(datadirectory+'Pokemon_sub*.csv')
pokemon_subset
```

[55]:

```
['../data/Pokemon_sub1.csv',
 '../data/Pokemon_sub2.csv',
 '../data/Pokemon_sub3.csv']
```

[56]:

```
## using concat call in all the files in glob
## since we are concateing our file based on the rows we call axis=rows
## if instead you wnated to concat your files with columns you could call␣
 ↪axis='columns'
```

```
## notice the index has repeated values
subset_together=pd.concat((pd.read_csv(file) for file in␣
 ↪pokemon_subset),axis='rows')
subset_together
```

[56]:

```
   Number                     Name Type 1  Type 2  Total  HP  Attack  \
0       1                Bulbasaur  Grass  Poison    318  45      49
1       2                  Ivysaur  Grass  Poison    405  60      62
2       3                 Venusaur  Grass  Poison    525  80      82
0       4               Charmander   Fire     NaN    309  39      52
1       5               Charmeleon   Fire     NaN    405  58      64
2       6                Charizard   Fire  Flying    534  78      84
3       6  CharizardMega Charizard X   Fire  Dragon    634  78     130
4       6  CharizardMega Charizard Y   Fire  Flying    634  78     104
0       7                 Squirtle  Water     NaN    314  44      48
1       8                Wartortle  Water     NaN    405  59      63
2       9                Blastoise  Water     NaN    530  79      83
3       9    BlastoiseMega Blastoise  Water     NaN    630  79     103

   Defense  Sp. Atk  Sp. Def  Speed  Generation  Legendary
0       49       65       65     45           1      False
1       63       80       80     60           1      False
2       83      100      100     80           1      False
0       43       60       50     65           1      False
1       58       80       65     80           1      False
2       78      109       85    100           1      False
3      111      130       85    100           1      False
4       78      159      115    100           1      False
0       65       50       64     43           1      False
1       80       65       80     58           1      False
2      100       85      105     78           1      False
3      120      135      115     78           1      False
```

[57]:

```
## using concat call in all the files in glob
## pass in ignore_index so the index values are unique
subset_together=pd.concat((pd.read_csv(file) for file in␣
 ↪pokemon_subset),ignore_index=True)
subset_together
```

[57]:

```
    Number                     Name Type 1  Type 2  Total  HP  Attack  \
0        1                Bulbasaur  Grass  Poison    318  45      49
1        2                  Ivysaur  Grass  Poison    405  60      62
2        3                 Venusaur  Grass  Poison    525  80      82
3        4               Charmander   Fire     NaN    309  39      52
4        5               Charmeleon   Fire     NaN    405  58      64
5        6                Charizard   Fire  Flying    534  78      84
6        6  CharizardMega Charizard X   Fire  Dragon    634  78     130
```

```
7         6  CharizardMega Charizard Y   Fire  Flying    634  78      104
8         7                  Squirtle  Water     NaN    314  44       48
9         8                 Wartortle  Water     NaN    405  59       63
10        9                 Blastoise  Water     NaN    530  79       83
11        9   BlastoiseMega Blastoise  Water     NaN    630  79      103

    Defense  Sp. Atk  Sp. Def  Speed  Generation  Legendary
0        49       65       65     45           1      False
1        63       80       80     60           1      False
2        83      100      100     80           1      False
3        43       60       50     65           1      False
4        58       80       65     80           1      False
5        78      109       85    100           1      False
6       111      130       85    100           1      False
7        78      159      115    100           1      False
8        65       50       64     43           1      False
9        80       65       80     58           1      False
10      100       85      105     78           1      False
11      120      135      115     78           1      False
```

Skill check

[58]:

```
my_df1=pd.DataFrame({'names':['Gohan','Naruto','Luffy'],'color':
 ↪['blue','orange','red']})
my_df2=pd.DataFrame({'names':['Gohan','Naruto','Luffy'],'power':
 ↪[9000,8000,7000]})
my_df3=pd.DataFrame({'power':[9000,8000,7000],'enemy':['Cell','Sasuke','Kaido']})
```

combine the three tables using the method you think is best

[59]:

```
#### your code
```

Answer

[60]:

```
###combine df1_df2
my_df12=pd.merge(my_df1,my_df2,on='names',how='outer')

## combine df12_3

my_df123=pd.merge(my_df12,my_df3,on='power',how='outer')

my_df123
```

[60]:

```
    names   color  power   enemy
0   Gohan    blue   9000    Cell
1  Naruto  orange   8000  Sasuke
2   Luffy     red   7000   Kaido
```

```
[61]: my_combined_df=pd.merge(my_df1,my_df2,on='names')
      my_combined_df_out=pd.merge(my_combined_df,my_df3,on=['power'])
      my_combined_df_out
```

```
[61]:     names   color  power   enemy
      0    Gohan    blue   9000    Cell
      1   Naruto  orange   8000  Sasuke
      2    Luffy     red   7000   Kaido
```

13. Data Analysis

There are many ways to organize the data you have and more often than not you will have to create your own functions to see the data as you want it. However there are some built in fucntions like pd.pivot_tableand groupby that you can use to organize your data. These are both complicated tools and I am only going to introduce the basics here. This stackoverflow response has a wonder explanation of how these two are different.

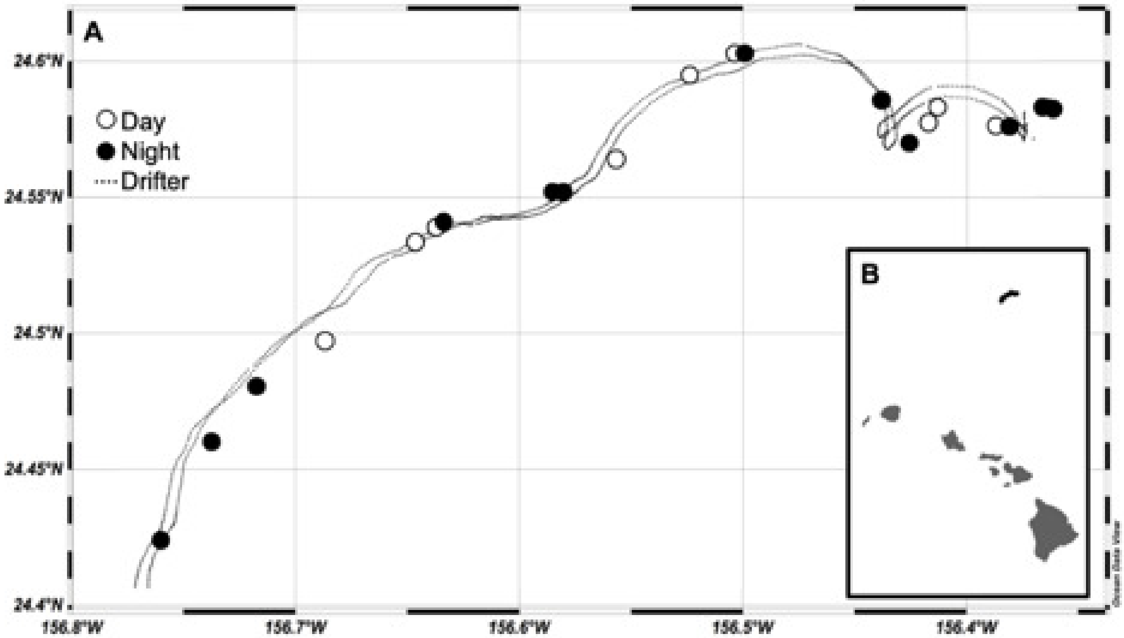
To explore data analysis and the process of data analysis I am going to walk you through a set of questions I answered for my first manuscript. This data explores gene expression patterns of a biochemically important phytoplankton called Emiliania huxleyi (Ehux). This organism makes calcium carbonate shells and so it is a key player in the global carbon cycle. Ehux is a phytoplankton meaning it uses photosynthesis for energy. For my research question I wanted to confirm that gene expression patterns of genes involved in processes related to light like photosynthesis followed the daily light cycles (diel cycles- light:dark).

Reference: Hernández Limón, María D., Gwenn MM Hennon, Matthew J. Harke, Kyle R. Frischkorn, Sheean T. Haley, and Sonya T. Dyhrman. "Transcriptional patterns of Emiliania huxleyi in the North Pacific Subtropical Gyre reveal the daily rhythms of its metabolic potential." Environmental microbiology 22, no. 1 (2020): 381-396.

