data-exploring-202007

July 9, 2020

[1]:
```python
import os
from IPython.display import display, Image
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from matplotlib import colors
from matplotlib.ticker import PercentFormatter
from scipy.stats import linregress
import math
from functools import reduce
import matplotlib
import argparse
# from Bio import SeqIO, Entrez, pairwise2
# Entrez.email = 'hongyingsun1101@gmail.com'
# from Bio.SeqRecord import SeqRecord
import re, time
import os, sys, glob
import random
import uuid
# from skbio.tree import TreeNode
# from skbio import read
# from skbio.stats.distance import DistanceMatrix
# from skbio.stats.distance import DissimilarityMatrix

from scipy import stats
from ast import literal_eval
import sqlite3
# roc curve and auc score
from sklearn.datasets import make_classification
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score
import warnings
warnings.filterwarnings("ignore")
```

[2]:
```python
import matplotlib.pyplot as plt
```

[3]:
```python
df = pd.read_csv("all_data.csv", index_col=0)
score= pd.read_csv("score_merged.csv", index_col=0)
```

[4]:
```python
reference ={'A':"RDP_10398", 'B':'RDP_5224', 'C':"RDP_1017", 'D':'RDP_92', 'E':
↪'RDP_12'}
```

[5]:
```python
def is_float(string):
  try:
    return float(string) and '.' in string  # True if string is a number␣
↪contains a dot
  except ValueError:  # String is not a number
    return False
```

[6]:
```python
def plot_pplacer(variable):
    fig, axes = plt.subplots(nrows=3, ncols=2)
    ax0, ax1, ax2, ax3, ax4, ax5 = axes.flatten()

    ax0.hist(df['A'+variable])
    ax0.set_title('A'+variable)
    ax0.set_ylim(0,5000)

    ax1.hist(df['B'+variable])
    ax1.set_title('B'+variable)
    ax1.set_ylim(0,5000)

    ax2.hist(df['C'+variable])
    ax2.set_title('C'+variable)
    ax2.set_ylim(0,5000)

    ax3.hist(df['D'+variable])
    ax3.set_title('D'+variable)
    ax3.set_ylim(0,5000)
    ax4.hist(df['E'+variable])
    ax4.set_title('E'+variable)
    ax4.set_ylim(0,5000)
```

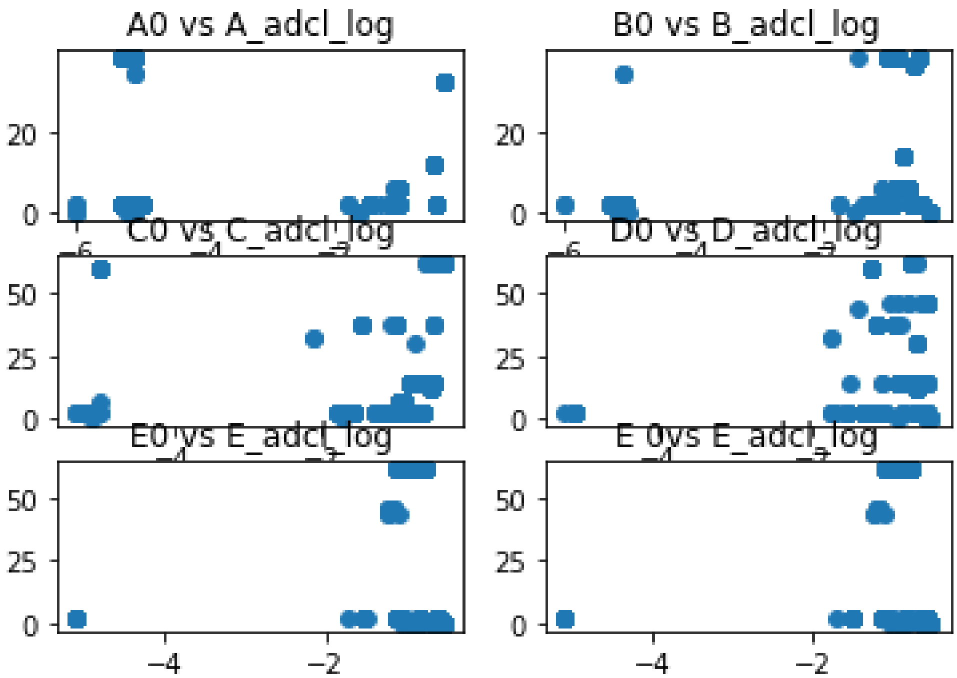
[7]:
```python
def plotScatter(reference,community):
    fig, axes = plt.subplots(nrows=2, ncols=2)
    ax0, ax1, ax2, ax3 = axes.flatten()

    ax0.scatter(df[reference+'_adcl_log'], df[reference+community])
    ax0.set_title(reference+community+' vs '+ reference + '_adcl_log')

    ax1.scatter(df[reference+'_edpl'], df[reference+community])
    ax1.set_title(reference+community+' vs '+ reference + '_edpl')
```

```python
    ax2.scatter(df[reference+'_mindistl'], df[reference+community])
    ax2.set_title(reference+community+' vs '+ reference + '_mindistl')

    ax3.scatter(df[reference+'_prichness'], df[reference+community])
    ax3.set_title(reference+community+' vs '+ reference + '_prichness')
```

[8]:
```python
# plotScatter('A','0')
```

[9]:
```python
# plotScatter('B','0')
```

[10]:
```python
def plotScatterRef(variable,community):
    fig, axes = plt.subplots(nrows=3, ncols=2)
    ax0, ax1, ax2, ax3, ax4, ax5 = axes.flatten()

    ax0.scatter(df['A'+variable], df['A'+community])
    ax0.set_title('A' + community +' vs A' + variable)
    ax1.scatter(df['B'+variable], df['B'+community])
    ax1.set_title('B' + community +' vs B' + variable)

    ax2.scatter(df['C'+variable], df['C'+community])
    ax2.set_title('C' + community +' vs C' + variable)

    ax3.scatter(df['D'+variable], df['D'+community])
    ax3.set_title('D' + community +' vs D' + variable)

    ax4.scatter(df['E'+variable], df['E'+community])
    ax4.set_title('E' + community +' vs E' + variable)

    ax5.scatter(df['E'+variable], df['E'+community])
    ax5.set_title('E ' + community +'vs E' + variable)




plotScatterRef('_adcl_log','0');
```



[11]:
```python

# plotScatterRef('_edpl','99');
```

[12]:
```python
cols=df.columns.tolist()
# cols[:20]
```

[13]:
```python
def plot_roc_curve(fpr, tpr):
    plt.plot(fpr, tpr, color='orange', label='ROC')
    plt.plot([0, 1], [0, 1], color='darkblue', linestyle='--')
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('Receiver Operating Characteristic (ROC) Curve')
    plt.legend()
    plt.show()
```

[14]:
```python
def plot_roc(data_X, class_label):
    trainX, testX, trainy, testy = train_test_split(data_X, class_label,␣
 ↪test_size=0.3, random_state=1)
    model = RandomForestClassifier()
    model.fit(trainX, trainy)
    probs = model.predict_proba(testX)
    probs = probs[:, 1]
    auc = roc_auc_score(testy, probs)
    fpr, tpr, thresholds = roc_curve(testy, probs)
```

```
    optimal_idx = np.argmax(tpr - fpr)
    optimal_threshold = thresholds[optimal_idx]
    print('optimal_threshold: %.2f' % optimal_threshold)
    print('AUC: %.2f' % auc)
    print( thresholds)
#     print( thresholds)
#     print('Model: ')
#     print(model)
    plot_roc_curve(fpr, tpr)
```

[15]:
```
def makeTable(headerRow,columnizedData,columnSpacing=2):
    """Creates a technical paper style, left justified table"""
    from numpy import array,max,vectorize

    cols = array(columnizedData,dtype=str)
    colSizes = [max(vectorize(len)(col)) for col in cols]

    header = ''
    rows = ['' for i in cols[0]]

    for i in range(0,len(headerRow)):
        if len(headerRow[i]) > colSizes[i]: colSizes[i]=len(headerRow[i])
        headerRow[i]+=' '*(colSizes[i]-len(headerRow[i]))
        header+=headerRow[i]
        if not i == len(headerRow)-1: header+=' '*columnSpacing

        for j in range(0,len(cols[i])):
            if len(cols[i][j]) < colSizes[i]:
                cols[i][j]+=' '*(colSizes[i]-len(cols[i][j])+columnSpacing)
            rows[j]+=cols[i][j]
            if not i == len(headerRow)-1: rows[j]+=' '*columnSpacing

    line = '-'*len(header)
    print(line)
    print(header)
    print(line)
    for row in rows: print(row)
    print(line)
header = ['AUROC','Categoroy']
cutoffs = ['0.9-1.0','0.8-0.9','0.7-0.8','0.6-0.7','0.5-0.6']
evalualtion = ['Very good','Good','Fair', 'Poor', 'Fail']
makeTable(header,[cutoffs,evalualtion])
```

```
------------------
AUROC    Categoroy
------------------
0.9-1.0  Very good
```

```
0.8-0.9  Good
0.7-0.8  Fair
0.6-0.7  Poor
0.5-0.6  Fail
------------------
```

[16]:

```python
def plot_roc_microbiome(data_X, class_label, x, y, data_test=False):
    if(not data_test):
#         print("data_set is False")
        trainX, testX, trainy, testy = train_test_split(data_X, class_label,␣
↪test_size=0.3, random_state=1)
        model = RandomForestClassifier()
        model.fit(trainX, trainy)
        probs = model.predict_proba(testX)
        probs = probs[:, 1]
        auc = roc_auc_score(testy, probs)
        fpr, tpr, thresholds = roc_curve(testy, probs)
        optimal_idx = np.argmax(tpr - fpr)
        optimal_threshold = thresholds[optimal_idx]
        print('optimal_threshold: %.2f' % optimal_threshold)
        print('AUC: %.2f' % auc)
        print('thresholds: ' + thresholds)

        plot_roc_curve(fpr, tpr)

    else:
        print("data_set is True")
        trainX, testX, trainy, testy = train_test_split(data_X, class_label,␣
↪test_size=0.3, random_state=1)
        model = RandomForestClassifier()
        model.fit(trainX, trainy)
        probs1 = model.predict_proba(testX)
        probs1 = probs1[:, 1]
        auc1 = roc_auc_score(testy, probs1)
        fpr1, tpr1, thresholds1 = roc_curve(testy, probs1)
        optimal_idx1 = np.argmax(tpr1 - fpr1)
        optimal_threshold1 = thresholds1[optimal_idx1]
        print('AUC1: %.2f' % auc1)
        print('optimal_threshold1: %.2f' % optimal_threshold1)
        print(thresholds1)
        plot_roc_curve(fpr1, tpr1)

        probs2 = model.predict_proba(x)
        probs2 = probs2[:, 1]
        auc2 = roc_auc_score(y, probs2)
        fpr2, tpr2, thresholds2 = roc_curve(y, probs2)
        optimal_idx2 = np.argmax(tpr2 - fpr2)
```

```
        optimal_threshold2 = thresholds2[optimal_idx2]
        print('AUC2: %.2f' % auc2)
        print('optimal_threshold2: %.2f' % optimal_threshold2)
        print( thresholds2)
        plot_roc_curve(fpr2, tpr2)
```

```
[17]: def plot_roc_curve_microbiome(pplacer_ref_list, pplacer_stats_list,␣
      ↪community_list, cutoff_list, scoreOption=True):
          for (refIndex,pplacer_ref) in enumerate(pplacer_ref_list):
      #     for refIndex in range(len(pplacer_ref_list)):
      #         pplacer_ref = pplacer_ref_list[refIndex]
              for (statsIndex,pplacer_stats) in enumerate(pplacer_stats_list):
      #         for statsIndex in range(len(pplacer_stats_list)):
      #             pplacer_stats = pplacer_stats_list[statsIndex]
                  for (communityIndex,community) in enumerate(community_list):
      #             for communityIndex in range(len(community_list)):
      #                 community = community_list[communityIndex]
                      for (i, cutoff) in enumerate(cutoff_list):
      #                 for i in range(len(cutoff_list)):
      #                     cutoff=cutoff_list[i]
                          if(is_float(cutoff)):
                              cutoff_binary=float(cutoff)
                          else:
                              if(scoreOption):
                                  cutoff_binary=float(df[pplacer_ref+community].
      ↪describe().loc[[cutoff]])

                              else:
                                  cutoff_binary = float(df[pplacer_ref+pplacer_stats].
      ↪describe().loc[[cutoff]])
                          if(scoreOption):
                              mask = df[pplacer_ref+community] <=  cutoff_binary
                              df.loc[mask, pplacer_ref+community+'_binary'] = 1
                              mask = df[pplacer_ref+community] >cutoff_binary
                              df.loc[mask, pplacer_ref+community+'_binary'] = 0
                              df_binary = df[[pplacer_ref+pplacer_stats,␣
      ↪pplacer_ref+community+'_binary']].dropna()
                              data_stats = df_binary[pplacer_ref+pplacer_stats].
      ↪to_numpy().reshape(-1,1)
                              binary_label = ␣
      ↪df_binary[pplacer_ref+community+'_binary'].to_numpy()
                              print(' The score cutoff '+ cutoff +' for Reference ' +␣
      ↪pplacer_ref +' community ' + community   + ' with pplacer_stats '+␣
      ↪pplacer_stats[1:] + ': %.2f' % cutoff_binary )
                              plot_roc(data_stats,binary_label)
                          else:
```

```
                        mask = df[pplacer_ref+pplacer_stats] <=  cutoff_binary
                        df.loc[mask, pplacer_ref+pplacer_stats+'_binary'] = 1
                        mask = df[pplacer_ref+pplacer_stats] >cutoff_binary
                        df.loc[mask, pplacer_ref+pplacer_stats+'_binary'] = 0
                        df_binary = df[[pplacer_ref+community,␣
↪pplacer_ref+pplacer_stats+'_binary']].dropna()
                        data_stats = df_binary[pplacer_ref+community].
↪to_numpy().reshape(-1,1)
                        binary_label = ␣
↪df_binary[pplacer_ref+pplacer_stats+'_binary'].to_numpy()
                        print(' The pplacer_stats_cutoff '+ cutoff +' for␣
↪Reference ' + pplacer_ref +' community ' + community + ' pplacer_stats '  +␣
↪pplacer_stats[1:]  + ': %.2f' % cutoff_binary )
                        plot_roc(data_stats,binary_label)
```

