StatsKurs_Uebung_Tag3

November 18, 2019

1 Einführung in die Statistik mit Python - Tag 3

1.1 Datenverarbeitung in Pandas

1.1.1 Apply Funktion

```
In [1]: # Import libraries
        #import pandas as pd
        #import numpy as np
        import seaborn as sns

        # Read dataset
        titanic = sns.load_dataset("titanic")

        # Create a new function:
        def num_missing(x): return sum(x.isnull())

        # Applying per column (axis=0)
        print(titanic.apply(num_missing, axis=0))
```

```
survived         0
pclass           0
sex              0
age            177
sibsp            0
parch            0
fare             0
embarked         2
class            0
who              0
adult_male       0
deck           688
embark_town      2
alive            0
alone            0
dtype: int64
```

```
In [2]: # Applying per row (axis=1)
        print(titanic.apply(num_missing, axis=1).head())
```

```
0    1
1    0
2    1
3    0
4    1
dtype: int64
```

1.1.2 Imputation von fehlenden Werten

```
In [3]: # Import function to determine the mode
        from scipy.stats import mode

        mode(titanic['deck']) # This returns both mode and count.
        # Mode can return multiple values with high frequency.

        # Take the first mode value
        mode(titanic['deck']).mode[0]

        # Impute the values:
        titanic['deck'].fillna(mode(titanic['deck']).mode[0], inplace=True)

        # Now check the missing values again to confirm:
        print(titanic.apply(num_missing, axis=0))
```

```
survived         0
pclass           0
sex              0
age            177
sibsp            0
parch            0
fare             0
embarked         2
class            0
who              0
adult_male       0
deck             0
embark_town      2
alive            0
alone            0
dtype: int64
```

```
/home/matt/anaconda3/lib/python3.7/site-packages/scipy/stats/stats.py:248: RuntimeWarning: The
  "values. nan values will be ignored.", RuntimeWarning)
```

1.1.3 Crosstab

```
In [4]: # Import library
        import pandas as pd

        # Create crosstab
        pd.crosstab(titanic["survived"],titanic["sex"], margins=True)
```

```
Out[4]: sex       female  male  All
        survived
        0             81   468  549
        1            233   109  342
        All          314   577  891
```

```
In [5]: def percConvert(ser): return ser/float(ser[-1])

        pd.crosstab(titanic["survived"],titanic["sex"], margins=True).apply(percConvert, axis=
```

```
Out[5]: sex         female      male  All
        survived
        0         0.147541  0.852459  1.0
        1         0.681287  0.318713  1.0
        All       0.352413  0.647587  1.0
```

1.1.4 Merging von DataFrames

```
In [6]: #?pd.merge

        # First we create some dummy data
        band = pd.DataFrame({"name":["Mick","John","Paul"],
                             "band":["Stones","Beatles","Beatles"]})
        print(band)
```

```
   name     band
0  Mick   Stones
1  John  Beatles
2  Paul  Beatles
```

```
In [7]: # Second dummy data
        instruments = pd.DataFrame({"name":["John","Paul","Keith"],
                                    "instrument":["guitar","bass","guitar"]})
        print(instruments)
```

```
    name instrument
0   John     guitar
1   Paul       bass
2  Keith     guitar
```

```
In [8]: # "Merge" to combine DataFrames by common variables
        pd.merge(band, instruments, on="name", how="inner")#, suffixes=('_left', '_right'))

Out[8]:    name     band instrument
        0  John  Beatles     guitar
        1  Paul  Beatles       bass

In [9]: pd.merge(band, instruments, how="left")

Out[9]:    name     band instrument
        0  Mick   Stones        NaN
        1  John  Beatles     guitar
        2  Paul  Beatles       bass

In [10]: pd.merge(band, instruments, how="right")

Out[10]:    name     band instrument
         0   John  Beatles     guitar
         1   Paul  Beatles       bass
         2  Keith      NaN     guitar

In [11]: pd.merge(band, instruments, how="outer")

Out[11]:    name     band instrument
         0   Mick   Stones        NaN
         1   John  Beatles     guitar
         2   Paul  Beatles       bass
         3  Keith      NaN     guitar

In [12]: # Use a named `left_on` and `right_on` if the join variables have different names
         instruments2 = pd.DataFrame({"artist": ["John", "Paul", "Keith"],
                                      "instrument": ["guitar","bass","guitar"]})
         instruments2

         pd.merge(band, instruments2, left_on="name", right_on= "artist")

Out[12]:   name     band artist instrument
         0  John  Beatles   John     guitar
         1  Paul  Beatles   Paul       bass
```

1.1.5 Pivot-Tabelle

```
In [13]: # Import library
         import seaborn as sns

         # Datensatz laden
         titanic = sns.load_dataset("titanic")

         # Pivot-Tabelle generieren
         titanic.pivot_table(columns="class", index="sex",
                             values="survived", aggfunc="mean")
```

```
Out[13]: class      First    Second     Third
         sex
         female  0.968085  0.921053  0.500000
         male    0.368852  0.157407  0.135447
```

```
In [14]: # Oder so
         params = {"columns": "class", "index": "sex",
                   "values": "survived", "aggfunc": "mean"}
         titanic_pivot = titanic.pivot_table(**params)

         print(titanic_pivot) # Show pivot table
```

```
class      First    Second     Third
sex
female  0.968085  0.921053  0.500000
male    0.368852  0.157407  0.135447
```

Versucht mal dasselbe mit der Funktion pivot()

```
In [15]: #?df.pivot

         #params = {
         #   "columns": "class",
         #   "index": "sex",
         #   "values": "survived"
         #}
         #titanic.pivot(**params)
```

Warum klappt das nicht?
Aber warum funktioniert es bei dem Beispiel unterhalb:

```
In [16]: import pandas as pd

         df = pd.DataFrame({'foo': ['one', 'one', 'one', 'two', 'two', 'two'],
                            'bar': ['A', 'B', 'C', 'A', 'B', 'C'],
                            'baz': [1, 2, 3, 4, 5, 6]})
         df
```

```
Out[16]:    foo bar  baz
         0  one   A    1
         1  one   B    2
         2  one   C    3
         3  two   A    4
         4  two   B    5
         5  two   C    6
```

```
In [17]: df_pivot = df.pivot(index='foo', columns='bar', values='baz')
         df_pivot
```

```
Out[17]: bar   A  B  C
         foo
         one   1  2  3
         two   4  5  6
```

1.1.6 Unpivot (melt)

```
In [18]: #?df.melt
```

```
In [19]: # Show column names
         df_pivot.columns.values
```

```
Out[19]: array(['A', 'B', 'C'], dtype=object)
```

```
In [20]: # Move row Index to column
         df_pivot.reset_index(inplace=True)
         df_pivot.columns.values
```

```
Out[20]: array(['foo', 'A', 'B', 'C'], dtype=object)
```

```
In [21]: df_orig = df_pivot.melt(id_vars=['foo'], value_vars=['A', 'B', 'C'],
                                 var_name='bar', value_name='baz')
         df_orig
```

```
Out[21]:    foo bar  baz
         0  one   A    1
         1  two   A    4
         2  one   B    2
         3  two   B    5
         4  one   C    3
         5  two   C    6
```

1.1.7 stack() und unstack()

```
In [22]: # Load numpy library
         import numpy as np

         # Row Multi-Index
         row_idx_arr = list(zip(['r0', 'r0'], ['r-00', 'r-01']))
         row_idx = pd.MultiIndex.from_tuples(row_idx_arr)

         # Column Multi-Index
         col_idx_arr = list(zip(['c0', 'c0', 'c1'], ['c-00', 'c-01', 'c-10']))
         col_idx = pd.MultiIndex.from_tuples(col_idx_arr)

         # Create the DataFrame
         d = pd.DataFrame(np.arange(6).reshape(2,3), index=row_idx, columns=col_idx)
         d = d.applymap(lambda x: (x // 3, x % 3))
         d
```

```
Out[22]:              c0              c1
                    c-00    c-01    c-10
         r0 r-00  (0, 0)  (0, 1)  (0, 2)
            r-01  (1, 0)  (1, 1)  (1, 2)
```

```
In [23]: # Stack
         s = d.stack()
         s
```

```
Out[23]:                   c0      c1
         r0 r-00 c-00  (0, 0)     NaN
                 c-01  (0, 1)     NaN
                 c-10     NaN  (0, 2)
            r-01 c-00  (1, 0)     NaN
                 c-01  (1, 1)     NaN
                 c-10     NaN  (1, 2)
```

```
In [24]: # Unstack
         u = d.unstack()
         u
```

```
Out[24]:         c0                              c1
               c-00            c-01            c-10
               r-00    r-01    r-00    r-01    r-00    r-01
         r0  (0, 0)  (1, 0)  (0, 1)  (1, 1)  (0, 2)  (1, 2)
```

```
In [25]: d = u.stack()
         d
```

```
Out[25]:              c0              c1
                    c-00    c-01    c-10
         r0 r-00  (0, 0)  (0, 1)  (0, 2)
            r-01  (1, 0)  (1, 1)  (1, 2)
```