```
[62]: ### recall gene_info_clean
      ## CAMNT is an ID for nucleotides-->gene
      ## WGCNA_Module_Num is the module/cluster from a clustering analysis
      ## RAIN_diel_Results is the output from an analysis on periodicty, so True mean␣
       ↪a 12hr period or diel, and False means no periodicty
      ## KEGG_annotation are genea annotations from another analysis

      gene_info_clean.head()
```

```
[62]:             CAMNT  WGCNA_Module_Num  RAIN_diel_Results  \
      0  CAMNT_0024302971                 7              False
      1  CAMNT_0024014877                 4              False
      2  CAMNT_0024014645                 9               True
      3  CAMNT_0023937169                 9               True
      4  CAMNT_0024335527                 9               True

                               KEGG_Annotations                KEGG_clean  \
      0      00910 Nitrogen metabolism [PATH:ko00910]       Nitrogen metabolism
```

```
1  00030 Pentose phosphate pathway [PATH:ko00030]  Pentose phosphate pathway
2  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation
3  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation
4  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation

                                 KEGG_clean1
0        Nitrogen metabolism [PATH:ko00910]
1  Pentose phosphate pathway [PATH:ko00030]
2  Oxidative phosphorylation [PATH:ko00190]
3  Oxidative phosphorylation [PATH:ko00190]
4  Oxidative phosphorylation [PATH:ko00190]
```



[63]:
```
### counts info
## the data we are looking at was collected in the North Pacific Subtropical␣
 ↪Gyre over a week and time samples were
## collected every 4hrs. This was A LOT of work!!!

#so we have 21 time points over a few days

gene_counts.head()
```

[63]:
```
               CAMNT    0    4    8   12   16   20   24   28   32  ...   40  \
0  CAMNT_0023928115  214  376  204  347  411  237  262  198  199  ...  411
1  CAMNT_0023928149   56   40   28   37   27  112   76   50   26  ...   27
2  CAMNT_0023928253   30   45   11   38   38   28   16   29   23  ...   38
3  CAMNT_0023928285   12   12   11   11   15   13    3   13    9  ...   15
4  CAMNT_0023928443  210  215  216  266  338  286  225  231  174  ...  338
```

```
    44   48   52   56   60   68   72   76   80
0  394  299  277  251  411  288  221  256  230
1  169   76   45   35   27   61   73   66   29
2   15    9   31   16   38   21   28   11   10
3    7    8    7   23   15   16   11    6   11
4  523  897  316  246  338  243  263  235  134

[5 rows x 21 columns]
```

13.1 coming up with questions

Possible questions:

1. What are the top 10 most abundant gene types (from the annotations) we find? How many photosynthesis genes do we find?
2. How many diel genes are there for each of these top 10 gene types?
3. Do the clusters/modules have the same type of genes in them? Are all the genes in a cluster either diel or not diel?
4. Do genes with annotations of interest show periodic patterns? even if we include the False diel? [annotations of interes: ‘Photosynthesis’, ‘Nitrogen metabolism’, ‘Carbon Metabolism’]

Introduction to groupby

Q1.

What are the top 10 most abundant gene types we find? How many photosynthesis genes do we find?

[64]:
```
#@title
## how many genes per pathway
## we can use groupby to group our rows based on the KEGG_clean pathway, by how␣
↪many there are
## this produces a table where all the columns have the same count
gene_info_clean.groupby('KEGG_clean').count()
```

[64]:
```
                                  CAMNT  WGCNA_Module_Num  RAIN_diel_Results  \
KEGG_clean
2-Oxocarboxylic acid metabolism      58                58                 58
ABC transporters                     47                47                 47
AMPK signaling pathway               42                42                 42
Acute myeloid leukemia                2                 2                  2
Adherens junction                    85                85                 85
...                                 ...               ...                ...
beta-Alanine metabolism               5                 5                  5
cGMP - PKG signaling pathway         62                62                 62
mRNA surveillance pathway            55                55                 55
```

```
mTOR signaling pathway                 18                 18                   18
p53 signaling pathway                  28                 28                   28

                                  KEGG_Annotations  KEGG_clean1
KEGG_clean
2-Oxocarboxylic acid metabolism                 58           58
ABC transporters                                47           47
AMPK signaling pathway                          42           42
Acute myeloid leukemia                           2            2
Adherens junction                               85           85
...                                            ...          ...
beta-Alanine metabolism                          5            5
cGMP - PKG signaling pathway                    62           62
mRNA surveillance pathway                       55           55
mTOR signaling pathway                          18           18
p53 signaling pathway                           28           28

[290 rows x 5 columns]
```

[65]:

```
## how many genes per pathway
## to only see one column we can specify what we want, in this case I want␣
 ↪CAMNT, but any column would work
gene_info_clean.groupby('KEGG_clean').count()
```

[65]:

```
                                  CAMNT  WGCNA_Module_Num  RAIN_diel_Results  \
KEGG_clean
2-Oxocarboxylic acid metabolism      58                58                 58
ABC transporters                     47                47                 47
AMPK signaling pathway               42                42                 42
Acute myeloid leukemia                2                 2                  2
Adherens junction                    85                85                 85
...                                 ...               ...                ...
beta-Alanine metabolism               5                 5                  5
cGMP - PKG signaling pathway         62                62                 62
mRNA surveillance pathway            55                55                 55
mTOR signaling pathway               18                18                 18
p53 signaling pathway                28                28                 28

                                  KEGG_Annotations  KEGG_clean1
KEGG_clean
2-Oxocarboxylic acid metabolism                 58           58
ABC transporters                                47           47
AMPK signaling pathway                          42           42
Acute myeloid leukemia                           2            2
Adherens junction                               85           85
...                                            ...          ...
beta-Alanine metabolism                          5            5
```

```
cGMP - PKG signaling pathway                            62           62
mRNA surveillance pathway                               55           55
mTOR signaling pathway                                  18           18
p53 signaling pathway                                   28           28

[290 rows x 5 columns]
```

[66]:

```
## how many genes per pathway
## to see which gene type is the most abundant we can sort our values
gene_info_clean.groupby('KEGG_clean').CAMNT.count().sort_values(ascending=False)
```

[66]:

```
KEGG_clean
Ribosome                                                 452
Carbon metabolism                                        313
Biosynthesis of amino acids                              297
Protein processing in endoplasmic reticulum              217
Huntington's disease                                     163
                                                        ...
C5-Branched dibasic acid metabolism                        1
Tropane, piperidine and pyridine alkaloid biosynthesis     1
Butirosin and neomycin biosynthesis                        1
Leishmaniasis                                              1
Ubiquinone and other terpenoid-quinone biosynthesis        1
Name: CAMNT, Length: 290, dtype: int64
```

[67]:

```
## let's make it a table so we can find things more easily
## we can create a new variable that holds the table we just made
annotation_counts=gene_info_clean.groupby('KEGG_clean').CAMNT.count().
 ↪sort_values(ascending=False)
annotation_counts.head(10)
```

[67]:

```
KEGG_clean
Ribosome                                       452
Carbon metabolism                              313
Biosynthesis of amino acids                    297
Protein processing in endoplasmic reticulum    217
Huntington's disease                           163
Epstein-Barr virus infection                   162
Oxidative phosphorylation                      160
Phagosome                                      155
Glycolysis / Gluconeogenesis                   151
Spliceosome                                    145
Name: CAMNT, dtype: int64
```

[68]:

```
## let's make it a table so we can find things more easily
annotation_counts_pretty=gene_info_clean.groupby('KEGG_clean').CAMNT.count().
 ↪sort_values(ascending=False).reset_index()
```

```
annotation_counts_pretty.head(10)
```

[68]:
```
                                      KEGG_clean  CAMNT
0                                      Ribosome     452
1                            Carbon metabolism      313
2                   Biosynthesis of amino acids     297
3  Protein processing in endoplasmic reticulum      217
4                          Huntington's disease     163
5                   Epstein-Barr virus infection    162
6                     Oxidative phosphorylation     160
7                                     Phagosome     155
8                   Glycolysis / Gluconeogenesis    151
9                                   Spliceosome     145
```

1. What are the top 10 most abundant genes we find? How many photosynthesis genes do we find?

[69]:
```
## make a list with the top 10 genes types
## since our annotations_counts table was sorted by the number of genes
## we just have to select the first 10 rows to get our answer
top10=list(annotation_counts.index[0:10])
top10
```

[69]:
```
['Ribosome ',
 'Carbon metabolism ',
 'Biosynthesis of amino acids ',
 'Protein processing in endoplasmic reticulum ',
 "Huntington's disease ",
 'Epstein-Barr virus infection ',
 'Oxidative phosphorylation ',
 'Phagosome ',
 'Glycolysis / Gluconeogenesis ',
 'Spliceosome ']
```

Skill check

Find how many photosynthesis genes there are, then add the name 'Photosynthesis' to the top10 list

[70]:
```
#### your code
```

Answer

[70]:
```
# let's add photosynthesis because we really care about it
top10.append('Photosynthesis ')
print (top10)
```