1 different reference same pplacer stats same community to test different cutoffs and different references for score

[18]:
```
# plot_roc_curve_microbiome(pplacer_ref_list =␣
↪['A','B','C','D','E'],pplacer_stats_list=['_adcl_log'],community_list=['A'],cutoff_list=['m
↪'min','25%','50%','75%'],scoreOption=False)
```

[19]:
```
df['E0'].describe()
```

[19]:
```
count    605.000000
mean      14.601653
std       25.354082
min        0.000000
25%        0.000000
50%        2.000000
75%        2.000000
max       62.000000
Name: E0, dtype: float64
```

2 Different reference same pplacer stats same community to test different cutoffs and different references for adcl_log

3 Fitting on large reference and test on small reference datasets

[20]:
```
def plot_roc_curve_microbiome_test2(pplacer_ref_list, pplacer_stats_list,␣
↪community_list, cutoff_list, test_data_list, scoreOption=True,␣
↪testOption=False):
    for refIndex in range(len(pplacer_ref_list)):
```

```
        pplacer_ref = pplacer_ref_list[refIndex]
        for statsIndex in range(len(pplacer_stats_list)):
            pplacer_stats = pplacer_stats_list[statsIndex]
            for communityIndex in range(len(community_list)):
                community = community_list[communityIndex]
                for i in range(len(cutoff_list)):
                    cutoff=cutoff_list[i]
                    if(is_float(cutoff)):
                        cutoff_binary=float(cutoff)
                    else:
                        if(scoreOption):
                            cutoff_binary=float(df[pplacer_ref+community].
↪describe().loc[[cutoff]])

                        else:
                            cutoff_binary = float(df[pplacer_ref+pplacer_stats].
↪describe().loc[[cutoff]])
                    # no test situation, which is the default option
                    if (not testOption):

                        if(scoreOption):
                            mask = df[pplacer_ref+community] <=  cutoff_binary
                            df.loc[mask, pplacer_ref+community+'_binary'] = 1
                            mask = df[pplacer_ref+community] >cutoff_binary
                            df.loc[mask, pplacer_ref+community+'_binary'] = 0
                            df_binary = df[[pplacer_ref+pplacer_stats,␣
↪pplacer_ref+community+'_binary']].dropna()
                            data_stats = df_binary[pplacer_ref+pplacer_stats].
↪to_numpy().reshape(-1,1)
                            binary_label = ␣
↪df_binary[pplacer_ref+community+'_binary'].to_numpy()
                            print(' The score cutoff '+ cutoff +' for Reference␣
↪' + pplacer_ref +' community ' + community   + ' with pplacer_stats '+␣
↪pplacer_stats[1:] + ': %.2f' % cutoff_binary )
                            # plot_roc(data_stats,binary_label)
                            ␣
↪plot_roc_microbiome(data_stats,binary_label,x=None,y=None,data_test=False)
                        else:
                            mask = df[pplacer_ref+pplacer_stats] <= ␣
↪cutoff_binary
                            df.loc[mask, pplacer_ref+pplacer_stats+'_binary'] =␣
↪1
                            mask = df[pplacer_ref+pplacer_stats] >cutoff_binary
                            df.loc[mask, pplacer_ref+pplacer_stats+'_binary'] =␣
↪0
```

```
                            df_binary = df[[pplacer_ref+community,␣
↪pplacer_ref+pplacer_stats+'_binary']].dropna()
                            data_stats = df_binary[pplacer_ref+community].
↪to_numpy().reshape(-1,1)
                            binary_label = ␣
↪df_binary[pplacer_ref+pplacer_stats+'_binary'].to_numpy()
                            print(' The pplacer_stats_cutoff '+ cutoff +' for␣
↪Reference ' + pplacer_ref +' community ' + community + ' pplacer_stats '  +␣
↪pplacer_stats[1:]  + ': %.2f' % cutoff_binary )
                            # plot_roc(data_stats,binary_label)
                           ␣
↪plot_roc_microbiome(data_stats,binary_label,x=None,y=None,data_test=False)

                    # if there is test
                    else:
                        for j in range(len(test_data_list)):
                            test=test_data_list[j]
                            if(scoreOption):
                                mask = df[pplacer_ref+community] <= ␣
↪cutoff_binary
                                df.loc[mask, pplacer_ref+community+'_binary'] =␣
↪1
                                mask = df[pplacer_ref+community] >cutoff_binary
                                df.loc[mask, pplacer_ref+community+'_binary'] =␣
↪0
                                df_binary = df[[pplacer_ref+pplacer_stats,␣
↪pplacer_ref+community+'_binary']].dropna()
                                data_stats =␣
↪df_binary[pplacer_ref+pplacer_stats].to_numpy().reshape(-1,1)
                                binary_label = ␣
↪df_binary[pplacer_ref+community+'_binary'].to_numpy()

                                mask_test = df[test+community] <=  cutoff_binary
                                df.loc[mask_test, test+community+'_binary'] = 1
                                mask_test = df[test+community] >cutoff_binary
                                df.loc[mask_test, test+community+'_binary'] = 0
                                df_binary = df[[test+pplacer_stats,␣
↪test+community+'_binary']].dropna()
                                x = df_binary[test+pplacer_stats].to_numpy().
↪reshape(-1,1)
                                y =  df_binary[test+community+'_binary'].
↪to_numpy()
```

```
                                print(' The score cutoff '+ cutoff +' for␣
↪Reference ' + pplacer_ref +' community ' + community   + ' with␣
↪pplacer_stats '+ pplacer_stats[1:] + ' compared with test ' + test +': %.2f'␣
↪% cutoff_binary )
                                ␣
↪plot_roc_microbiome(data_stats,binary_label,x,y,data_test=True)
                            else:

                                mask = df[pplacer_ref+pplacer_stats] <= ␣
↪cutoff_binary
                                df.loc[mask,␣
↪pplacer_ref+pplacer_stats+'_binary'] = 1
                                mask = df[pplacer_ref+pplacer_stats]␣
↪>cutoff_binary
                                df.loc[mask,␣
↪pplacer_ref+pplacer_stats+'_binary'] = 0
                                df_binary = df[[pplacer_ref+community,␣
↪pplacer_ref+pplacer_stats+'_binary']].dropna()
                                data_stats = df_binary[pplacer_ref+community].
↪to_numpy().reshape(-1,1)
                                binary_label = ␣
↪df_binary[pplacer_ref+pplacer_stats+'_binary'].to_numpy()

                                mask_test = df[test+pplacer_stats] <= ␣
↪cutoff_binary
                                df.loc[mask_test, test+pplacer_stats+'_binary']␣
↪= 1
                                mask_test = df[test+pplacer_stats]␣
↪>cutoff_binary
                                df.loc[mask_test, test+pplacer_stats+'_binary']␣
↪= 0
                                df_binary = df[[test+community,␣
↪test+pplacer_stats+'_binary']].dropna()
                                x = df_binary[test+community].to_numpy().
↪reshape(-1,1)
                                y =  df_binary[test+pplacer_stats+'_binary'].
↪to_numpy()

                                print(' The pplacer_stats_cutoff '+ cutoff +'␣
↪for Reference ' + pplacer_ref +' community ' + community + ' pplacer_stats '␣
↪ + pplacer_stats[1:] + ' compared with test ' + test  + ': %.2f' %␣
↪cutoff_binary )
                                ␣
↪plot_roc_microbiome(data_stats,binary_label,x,y,data_test=True)
```

3.1 Model from larger reference sets to fit data used small reference set. Could be worse on both directions

[21]:
```
# plot_roc_curve_microbiome_test2(pplacer_ref_list =␣
↪['A'],pplacer_stats_list=['_adcl_log','_edpl','_prichness','_mindistl'],community_list=['0'
↪00'], test_data_list=['B','C','D','E'],testOption=True, scoreOption=True)
```

[22]:
```
# plot_roc_curve_microbiome_test2(pplacer_ref_list =␣
↪['A'],pplacer_stats_list=['_adcl_log'],community_list=['0'],cutoff_list=['-4.
↪00'], test_data_list=['B','C','D','E'],testOption=True, scoreOption=False)
```

[23]:
```
# plot_roc_curve_microbiome_test2(pplacer_ref_list =␣
↪['A'],pplacer_stats_list=['_adcl_log'],community_list=['0'],cutoff_list=['25%'],␣
↪test_data_list=['B','C'],testOption=True, scoreOption=False)
```

[24]:
```
# plot_roc_curve_microbiome_test2(pplacer_ref_list =␣
↪['B'],pplacer_stats_list=['_adcl_log'],community_list=['0'],cutoff_list=['25%'],␣
↪test_data_list=['A','C'],testOption=True, scoreOption=False)
```

[25]:
```
# print("the head for df is {}".format(df.head)+ " the columns of the df is {}".
↪format(df.columns))
#
```

[26]:
```
# df['A0'].describe(), df['B0'].describe(), df['C0'].describe(), df['D0'].
↪describe(),df['E0'].describe()
```

[27]:
```
# for community in ['A','B','C','D','E']:
#     for i in range(10):
#             print(df[community+str(i)].describe())
```

[28]:
```
df_0 = df
```

[29]:
```
# plot_pplacer('90')
```

[30]:
```
# plotScatter('B','0')
```

[31]:
```
# plotScatterRef('_adcl_log','0')
```

[32]:
```
# plot_pplacer('_adcl_log')
```

[33]:
```
df['A_adcl_log'].describe()
```

[33]:
```
count    5974.000000
mean       -4.083366
std         1.837510
min        -5.995679
25%        -5.221126
```

```
50%        -5.096367
75%        -1.706947
max        -0.344675
Name: A_adcl_log, dtype: float64
```

[34]:
```
# plot_pplacer('0')
```

[35]:
```
df['A0'].describe()
```

[35]:
```
count    605.000000
mean       6.390083
std       10.778008
min        0.000000
25%        2.000000
50%        2.000000
75%        2.000000
max       38.000000
Name: A0, dtype: float64
```

[36]:
```
df1 = df[(df['A0']>10)]
```

[37]:
```
df1['A0'].describe()
```

[37]:
```
count    99.000000
mean     28.626263
std      10.791707
min      12.000000
25%      12.000000
50%      32.000000
75%      38.000000
max      38.000000
Name: A0, dtype: float64
```

[38]:
```
99/605
```

[38]:
```
0.16363636363636364
```

[39]:
```
df1['B0'].describe()
```

[39]:
```
count    99.000000
mean     25.070707
std      17.438670
min       0.000000
25%       0.000000
50%      36.000000
75%      38.000000
max      38.000000
```

```
Name: B0, dtype: float64
```

[40]:
```
df2=df[['seqID','A0','B0', 'C0','D0','E0']].dropna()
```

[41]:
```
df3 = df2[(df2['A0']>10) & (df2['B0']>10)  & (df2['C0']>10)  & (df2['D0']>10) &␣
↪(df2['E0']>10)]
```

[42]:
```
# df2.describe(), df3.describe()
```

[43]:
```
df3
```

[43]:

	seqID	A0	B0	C0	D0	E0
5313	CC11CM5SCR137ef78188b94db7b59504dc64363aa3	34.0	34.0	32.0	32.0	44.0
5314	CC11CM0SCR35529da454f0497fa16e04841e8e1639	34.0	34.0	32.0	32.0	44.0

[44]:
```
2/605
```

[44]:
```
0.003305785123966942
```

[45]:
```
dfc90 = df[(df['A90']>10) & (df['B90']>10)  & (df['C90']>10)  & (df['D90']>10)␣
↪& (df['E90']>10)]
```

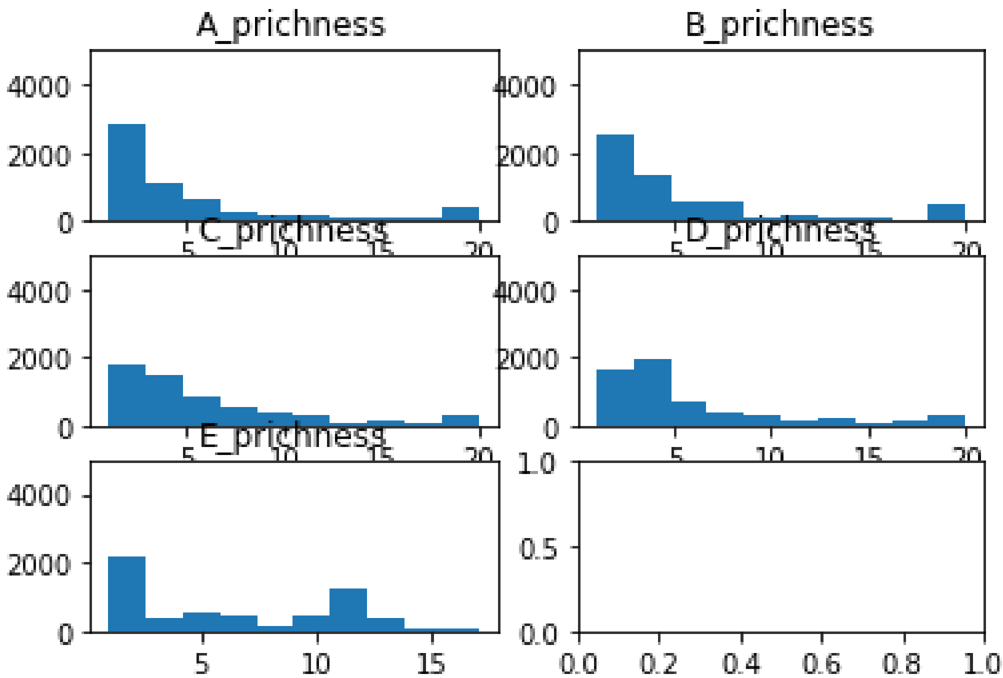
[46]:
```
dfc90['B0'].describe()
```

[46]:
```
count    0.0
mean     NaN
std      NaN
min      NaN
25%      NaN
50%      NaN
75%      NaN
max      NaN
Name: B0, dtype: float64
```