1.2 Nachtrag - Tag 2

1.2.1 Namensräume verbinden

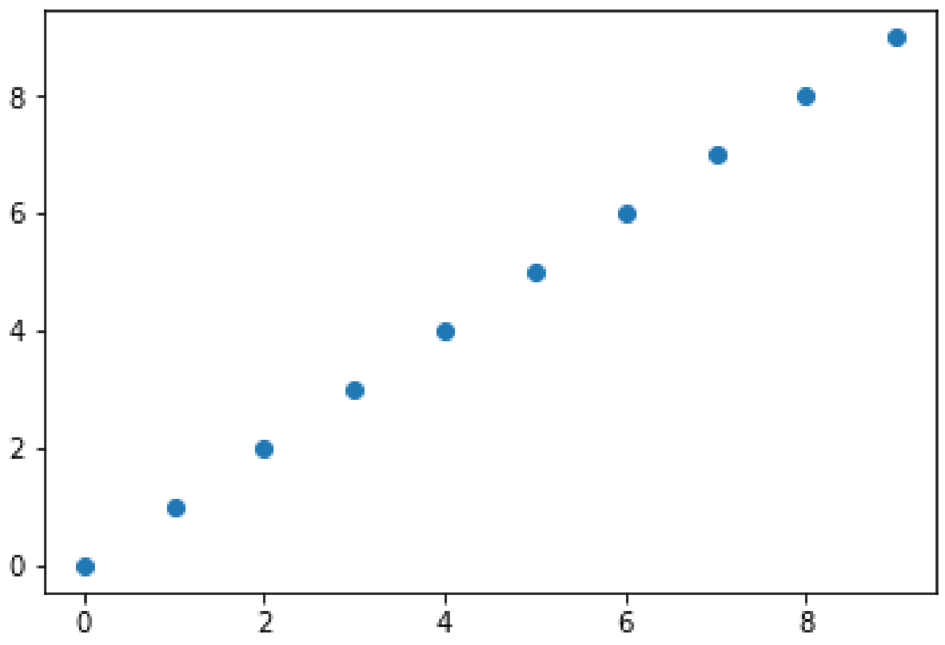
```
In [26]: list1 = ['1','2','3','4']
         s = "-"

         # joins elements of list1 by '-' and stores in string s
         s.join(list1)
```

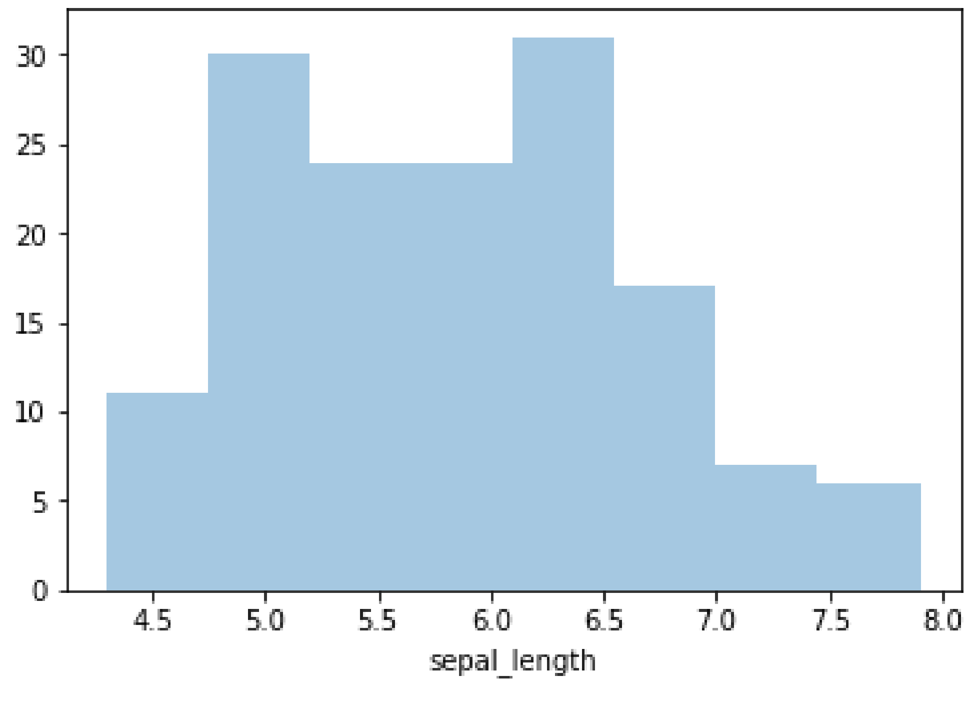
```
Out[26]: '1-2-3-4'
```

```
In [27]: # Create filename from basename and format
         base_filename='my_figure'
         format = 'pdf'
         filename = ".".join([base_filename, format])
         # Specify full path of file directory, please change accordingly
         dir_name='/home/matt/Documents/Github/pyStats/'

         # Create filename with full path
         "".join([dir_name, filename])

Out[27]: '/home/matt/Documents/Github/pyStats/my_figure.pdf'

In [28]: # Alternative approach using the os package
         import os
         os.path.join(dir_name, base_filename + "." + format)

Out[28]: '/home/matt/Documents/Github/pyStats/my_figure.pdf'
```

1.2.2 Speichern von bestimmten Abbildungen

```
In [29]: import matplotlib.pyplot as plt

         f1 = plt.figure()
         plt.plot(range(10), range(10), "o")
         plt.show()

         # Import library and dataset
         iris = sns.load_dataset('iris')

         # Hist only
         f2 = plt.figure()
         sns.distplot(a=iris["sepal_length"], hist=True, kde=False, rug=False )
         plt.show()

         # Save with combined dir_name and filename
         file = "".join([dir_name, filename])
         file # Make sure the path is correct, before saving!!!

         #f1.savefig(file, bbox_inches='tight')

         # Save to working directory
         #f2.savefig("hist_sepal_length.pdf", bbox_inches='tight')
```





```
Out[29]: '/home/matt/Documents/Github/pyStats/my_figure.pdf'
```

1.3 Übung

Ladet den Datensatz schoko.csv in Python:

```
In [30]: import pandas as pd

         # Load your dataset
         schoko = pd.read_csv("/home/matt/Documents/Github/pyStats/data/schoko.csv")

         # If you have opened the Jupyter Notebook from your local directory,
         # this should also work:
         schoko = pd.read_csv("data/schoko.csv")
```

Verschafft euch einen Überblick über den Datensatz:

```
In [31]: #schoko.dtypes
         schoko.head()
         #schoko.shape
```

```
Out[31]:                        me      Marke Einkaufsort  Preis  Kategorie   Bio  \
         0    Choceur Weisse Crisp    Choceur        Aldi     99      weiss  nein
         1  Choceur Alpenvollmilch    Choceur        Aldi     35  vollmilch  nein
         2       Choceur Haselnuss    Choceur        Aldi     35  vollmilch  nein
         3               Nusskcker  Nusskcker        Aldi     55  vollmilch  nein
         4         Happy Halloween      Meybo     Bio Bio    199  vollmilch    ja

            Fair  crisp  nuss  traube  rum  chili  echte.vanille  cocos  Kakaogehalt  \
         0  nein      1     0       0    0      0              0      0         28.0
         1  nein      0     0       0    0      0              0      0         30.0
         2  nein      0     1       0    0      0              0      0         30.0
         3  nein      0     1       0    0      0              0      0         32.0
         4  nein      0     0       0    0      0              1      0         35.0

            Gewicht  Anzahl.der.Inhaltsstoffe  Nussanteil  Crisps  Verfallsdatum
         0      200                        15        12.0       6            5.0
         1      100                        10         0.0       0            9.0
         2      100                        10        12.0       0            9.0
         3      100                         9        25.0       0            6.0
         4      100                         6         0.0       0           15.0
```

Findet sämtliche Bio-Schokolade mit einem Preis nicht teurer als 1,6 :

```
In [32]: schoko[(schoko.Bio == "ja") & (schoko.Preis <= 160)]
```

```
Out[32]:                          me   Marke Einkaufsort  Preis  Kategorie Bio  Fair  \
         9            Weisse Knusper  Vivani     Bio Bio    159      weiss  ja  nein
         11           Vollmilch Nuss  Vivani     Bio Bio    159  vollmilch  ja  nein
         13          LacoaZartbitter   Lacoa     Bio Bio    119  vollmilch  ja  nein
         14  LacoaVollmichschokolade   Lacoa     Bio Bio    119  vollmilch  ja  nein
```

```
19              FeineBitter  Vivani     Bio Bio    159     bitter  ja  nein
21                     Kids  Vivani     Bio Bio    159  vollmilch  ja  nein

    crisp  nuss  traube  rum  chili  echte.vanille  cocos  Kakaogehalt  \
9       1     0       0    0      0              1      0         29.0
11      0     1       0    0      0              1      0         33.0
13      0     0       0    0      0              0      0         70.0
14      0     0       0    0      0              1      0         33.0
19      0     0       0    0      0              0      0         72.0
21      0     0       0    0      0              1      0         33.0

    Gewicht  Anzahl.der.Inhaltsstoffe  Nussanteil  Crisps  Verfallsdatum
9       100                         6         0.0       5           15.0
11      100                         8        10.0       0            6.0
13      100                         3         0.0       0           21.0
14      100                         7         0.0       0           16.0
19      100                         3         0.0       0           19.0
21      100                        10         0.0       0            2.0
```

Sortiert den Datensatz nach Bio und Preis:

```
In [33]: schoko.sort_values(by=["Bio", "Preis"], inplace=True)
         schoko.head()
```

```
Out[33]:                          me   Marke Einkaufsort  Preis  Kategorie Bio  Fair  \
         13          LacoaZartbitter   Lacoa     Bio Bio    119  vollmilch  ja  nein
         14  LacoaVollmichschokolade   Lacoa     Bio Bio    119  vollmilch  ja  nein
         9            Weisse Knusper  Vivani     Bio Bio    159      weiss  ja  nein
         11           Vollmilch Nuss  Vivani     Bio Bio    159  vollmilch  ja  nein
         19              FeineBitter  Vivani     Bio Bio    159     bitter  ja  nein

             crisp  nuss  traube  rum  chili  echte.vanille  cocos  Kakaogehalt  \
         13      0     0       0    0      0              0      0         70.0
         14      0     0       0    0      0              1      0         33.0
         9       1     0       0    0      0              1      0         29.0
         11      0     1       0    0      0              1      0         33.0
         19      0     0       0    0      0              0      0         72.0

             Gewicht  Anzahl.der.Inhaltsstoffe  Nussanteil  Crisps  Verfallsdatum
         13      100                         3         0.0       0           21.0
         14      100                         7         0.0       0           16.0
         9       100                         6         0.0       5           15.0
         11      100                         8        10.0       0            6.0
         19      100                         3         0.0       0           19.0
```