```
['Ribosome ', 'Carbon metabolism ', 'Biosynthesis of amino acids ', 'Protein
processing in endoplasmic reticulum ', "Huntington's disease ", 'Epstein-Barr
```

```
virus infection ', 'Oxidative phosphorylation ', 'Phagosome ', 'Glycolysis /
Gluconeogenesis ', 'Spliceosome ', 'Photosynthesis ']
```

[71]:
```
## but we still care about photosynthesis
##how many photosythesis genes
## we can use indexing to find this value
annotation_counts.loc[annotation_counts.index =='Photosynthesis ',]
```

[71]:
```
KEGG_clean
Photosynthesis     71
Name: CAMNT, dtype: int64
```

Sweet!! we were able to leverage groupby to answer our question!

13.2 Introduction to pivot tables

Q2.

How many diel genes are there for each of these top 10 gene types? We can use pivot table to answer this.

[72]:
```
## let's see that table once again
gene_info_clean.head()
```

[72]:
```
              CAMNT  WGCNA_Module_Num  RAIN_diel_Results  \
0  CAMNT_0024302971                 7              False
1  CAMNT_0024014877                 4              False
2  CAMNT_0024014645                 9               True
3  CAMNT_0023937169                 9               True
4  CAMNT_0024335527                 9               True

                                   KEGG_Annotations                  KEGG_clean  \
0        00910 Nitrogen metabolism [PATH:ko00910]         Nitrogen metabolism
1  00030 Pentose phosphate pathway [PATH:ko00030]  Pentose phosphate pathway
2  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation
3  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation
4  00190 Oxidative phosphorylation [PATH:ko00190]  Oxidative phosphorylation

                             KEGG_clean1
0        Nitrogen metabolism [PATH:ko00910]
1  Pentose phosphate pathway [PATH:ko00030]
2  Oxidative phosphorylation [PATH:ko00190]
3  Oxidative phosphorylation [PATH:ko00190]
4  Oxidative phosphorylation [PATH:ko00190]
```

[73]:
```
## let's make a pivot table with the summary
## to make a pivot table you need to specify what you want in the index and␣
↪columns and how you want to aggregare your values
```

```
## I am telling pivot_table to make me a table where my annotations␣
 ↪('KEGG_clean') are the index,
## my columns are the values in RAIN_diel_Results (True or False)
## and I want the values to be aggregated by count
diel_count_genetype=gene_info_clean.
 ↪pivot_table(values='CAMNT',index='KEGG_clean',columns='RAIN_diel_Results',aggfunc='count')
diel_count_genetype
```

```
[73]: RAIN_diel_Results                  False  True
      KEGG_clean
      2-Oxocarboxylic acid metabolism     40.0  18.0
      ABC transporters                    43.0   4.0
      AMPK signaling pathway              34.0   8.0
      Acute myeloid leukemia               2.0   NaN
      Adherens junction                   65.0  20.0
      ...                                  ...   ...
      beta-Alanine metabolism              4.0   1.0
      cGMP - PKG signaling pathway        49.0  13.0
      mRNA surveillance pathway           39.0  16.0
      mTOR signaling pathway              16.0   2.0
      p53 signaling pathway               21.0   7.0

      [290 rows x 2 columns]
```

```
[74]: #to select the genes types in our top10 list we can use indexing again
      diel_count_genetype.loc[diel_count_genetype.index.isin(top10),]
```

```
[74]: RAIN_diel_Results                             False   True
      KEGG_clean
      Biosynthesis of amino acids                   191.0  106.0
      Carbon metabolism                             157.0  156.0
      Epstein-Barr virus infection                  118.0   44.0
      Glycolysis / Gluconeogenesis                   83.0   68.0
      Huntington's disease                          121.0   42.0
      Oxidative phosphorylation                      96.0   64.0
      Phagosome                                      99.0   56.0
      Photosynthesis                                 10.0   61.0
      Protein processing in endoplasmic reticulum   139.0   78.0
      Ribosome                                      353.0   99.0
      Spliceosome                                   126.0   19.0
```

Q3.

Do the clusters/modules have the same type of genes in them? Are all the genes in a cluster either diel or not diel?

I made clusters for my genes using a program called WGCNA, you don't need to know what it is. The program gathers genes into clusters based on their expression patterns. I want to know if each cluster (called module by the program) has the same kind of genes in it? or if the clusters are a mixed of genes? But I only care about the clusters with a lot of diel genes.

Skill check

Make a new pivot table called modules_diel that has the counts of the CAMNT. I want 'WGCNA_Module_Num' as the index and on the columns I want 'RAIN_diel_Results'

[75]:

```
#### your code here

##modules_diel=
```

Answer

[76]:

```
## which modules have the most diel genes
## make a new pivot tables, this time the index is the WGCNA_modules and my␣
 ↪columns is the diel results
modules_diel=gene_info_clean.
 ↪pivot_table(values='CAMNT',index='WGCNA_Module_Num',columns=['RAIN_diel_Results'],aggfunc='co
modules_diel
```

[76]:

```
RAIN_diel_Results   False  True
WGCNA_Module_Num
0                  2239.0   28.0
1                  1393.0  688.0
2                   495.0  621.0
3                  1110.0  943.0
4                   321.0  267.0
5                   327.0   12.0
6                   351.0  372.0
7                   154.0    1.0
8                    93.0   15.0
9                   148.0  164.0
10                  105.0   79.0
11                  583.0  203.0
12                   93.0    NaN
13                  123.0    NaN
14                   40.0    5.0
15                   75.0   16.0
16                  113.0    NaN
17                   54.0    NaN
```

Continue

[77]:

```
## I only care about the modules with a lot of diel genes,
## for this case let's say more than 250 diel is of interest to us
modules_diel_clean=modules_diel.loc[modules_diel[True]>250,]
modules_diel_clean
```

[77]:

```
RAIN_diel_Results   False   True
WGCNA_Module_Num
1                  1393.0  688.0
2                   495.0  621.0
3                  1110.0  943.0
4                   321.0  267.0
6                   351.0  372.0
```

okay so there are 5 modules with more than 250 diel==True gens, they also have a lot that are not diel but that's ok

[78]:

```
##What pathways are on these modules and how many are diel

##this is a complicated run but really useufl
## I am telling pivot table to separate True/False diel, then give me how much␣
 ↪of each annotation of each, and tell
## me the distribution per module

modules_diel_genes=gene_info_clean.loc[((gene_info_clean['WGCNA_Module_Num'].
 ↪isin(modules_diel_clean.index)) &
                                         (gene_info_clean['KEGG_clean'].
 ↪isin(top10))) ,]
modules_diel_genes.
 ↪pivot_table(values='CAMNT',columns='WGCNA_Module_Num',index=['RAIN_diel_Results','KEGG_clean'
```

[78]:

```
WGCNA_Module_Num                                                     1     2  \
RAIN_diel_Results KEGG_clean
False             Biosynthesis of amino acids                     14.0  21.0
                  Carbon metabolism                               18.0  23.0
                  Epstein-Barr virus infection                    42.0   4.0
                  Glycolysis / Gluconeogenesis                     5.0  15.0
                  Huntington's disease                            16.0   3.0
                  Oxidative phosphorylation                       16.0   3.0
                  Phagosome                                        8.0   1.0
                  Photosynthesis                                   NaN   1.0
                  Protein processing in endoplasmic reticulum     43.0   8.0
                  Ribosome                                       197.0   1.0
                  Spliceosome                                     40.0  10.0
True              Biosynthesis of amino acids                      7.0  63.0
                  Carbon metabolism                               14.0  68.0
                  Epstein-Barr virus infection                    28.0   NaN
                  Glycolysis / Gluconeogenesis                     2.0  49.0
                  Huntington's disease                            12.0   NaN
```

```
                  Oxidative phosphorylation                      13.0  18.0
                  Phagosome                                      12.0   1.0
                  Photosynthesis                                  NaN  39.0
                  Protein processing in endoplasmic reticulum    47.0   1.0
                  Ribosome                                       44.0  31.0
                  Spliceosome                                    13.0   2.0