[47]:
```
df[(df.community=='CC11CM0')]['C_adcl_log'].dropna().describe()
```

[47]:
```
count    55.000000
mean     -1.885119
std       1.762885
min      -5.300162
25%      -1.773077
50%      -1.040954
75%      -0.682030
max      -0.373058
Name: C_adcl_log, dtype: float64
```

[48]:
```
plot_pplacer('_prichness')
```



[49]:
```
df['A_prichness'].describe()
```

[49]:
```
count    5974.000000
mean        4.727653
std         5.465596
min         1.000000
25%         1.000000
50%         3.000000
75%         5.000000
max        20.000000
Name: A_prichness, dtype: float64
```

[50]:
```
df[df.A0>10].A0.count()
```

[50]: 99

[51]:
```
df[df.A0>10].A0.count()/df.A0.count()
```

[51]: 0.16363636363636364

[52]:
```
# df.head()
```

[53]:
```
df.A_adcl.count()
```

[53]: 5974

```
[54]: d={"a":1, "b":2}
```

```
[55]: d
```

[55]: {'a': 1, 'b': 2}

```
[56]: dd = pd.Series(d, name='score')
```

```
[57]: dd.index.name="community"
```

```
[58]: dd.reset_index()
```

[58]:

	community	score
0	a	1
1	b	2

```
[59]: "CC11CM"+str(0)
```

[59]: 'CC11CM0'

```
[60]: c0=df['A0'][df['community']=='CC11CM0']
```

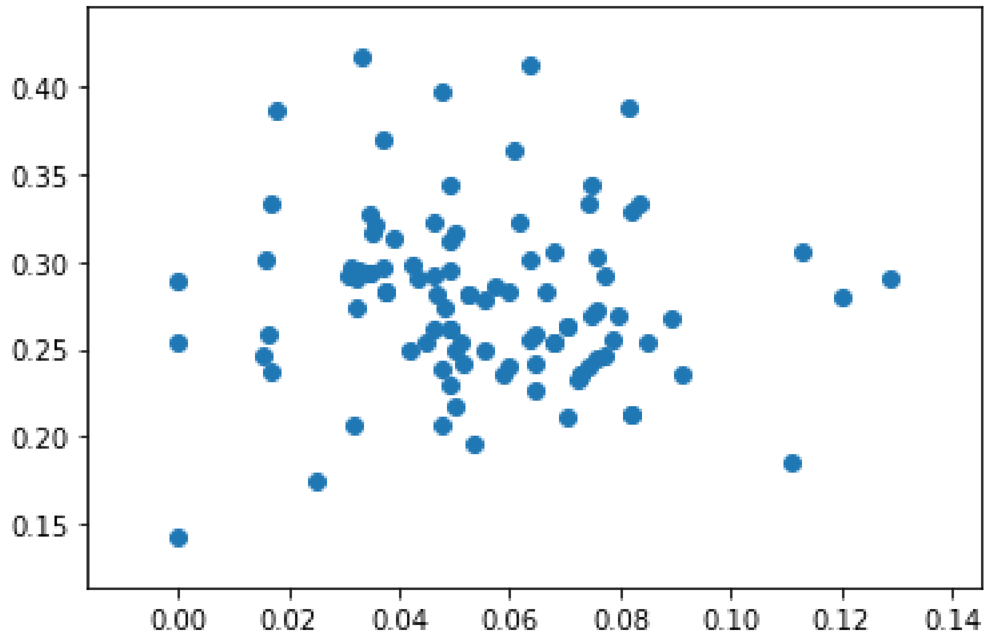
```
[61]: per=c0[c0>10].count()/c0.count()
```

```
[62]: def generateScore(stats, referenceID,scorecutoff,statscutoff):
          d1={}
          d2={}
          for i in range(100):
              values = df[referenceID+str(i)][df.community=='CC11CM'+str(i)]
              statsvalues = df[stats][df['community']=='CC11CM'+str(i)]
              d1['CC11CM'+str(i)] = values[values>scorecutoff].count()/values.count()
              d2['CC11CM'+str(i)] =statsvalues[statsvalues>statscutoff].count()/
       ↪statsvalues.count()
          d1=pd.Series(d1, name=referenceID)
          d1.index.name='community'
          d1=d1.reset_index()
          d2=pd.Series(d2, name=stats)
          d2.index.name='community'
          d2=d2.reset_index()
          dt = pd.concat([d1,d2], axis=1)
      #     dt=dt.set_index('community')
          return (dt)
```

```
[63]: dt=generateScore('A_adcl', 'A', 10, 0.001)
```

[64]:
```
plt.scatter(dt.A, dt.A_adcl)
```

[64]: <matplotlib.collections.PathCollection at 0x7faec03dc450>



[65]:
```
t=[]
for referenceID in ['A','B','C','D','E']:
    t.append(generateScore('A_adcl', referenceID, 10, 0.001))
```

[66]:
```
t[0].head()
```

[66]:

	community	A	community	A_adcl
0	CC11CM0	0.090909	CC11CM0	0.236364
1	CC11CM1	0.082192	CC11CM1	0.328767
2	CC11CM2	0.025000	CC11CM2	0.175000
3	CC11CM3	0.050847	CC11CM3	0.254237
4	CC11CM4	0.000000	CC11CM4	0.288462

[67]:
```
tt = pd.concat([t[0],t[1],t[2],t[3],t[4]], axis=1)
```

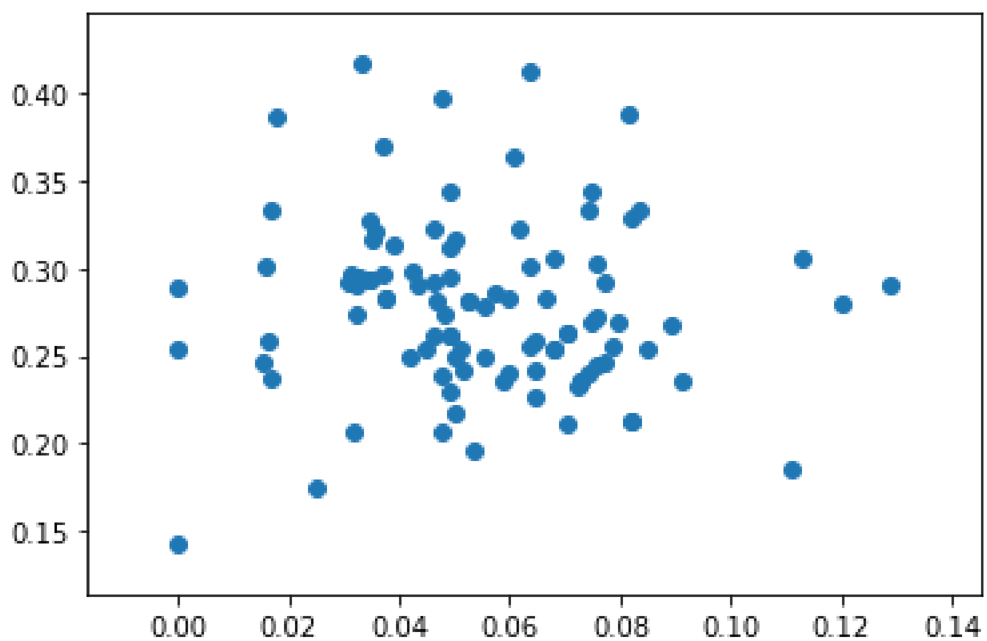
[68]:
```
def generateScoreu(stats, referenceID,scorecutoff,statscutoff):
    d1={}
    d2={}
    for i in range(100):
        values = df[referenceID+str(i)][df.community=='CC11CM'+str(i)]
        statsvalues = df[referenceID+stats][df['community']=='CC11CM'+str(i)]
        d1['CC11CM'+str(i)] = values[values>scorecutoff].count()/values.count()
```

```
        d2['CC11CM'+str(i)] =statsvalues[statsvalues>statscutoff].count()/
↪statsvalues.count()
    d1=pd.Series(d1, name=referenceID)
    d1.index.name='community'
    d1=d1.reset_index()
    d2=pd.Series(d2, name=referenceID+stats)
    d2.index.name='community'
    d2=d2.reset_index()
    dt = pd.concat([d1,d2], axis=1)
    dt=dt.loc[:, ~dt.columns.duplicated()]
    dt=dt.set_index('community')
    return (dt)
```

[69]:
```
dtu=generateScoreu('_adcl', 'A', 10, 0.001)
```

[70]:
```
plt.scatter(dtu.A, dtu.A_adcl)
```

[70]: <matplotlib.collections.PathCollection at 0x7faea6a1c390>



[ ]:
```

```

[71]:
```
t=[]
statsdir= {'_adcl':0.0001, '_edpl':0,'_prichness':10,'_mindistl':0.05}
for stats in statsdir.keys():
```

```
    for referenceID in ['A','B','C','D','E']:
        t.append(generateScoreu(stats, referenceID, 10, statsdir[stats]))
```

[ ]:

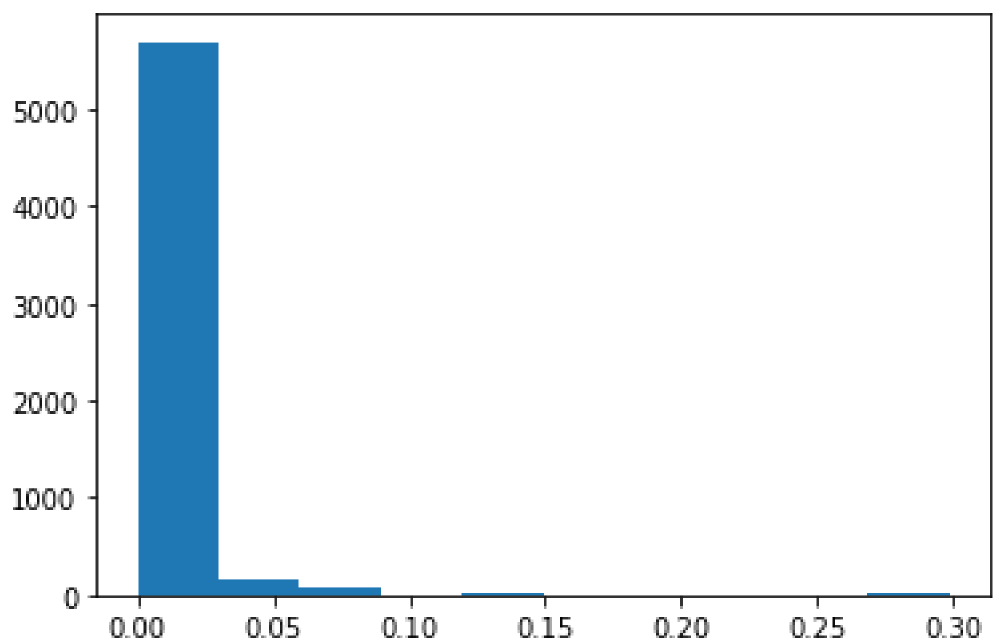
[72]:
```
ttt = pd.
 ↪concat([t[0],t[1],t[2],t[3],t[4],t[5],t[6],t[7],t[8],t[9],t[10],t[11],t[12],t[13],t[14],t[1
 ↪axis=1)
ttt=ttt.loc[:, ~ttt.columns.duplicated()]
```

[73]:
```
# ttt.describe()
```

[74]:
```
ttt.to_csv("community-based.csv")
```

[75]:
```
plt.hist(df.A_mindistl)
```

[75]:
```
(array([5.696e+03, 1.570e+02, 6.800e+01, 0.000e+00, 2.200e+01, 0.000e+00,
        0.000e+00, 5.000e+00, 0.000e+00, 2.600e+01]),
 array([3.48920365e-07, 2.98496853e-02, 5.96990217e-02, 8.95483581e-02,
        1.19397695e-01, 1.49247031e-01, 1.79096367e-01, 2.08945704e-01,
        2.38795040e-01, 2.68644377e-01, 2.98493713e-01]),
 <a list of 10 Patch objects>)
```



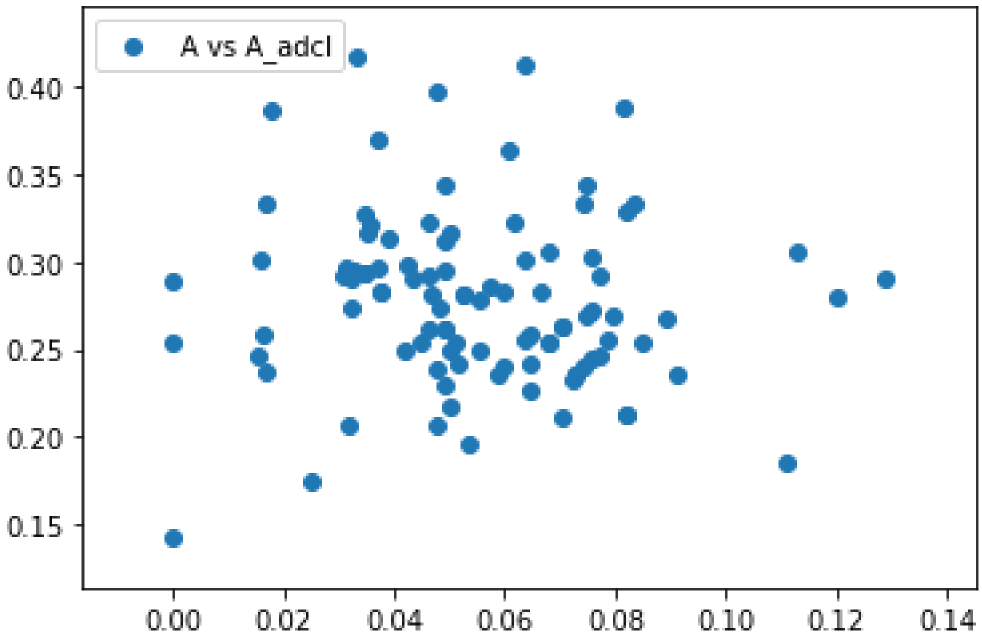
[76]:
```
dp =pd.read_csv("community-based.csv", index_col=0)
```