Erstellt eine Pivot-Tabelle für Marke, Kategorie und Preis (pivot_table()):

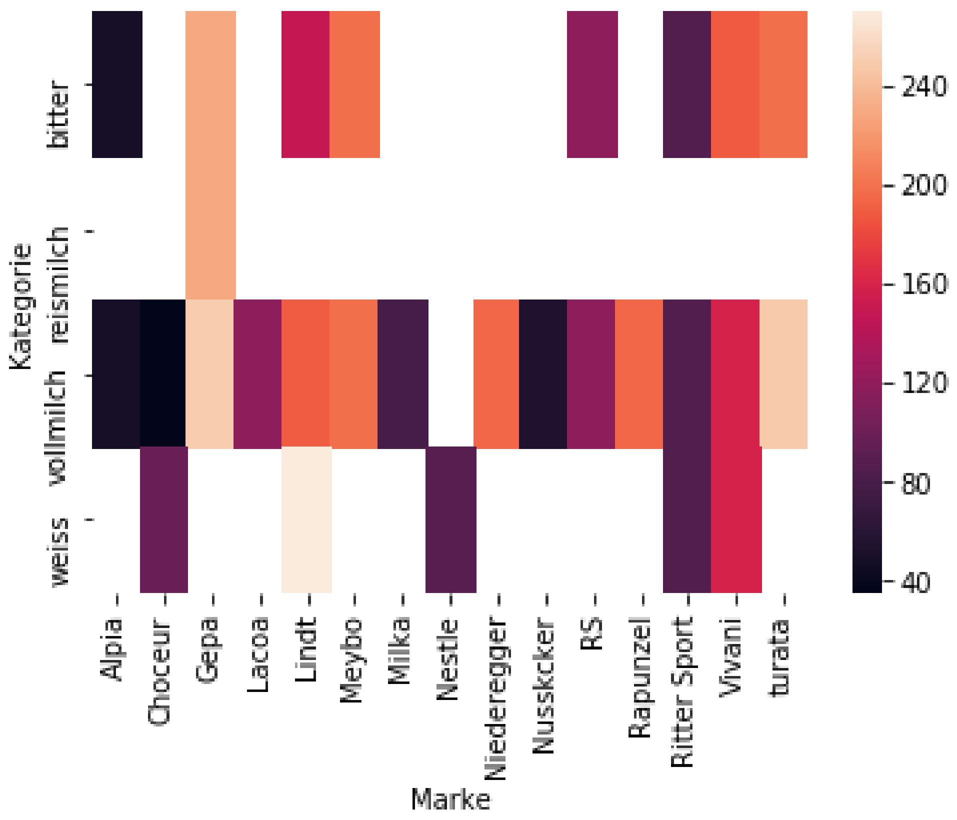
```
In [34]: schoko_pivot = schoko.pivot_table(columns="Marke", index="Kategorie", values="Preis")
         schoko_pivot
```

```
Out[34]: Marke       Alpia  Choceur   Gepa  Lacoa       Lindt  Meybo  Milka  Nestle  \
         Kategorie
         bitter       49.0      NaN  230.0    NaN  149.000000  199.0    NaN     NaN
         reismilch     NaN      NaN  230.0    NaN         NaN    NaN    NaN     NaN
         vollmilch    49.0     35.0  250.0  119.0  189.333333  199.0   79.0     NaN
         weiss         NaN     99.0    NaN    NaN  270.000000    NaN    NaN    89.0

         Marke       Niederegger  Nusskcker     RS  Rapunzel  Ritter Sport  Vivani  \
         Kategorie
         bitter              NaN        NaN  119.0       NaN          85.0   189.0
         reismilch           NaN        NaN    NaN       NaN           NaN     NaN
         vollmilch         195.0       55.0  119.0     195.0          85.0   159.0
         weiss               NaN        NaN    NaN       NaN          85.0   159.0

         Marke       turata
         Kategorie
         bitter       199.0
         reismilch      NaN
         vollmilch    249.0
         weiss          NaN
```

Erstellt eine Heatmap von der Pivot-Tabelle (sns.heatmap()):

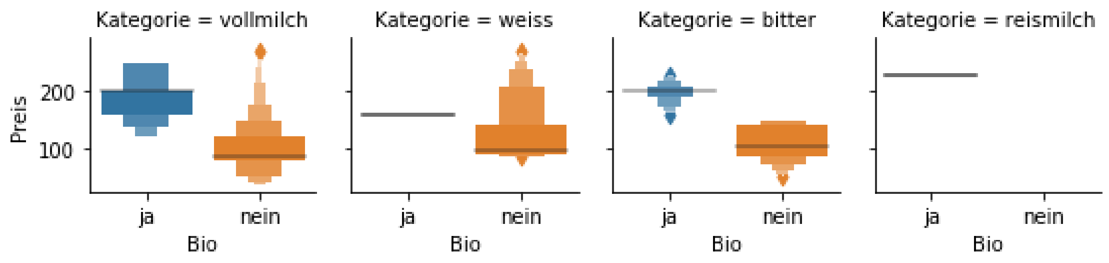
```
In [35]: # Import your libraries
         import matplotlib.pyplot as plt
         import seaborn as sns

         # Hist only
         sns.heatmap(schoko_pivot)
         #plt.savefig('/home/matt/Desktop/plot.png')
```

```
Out[35]: <matplotlib.axes._subplots.AxesSubplot at 0x7f429a0d4c88>
```



Erstellt eine Grafik (sns.catplot()) mit Bio, Preis & Kategorie:

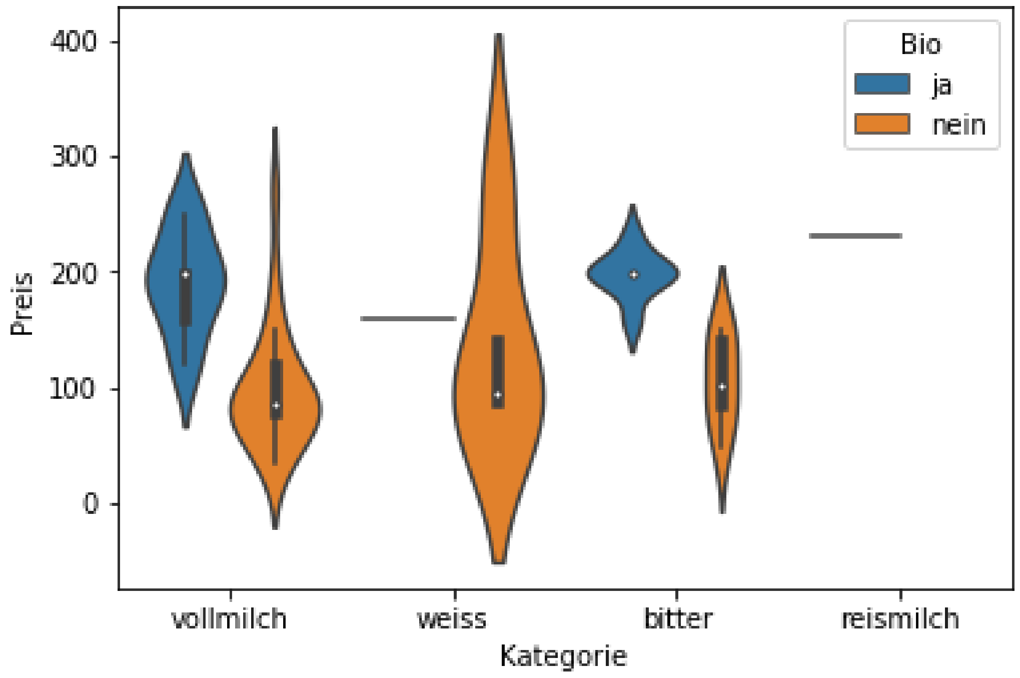
```
In [36]: conf = {
         "x": "Bio",
         "y": "Preis",
         "col": "Kategorie",
         "kind": "boxen",
         "data": schoko,
         "height": 2,
         "sharex": False,
         "dodge": False,
         }

         f = sns.catplot(**conf)
         f

Out[36]: <seaborn.axisgrid.FacetGrid at 0x7f429a0d44e0>
```



Und nun nochmal mit sns.violinplot():

```
In [37]: sns.violinplot(x="Kategorie", y="Preis", hue="Bio", data=schoko)
```