WGCNA_Module_Num                                                   3     4  \
RAIN_diel_Results KEGG_clean
False             Biosynthesis of amino acids                   25.0  14.0
                  Carbon metabolism                             15.0  14.0
                  Epstein-Barr virus infection                  15.0   2.0
                  Glycolysis / Gluconeogenesis                   8.0  10.0
                  Huntington's disease                          28.0   2.0
                  Oxidative phosphorylation                     18.0   6.0
                  Phagosome                                     13.0   3.0
                  Photosynthesis                                 NaN   1.0
                  Protein processing in endoplasmic reticulum   15.0  11.0
                  Ribosome                                      70.0   1.0
                  Spliceosome                                    9.0   2.0
True              Biosynthesis of amino acids                   22.0   6.0
                  Carbon metabolism                             51.0  13.0
                  Epstein-Barr virus infection                  10.0   NaN
                  Glycolysis / Gluconeogenesis                   6.0   8.0
                  Huntington's disease                          12.0   NaN
                  Oxidative phosphorylation                     19.0   NaN
                  Phagosome                                     12.0   1.0
                  Photosynthesis                                 NaN  19.0
                  Protein processing in endoplasmic reticulum    7.0   5.0
                  Ribosome                                      21.0   1.0
                  Spliceosome                                    NaN   NaN

WGCNA_Module_Num                                                   6
RAIN_diel_Results KEGG_clean
False             Biosynthesis of amino acids                    6.0
                  Carbon metabolism                              6.0
                  Epstein-Barr virus infection                   9.0
                  Glycolysis / Gluconeogenesis                   NaN
                  Huntington's disease                           5.0
                  Oxidative phosphorylation                      2.0
                  Phagosome                                      NaN
                  Photosynthesis                                 3.0
                  Protein processing in endoplasmic reticulum   16.0
                  Ribosome                                       NaN
                  Spliceosome                                    8.0
True              Biosynthesis of amino acids                    4.0
                  Carbon metabolism                              7.0
```

```
Epstein-Barr virus infection                    4.0
Glycolysis / Gluconeogenesis                    1.0
Huntington's disease                            6.0
Oxidative phosphorylation                       5.0
Phagosome                                       NaN
Photosynthesis                                  2.0
Protein processing in endoplasmic reticulum    18.0
Ribosome                                        NaN
Spliceosome                                     3.0
```

My question: I want to know if each cluster (called module by the program) has the same kind of genes in it? or if the clusters are a mixed of genes? what are the bilogical implications?

Answer: The clusters have a mixed of gene types in them both in terms of diel type (true or false) and gene annotations (multiple pathways). The biological explanation for this is that cells are doing a little bit of the same processes throughout the day. That is they don't stop and do one process at a time.

However there are some processes that see time dependant perhaps because of their requiremnt for light. Based on these observations we can hypothesise that processes like photosynthesis and carbon metabolism are dependent on light because these pathways have more true diel than non diel genes. The majority of these genes are in module 2 which has a peak in the middle of the day. (See WGCNA_clusters.tiff in data folder) These hypotheses conincide with what we know about photosynthesis in plants.

The fact that we observe the patterns we expected for photosynthesis and carbon metabolism validates our analysis methods. We can now explore genes whose behavior we don't know and trust what we find.

13.3 Combining our skills

Q4.

Do genes with annotations of interest show periodic patterns? even if we include the False diel? [annotations of interest: 'Photosynthesis', 'Carbon Metabolism']

[79]:
```
def get_gene_wanted(some_pathway):
    """This fucntion makes a plot of the pathway we choose"""

    ### find contigs with these annotations
    genes_wanted=gene_info_clean.
 ↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()
    print (genes_wanted)

    #find the counts for the genes with the annotations we want
    counts_wanted=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted.CAMNT)].
 ↪copy()
    return (counts_wanted)
```

```
get_gene_wanted('Nitrogen metabolism ')
```

```
                CAMNT  WGCNA_Module_Num  RAIN_diel_Results  \
0     CAMNT_0024302971                 7              False
294   CAMNT_0041672563                 2              False
295   CAMNT_0041652847                 4              False
296   CAMNT_0041714545                 4              False
1242  CAMNT_0041766699                 8              False
...                ...               ...                ...
4525  CAMNT_0041672429                 8              False
4526  CAMNT_0041713339                 3              False
4527  CAMNT_0041714151                 4              False
4528  CAMNT_0041792197                 1              False
4529  CAMNT_0041886015                 3              False

                               KEGG_Annotations           KEGG_clean  \
0     00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
294   00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
295   00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
296   00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
1242  00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
...                                         ...                  ...
4525  00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
4526  00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
4527  00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
4528  00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism
4529  00910 Nitrogen metabolism [PATH:ko00910]  Nitrogen metabolism

                               KEGG_clean1
0     Nitrogen metabolism [PATH:ko00910]
294   Nitrogen metabolism [PATH:ko00910]
295   Nitrogen metabolism [PATH:ko00910]
296   Nitrogen metabolism [PATH:ko00910]
1242  Nitrogen metabolism [PATH:ko00910]
...                                    ...
4525  Nitrogen metabolism [PATH:ko00910]
4526  Nitrogen metabolism [PATH:ko00910]
4527  Nitrogen metabolism [PATH:ko00910]
4528  Nitrogen metabolism [PATH:ko00910]
4529  Nitrogen metabolism [PATH:ko00910]

[124 rows x 6 columns]
```

[79]:

```
                CAMNT   0   4   8  12  16  20  24  28  32  ...  40  \
113  CAMNT_0023937163  52  37  20  38  51  62  23  36  33  ...  51
136  CAMNT_0023937581  47  38  23  30  27   9  16  17  24  ...  27
210  CAMNT_0023939041  32  59  38  28  31  36  35  69  16  ...  31
```

```
260   CAMNT_0023940979  115  275  107  117   76  118  146  175  46  ...   76
309   CAMNT_0023943767   94   98   45   63   69   73   31   76  52  ...   69
...                ...  ...  ...  ...  ...  ...  ...  ...  ...  ..  ...  ...
8722  CAMNT_0041857789  141  259  102  110   84  114  128  185  49  ...   84
8778  CAMNT_0041860069  117  140   99  134  115  180   98  122  71  ...  115
8914  CAMNT_0041884157   42   79   37   32   20   40   27   33  14  ...   20
9005  CAMNT_0041885089   47   36   25   36   21   14   17   35  17  ...   21
9055  CAMNT_0041886015   24   24   10   28   27   19   22   28   2  ...   27

       44   48   52   56   60   68   72  76  80
113    35   22   36   21   51   32   31  30  17
136    19   20   21   27   27   14   26  23  14
210    54   29   26   31   31   44   44  31  11
260   101  122  110  102   76  133  120  71  76
309   103   74   74   89   69   67   65  56  46
...   ...  ...  ...  ...  ...  ...  ...  ..  ..
8722  107   77  114  104   84  128  116  70  62
8778  135  101   91  105  115  116  101  97  74
8914   21   18   21   24   20   27   30  18  13
9005   12   27   28   24   21   15   19  20  14
9055   21   17   20   11   27   18   27   5  13

[124 rows x 21 columns]
```

[86]:
```
def get_gene_wanted(some_pathway):
    """This fucntion makes a plot of the pathway we choose"""

    ### find contigs with these annotations
    genes_wanted=gene_info_clean.
 ↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()

    #find the counts for the genes with the annotations we want
    counts_wanted=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted.CAMNT)].
 ↪copy()

    #add a column to our table
    counts_wanted['pathway']=some_pathway
    del counts_wanted['CAMNT']

    return counts_wanted

get_gene_wanted('Nitrogen metabolism ')
```

[86]:
```
      index   0   4   8  12  16  20  24  28  32  ...  44  48  52  \
113     113  52  37  20  38  51  62  23  36  33  ...  35  22  36
136     136  47  38  23  30  27   9  16  17  24  ...  19  20  21
210     210  32  59  38  28  31  36  35  69  16  ...  54  29  26
```

```
260      260  115  275  107  117   76  118  146  175  46  ...  101  122  110
309      309   94   98   45   63   69   73   31   76  52  ...  103   74   74
...      ...  ...  ...  ...  ...  ...  ...  ...  ...  ..  ...  ...  ...  ...
8722    8722  141  259  102  110   84  114  128  185  49  ...  107   77  114
8778    8778  117  140   99  134  115  180   98  122  71  ...  135  101   91
8914    8914   42   79   37   32   20   40   27   33  14  ...   21   18   21
9005    9005   47   36   25   36   21   14   17   35  17  ...   12   27   28
9055    9055   24   24   10   28   27   19   22   28   2  ...   21   17   20