[77]:
```
dp.describe()
```

[77]:
```
                A       A_adcl           B       B_adcl           C       C_adcl  \
count  100.000000  100.000000  100.000000  100.000000  100.000000  100.000000
mean     0.055034    0.277586    0.116043    0.557102    0.318386    0.799584
std      0.024318    0.049060    0.032415    0.054352    0.048526    0.044362
min      0.000000    0.142857    0.051724    0.406780    0.216667    0.666667
25%      0.037736    0.246154    0.095238    0.516532    0.285119    0.773585
50%      0.052178    0.275986    0.112007    0.563333    0.315789    0.800000
75%      0.072530    0.301587    0.136310    0.600000    0.346392    0.830769
max      0.129032    0.416667    0.209677    0.682540    0.448980    0.888889

                D       D_adcl           E       E_adcl  …  A_prichness  \
count  100.000000  100.000000  100.000000  100.000000  …   100.000000
mean     0.647292    0.962263    0.229600    0.989559  …     0.140234
std      0.051736    0.017520    0.045910    0.008343  …     0.035764
min      0.491803    0.916667    0.097222    0.975000  …     0.052632
25%      0.612455    0.949788    0.193768    0.983051  …     0.118395
50%      0.649561    0.966667    0.229508    0.984615  …     0.137147
75%      0.682738    0.978723    0.261943    1.000000  …     0.164801
max      0.786885    1.000000    0.339623    1.000000  …     0.235294

       B_prichness  C_prichness  D_prichness  E_prichness  A_mindistl  \
count   100.000000   100.000000   100.000000   100.000000  100.000000
mean      0.147809     0.142149     0.160060     0.304304    0.025369
std       0.041895     0.037576     0.034324     0.042562    0.018591
min       0.042553     0.056604     0.080645     0.190476    0.000000
25%       0.123077     0.120690     0.144585     0.274194    0.015873
50%       0.146257     0.140351     0.155048     0.306452    0.020221
75%       0.179410     0.157540     0.180082     0.338524    0.034044
max       0.240741     0.254545     0.244898     0.393443    0.096774

       B_mindistl  C_mindistl  D_mindistl  E_mindistl
count  100.000000  100.000000  100.000000  100.000000
mean     0.114361    0.097589    0.198869    0.290481
std      0.030794    0.030017    0.042808    0.047167
min      0.037037    0.033333    0.109091    0.156863
25%      0.095013    0.079132    0.172414    0.265789
50%      0.111111    0.096774    0.196400    0.298507
75%      0.134615    0.114754    0.229823    0.323077
max      0.187500    0.203390    0.333333    0.387755

[8 rows x 25 columns]
```

[78]:
```
for score in ['A','B','C','D','E'][0:1]:
    for stats in ['_adcl', '_edpl','_prichness','_mindistl'][0:1]:
```

```
        plt.scatter(dp[score], dp[score+stats], label=score + ' vs '+␣
↪score+stats)
        plt.legend(loc='upper left')
        plt.show
```

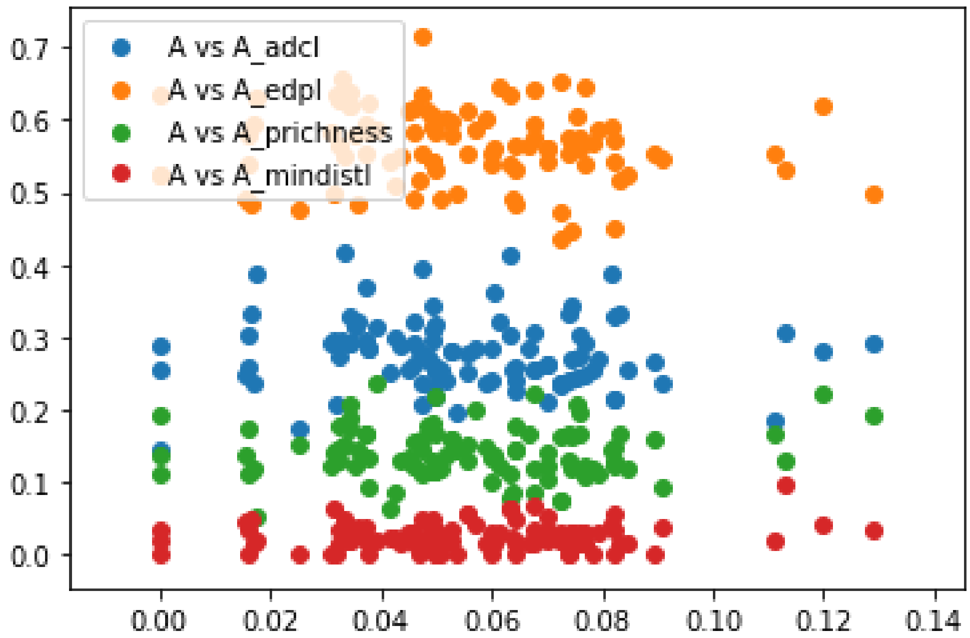


[ ]:

```

```

[79]:

```
for score in ['A','B','C','D','E'][0:1]:
    for stats in ['_adcl', '_edpl','_prichness','_mindistl'][0:5]:
        plt.scatter(dp[score], dp[score+stats], label=score + ' vs '+␣
↪score+stats)
        plt.legend(loc='upper left')
        plt.show
```

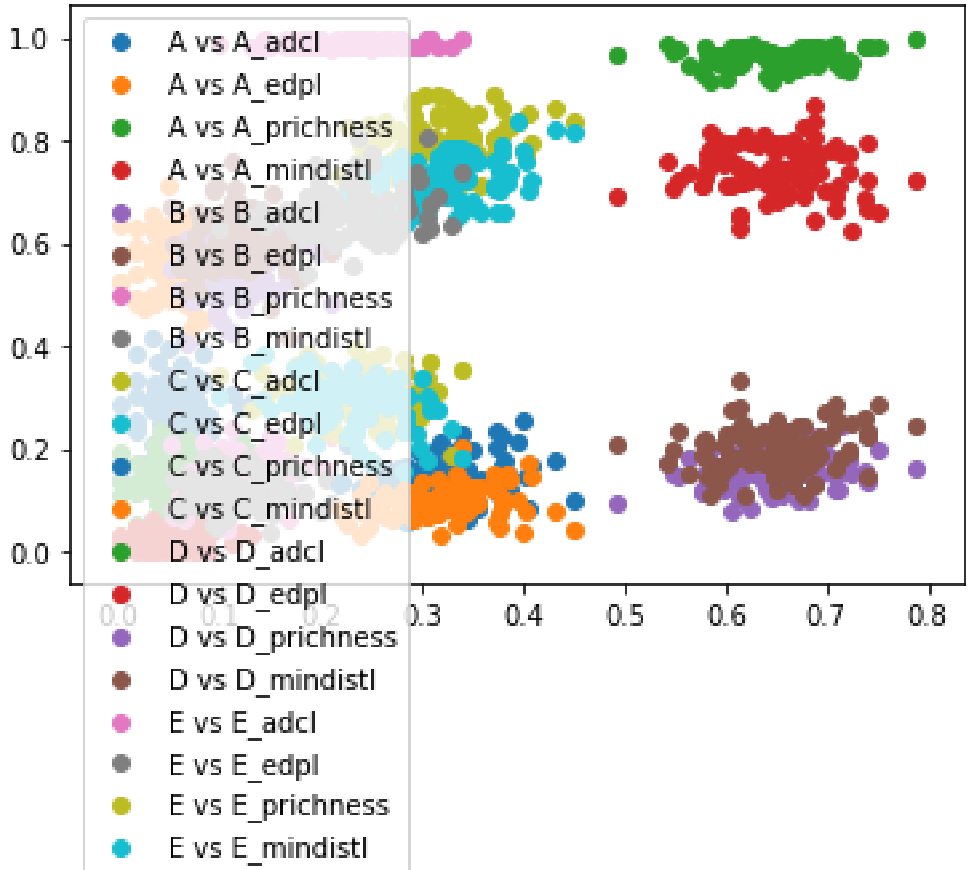


[ ]:

```
```

[80]:

```
for score in ['A','B','C','D','E']:
    for stats in ['_adcl', '_edpl','_prichness','_mindistl']:
        plt.scatter(dp[score], dp[score+stats], label=score + ' vs '+␣
↪score+stats)
        plt.legend(loc='upper left')
        plt.show
```



[81]:
```
# dp.describe()
```

4 Bray-Curtis distance

[82]:
```
>>> from scipy.spatial import distance
>>> distance.braycurtis([1, 0, 0], [0, 1, 0])
1.0
>>> distance.braycurtis([1, 1, 0], [0, 1, 0])
0.33333333333333331
```

[82]: 0.3333333333333333

[83]:
```
distance.braycurtis([1, 0, 0], [0, 1, 0])
```

[83]: 1.0

[84]:
```
>>> distance.braycurtis([1, 1, 0], [0, 1, 0])
```

[84]: 0.3333333333333333

5 Association between Bray-Curtis Distance and Sensitivity

[85]:
```
bcd = pd.read_csv("Bray-Curtis-Distance-HS.csv", index_col=0)
sensitivity = pd.read_csv("alphaDiversity_phyloEntropy.csv", index_col=0)
```

[86]:
```
bcd.head(),sensitivity.head()
```

[86]:
```
(          rdp10398   rdp5224   rdp1017     rdp92     rdp12
 CC11CM0  0.000000  0.000000  0.000000  0.032523  0.000000
 CC11CM1  0.012653  0.012653  0.012653  0.025961  0.017573
 CC11CM2  0.002196  0.002196  0.002196  0.002196  0.002196
 CC11CM3  0.009952  0.009952  0.009952  0.009952  0.009952
 CC11CM4  0.006173  0.006173  0.011572  0.006173  0.006173,
            RDP_10398  RDP_5224  RDP_1017    RDP_92    RDP_12
 CC11CM0     3.52104   3.02461   2.01612  0.866728  0.247681
 CC11CM1     3.53484   2.95072   2.18432  0.838860  0.217677
 CC11CM10    3.51104   3.05156   2.18018  0.878181  0.245779
 CC11CM11    3.44639   2.93488   2.17424  0.900507  0.237034
 CC11CM12    3.57253   3.02328   2.22683  0.908349  0.248668)
```

[87]:
```
# bcd-sen = pd.merge(bcd, sensitivity, left_index=True, right_index=True)
bcdsen = pd.concat([bcd, sensitivity], axis=1)
```

[88]:
```
bcdsen.head()
```

[88]:
```
         rdp10398   rdp5224   rdp1017     rdp92     rdp12  RDP_10398  \
CC11CM0  0.000000  0.000000  0.000000  0.032523  0.000000    3.52104
CC11CM1  0.012653  0.012653  0.012653  0.025961  0.017573    3.53484
CC11CM2  0.002196  0.002196  0.002196  0.002196  0.002196    3.36317
CC11CM3  0.009952  0.009952  0.009952  0.009952  0.009952    3.51643
CC11CM4  0.006173  0.006173  0.011572  0.006173  0.006173    3.43322

         RDP_5224  RDP_1017    RDP_92    RDP_12
CC11CM0   3.02461   2.01612  0.866728  0.247681
CC11CM1   2.95072   2.18432  0.838860  0.217677
CC11CM2   2.86013   2.02162  0.869733  0.243896
CC11CM3   3.00732   2.20913  0.864256  0.234243
CC11CM4   3.05337   2.20913  0.889513  0.219864
```

[89]:
```
# df_new = df.rename(columns={'A': 'a'}, index={'ONE': 'one'})
```

```
bcdsen = bcdsen.rename(columns={'rdp10398':'bcd_rdp10398', 'rdp10398':
↪'bcd_rdp10398','rdp5224':'bcd_rdp5224','rdp1017':'bcd_rdp1017','rdp92':
↪'bcd_rdp92','rdp12':'bcd_rdp12','RDP_10398':
↪'sensitivity_rdp10398','RDP_5224':'sensitivity_rdp5224','RDP_1017':
↪'sensitivity_rdp1017','RDP_92':'sensitivity_rdp92','RDP_12':
↪'sensitivity_rdp12'})
```

[90]:
```
bcdsen.head()
```

[90]:
```
         bcd_rdp10398  bcd_rdp5224  bcd_rdp1017  bcd_rdp92  bcd_rdp12  \
CC11CM0      0.000000     0.000000     0.000000   0.032523   0.000000
CC11CM1      0.012653     0.012653     0.012653   0.025961   0.017573
CC11CM2      0.002196     0.002196     0.002196   0.002196   0.002196
CC11CM3      0.009952     0.009952     0.009952   0.009952   0.009952
CC11CM4      0.006173     0.006173     0.011572   0.006173   0.006173

         sensitivity_rdp10398  sensitivity_rdp5224  sensitivity_rdp1017  \
CC11CM0               3.52104              3.02461              2.01612
CC11CM1               3.53484              2.95072              2.18432
CC11CM2               3.36317              2.86013              2.02162
CC11CM3               3.51643              3.00732              2.20913
CC11CM4               3.43322              3.05337              2.20913

         sensitivity_rdp92  sensitivity_rdp12
CC11CM0           0.866728           0.247681
CC11CM1           0.838860           0.217677
CC11CM2           0.869733           0.243896
CC11CM3           0.864256           0.234243
CC11CM4           0.889513           0.219864
```

[91]:
```
# objects = ('Python', 'C++', 'Java', 'Perl', 'Scala', 'Lisp')
# y_pos = np.arange(len(objects))
# performance = [10,8,6,4,2,1]
# plt.bar(y_pos, performance, align='center', alpha=0.5)
# plt.xticks(y_pos, objects)
# plt.ylabel('Usage')
# plt.title('Programming language usage')
# plt.show()
```

[92]:
```
#␣
↪objects=('bcd_rdp10398','bcd_rdp5224','bcd_rdp1017','bcd_rdp92','bcd_rdp12','sensitivity_rd
# plt.bar(bcdsen.bcd_rdp10398, )
```

[93]:
```
#         plt.scatter(bcdsen['bcd_rdp10398'], bcdsen['sensitivity_rdp10398'],␣
↪label='BCD vs Sensitivity' )
#         plt.legend(loc='upper left')
#         plt.show
```

[94]:
```
# plt.scatter(bcdsen['bcd_rdp5224'], bcdsen['sensitivity_rdp5224'], label='BCD␣
↪vs Sensitivity' )
# plt.legend(loc='upper left')
# plt.show
```

[95]:
```
# plt.scatter(bcdsen['bcd_rdp12'], bcdsen['sensitivity_rdp12'], label='BCD vs␣
↪Sensitivity' )
# plt.legend(loc='upper left')
# plt.show
```