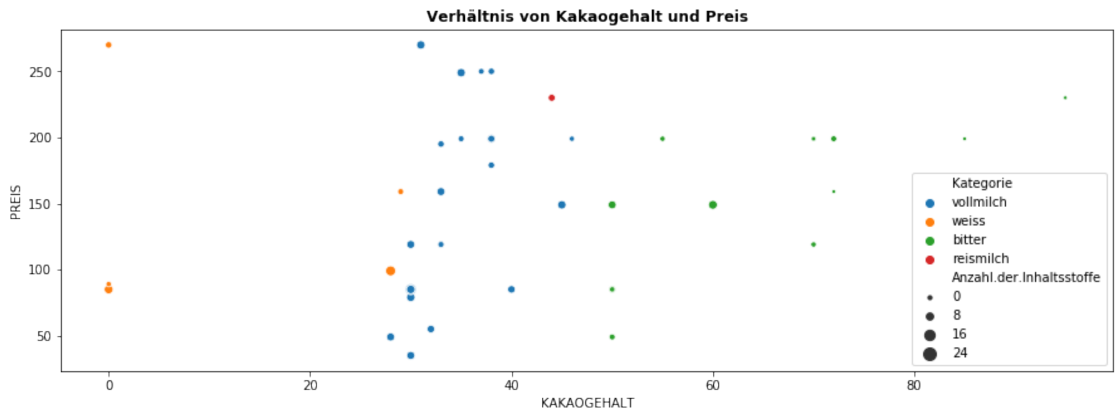
```
Out[37]: <matplotlib.axes._subplots.AxesSubplot at 0x7f4299ee2be0>
```



Erstellt nun noch einen Scatterplot (sns.scatterplot()) mit Kakaogehalt, Preis, Kategorie & Anzahl der Inhaltsstoffe:

```
In [38]: # Figure und Axes Objekt anlegen
         fig, ax = plt.subplots(figsize=(15, 5))

         # Grafik anlegen
         conf = {
         "x": "Kakaogehalt",
         "y": "Preis",
         "hue": "Kategorie",
         "size": "Anzahl.der.Inhaltsstoffe",
         "sizes": (10, 100),
         "data": schoko,
         "ax": ax
         }
         sns.scatterplot(**conf)

         # Beschriftung formatieren und festlegen
         font = {"weight": "bold"}
         ax.set(xlabel=conf["x"].upper(), ylabel=conf["y"].upper())
         title = ("Verhältnis von Kakaogehalt und Preis")

         plt.title(title, **font)
```

```
Out[38]: Text(0.5, 1.0, 'Verhältnis von Kakaogehalt und Preis')
```



1.4 Verteilungs- & Dichtefunktionen

1.4.1 Bernoulli-Verteilung

```
In [39]: from scipy import stats

        p = 0.5
        bernoulliDist = stats.bernoulli(p)

        # In Python this is called a frozen distribution function,
        # and it allows us to calculate everything we want for this distribution.
        # For example, the probability if head comes up zero or one times is given by the pro

        # Probability mass function
        p_tails = bernoulliDist.pmf(0)
```

```
         p_heads = bernoulliDist.pmf(1)

         # And we can simulate 10 Bernoulli trials with
         trials = bernoulliDist.rvs(10) # rvs = random variates
         trials
```

```
Out[39]: array([1, 1, 1, 0, 0, 0, 0, 0, 0, 0])
```

1.4.2 Binomial-Verteilung

```
In [40]: from scipy import stats
         import numpy as np

         # Frozen distribution function
         (p, num) = (0.5, 4)
         binomDist = stats.binom(num, p)

         # Calculate the probabilities how often heads come up
         # during four tosses, given by the PMF
         binomDist.pmf(np.arange(5))
```

```
Out[40]: array([0.0625, 0.25  , 0.375 , 0.25  , 0.0625])
```

1.4.3 Poisson-Verteilung

```
In [41]: # Generate the distribution.
         # Watch out NOT to divide integers,
         # as "3/4" gives "0" in Python 2.x!
         prob = 62./(365./7)
         pd = stats.poisson(prob)

         # Select the interesting numbers,
         # calculate the PMF, and print the results
         x = [0,2,5]
         y = pd.pmf(x)*100
         for num, solution in zip(x,y):
           print('''The chance of having {0} fatal accidents in one
                 week is {1:4.1f}%.'''.format(num,solution))
```

```
The chance of having 0 fatal accidents in one
        week is 30.5%.
The chance of having 2 fatal accidents in one
        week is 21.5%.
The chance of having 5 fatal accidents in one
        week is  0.6%.
```

1.4.4 Normalverteilung

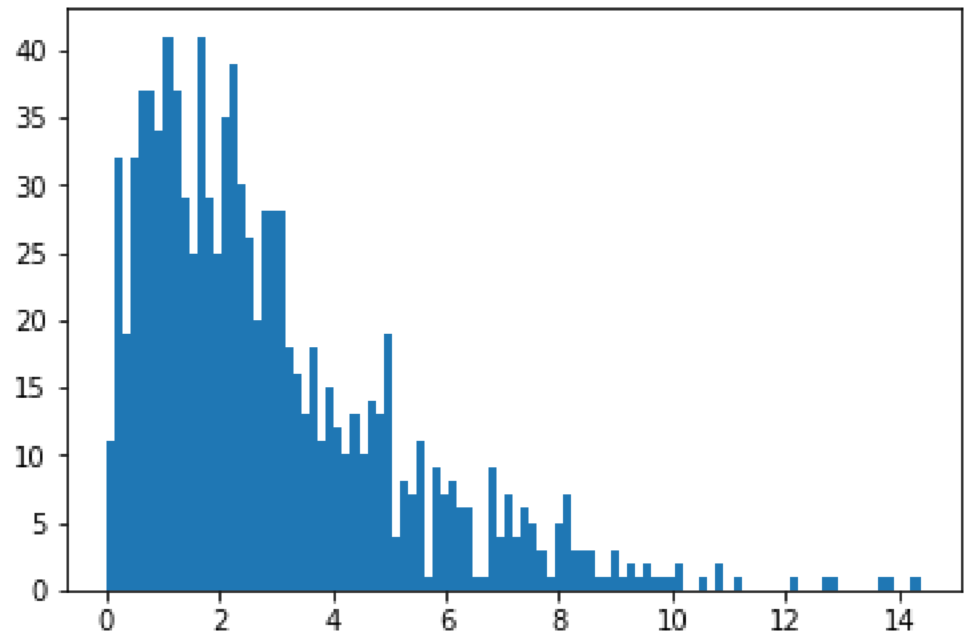
```
In [42]: import numpy as np
         from scipy import stats

         mu = -2
         sigma = 0.7
         myDistribution = stats.norm(mu, sigma)
         significanceLevel = 0.05

         myDistribution.ppf([significanceLevel/2, 1-significanceLevel/2])

Out[42]: array([-3.37197479, -0.62802521])
```

1.4.5 t-Verteilung

```
In [43]: import numpy as np
         import matplotlib.pyplot as plt
         from scipy import stats

         x = [52, 70, 65, 85, 62, 83, 59] # Enter the data

         # Generate the t-distribution: DOF = length data minus 1.
         td = stats.t(len(x)-1); alpha = 0.01

         # From the t-distribution, you use the "PPF" function and
         # multiply it with the standard error
         tval = abs(td.ppf(alpha/2)*stats.sem(x))
         print('mean +/- 99%CI = {0:3.1f} +/- {1:3.1f}'.format(np.mean(x),tval))

mean +/- 99%CI = 68.0 +/- 17.2
```

1.4.6 Chi-Quadratverteilung

```
In [44]: # Define the normal distribution
         nd = stats.norm()

         # Generate three sets of random variates from this distribution
         numData = 1000
         data1 = nd.rvs(numData)
         data2 = nd.rvs(numData)
         data3 = nd.rvs(numData)

         # Show a histogram of the sum of the squares of
         # these random data
         plt.hist(data1**2+data2**2 +data3**2, 100)
         plt.show()
```



1.4.7 F-Verteilung

```
In [45]: apples1 = [110, 121, 143]
         apples2 = [88, 93, 105, 124]

         fval = np.std(apples1, ddof=1)/np.std(apples2, ddof=1)
         fd = stats.distributions.f(len(apples1),len(apples2))
         pval = fd.cdf(fval)

         print('The p-value of the F-distribution = {0}.'.format(pval))
         if pval>0.025 and pval<0.975:
           print('The variances are equal.')
```

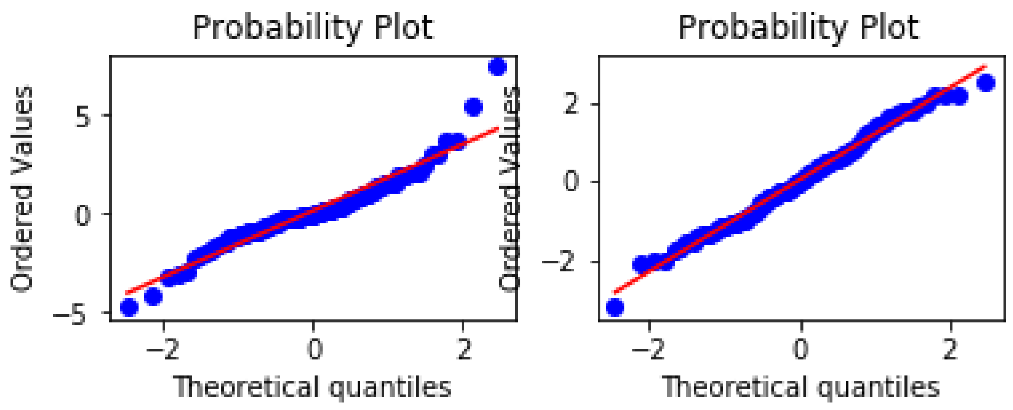
```
The p-value of the F-distribution = 0.537640478466751.
The variances are equal.
```

1.5 Normality check

1.5.1 Probability plots

```
In [46]: from scipy import stats
         import matplotlib.pyplot as plt
         nsample = 100
         np.random.seed(7654321)
```