         56   60   68   72  76  80               pathway
113      21   51   32   31  30  17  Nitrogen metabolism
136      27   27   14   26  23  14  Nitrogen metabolism
210      31   31   44   44  31  11  Nitrogen metabolism
260     102   76  133  120  71  76  Nitrogen metabolism
309      89   69   67   65  56  46  Nitrogen metabolism
...     ...  ...  ...  ...  ..  ..                   ...
8722    104   84  128  116  70  62  Nitrogen metabolism
8778    105  115  116  101  97  74  Nitrogen metabolism
8914     24   20   27   30  18  13  Nitrogen metabolism
9005     24   21   15   19  20  14  Nitrogen metabolism
9055     11   27   18   27   5  13  Nitrogen metabolism

[124 rows x 22 columns]
```

[80]:

```
def get_gene_wanted(some_pathway):
    """This fucntion makes a plot of the pathway we choose"""

    ### find contigs with these annotations
    genes_wanted=gene_info_clean.
 ↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()

    #find the counts for the genes with the annotations we want
    counts_wanted=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted.CAMNT)].
 ↪copy()

    #add a column to our table
    counts_wanted['pathway']=some_pathway
    del counts_wanted['CAMNT']

    mean=counts_wanted.groupby('pathway').mean()
    return mean

get_gene_wanted('Nitrogen metabolism ')
```

[80]:

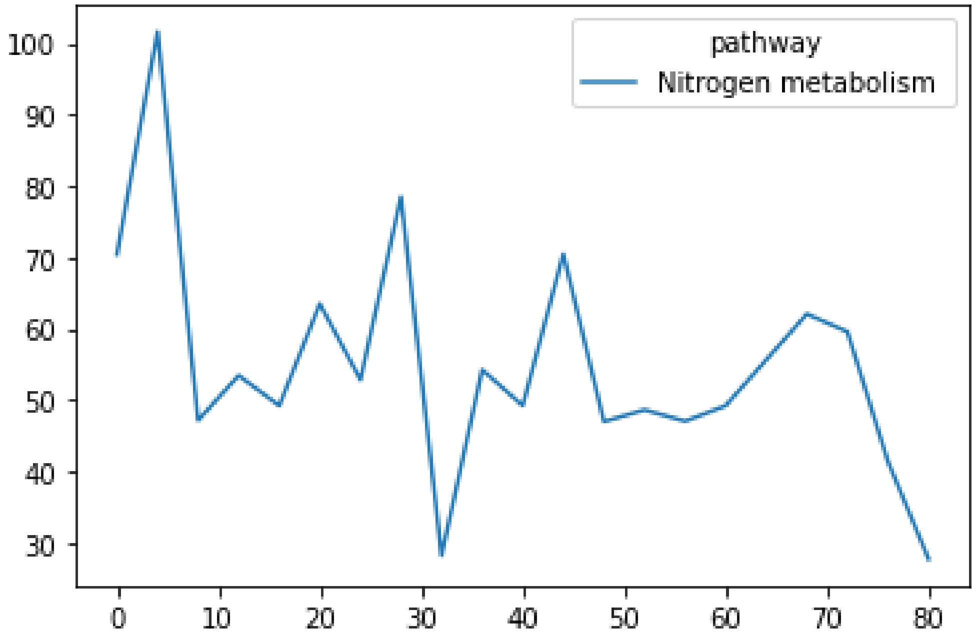
```
                             0           4         8          12         16  \
pathway
Nitrogen metabolism   70.41129  101.604839  47.16129  53.419355  49.193548
```

```
                             20         24         28         32         36  \
pathway
Nitrogen metabolism   63.475806  52.830645  78.451613  28.185484  54.225806

                             40         44         48         52         56  \
pathway
Nitrogen metabolism   49.193548  70.491935  46.967742  48.620968  47.032258

                             60         68         72         76         80
pathway
Nitrogen metabolism   49.193548  62.048387  59.564516  41.362903  27.693548
```

Let's flip this to make it easier to plot and make a quick plot

```
[81]: def get_gene_wanted(some_pathway):
          """This fucntion makes a plot of the pathway we choose"""

          ### find contigs with these annotations
          genes_wanted=gene_info_clean.
       ↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()

          #find the counts for the genes with the annotations we want
          counts_wanted=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted.CAMNT)].
       ↪copy()

          #add a column to our table
          counts_wanted['pathway']=some_pathway
          del counts_wanted['CAMNT']

          mean=counts_wanted.groupby('pathway').mean().transpose()
          return mean.plot()

          plt.close()

      get_gene_wanted('Nitrogen metabolism ')
```

```
[81]: <AxesSubplot:>
```



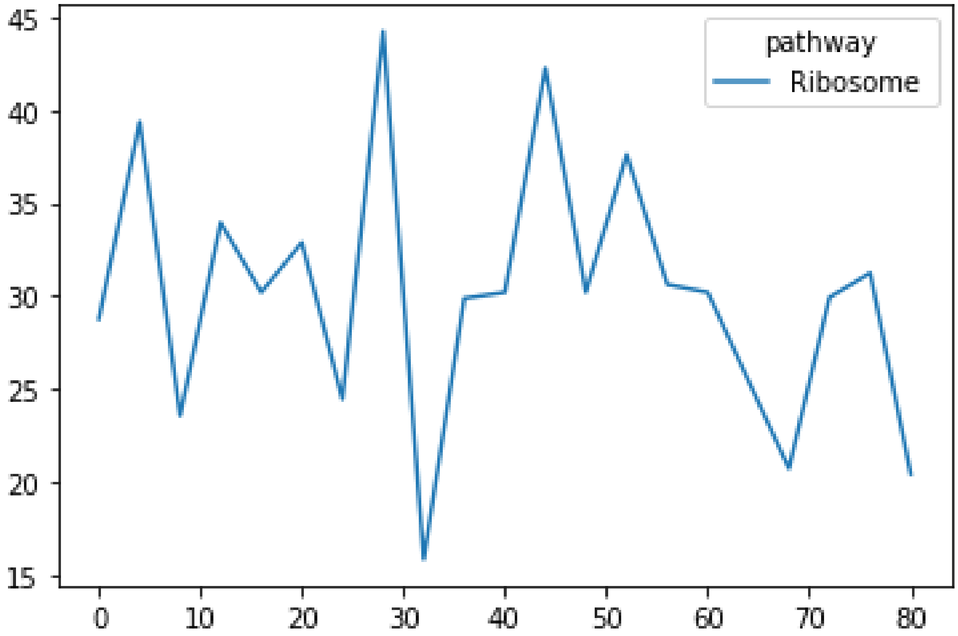
But we need to add an option to see the diel

[82]:
```
def get_gene_wanted(some_pathway, diel):

    ### find contigs with these annotations and the diel category wanted

    if diel== True:
        genes_wanted=gene_info_clean.
↪loc[((gene_info_clean['KEGG_clean']==some_pathway) &␣
↪(gene_info_clean['RAIN_diel_Results']==True)),].copy()
    elif diel == False:
        genes_wanted=gene_info_clean.
↪loc[((gene_info_clean['KEGG_clean']==some_pathway) &␣
↪(gene_info_clean['RAIN_diel_Results']==False)),].copy()
    else:
        genes_wanted=gene_info_clean.
↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()

    #find the counts for the genes with the annotations we want
    counts_wanted=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted.CAMNT)].
↪copy()

    #add a column to our table
    counts_wanted['pathway']=some_pathway
    del counts_wanted['CAMNT']
```

```
    #groupby the mean
    mean=counts_wanted.groupby('pathway').mean().transpose()
    return mean.plot()

    plt.close()

get_gene_wanted('Ribosome ', True)
```

[82]:

```
<AxesSubplot:>
```



let's add some shading so we can tell day and night apart

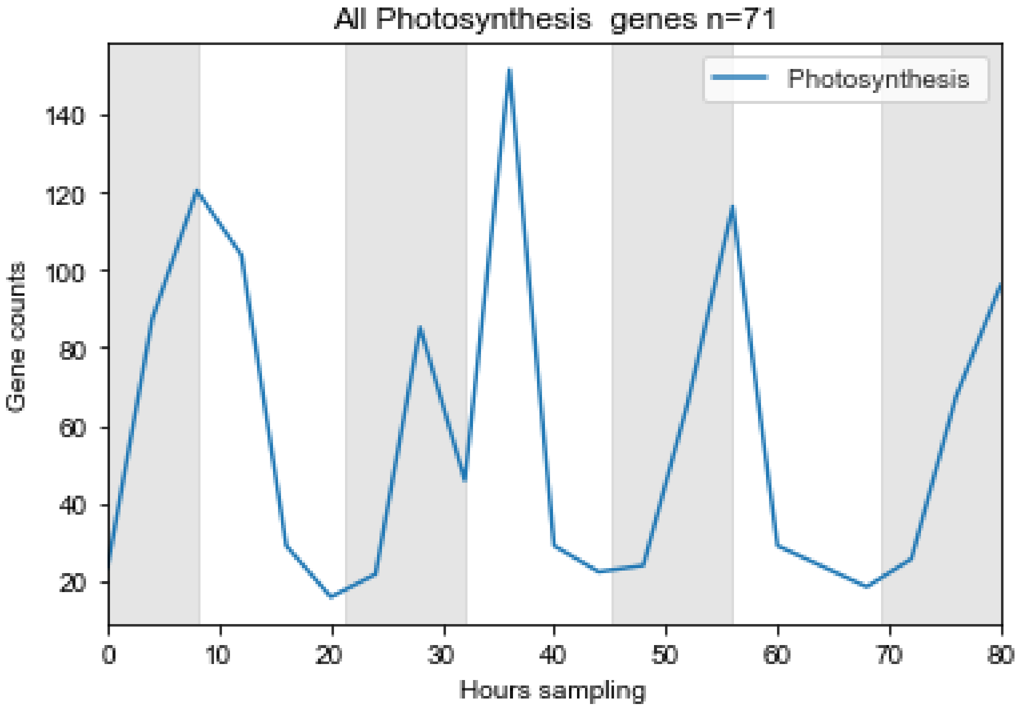
[83]:

```
def get_gene_wanted(some_pathway, diel):

    ### find contigs with these annotations and the diel category wanted

    if diel== True:
        genes_wanted=gene_info_clean.
 ↪loc[((gene_info_clean['KEGG_clean']==some_pathway) &␣
 ↪(gene_info_clean['RAIN_diel_Results']==True)),].copy()
    elif diel == False:
        genes_wanted=gene_info_clean.
 ↪loc[((gene_info_clean['KEGG_clean']==some_pathway) &␣
 ↪(gene_info_clean['RAIN_diel_Results']==False)),].copy()
    else:
```

```
        genes_wanted=gene_info_clean.
 ↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()

    #find the counts for the genes with the annotations we want
    counts_wanted=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted.CAMNT)].
 ↪copy()

    #add a column to our table
    counts_wanted['pathway']=some_pathway
    del counts_wanted['CAMNT']

    mean=counts_wanted.groupby('pathway').mean().transpose()
    #return mean

    ###make my plot pretty
    fig, ax= plt.subplots()
    sns.set_style('white')
    print(some_pathway)
    print(mean)
    ax.plot(mean,label=some_pathway)
    plt.xlim(0,80)

    plt.axvspan(0, 8, alpha=.2, color='grey',zorder=1)
    plt.axvspan(21.25, 32, alpha=.2, color='grey',zorder=1)
    plt.axvspan(45.25, 56, alpha=.2, color='grey',zorder=1)
    plt.axvspan(69.25, 80, alpha=.2, color='grey',zorder=1)

    ax.set_title('{} {} genes n={}'.format(diel, some_pathway,counts_wanted.
 ↪shape[0]))
    ax.set_xlabel('Hours sampling')
    ax.set_ylabel('Gene counts')
    plt.legend()

    plt.savefig(data_out_directory+'{}_{}.pdf'.format(some_pathway,diel))
    plt.show()
    plt.close()

get_gene_wanted('Photosynthesis ', 'All')
```

```
Photosynthesis
pathway  Photosynthesis
0             23.422535
4             87.281690
8            120.408451
12           103.830986
16            29.070423
20            15.830986
```

```
24               21.718310
28               85.197183
32               45.901408
36              151.507042
40               29.070423
44               22.309859
48               23.971831
52               66.028169
56              116.267606
60               29.070423
68               18.450704
72               25.647887
76               67.394366
80               96.140845
```

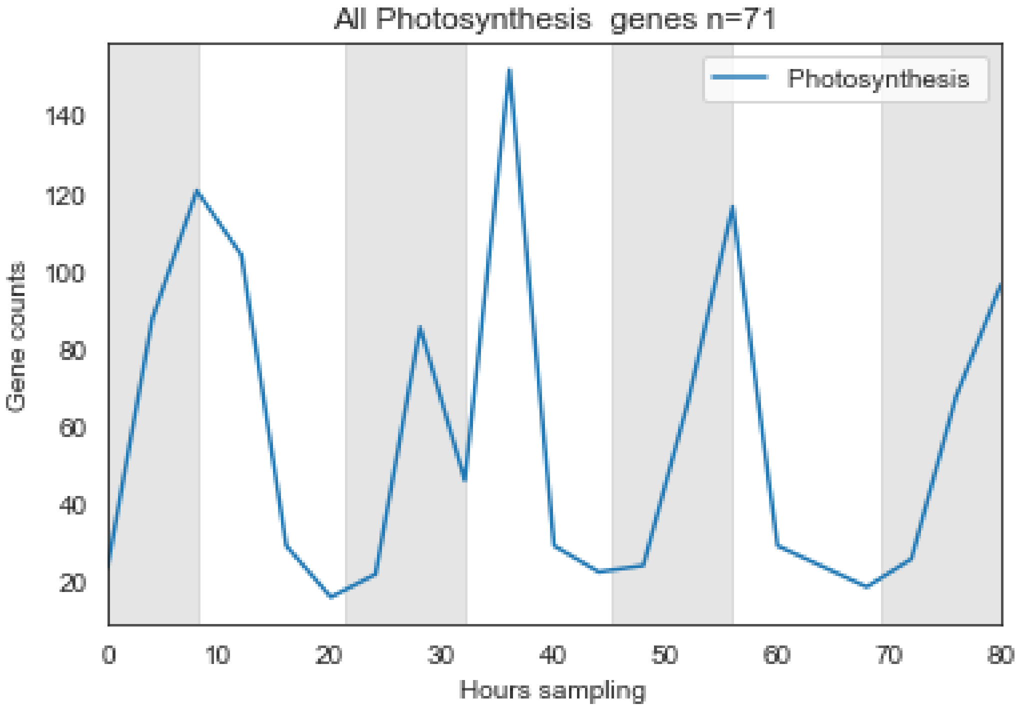


let's compare photosynthesis true, false and all

[85]:
```
get_gene_wanted('Photosynthesis ', 'All')
get_gene_wanted('Photosynthesis ', True)
get_gene_wanted('Photosynthesis ', False)
```

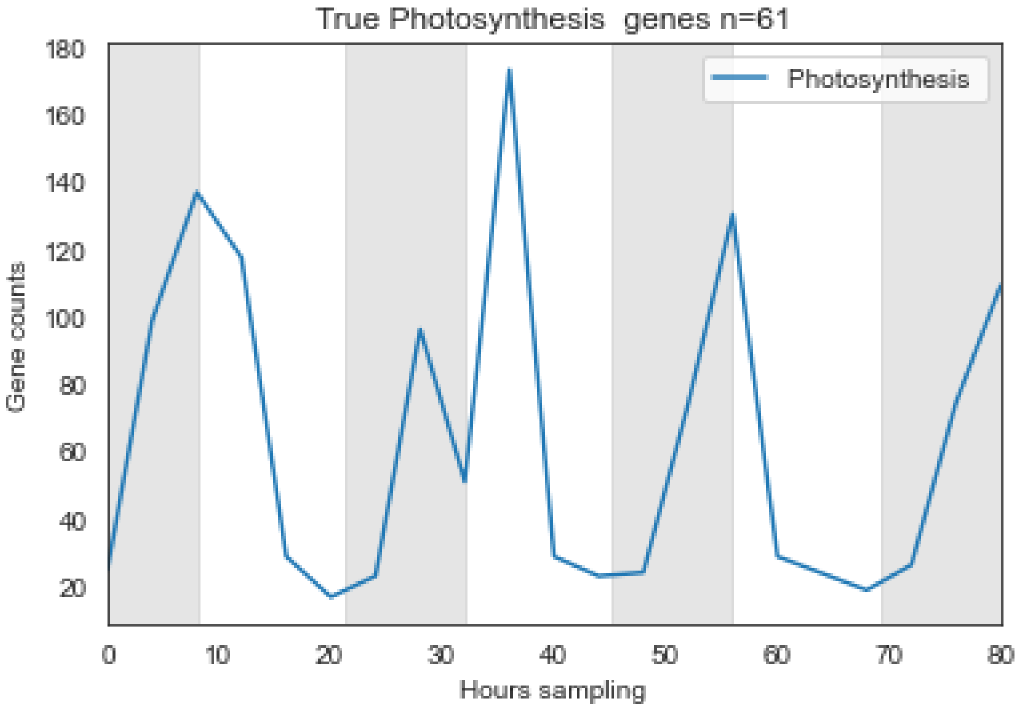
```
Photosynthesis
pathway  Photosynthesis
0               23.422535
4               87.281690
```