[96]:
```
# for refindex in ['10398', '5224','1017','92','12']:
#     plt.scatter(bcdsen['bcd_rdp'+refindex], bcdsen['sensitivity_rdp' +␣
↪refindex ], label='RDP'  + refindex)
#     plt.legend(loc='lower right')
#     plt.show;
#     plt.savefig('bcd-sen.png')
```

6 Exploring data

7 Adcl

8 Adcl plot all sequences in 5 reference sets

[ ]:
```

```

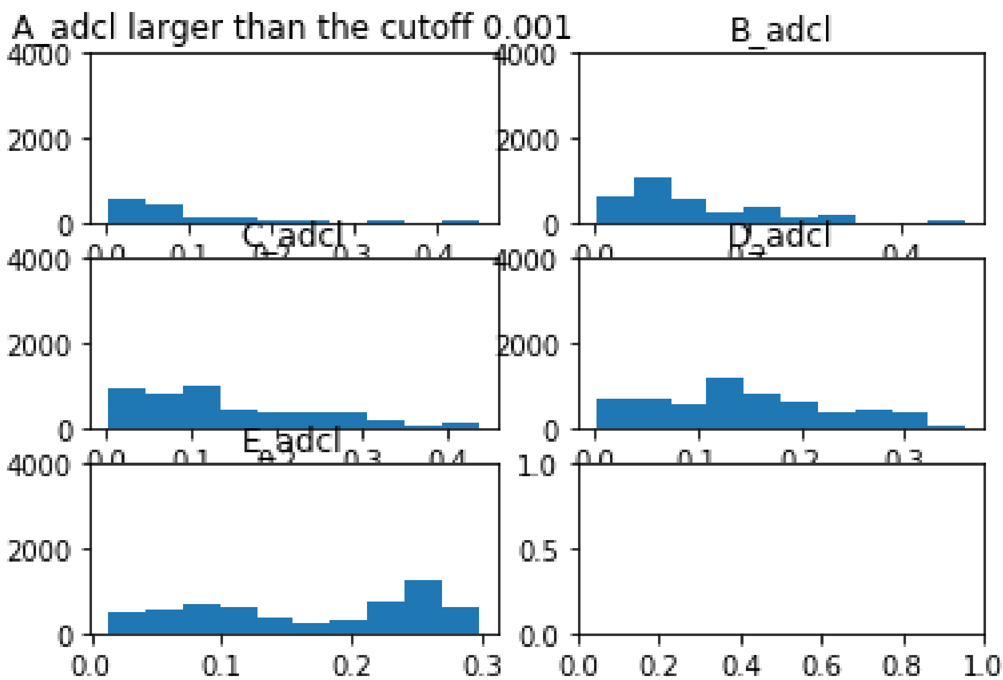
9 setting y axis to have the same range

[159]:
```
def plot_pplacer_cutoff(variable, cutoff):

    fig, axes = plt.subplots(nrows=3, ncols=2)
    ax0, ax1, ax2, ax3, ax4, ax5 = axes.flatten()

    ax0.hist(df['A'+variable][df['A'+variable]>cutoff])
    ax0.set_title('A'+variable + ' larger than the cutoff '+ str(cutoff) )
    ax0.set_ylim(0,4000)

    ax1.hist(df['B'+variable][df['B'+variable]>cutoff])
    ax1.set_title('B'+variable)
    ax1.set_ylim(0,4000)

    ax2.hist(df['C'+variable][df['C'+variable]>cutoff])
    ax2.set_title('C'+variable)
    ax2.set_ylim(0,4000)
```

```
    ax3.hist(df['D'+variable][df['D'+variable]>cutoff])
    ax3.set_title('D'+variable)
    ax3.set_ylim(0,4000)
    ax4.hist(df['E'+variable][df['E'+variable]>cutoff])
    ax4.set_title('E'+variable)
    ax4.set_ylim(0,4000)
```

10 Plot adcl with bad values larger than 0.001

[160]:
```
plot_pplacer_cutoff('_adcl', 0.001)
```



11 Plot adcl with bad values larger than 0.15

[ ]:
```
```

[ ]:
```
```

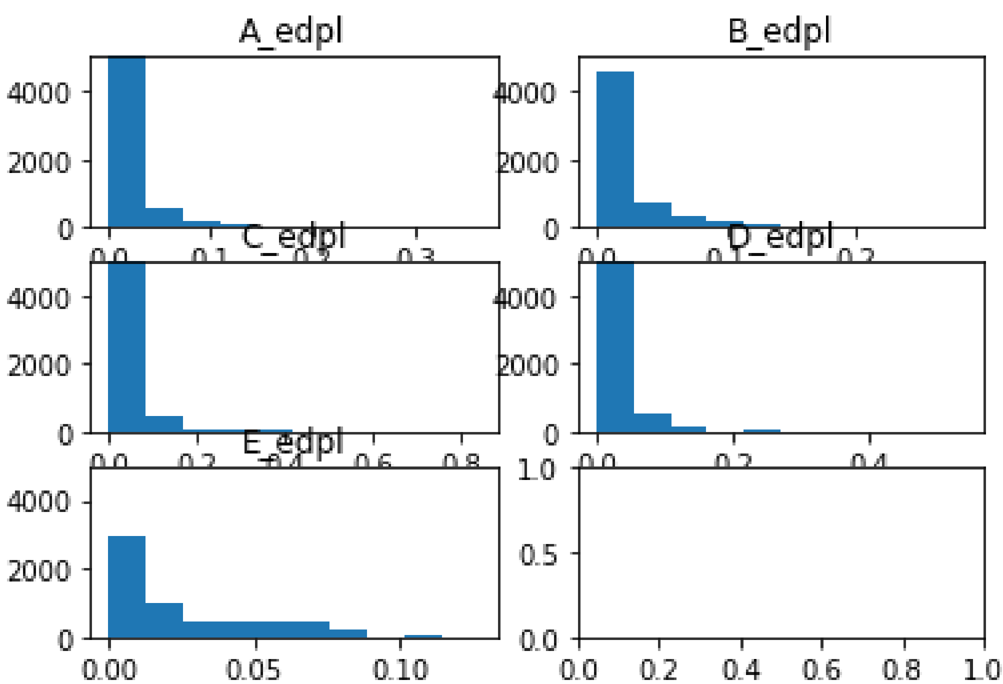
[99]:
```
# stats.percentileofscore(df.A_adcl,0.001),stats.percentileofscore(df.B_adcl,0.
↪001),stats.percentileofscore(df.C_adcl,0.001),stats.percentileofscore(df.
↪D_adcl,0.001),stats.percentileofscore(df.E_adcl,0.001)
```

[100]:
```
# stats.percentileofscore(df.A_adcl,0.15),stats.percentileofscore(df.B_adcl,0.
↪15),stats.percentileofscore(df.C_adcl,0.15),stats.percentileofscore(df.
↪D_adcl,0.15),stats.percentileofscore(df.E_adcl,0.15)
```

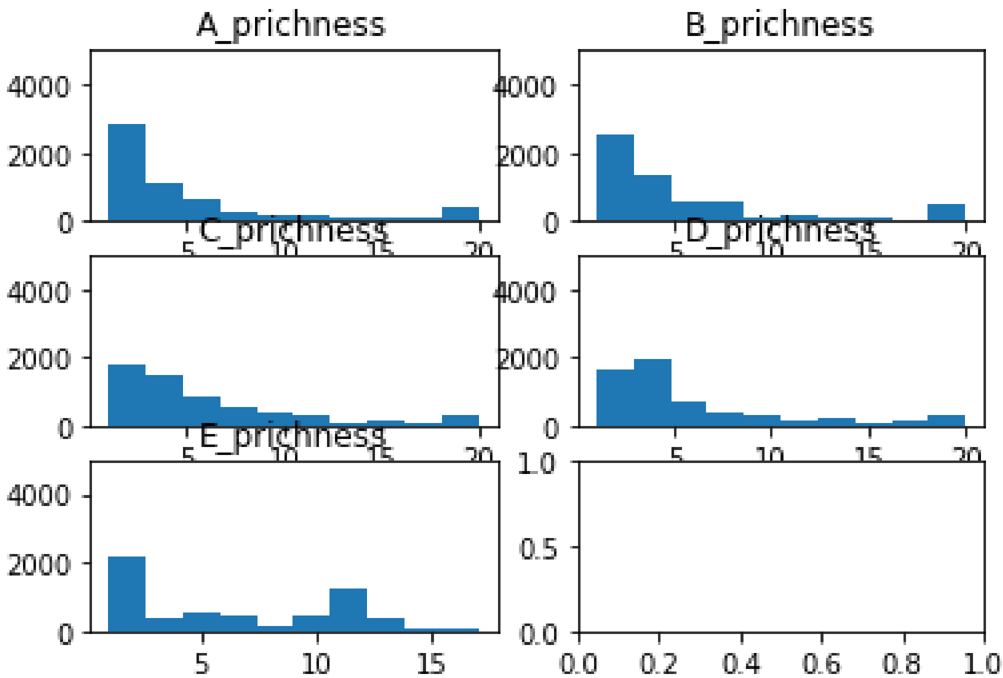
12 edpl

[101]:
```
from scipy.stats import median_test
from scipy.stats import skew
# stat, p, med, tbl = median_test(g1, g2, g3)
```

[102]:
```
plot_pplacer('_edpl')
```



[103]:
```
plot_pplacer('_prichness')
```



[104]:
```
df.A_prichness.describe()
```

[104]:
```
count    5974.000000
mean        4.727653
std         5.465596
min         1.000000
25%         1.000000
50%         3.000000
75%         5.000000
max        20.000000
Name: A_prichness, dtype: float64
```

[105]:
```
stat, p, med, tbl = median_test(df['A_edpl'], df['B_edpl'],␣
↪df['C_edpl'],df['D_edpl'],df['E_edpl'])
```

[106]:
```
stat,p,med,tbl
```

[106]:
```
(884.8049200597882,
 3.2647574897641094e-190,
 0.00624063,
 array([[2160, 2623, 3293, 3537, 3317],
        [3814, 3351, 2681, 2437, 2657]]))
```

[107]:
```
# stats.scoreatpercentile(df.A_edpl,95),stats.scoreatpercentile(df.
↪B_edpl,95),stats.scoreatpercentile(df.C_edpl,95),stats.scoreatpercentile(df.
↪D_edpl,95),stats.scoreatpercentile(df.E_edpl,95)
```

[108]:
```
stat, p, med, tbl = median_test(df['A_edpl'][df['A_edpl']>0.09], df['B_edpl'],␣
↪df['C_edpl'],df['D_edpl'],df['E_edpl'])
```

[109]:
```
# stats.scoreatpercentile(df.A_edpl,95),stats.scoreatpercentile(df.
↪B_edpl,95),stats.scoreatpercentile(df.C_edpl,95),stats.scoreatpercentile(df.
↪D_edpl,95),stats.scoreatpercentile(df.E_edpl,95)
```

[110]:
```
# stat is The default is Pearson's chi-squared statistic.
# tbl: contingency table is the number of counts above (first) or below␣
↪(second) the median
# median is the grand median of all the data
```

[111]:
```
# stats.scoreatpercentile(df.A_edpl,95),stats.scoreatpercentile(df.
↪B_prichness,25),stats.scoreatpercentile(df.C_prichness,25),stats.
↪scoreatpercentile(df.D_prichness,25),stats.scoreatpercentile(df.
↪E_prichness,25)
```

[112]:
```
stat_prichness, p_prichness, med_prichness, tbl_prichness =␣
↪median_test(df['A_prichness'], df['B_prichness'],␣
↪df['C_prichness'],df['D_prichness'],df['E_prichness'])
```

[113]:
```
stat_prichness, p_prichness, med_prichness, tbl_prichness
```

[113]:
```
(714.3998925689131,
 2.6555831779866207e-153,
 3.0,
 array([[2166, 2404, 2848, 2695, 3517],
        [3808, 3570, 3126, 3279, 2457]]))
```

[114]:
```
skew(df.A_prichness),skew(df.B_prichness),skew(df.C_prichness),skew(df.
↪D_prichness),skew(df.E_prichness)
```

[114]:
```
(1.7223937315812259,
 1.655081662276798,
 1.4447455865352592,
 1.5041655669763299,
 0.27329743773080667)
```

[115]:
```
skew(df.A_edpl),skew(df.B_edpl),skew(df.C_edpl),skew(df.D_edpl),skew(df.E_edpl)
```

[115]:
```
(4.7967506095623875,
 3.5506023182231856,
 4.587433148956383,
```

 4.529095610041163,
 1.048243259502774)

[116]:
```
from scipy import stats
#  stats.percentileofscore([1, 2, 3, 4], 3)
```

[117]:
```
stats.percentileofscore(df.A_prichness,3),stats.percentileofscore(df.
↪B_prichness,3),stats.percentileofscore(df.C_prichness,3),stats.
↪percentileofscore(df.D_prichness,3),stats.percentileofscore(df.E_prichness,3)
```

[117]:
```
(55.4820890525611,
 50.77837294944761,
 41.58018078339471,
 41.1700703046535,
 38.95212587880817)
```

[118]:
```
stats.percentileofscore(df.A_prichness,10),stats.percentileofscore(df.
↪B_prichness,10),stats.percentileofscore(df.C_prichness,10),stats.
↪percentileofscore(df.D_prichness,10),stats.percentileofscore(df.
↪E_prichness,10)
```

[118]:
```
(85.40341479745564,
 84.96819551389353,
 84.32373619015735,
 83.17710077000335,
 68.58888516906595)
```

[119]:
```
stats.percentileofscore(df.A_prichness,5),stats.percentileofscore(df.
↪B_prichness,5),stats.percentileofscore(df.C_prichness,5),stats.
↪percentileofscore(df.D_prichness,5),stats.percentileofscore(df.E_prichness,5)
```

[119]:
```
(70.99933043187144,
 67.71007700033478,
 59.943086709072645,
 64.32875795112153,
 47.94107800468698)
```

[120]:
```
stats.percentileofscore(df.A_edpl,0.01),stats.percentileofscore(df.B_edpl,0.
↪01),stats.percentileofscore(df.C_edpl,0.01),stats.percentileofscore(df.
↪D_edpl,0.01),stats.percentileofscore(df.E_edpl,0.01)
```