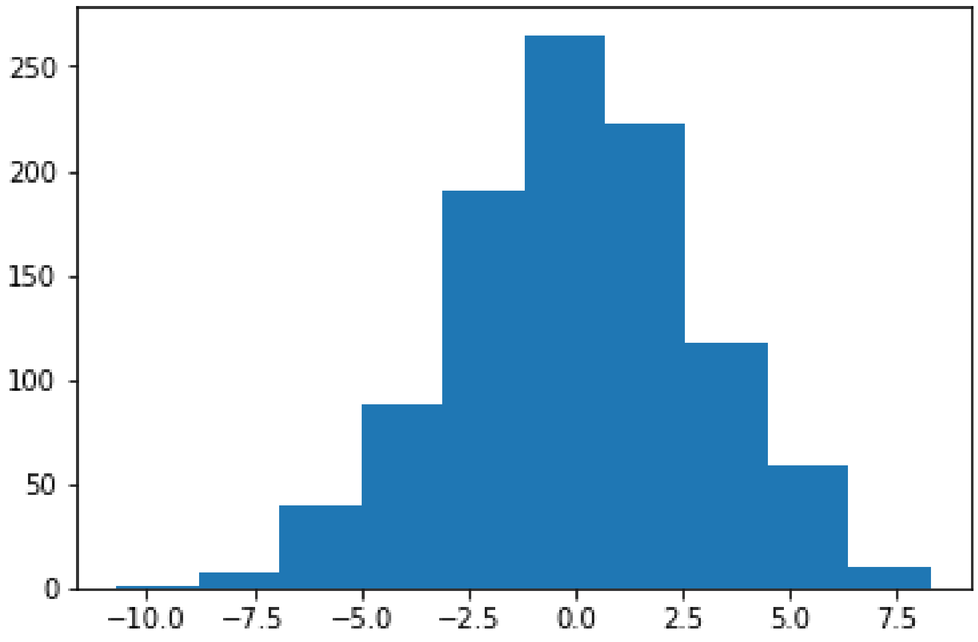
```
# A t distribution with small degrees of freedom:
ax1 = plt.subplot(221)
x = stats.t.rvs(3, size=nsample)
res = stats.probplot(x, plot=plt)

# A t distribution with larger degrees of freedom:
ax2 = plt.subplot(222)
x = stats.t.rvs(25, size=nsample)
res = stats.probplot(x, plot=plt)
plt.show()
```

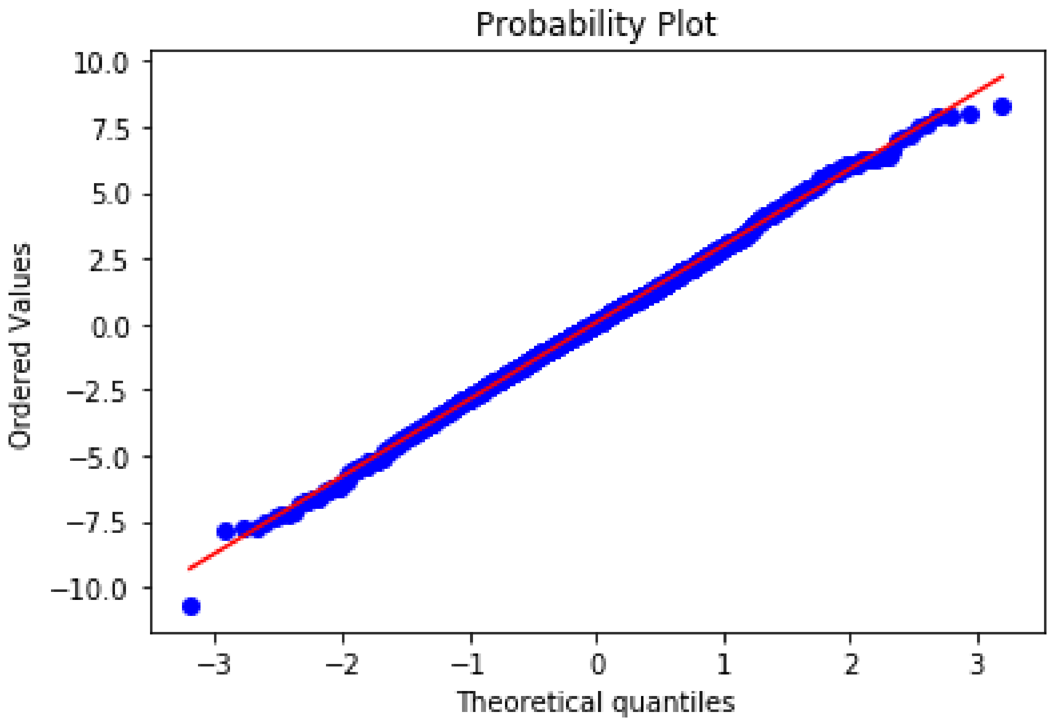


1.5.2 Tests for Normality

D'Agostino-Pearson Omnibus-Test

```
In [47]: # Import standard packages
         import numpy as np
         import matplotlib.pyplot as plt
         import scipy.stats as stats
         import pandas as pd

         # Set the parameters
         numData = 1000
         myMean = 0
         mySD = 3

         # To get reproducable values, I provide a seed value
         np.random.seed(1234)

         # Generate and show random data
         data = stats.norm.rvs(myMean, mySD, size=numData)
         fewData = data[:100]
         plt.hist(data)
         plt.show()

         # Graphical test: if the data lie on a line, they are pretty much
         # normally distributed
         stats.probplot(data, plot=plt)
         plt.show()

         # The scipy normaltest is based on D-Agostino and Pearsons test that
         # combines skew and kurtosis to produce an omnibus test of normality.
         print(stats.normaltest(data))
         print(stats.normaltest(fewData))
```





```
NormaltestResult(statistic=0.1805408823000446, pvalue=0.913684054089169)
NormaltestResult(statistic=10.794182887834198, pvalue=0.004529736794579303)
```

Shapiro-Wilk normality test

```
In [48]: # Shapiro-Wilk test
         print(stats.shapiro(data))
         print(stats.shapiro(fewData))
```

```
(0.9985058903694153, 0.5584741830825806)
(0.9742451906204224, 0.0471017062664032)
```

Kolmogorov-Smirnov normality test

```
In [49]: # Kolmogorov-Smirnov test
         print(stats.kstest((data-np.mean(data))/np.std(data,ddof=1), 'norm'))
         print(stats.kstest((fewData-np.mean(fewData))/np.std(fewData,ddof=1), 'norm'))
```

```
KstestResult(statistic=0.018090443026108516, pvalue=0.8989669136577692)
KstestResult(statistic=0.07383212034840342, pvalue=0.6406771608350166)
```

1.5.3 Daten-Transformation

log-Transformation

```
In [50]: # example dataframe
         df = pd.DataFrame({'a': [0, 1, 2, 3],
                            'b': [4, 5, np.nan, 7],
                            'c': [8, 9, 10, 11]})

         # apply log(x+1) element-wise to a subset of columns
         df_log = df[['a', 'b']].applymap(lambda x: np.log(x+1))

         # rename columns
         df_log.columns = 'log_' + df_log.columns

         # shift the index
         df_log.index = df_log.index + 1

         # If you want a special treatment for missing values, you can do:
         df_log[df_log.isnull()] = -1

         # Print DataFrame
         df_log
```

```
Out[50]:       log_a     log_b
         1  0.000000  1.609438
         2  0.693147  1.791759
         3  1.098612 -1.000000
         4  1.386294  2.079442
```

1.5.4 Sample size

StichprobengröSSe bei bekannter Population

```
In [51]: from scipy import stats
         import math

         def sample_size_pop(N, e=0.05, c=0.95, p=0.5, extra=None):
           """Stichprobengröe bei bekannter Population.
              N: Population / Grundgesamtheit
              e: Fehlertoleranz
              c: Konfidenzniveau
              p: geschätzter Anteilswert
              extra: Zusatz für fehlenden Rücklauf [0, 1]
           """

           z = stats.norm.ppf((1 + c) / 2)
           frac_n = (z**2 * p*(1-p)) / e**2
           frac_d = 1 + ((z**2 * p*(1-p)) / (e**2 * N))
```

```
      n = frac_n / frac_d
      if extra:
        n = n + n * extra
        # Werte aufrunden
      return math.ceil(n)

    # Beispiel
    n = 4000
    sample_size_pop(n, c=0.99, e=0.03, p=0.5, extra=0.05) #out: 1325
    sample_size_pop(n, c=0.95, e=0.05, p=0.8, extra=0.05) #out: 244
```

```
Out[51]: 244
```

StichprobengröSSe für den Vergleich von zwei bekannten Gruppen

```
In [52]: #Calculate the sample size for experiments, for normally distributed groups, for comp

         # Import standard packages
         import numpy as np

         # additional packages
         from scipy.stats import norm

         def sampleSize_twoGroups(D, alpha=0.05, beta=0.2, sigma1=1, sigma2=1):
             '''Sample size for two groups. The formula corresponds to Eq 6.4 in the book.'''

             n = np.round((norm.ppf(1-alpha/2.) + norm.ppf(1-beta))**2 * (sigma1**2 + sigma2**

             print(('In order to detect a change of {0} between groups with an SD of {1} and {
             print(('''with significance {0} and test-power {1},
                    you need in each group at least {2:d} subjects.'''.format(alpha, 100*(1-be
             return n

         sampleSize_twoGroups(0.4, sigma1=0.6, sigma2=0.6)
```

```
In order to detect a change of 0.4 between groups with an SD of 0.6 and 0.6,
with significance 0.05 and test-power 80.0,
           you need in each group at least 35 subjects.
```

```
Out[52]: 35.0
```