```
8               120.408451
12              103.830986
16               29.070423
20               15.830986
24               21.718310
28               85.197183
32               45.901408
36              151.507042
40               29.070423
44               22.309859
48               23.971831
52               66.028169
56              116.267606
60               29.070423
68               18.450704
72               25.647887
76               67.394366
80               96.140845
```



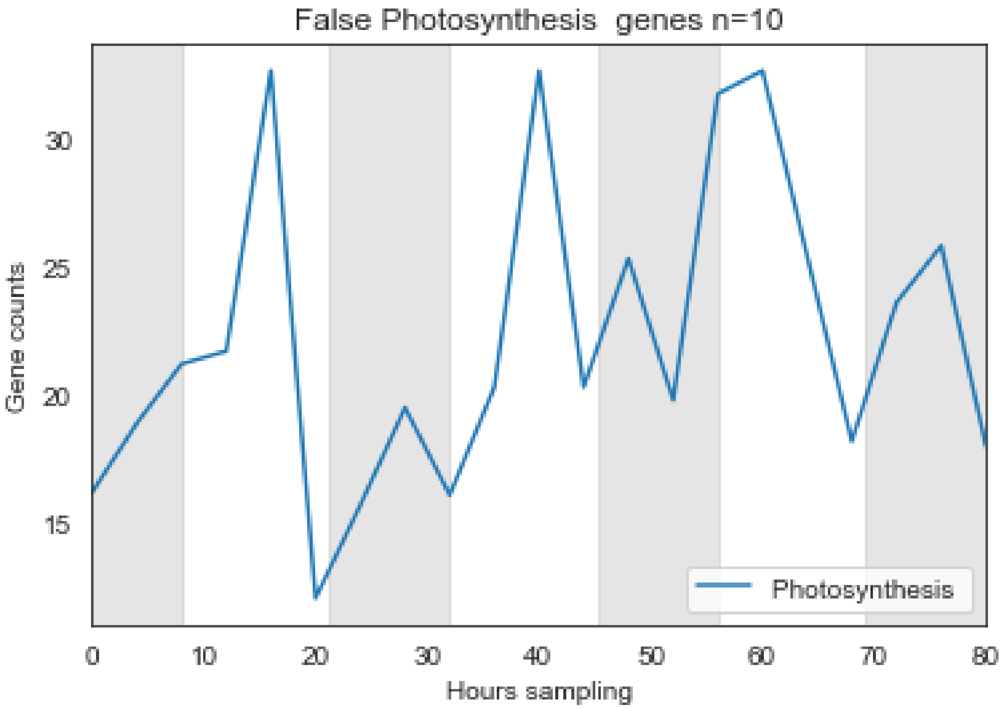
```
Photosynthesis
pathway  Photosynthesis
0                24.606557
4                98.491803
8               136.672131
```

```
12            117.295082
16             28.491803
20             16.442623
24             22.704918
28             95.967213
32             50.786885
36            173.016393
40             28.491803
44             22.639344
48             23.754098
52             73.606557
56            130.131148
60             28.491803
68             18.491803
72             25.983607
76             74.213115
80            108.950820
```



```
Photosynthesis
pathway  Photosynthesis
0                   16.2
4                   18.9
8                   21.2
12                  21.7
```

```
16                    32.6
20                    12.1
24                    15.7
28                    19.5
32                    16.1
36                    20.3
40                    32.6
44                    20.3
48                    25.3
52                    19.8
56                    31.7
60                    32.6
68                    18.2
72                    23.6
76                    25.8
80                    18.0
```



As expected photosynthesis related genes show a diel pattern. The majority of the genes 61/71 are diel. When we look at the pattern of all the genes together we see that the diel genes dominate the patterns we see.

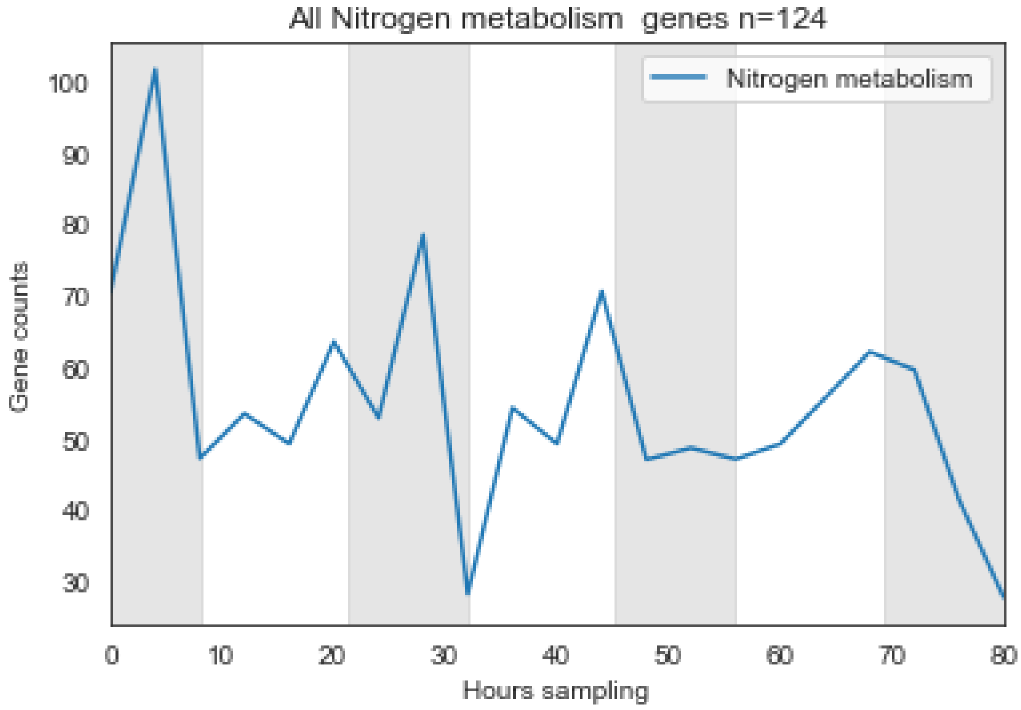
Let's check a set of genes we don't know much about and see what we learn

[86]:

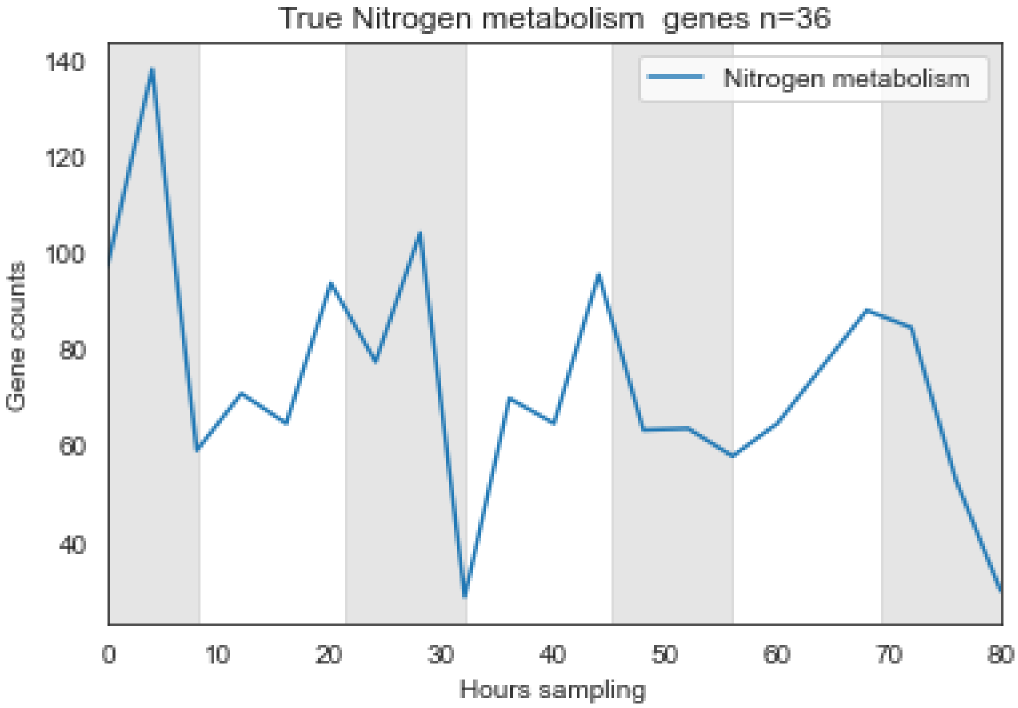
```
get_gene_wanted('Nitrogen metabolism ', 'All')
get_gene_wanted('Nitrogen metabolism ', True)
```