[120]:
```
(66.27050552393706,
 60.964178105122194,
 52.57783729494476,
 44.19149648476733,
 45.915634415801804)
```

13 D is larger C. A is the best and E is the worst. This indicates that percentile at score of 5 is a good metric.

[121]:
```
stats.percentileofscore(df.A_prichness,15),stats.percentileofscore(df.
↪B_prichness,15),stats.percentileofscore(df.C_prichness,15),stats.
↪percentileofscore(df.D_prichness,15),stats.percentileofscore(df.
↪E_prichness,15)
```

[121]:
```
(91.04452628054905,
 90.23267492467359,
 92.74355540676264,
 90.7348510210914,
 98.58553732842317)
```

[122]:
```
stats.scoreatpercentile(df.A_prichness,25),stats.scoreatpercentile(df.
↪B_prichness,25),stats.scoreatpercentile(df.C_prichness,25),stats.
↪scoreatpercentile(df.D_prichness,25),stats.scoreatpercentile(df.
↪E_prichness,25)
```

[122]:
```
(1.0, 1.0, 1.0, 1.0, 1.0)
```

[123]:
```
stats.scoreatpercentile(df.A_prichness,75),stats.scoreatpercentile(df.
↪B_prichness,75),stats.scoreatpercentile(df.C_prichness,75),stats.
↪scoreatpercentile(df.D_prichness,75),stats.scoreatpercentile(df.
↪E_prichness,75)
```

[123]:
```
(5.0, 7.0, 7.0, 7.0, 11.0)
```

[124]:
```
aa=stats.scoreatpercentile(df.A_prichness,75),stats.scoreatpercentile(df.
↪B_prichness,75),stats.scoreatpercentile(df.C_prichness,75),stats.
↪scoreatpercentile(df.D_prichness,75),stats.scoreatpercentile(df.
↪E_prichness,75)
```

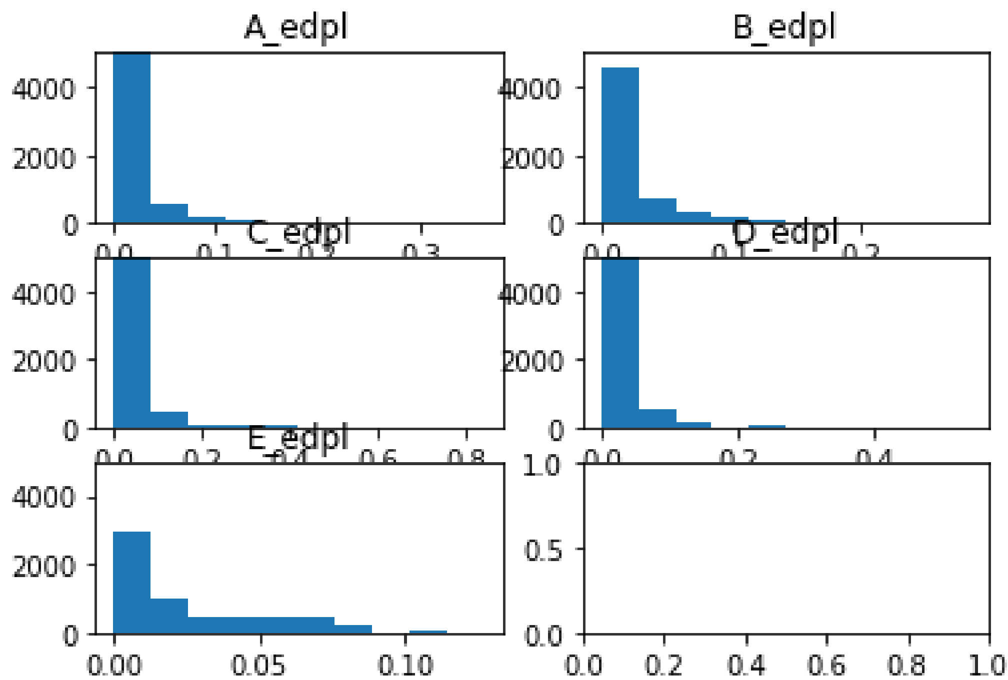
[125]:
```
stats.scoreatpercentile(df.A_prichness,50),stats.scoreatpercentile(df.
↪B_prichness,50),stats.scoreatpercentile(df.C_prichness,50),stats.
↪scoreatpercentile(df.D_prichness,50),stats.scoreatpercentile(df.
↪E_prichness,50)
```

[125]:
```
(3.0, 3.0, 3.0, 3.0, 5.0)
```

[ ]:
```

```

14 Plot

[126]:
```
plot_pplacer('_edpl')
```



[127]:
```
df.A_edpl.describe()
```

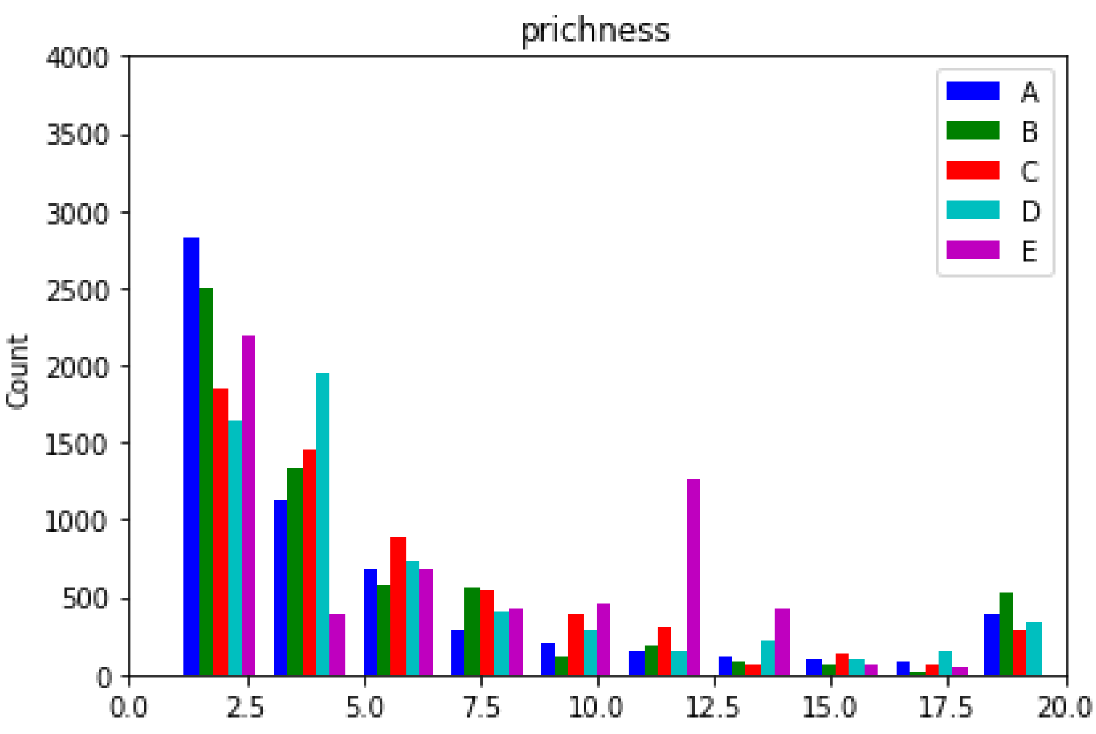
[127]:
```
count    5974.000000
mean        0.019395
std         0.044893
min         0.000000
25%         0.000000
50%         0.000617
75%         0.019254
max         0.361655
Name: A_edpl, dtype: float64
```

15 Plotting prichness in bins

[195]:
```
# #makes the data
# y1 = np.random.normal(-2, 2, 1000)
# y2 = np.random.normal(2, 2, 5000)
# colors = ['b','g']

# #plots the histogram
```

```
# fig, ax1 = plt.subplots()
# ax1.hist([y1,y2],color=colors)
# ax1.set_xlim(-10,10)
# ax1.set_ylabel("Count")
# plt.tight_layout()
# plt.show()
```

[192]:
```
fig, ax1=plt.subplots()
ax1.hist([df.A_prichness, df.B_prichness,df.C_prichness, df.D_prichness,df.
 ↪E_prichness], color=['b','g','r','c','m'],label=['A','B','C','D','E'])
ax1.set_ylim(0,4000)

ax1.set_xlim(0,max(df.A_prichness.max(), df.B_prichness.max(),df.C_prichness.
 ↪max(), df.D_prichness.max(), df.E_prichness.max()))
ax1.set_ylabel("Count")
plt.title("prichness")
plt.legend(loc='upper right')
plt.tight_layout()
# plt.show()
plt.savefig('prichness.png',dpi=1000)
```



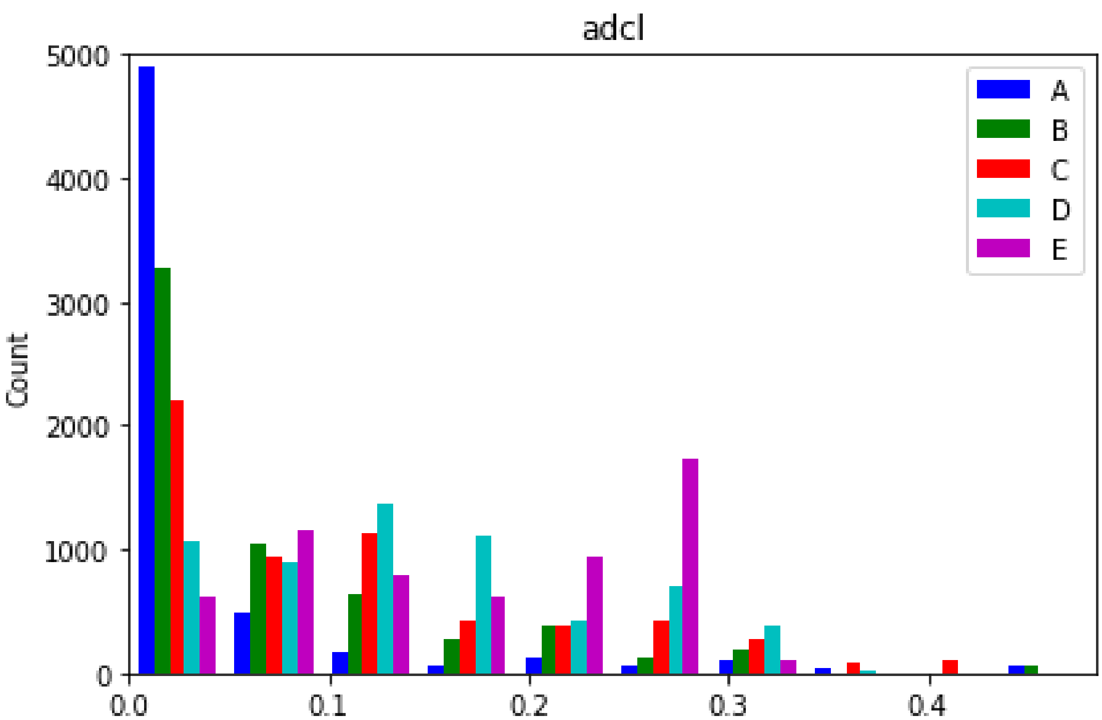
[194]:

```
stats.percentileofscore(df.A_prichness,5),stats.percentileofscore(df.
↪B_prichness,5),stats.percentileofscore(df.C_prichness,5),stats.
↪percentileofscore(df.D_prichness,5),stats.percentileofscore(df.E_prichness,5)
```

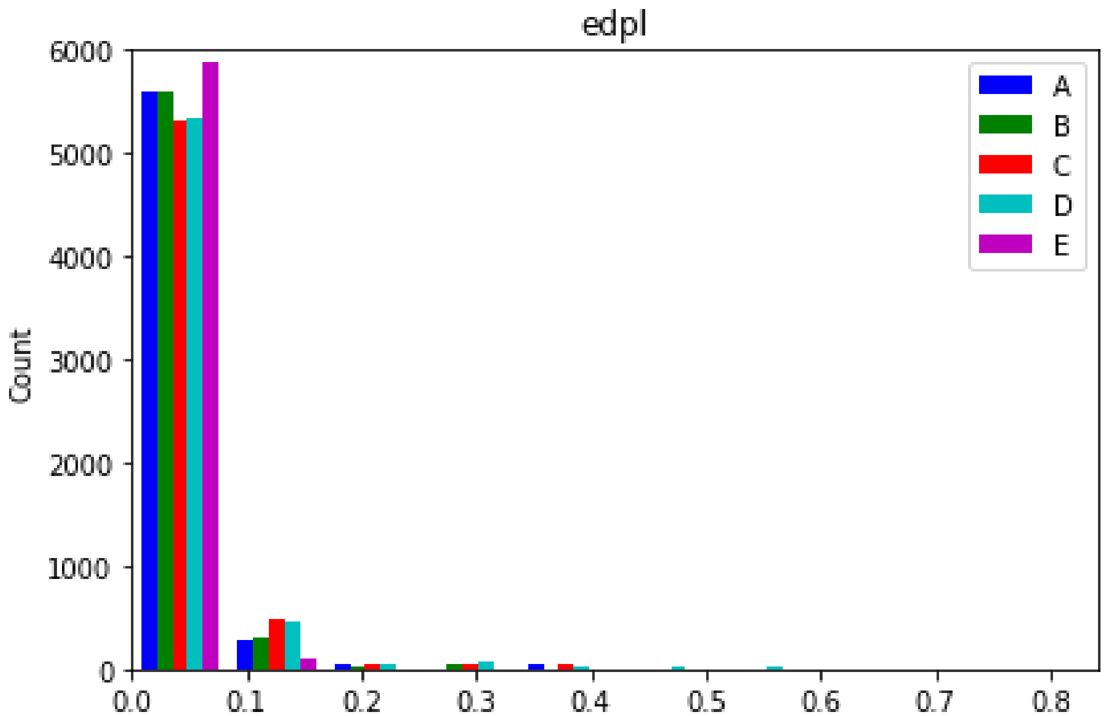
[194]:
```
(70.99933043187144,
 67.71007700033478,
 59.943086709072645,
 64.32875795112153,
 47.94107800468698)
```