StichprobengröSSe bei unbekannter Population

```
In [53]: from scipy import stats
         import math
         def sample_size(e=0.05, c=0.95, p=0.5, extra=None):
           """
           Stichprobengröe, unbekannte Population.
```

```
    Parameter
    ---------
      e: Fehlertoleranz
      c: Konfidenzniveau
      p: geschätzter Anteilswert
      extra: Zusatz für fehlenden Rücklauf
    Returns
    -------
      n, sample size -> int
    """
    z = stats.norm.ppf((1 + c) / 2)
    n = (z**2 * p * (1-p)) / e**2
    if extra:
     n = n + n * extra
    return math.ceil(n)

sample_size(p=0.09, e=0.01, c=0.95) #out: 3147
```

```
Out[53]: 3147
```

Poweranalyse mit statsmodels für eine Gruppe

```
In [54]: from statsmodels.stats import power
         nobs = power.tt_solve_power(effect_size = 0.5, alpha =0.05, power=0.8)
         print(nobs)
```

```
33.3671314275208
```

für zwei Gruppen

```
In [55]: nobs = power.tt_ind_solve_power(effect_size = 0.5, alpha =0.05, power=0.8)
         print(nobs)
```

```
63.765611775409525
```

```
In [56]: effect_size = power.tt_ind_solve_power(alpha =0.05, power=0.8, nobs1=25)
         print(effect_size)
```

```
0.8087077886680412
```

1.6 Induktive Statistik

1.6.1 Verteilungs-Tests

Einstichproben-t-Test

```
In [57]: # One-sample t-Test
         from scipy import stats

         np.random.seed(7654567)  # fix seed to get the same result
         rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))

         # Test if mean of random sample is equal to true mean
         t, pVal = stats.ttest_1samp(rvs,5.0)
         print(t); print(pVal)
```

```
[-0.68014479 -0.04323899]
[0.49961383 0.96568674]
```

```
In [58]: # Test if mean of random sample is equal to different mean (0)
         t, pVal = stats.ttest_1samp(rvs,0.0)
         print(t); print(pVal)
```

```
[2.77025808 4.11038784]
[0.00789095 0.00014999]
```

We reject the null hypothesis in the second case and don't reject it in the first case.

Wilcoxon-Vorzeichen-Rang-Test

```
In [59]: # Wilcoxon Signed Rank Sum test
         d = [6, 8, 14, 16, 23, 24, 28, 29, 41, -48, 49, 56, -60]
         rank, pVal = stats.wilcoxon(d)
         print(rank); print(pVal)
```

```
23.0
0.11585149752593009
```

1.6.2 Vergleich von zwei abhängigen Verteilungen

(gepaarter t-Test)

```
In [60]: # paired t-test

         import numpy as np
         from scipy import stats

         np.random.seed(1234)
         data = np.random.randn(10)+0.1
         data1 = np.random.randn(10)*5 # dummy data
         data2 = data1 + data
         # paired t-test
         print(stats.ttest_rel(data2, data1))
         # same group-difference as "data"

         # one-sample t-test on data
         print(stats.ttest_1samp(data, 0))

Ttest_relResult(statistic=-0.1245849229873135, pvalue=0.9035904508547089)
Ttest_1sampResult(statistic=-0.12458492298731401, pvalue=0.9035904508547086)
```

1.6.3 Vergleich von zwei unabhängigen Verteilungen

Zweistichproben-t-Test (ungepaart)

```
In [61]: # two-sample t-Test
         rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
         rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)

         stats.ttest_ind(rvs1,rvs2)

Out[61]: Ttest_indResult(statistic=0.37253970303059, pvalue=0.7095701552042009)

In [62]: # `ttest_ind` underestimates p for unequal variances:

         rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
         stats.ttest_ind(rvs1, rvs3, equal_var = False)

Out[62]: Ttest_indResult(statistic=-0.3985984494918709, pvalue=0.6903088057124194)

In [63]: # When n1 != n2, the equal variance t-statistic is no longer equal to the
         # unequal variance t-statistic:

         rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
         print(stats.ttest_ind(rvs1, rvs4))
         print(stats.ttest_ind(rvs1, rvs4, equal_var = False))

Ttest_indResult(statistic=-1.8714304469876069, pvalue=0.06177345109934761)
Ttest_indResult(statistic=-1.181542065426572, pvalue=0.23998895128328585)


In [64]: # T-test with different means, variance, and n:

         rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
         stats.ttest_ind(rvs1, rvs5)

Out[64]: Ttest_indResult(statistic=-2.0228467894259325, pvalue=0.04353343278712891)
```

Non-parametrischer Vergleich von zwei Gruppen Mann-Whitney test

```
In [65]: # Mann-Whitney test
         import numpy as np
         import scipy.stats as stats

         # Create two groups of data
         group1 = [1, 5 ,7 ,3 ,5 ,8 ,34 ,1 ,3 ,5 ,200, 3]
         group2 = [10, 18, 11, 12, 15, 19, 9, 17, 1, 22, 9, 8]

         # Calculate u and probability of a difference
         u_statistic, pVal = stats.mannwhitneyu(group1, group2)

         # Print p-Value
         print (pVal)
```

```
0.013880800754602955
```

1.6.4 Vergleich von mehreren Gruppen

ANOVA

```
In [66]: # 1-way ANOVA
         import scipy.stats as stats

         # Here are some data on a shell measurement (the length of the anterior adductor musc
         # Mytilus trossulus from five locations: Tillamook, Oregon; Newport, Oregon; Petersbu
         # much larger data set used in McDonald et al. (1991).

         tillamook = [0.0571, 0.0813, 0.0831, 0.0976, 0.0817, 0.0859, 0.0735, 0.0659, 0.0923, 0
         newport = [0.0873, 0.0662, 0.0672, 0.0819, 0.0749, 0.0649, 0.0835, 0.0725]
         petersburg = [0.0974, 0.1352, 0.0817, 0.1016, 0.0968, 0.1064, 0.105]
         magadan = [0.1033, 0.0915, 0.0781, 0.0685, 0.0677, 0.0697, 0.0764, 0.0689]
         tvarminne = [0.0703, 0.1026, 0.0956, 0.0973, 0.1039, 0.1045]

         stats.f_oneway(tillamook, newport, petersburg, magadan, tvarminne)

Out[66]: F_onewayResult(statistic=7.121019471642447, pvalue=0.0002812242314534544)
```

```
In [67]: # Varianz Analyse (ANOVA)

         # Import libraries
         import pandas as pd
         import seaborn as sns
         import statsmodels.api as sm
         from statsmodels.formula.api import ols

         # Load data
```

```
        iris = sns.load_dataset("iris")

        # Perform ANOVA
        model = ols('sepal_length ~ C(species)', iris).fit()
        anovaResults = sm.stats.anova_lm(model)
        print(anovaResults)
```

```
               df     sum_sq    mean_sq           F        PR(>F)
C(species)    2.0  63.212133  31.606067  119.264502  1.669669e-31
Residual    147.0  38.956200   0.265008         NaN           NaN
```

Post-Hoc Analyse Tukey HSD

```
In [68]: # Tukey HSD test
         from statsmodels.stats.multicomp import pairwise_tukeyhsd
         res2 = pairwise_tukeyhsd(iris['sepal_length'], iris['species'])
         print(res2)
```

```
 Multiple Comparison of Means - Tukey HSD,FWER=0.05
===================================================
  group1     group2   meandiff lower  upper  reject
---------------------------------------------------
  setosa   versicolor   0.93   0.6862 1.1738  True
  setosa   virginica   1.582   1.3382 1.8258  True
versicolor virginica   0.652   0.4082 0.8958  True
---------------------------------------------------
```

```
In [69]: # Load multicomparison
         from statsmodels.stats.multicomp import MultiComparison

         # Compare models
         mod = MultiComparison(iris['sepal_length'], iris['species'])

         # Run TukeyHSD
         print(mod.tukeyhsd())
```

```
 Multiple Comparison of Means - Tukey HSD,FWER=0.05
===================================================
  group1     group2   meandiff lower  upper  reject
---------------------------------------------------
  setosa   versicolor   0.93   0.6862 1.1738  True
  setosa   virginica   1.582   1.3382 1.8258  True
versicolor virginica   0.652   0.4082 0.8958  True
---------------------------------------------------
```

From the result, we see that we cannot reject the hypothesis that any of the groups have the same mean.

Bonferroni Korrektur

```
In [70]: # Compare models, same as above
         mod = MultiComparison(iris['sepal_length'], iris['species'])

         # Bonferroni Correction
         rtp = mod.allpairtest(stats.ttest_rel, method='b')
         print(rtp[0])
```

```
Test Multiple Comparison ttest_rel
FWER=0.05 method=b
alphacSidak=0.02, alphacBonf=0.017
====================================================
  group1     group2     stat   pval pval_corr reject
----------------------------------------------------
  setosa   versicolor -10.1459 0.0     0.0     True
  setosa   virginica  -16.3441 0.0     0.0     True
versicolor virginica  -5.2753  0.0     0.0     True
----------------------------------------------------
```

Holm Korrektur

```
In [71]: # Compare models, same as above
         mod = MultiComparison(iris['sepal_length'], iris['species'])

         # Holm correction
         rtp = mod.allpairtest(stats.ttest_rel, method='Holm')
         print(rtp[0])
```

```
Test Multiple Comparison ttest_rel
FWER=0.05 method=Holm
alphacSidak=0.02, alphacBonf=0.017
====================================================
  group1     group2     stat   pval pval_corr reject
----------------------------------------------------
  setosa   versicolor -10.1459 0.0     0.0     True
  setosa   virginica  -16.3441 0.0     0.0     True
versicolor virginica  -5.2753  0.0     0.0     True
----------------------------------------------------
```