```
get_gene_wanted('Nitrogen metabolism ', False)
```

```
Nitrogen metabolism
pathway  Nitrogen metabolism
0                  70.411290
4                 101.604839
8                  47.161290
12                 53.419355
16                 49.193548
20                 63.475806
24                 52.830645
28                 78.451613
32                 28.185484
36                 54.225806
40                 49.193548
44                 70.491935
48                 46.967742
52                 48.620968
56                 47.032258
60                 49.193548
68                 62.048387
72                 59.564516
76                 41.362903
80                 27.693548
```



```
Nitrogen metabolism
pathway  Nitrogen metabolism
0                  97.166667
4                 137.944444
8                  58.833333
12                 70.638889
16                 64.444444
20                 93.555556
24                 77.250000
28                104.000000
32                 28.527778
36                 69.638889
40                 64.444444
44                 95.361111
48                 63.083333
52                 63.388889
56                 57.638889
60                 64.444444
68                 87.916667
72                 84.333333
76                 52.638889
80                 29.722222
```



```
Nitrogen metabolism
```

```
pathway  Nitrogen metabolism
0                  59.465909
4                  86.738636
8                  42.386364
12                 46.375000
16                 42.954545
20                 51.170455
24                 42.840909
28                 68.000000
32                 28.045455
36                 47.920455
40                 42.954545
44                 60.318182
48                 40.375000
52                 42.579545
56                 42.693182
60                 42.954545
68                 51.465909
72                 49.431818
76                 36.750000
80                 26.863636
```

For genes related to nitrogen metabolism we see that the majority are not diel. This may suggest that given the low concentrations of nitrogen in the North Pacific Sunbtropical Gyre that the cells take up nitrogen whenever they can.

Homework

Can you make a function to print all three lines, (all, true, false) in one plot?

[87]:

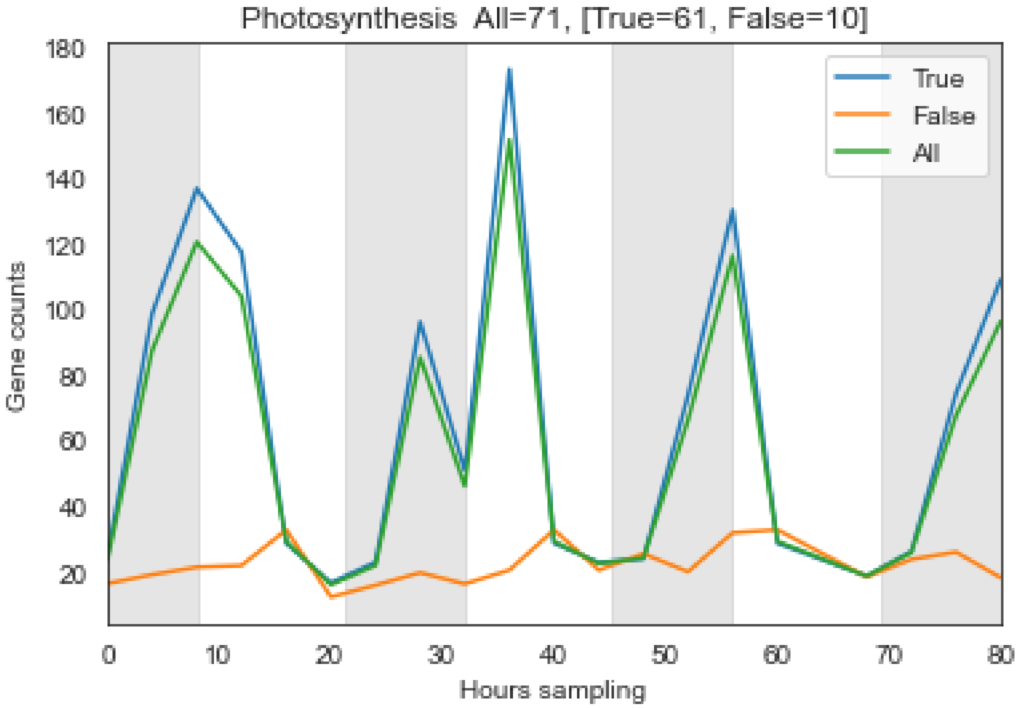
```
#### your work###
###Hint: use the skills you learned from Katie
### hint: I already did most of the work for you so use the function I made as a␣
 ↪spring board
```

Answer

[88]:

```
#### I will add on Fri morning :)

def get_gene_wanted(some_pathway):

    ### find contigs with these annotations and the diel category wanted

    #true
    genes_wanted_true=gene_info_clean.
 ↪loc[((gene_info_clean['KEGG_clean']==some_pathway) &␣
 ↪(gene_info_clean['RAIN_diel_Results']==True)),].copy()
    counts_wanted_true=gene_counts.loc[gene_counts['CAMNT'].
 ↪isin(genes_wanted_true.CAMNT)].copy()
    counts_wanted_true['pathway']=some_pathway
    del counts_wanted_true['CAMNT']
    mean_true=counts_wanted_true.groupby('pathway').mean().transpose()

    ##counts for the label
    counts_true=counts_wanted_true.shape[0]

    #false
    genes_wanted_false=gene_info_clean.
 ↪loc[((gene_info_clean['KEGG_clean']==some_pathway) &␣
 ↪(gene_info_clean['RAIN_diel_Results']==False)),].copy()
    counts_wanted_false=gene_counts.loc[gene_counts['CAMNT'].
 ↪isin(genes_wanted_false.CAMNT)].copy()
    counts_wanted_false['pathway']=some_pathway
    del counts_wanted_false['CAMNT']
    mean_false=counts_wanted_false.groupby('pathway').mean().transpose()

    ##counts for the label
    counts_false=counts_wanted_false.shape[0]

    #all
```

```
    genes_wanted_all=gene_info_clean.
 ↪loc[gene_info_clean['KEGG_clean']==some_pathway,].copy()
    counts_wanted_all=gene_counts.loc[gene_counts['CAMNT'].isin(genes_wanted_all.
 ↪CAMNT)].copy()
    counts_wanted_all['pathway']=some_pathway
    del counts_wanted_all['CAMNT']
    mean_all=counts_wanted_all.groupby('pathway').mean().transpose()

    ##counts for the label
    counts_all=counts_wanted_all.shape[0]

    ###make my plot pretty
    fig, ax= plt.subplots()
    sns.set_style('white')

    ax.plot(mean_true, label='True')
    ax.plot(mean_false, label='False')
    ax.plot(mean_all, label='All')

    ax.set_title('{} All={}, [True={}, False={}]'.
 ↪format(some_pathway,counts_all,counts_true,counts_false))
    ax.set_xlabel('Hours sampling')
    ax.set_ylabel('Gene counts')
    ax.legend()

    plt.xlim(0,80)
    plt.axvspan(0, 8, alpha=.2, color='grey',zorder=1)
    plt.axvspan(21.25, 32, alpha=.2, color='grey',zorder=1)
    plt.axvspan(45.25, 56, alpha=.2, color='grey',zorder=1)
    plt.axvspan(69.25, 80, alpha=.2, color='grey',zorder=1)
    plt.show()

    plt.close()

get_gene_wanted('Photosynthesis ')
```


Photosynthesis All=71, [True=61, False=10]
180
160
140
120
100
80
60
40
20
Gene counts
0
10
20
30
40
50
60
70
80
Hours sampling
True
False
All