prichness: the percentile at value 5 is a good indicator

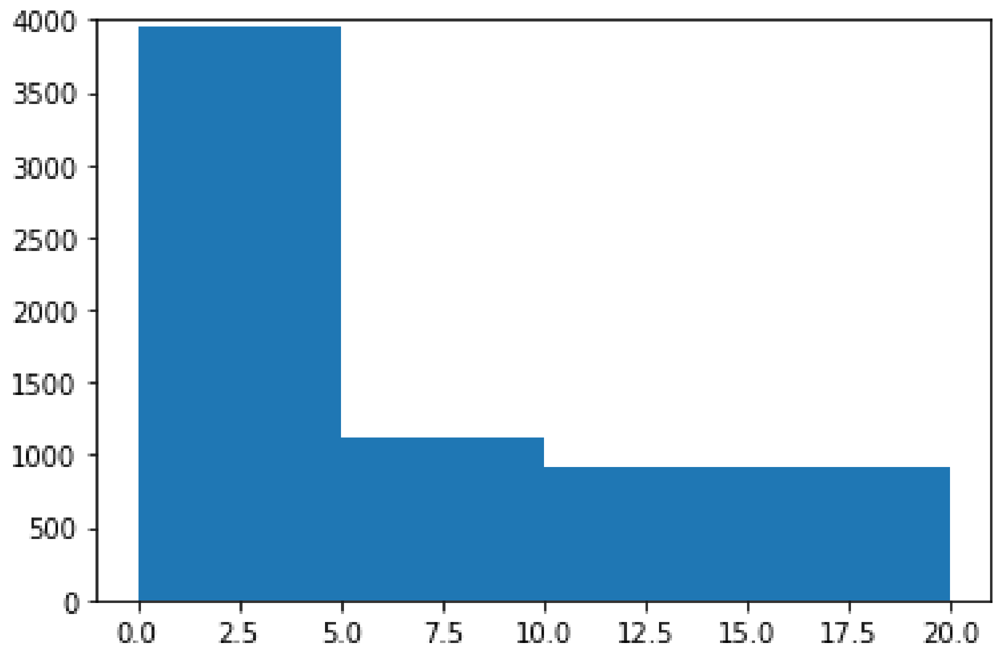
[190]:
```
```



[193]:
```
```

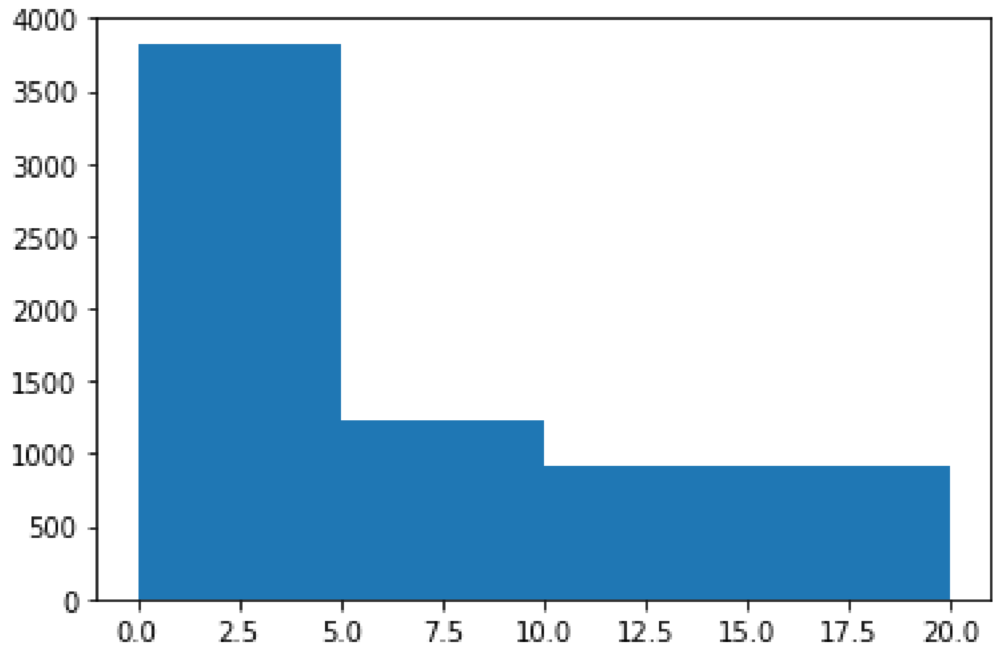


[165]:
```
plt.hist(df.A_prichness, bins=[0, 5, 10, df.A_prichness.max()]),
plt.ylim((0,4000))
plt.savefig('prichnessbin.png',dpi=500)
```

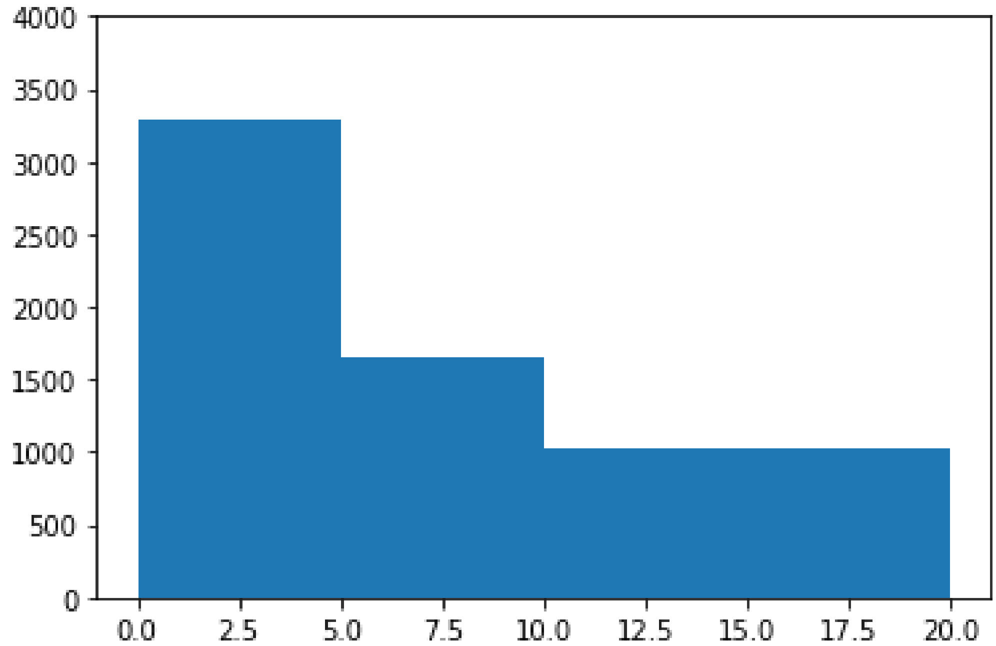


[ ]:

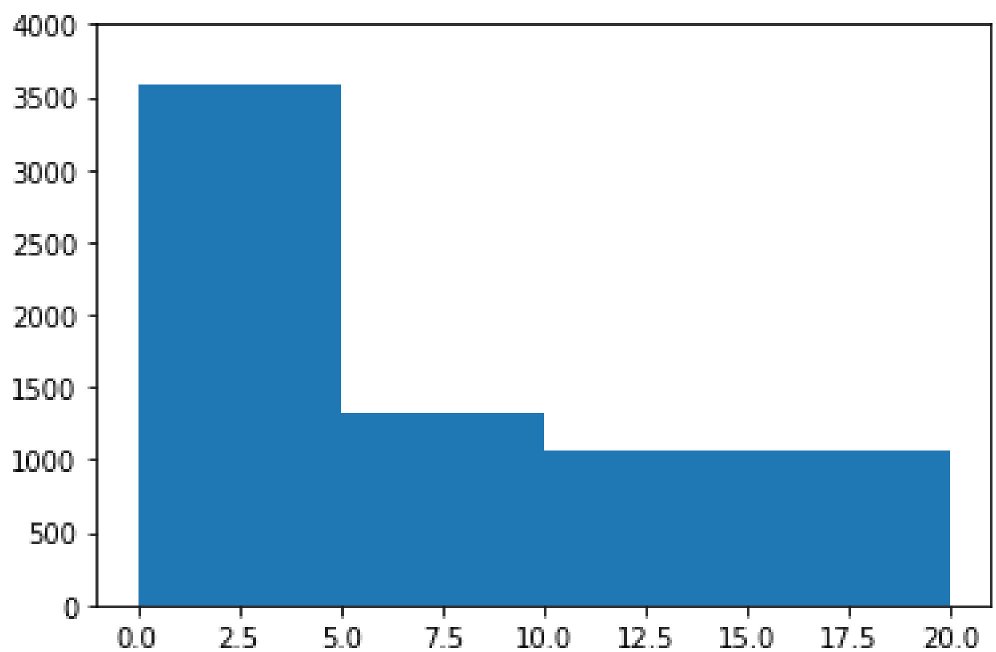
[151]:
```
plt.hist(df.B_prichness, bins=[0, 5, 10, df.B_prichness.max()])
plt.ylim((0,4000))
plt.savefig('B_prichnessbin.png',dpi=500)
```



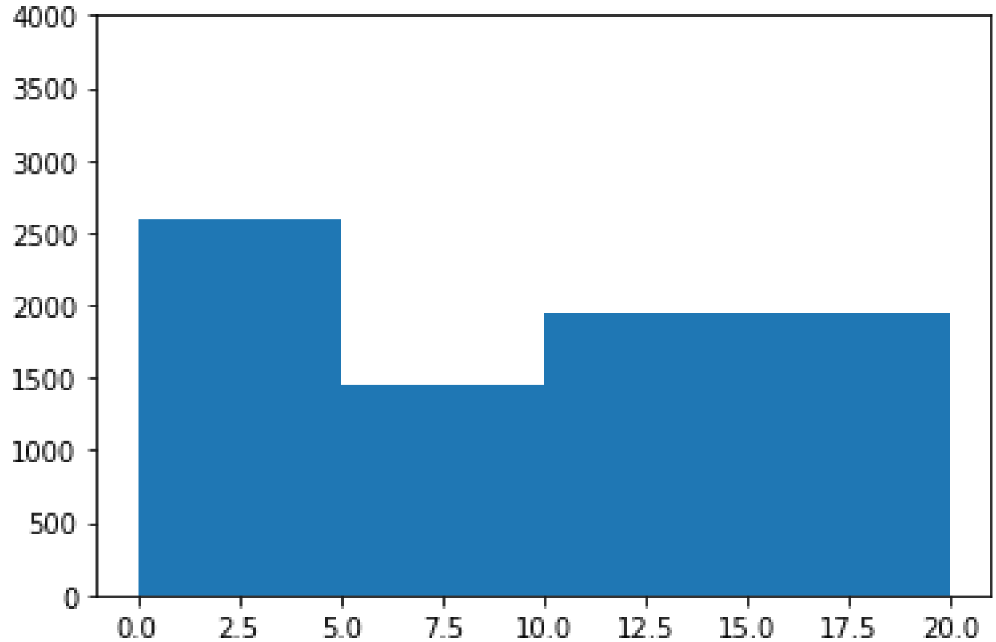
[152]:
```
plt.hist(df.C_prichness, bins=[0, 5, 10, df.C_prichness.max()])
plt.ylim((0,4000))
plt.savefig('C_prichnessbin.png',dpi=500)
```



[153]:
```
plt.hist(df.D_prichness, bins=[0, 5, 10, df.D_prichness.max()])
plt.ylim((0,4000))
plt.savefig('D_prichnessbin.png',dpi=500)
```



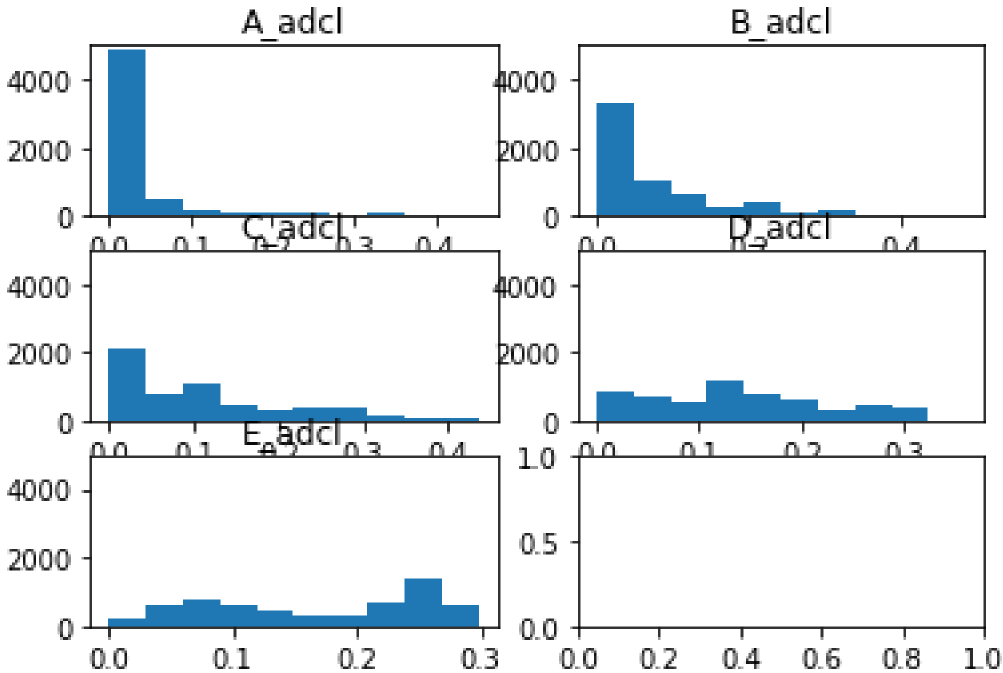
[154]:
```
plt.hist(df.E_prichness, bins=[0, 5, 10, 20])
plt.ylim((0,4000))
plt.savefig('E_prichnessbin.png',dpi=500)
```