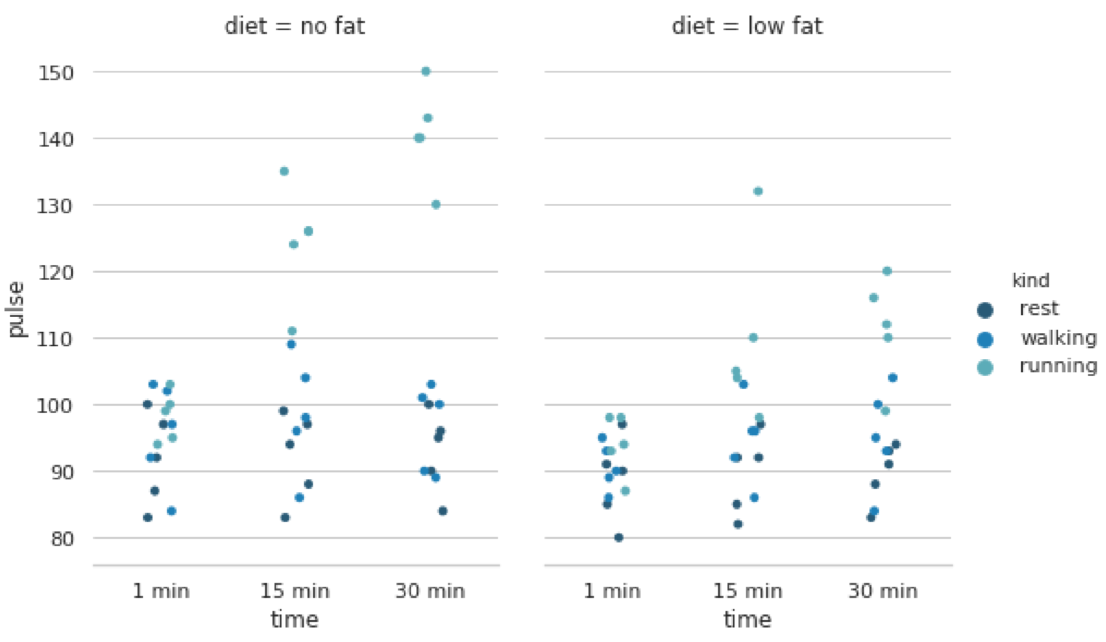
1.6.5 Nicht-parametrischer Vergleich von mehreren Gruppen

Kurskal-Wallis Test

```
In [72]: # Load stats library
         from scipy import stats

         # Create dummy data
         x = [1, 1, 1]
         y = [2, 2, 2]
         z = [2, 2]

         # Perform Kruskal-Wallis test
         stats.kruskal(x, y, z)

Out[72]: KruskalResult(statistic=7.0, pvalue=0.0301973834223185)
```

1.6.6 Vergleich von mehreren Faktoren

```
In [73]: # Two-way ANOVA

         # Load libraries
         import seaborn as sns
         import pandas as pd
         from statsmodels.formula.api import ols
         from statsmodels.stats.anova import anova_lm

         # Load data
         titanic = sns.load_dataset("titanic")
         titanic.head()

         # Determine the ANOVA with interaction
         formula = 'age ~ C(sex) + C(pclass) + C(pclass):C(sex)'
         lm = ols(formula, titanic).fit()
         anovaResults = anova_lm(lm)

         #print(anovaResults)

In [74]: # Three-way ANOVA (just visual)

         import matplotlib.pyplot as plt
         import seaborn as sns
         sns.set(style="whitegrid")
         df = sns.load_dataset("exercise")

         sns.catplot("time", "pulse", hue="kind",
                        col="diet", data=df,
                        hue_order=["rest", "walking", "running"],
                        palette="YlGnBu_d",
                        aspect=.75).despine(left=True)
         plt.show()
```



1.7 Tests an Kategorischen Daten

1.7.1 One-Way Chi-Square test

```
In [75]: import pandas as pd
         df = pd.DataFrame({"name":["You", "Peter", "Hans", "Paul"],
                            "dishes":[10, 7, 6, 5]})

         from scipy import stats
         V, p = stats.chisquare(df["dishes"])
         print(p) # 0.5724067044708798
```

```
0.5724067044708798
```

1.7.2 Chi-Quadrat-Kontingenztest

```
In [76]: data = np.array([[43,9], [44,4]])
         V, p, dof, expected = stats.chi2_contingency(data)
         print(p) # 0.300384770391
```

```
0.300384770390566
```

1.7.3 Fishers exact Test

```
In [77]: import scipy.stats as stats
         oddsratio, pvalue = stats.fisher_exact(data)
```

```
        pvalue # 0.23915695682

Out[77]: 0.23915695682224306
```

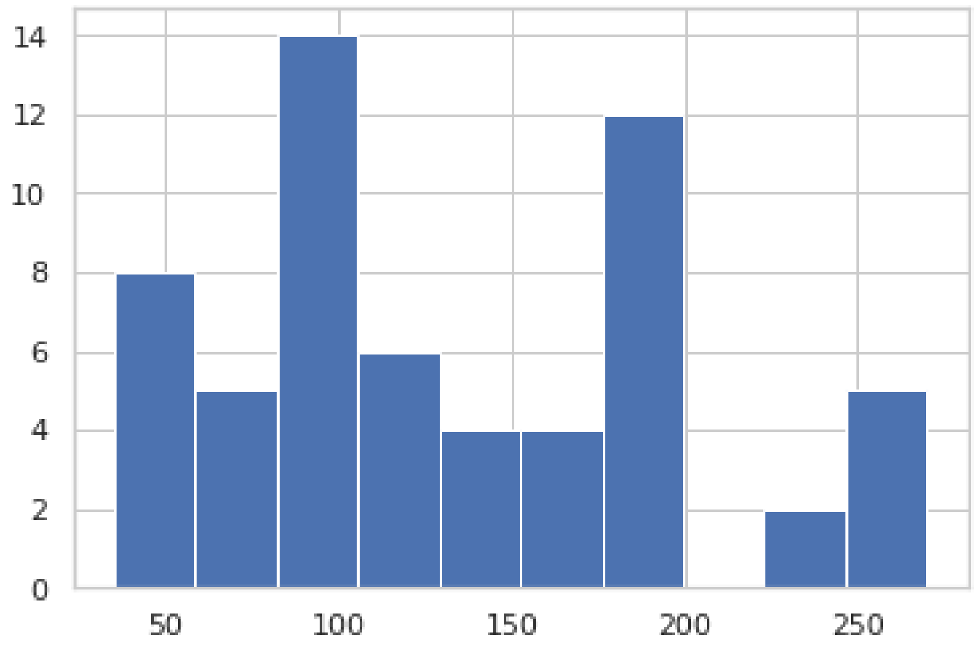
1.8 Übung II

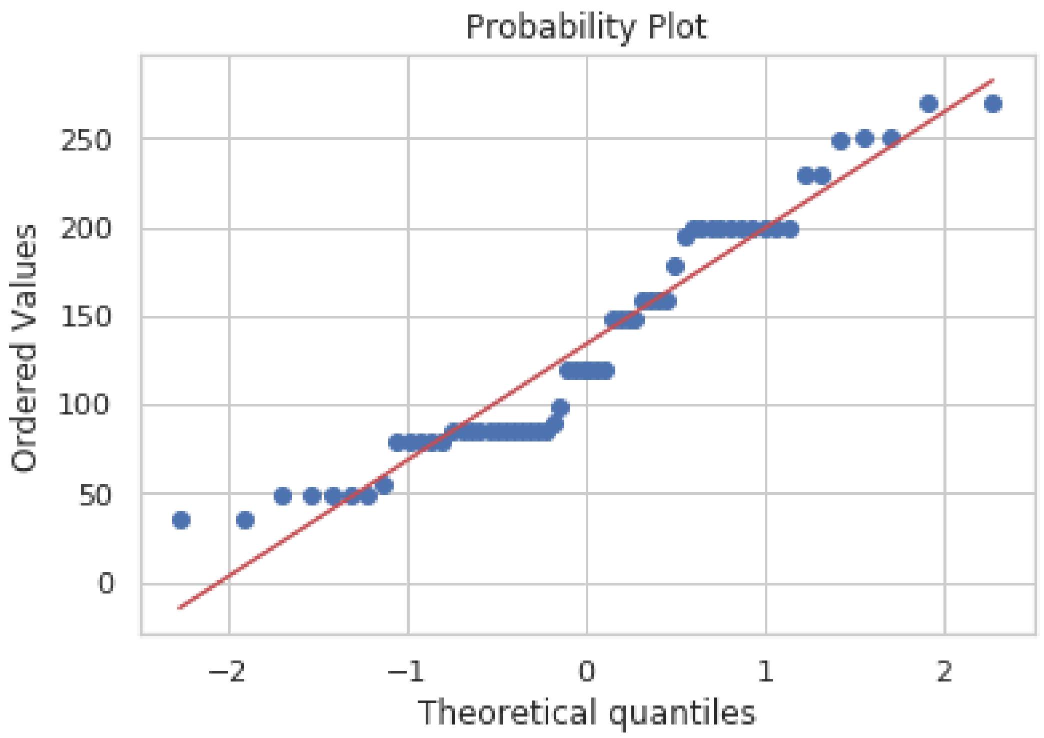
Lade den Datensatz **schoko.csv** in Python

```
In [78]: import pandas as pd

         # Load your dataset
         schoko = pd.read_csv("/home/matt/Documents/Github/pyStats/data/schoko.csv")
         schoko.head()

Out[78]:                         me      Marke Einkaufsort  Preis  Kategorie   Bio  \
         0    Choceur Weisse Crisp    Choceur        Aldi     99      weiss  nein
         1  Choceur Alpenvollmilch    Choceur        Aldi     35  vollmilch  nein
         2       Choceur Haselnuss    Choceur        Aldi     35  vollmilch  nein
         3               Nusskcker  Nusskcker        Aldi     55  vollmilch  nein
         4         Happy Halloween      Meybo     Bio Bio    199  vollmilch    ja

           Fair  crisp  nuss  traube  rum  chili  echte.vanille  cocos  Kakaogehalt  \
         0  nein      1     0       0    0      0              0      0         28.0
         1  nein      0     0       0    0      0              0      0         30.0
         2  nein      0     1       0    0      0              0      0         30.0
         3  nein      0     1       0    0      0              0      0         32.0
         4  nein      0     0       0    0      0              1      0         35.0

           Gewicht  Anzahl.der.Inhaltsstoffe  Nussanteil  Crisps  Verfallsdatum
         0      200                        15        12.0       6            5.0
         1      100                        10         0.0       0            9.0
         2      100                        10        12.0       0            9.0
         3      100                         9        25.0       0            6.0
         4      100                         6         0.0       0           15.0
```

