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In [3]: 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

%matplotlib inline
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In [4]: wine_data = pd.read_csv('wine.data', header = None, sep=',')
wine_data.head()

sample = wine_data.values[:,4]
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In [17]: def normility(sample, alpha = 0.05, method='bonferroni'):
    num_tests = 5
    p_val = np.zeros(num_tests)
    st, p_val[0] = sps.kstest(sample, sps.norm.cdf)
    st, p_val[1] = sps.jarque_bera(sample)
    st, p_val[2] = sps.skewtest(sample)
    st, p_val[3] = sps.shapiro(sample)
    st, p_val[4] = sps.normaltest(sample)
    return multipletests(p_val, alpha=alpha, method=method)

for method in ['hs', 'bonferroni', 'sidak', 'holm', 'fdr_bh', 'fdr_by']:
    reject, pvals_corrected = normility(sample, alpha=0.05, method=method)
    print("method %s, p_value is: %2.f" % (method, reject.sum()))
```

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method hs, p_value is: 1
method bonferroni, p_value is: 1
method sidak, p_value is: 1
method holm, p_value is: 1
method fdr_bh, p_value is: 1
method fdr_by, p_value is: 1
```

Смысла выбирать между процедурами нет, так как все из изученных(в том числе для FDR) дали один ответ о принятии гипотезы.