```
In [67]: import numpy as np
          import matplotlib.pyplot as plt
          import scipy.stats as sps
          import pandas as pd
          from statsmodels.distributions.empirical distribution import ECDF
          from sklearn.neighbors import KernelDensity
          import statsmodels.api as sm
          from statsmodels.sandbox.stats.multicomp import multipletests
          from skidmarks import wald wolfowitz
          %matplotlib inline
In [70]: wine data = pd.read csv('wine.data', header = None, sep=',')
          wine data.head()
          sample = np.array(wine_data.values[:,1])
In [71]: def chi_sq(distr, sample, K):
              frequance = np.array([np.sum([1 for x in sample if
                             ((x > np.percentile(sample, j * 100 / K))
              and (x \le np.percentile(sample, (j+1) * 100 / K))) for bounds = np.array([np.percentile(sample, q=i * 100 / K) for i in range()
              theory_fr = np.array([distr(bounds[i + 1]) - distr(bounds[i]) for i in
              print (frequance)
              print (theory fr)
              return sps.chisquare(frequance, theory_fr, ddof=K)
          chi_sq(sps.norm(np.mean(sample),np.var(sample)).cdf,sample, 8)
          [29 30 33 26 29 30]
          [ 17.6691722
                         23.10248704 52.81049983 42.07723087 23.1451848
           17.4974407 1
Out[71]: Power_divergenceResult(statistic=33.314424049484806, pvalue=nan)
In [72]:
          def normility(sample, alpha = 0.05, method='bonferroni'):
              num tests = 6
              p val = np.zeros(num tests)
              sequence = np.sign(sample - np.mean(sample))
              p_val[0] = wald_wolfowitz(sequence)['p']
              p val[1] = sps.kstest(sample, sps.norm(np.mean(sample),np.var(sample)).
              p val[2] = sps.jarque bera(sample)[1]
              p val[3] = sps.skewtest(sample)[1]
              p_val[4] = sps.shapiro(sample)[1]
              p_val[5] = sps.normaltest(sample)[1]
              return multipletests(p_val, alpha=alpha, method=method)
          for method in ['bonferroni', 'holm']:
    reject, pvals_corrected = normility(sample, alpha=0.05, method=method)
              print("method %s" % (method))
              print(reject)
         method bonferroni
          [ True False False False True]
         method holm
          [ True True False False True]
```

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Наиболее мощный без предположений о независимости - метод Холма, отвергает гипотезу о том, что эта выборка распределена нормально. Но зато это выборка:)

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