Prüfe ob der Preis von Schokolade normalverteilt ist (visuell und statistisch)

```
In [79]: from scipy import stats
         import matplotlib.pyplot as plt

         plt.hist(schoko["Preis"])
         plt.show()

         stats.probplot(schoko["Preis"], plot=plt)
         plt.show()
```





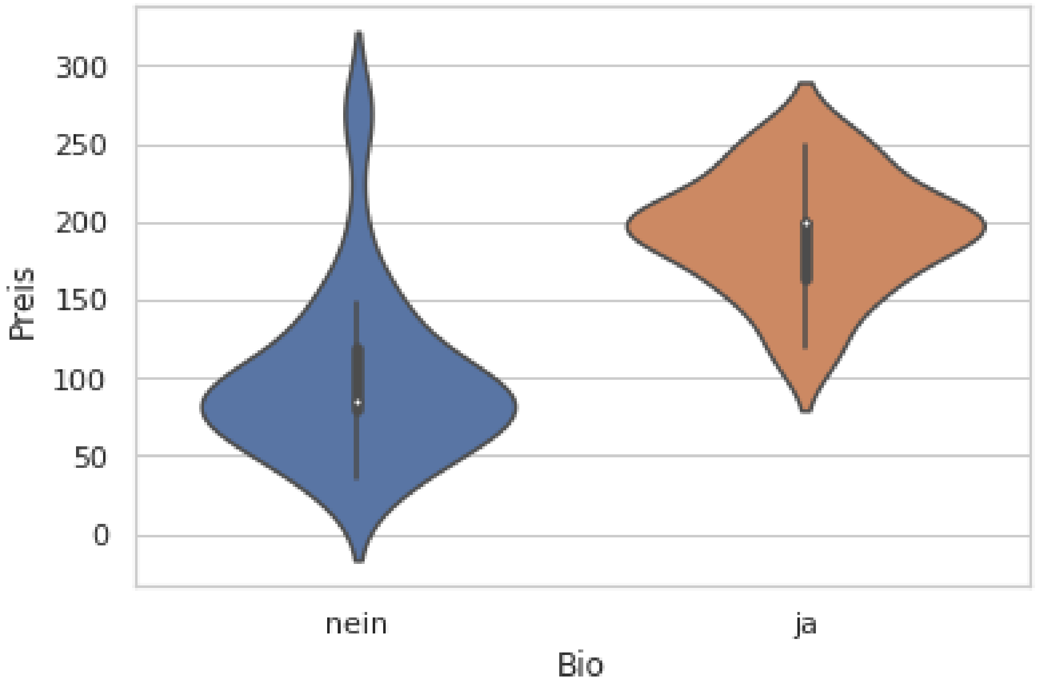
```
In [80]: # Shapiro-Wilk test
         print(stats.shapiro(schoko["Preis"]))
```

```
(0.9231991171836853, 0.0010341410525143147)
```

Prüfe ob Bio-Schokolade signifikant teurer/billiger als normale Schokolade ist

```
In [81]: # Mann-Whitney test
         import seaborn as sns

         group1 = schoko[(schoko.Bio == "ja")]
         group2 = schoko[(schoko.Bio == "nein")]

         sns.violinplot(x="Bio", y="Preis", data=schoko)

         # Calculate u and probability of a difference
         u_statistic, pVal = stats.mannwhitneyu(group1["Preis"], group2["Preis"])

         # Print p-Value
         print(pVal)
```

```
2.1262781683610106e-08
```

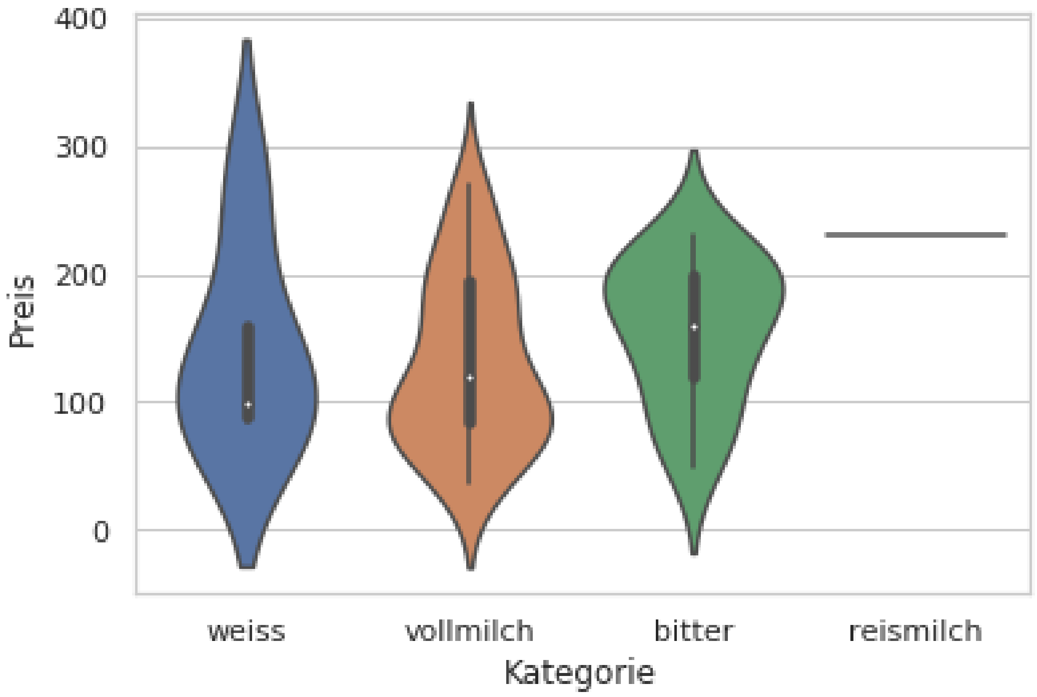


Prüfe ob der Schokoladen-Preis von der Kategorie abhängig ist

```
In [82]: # Load stats library
         from scipy import stats
```

```
        # Create dummy data
        group1 = schoko[(schoko.Kategorie == "weiss")]
        group2 = schoko[(schoko.Kategorie == "vollmilch")]
        group3 = schoko[(schoko.Kategorie == "bitter")]
        group4 = schoko[(schoko.Kategorie == "reismilch")]

        sns.violinplot(x="Kategorie", y="Preis", data=schoko)

        # Perform Kruskal-Wallis test
        stats.kruskal(group1.Preis, group2.Preis, group3.Preis, group4.Preis)
```

```
Out[82]: KruskalResult(statistic=4.0335955677598365, pvalue=0.2578591925608929)
```



Erstelle eine Kontingenztabelle mit Bio & Fair und prüft ob es möglich ist, dass die Verteilung durch Zufall zustande kam

```
In [83]: # Import library
         import pandas as pd

         # Create crosstab
         schoko_tab = pd.crosstab(schoko["Bio"], schoko["Fair"], margins=True)
         schoko_tab
```

```
Out[83]: Fair  ja  nein  All
         Bio
```

```
        ja     4    18   22
        nein   0    38   38
        All    4    56   60
```

```
In [84]: def percConvert(ser): return ser/float(ser[-1])

         pd.crosstab(schoko["Bio"], schoko["Fair"], margins=True).apply(percConvert, axis=1)
```

```
Out[84]: Fair        ja      nein  All
         Bio
         ja    0.181818  0.818182  1.0
         nein  0.000000  1.000000  1.0
         All   0.066667  0.933333  1.0
```

```
In [85]: import scipy.stats as stats
         oddsratio, pvalue = stats.fisher_exact(schoko_tab.iloc[0:2,0:2])
         pvalue
```

```
Out[85]: 0.015000974089226525
```

```
In [86]: V, p, dof, expected = stats.chi2_contingency(schoko_tab.iloc[0:2,0:2])
         print(p)
```

```
0.0289786309279283
```

Erstelle eine Kontingenztabelle mit Bio & Kategorie und prüft ob es möglich ist, dass die Verteilung durch Zufall zustande kam

```
In [87]: schoko_tab = pd.crosstab(schoko["Bio"], schoko["Kategorie"], margins=False)
         # margins=False, otherwise "All" values are included in the chi2-contingency test

         schoko_tab#.iloc[0:2,0:4]
```

```
Out[87]: Kategorie  bitter  reismilch  vollmilch  weiss
         Bio
         ja              7          1         13      1
         nein            6          0         24      4
```

```
In [88]: V, p, dof, expected = stats.chi2_contingency(schoko_tab)
         print(p)
```

```
0.290009367111933
```

```
In [89]: V, p, dof, expected = stats.chi2_contingency(schoko_tab.iloc[0:2,0:4])
         print(p)
```

```
0.290009367111933
```