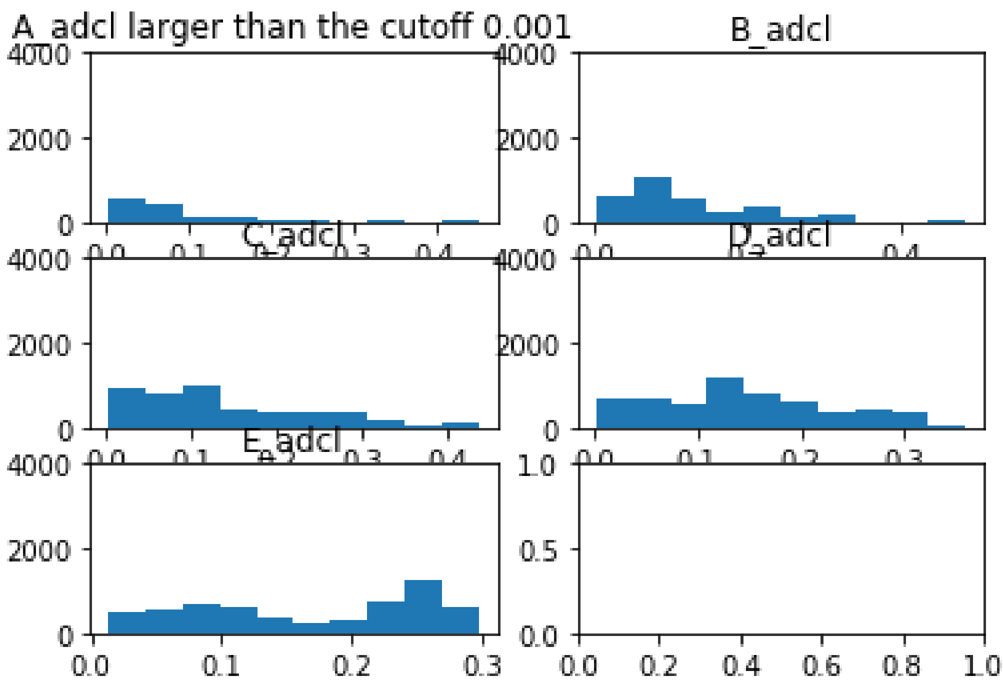


[133]:
```
df.E_prichness.describe()
```

[133]:
```
count    5974.000000
mean        6.038165
std         4.627806
min         1.000000
25%         1.000000
50%         5.000000
75%        11.000000
max        17.000000
Name: E_prichness, dtype: float64
```

[163]:
```
plot_pplacer('_adcl'),plot_pplacer_cutoff('_adcl', 0.001)
plt.savefig('adcl.png', bbox_inches='tight', dpi=500)
```

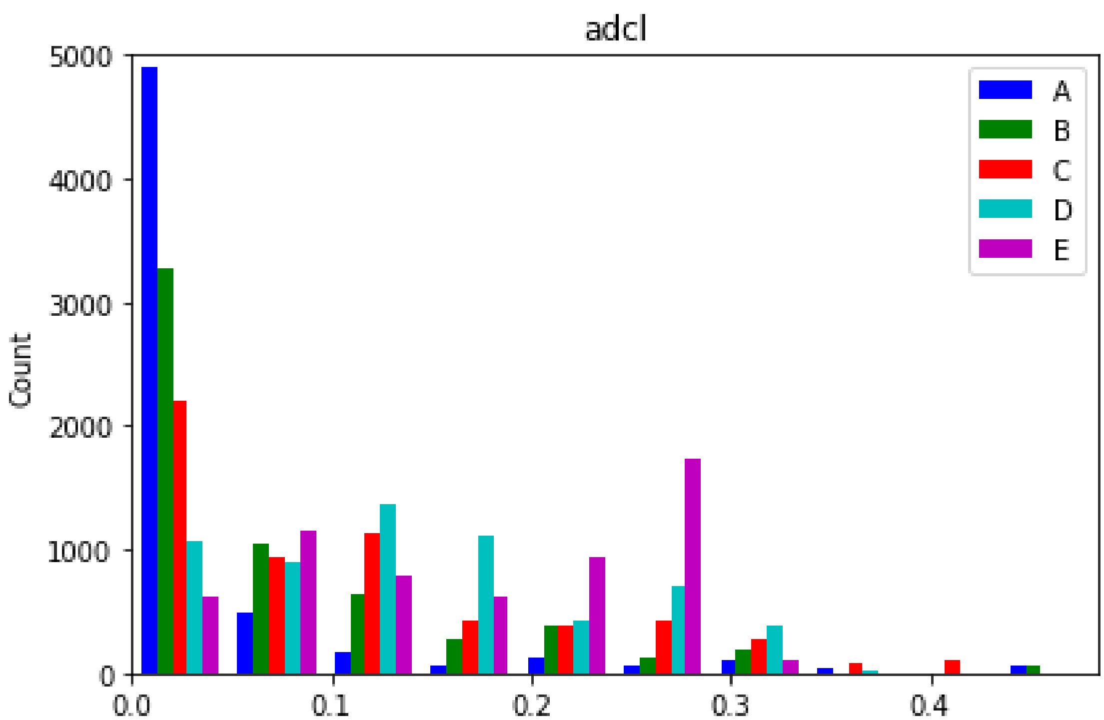

A_adcl
B_adcl
C_adcl
D_adcl
E_adcl
4000
2000
0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.8
1.0


A_adcl larger than the cutoff 0.001
B_adcl
C_adcl
D_adcl
E_adcl
4000
2000
0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.8
1.0

16 2020-07-09

17 adcl: subsetting data with the cutoff 0.001. 1st:percentile at score, 2nd: median

[196]:
```
fig, ax1=plt.subplots()
ax1.hist([df.A_adcl, df.B_adcl,df.C_adcl, df.D_adcl,df.E_adcl],␣
 ↪color=['b','g','r','c','m'],label=['A','B','C','D','E'])
ax1.set_ylim(0,5000)
ax1.set_xlim(0,max(df.A_adcl.max(), df.B_adcl.max(),df.C_adcl.max(), df.D_adcl.
 ↪max(), df.E_adcl.max()))
ax1.set_ylabel("Count")
plt.title("adcl")
plt.legend(loc='upper right')
plt.tight_layout()
# plt.show()
plt.savefig('adcl.png',dpi=1000)
```



[135]:
```
[stats.percentileofscore(df.A_adcl,0.001),stats.percentileofscore(df.B_adcl,0.
 ↪001),stats.percentileofscore(df.C_adcl,0.001),stats.percentileofscore(df.
 ↪D_adcl,0.001),stats.percentileofscore(df.E_adcl,0.001)]
```

[135]: [72.19618346166722,
 44.27519250083696,
 20.070304653498493,
 3.7663207231335787,
 1.037830599263475]

[136]:
```
[df.A_adcl[df.A_adcl>0.001].median(),
df.B_adcl[df.B_adcl>0.001].median(),
df.C_adcl[df.C_adcl>0.001].median(),
df.D_adcl[df.D_adcl>0.001].median(),
df.E_adcl[df.E_adcl>0.001].median()]
```

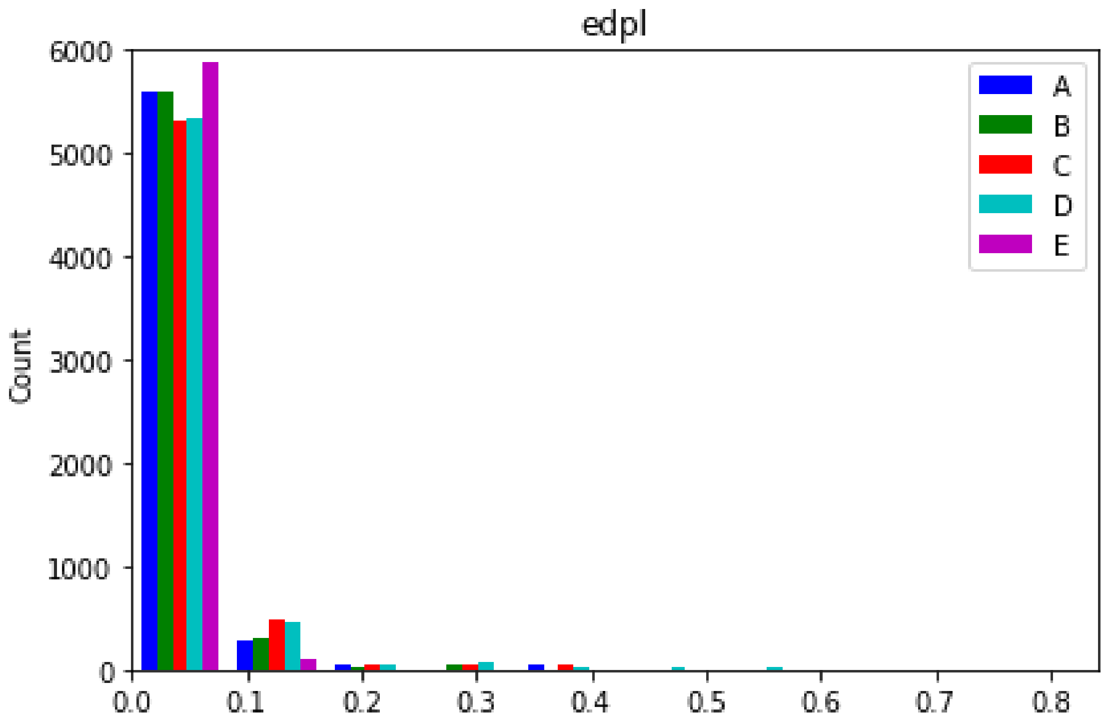
[136]: [0.06385, 0.095206, 0.11277100000000001, 0.13653800000000002, 0.17937]

[ ]:

[ ]:

18 edpl: use 75% pertenctile of the tail (tail defined as those with the values larger than the cutoff 0.01)

[197]:
```
fig, ax1=plt.subplots()
ax1.hist([df.A_edpl, df.B_edpl,df.C_edpl, df.D_edpl,df.E_edpl],␣
↪color=['b','g','r','c','m'],label=['A','B','C','D','E'])
ax1.set_ylim(0,6000)
ax1.set_xlim(0,max(df.A_edpl.max(), df.B_edpl.max(),df.C_edpl.max(), df.D_edpl.
↪max(), df.E_edpl.max()))
ax1.set_ylabel("Count")
plt.title("edpl")
plt.legend(loc='upper right')
plt.tight_layout()
# plt.show()
plt.savefig('edpl.png',dpi=1000)
```



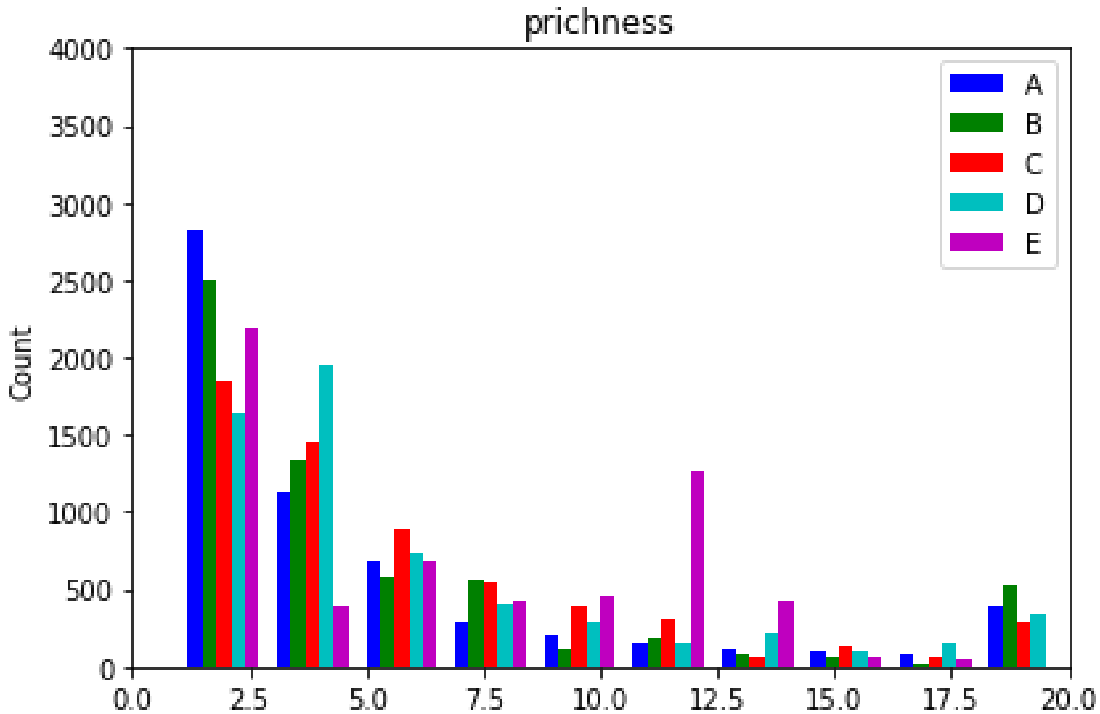
[138]:
```
[stats.scoreatpercentile(df.A_edpl[df.A_edpl>0.01],75),
stats.scoreatpercentile(df.B_edpl[df.B_edpl>0.01],75),
stats.scoreatpercentile(df.C_edpl[df.C_edpl>0.01],75),
stats.scoreatpercentile(df.D_edpl[df.D_edpl>0.01],75),
stats.scoreatpercentile(df.E_edpl[df.E_edpl>0.01],75)]
```

[138]:
```
[0.05812195, 0.065444, 0.08109119999999999, 0.059724, 0.0609513]
```

19 prichness: percentile at score 5 is a good indicator

[200]:
```
fig, ax1=plt.subplots()
ax1.hist([df.A_prichness, df.B_prichness,df.C_prichness, df.D_prichness,df.
↪E_prichness], color=['b','g','r','c','m'],label=['A','B','C','D','E'])
ax1.set_ylim(0,4000)

ax1.set_xlim(0,max(df.A_prichness.max(), df.B_prichness.max(),df.C_prichness.
↪max(), df.D_prichness.max(), df.E_prichness.max()))
ax1.set_ylabel("Count")
plt.title("prichness")
plt.legend(loc='upper right')
plt.tight_layout()
# plt.show()
```

```
plt.savefig('prichness.png',dpi=1000)
```



[201]:
```
stats.percentileofscore(df.A_prichness,5),stats.percentileofscore(df.
→B_prichness,5),stats.percentileofscore(df.C_prichness,5),stats.
→percentileofscore(df.D_prichness,5),stats.percentileofscore(df.E_prichness,5)
```

[201]:
```
(70.99933043187144,
 67.71007700033478,
 59.943086709072645,
 64.32875795112153,
 47.94107800468698)
```

[ ]: