

Data Standardization

July 10, 2024

The process of standardizing the data to a common format and common range

```
[4]: import numpy as np
import pandas as pd
import sklearn.datasets
from sklearn.preprocessing import StandardScaler #function that will be use to
    ↪standardize our data set
from sklearn.model_selection import train_test_split #it helps to split the
    ↪data into train and test dataset
```

```
[22]: #loading the dataset

data = pd.read_csv('breast_cancer_data.csv')
data.head()
```

```
[22]:
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave	points_mean	\
0	0.11840	0.27760	0.3001		0.14710	
1	0.08474	0.07864	0.0869		0.07017	
2	0.10960	0.15990	0.1974		0.12790	
3	0.14250	0.28390	0.2414		0.10520	
4	0.10030	0.13280	0.1980		0.10430	

	texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	17.33	184.60	2019.0	0.1622	
1	23.41	158.80	1956.0	0.1238	
2	25.53	152.50	1709.0	0.1444	
3	26.50	98.87	567.7	0.2098	
4	16.67	152.20	1575.0	0.1374	

	compactness_worst	concavity_worst	concave	points_worst	symmetry_worst	\
0	0.6656	0.7119		0.2654	0.4601	

1	0.1866	0.2416	0.1860	0.2750
2	0.4245	0.4504	0.2430	0.3613
3	0.8663	0.6869	0.2575	0.6638
4	0.2050	0.4000	0.1625	0.2364

	fractal_dimension_worst	Unnamed: 32
0	0.11890	NaN
1	0.08902	NaN
2	0.08758	NaN
3	0.17300	NaN
4	0.07678	NaN

[5 rows x 33 columns]

```
[14]: dataset = sklearn.datasets.load_breast_cancer()
```

```
[15]: print(dataset)
```

```
{'data': array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01, 4.601e-01,
1.189e-01],
[2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
8.902e-02],
[1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
8.758e-02],
...,
[1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
7.820e-02],
[2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
1.240e-01],
[7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
7.039e-02]]), 'target': array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 0, 0, 0, 0, 1, 1, 1,
0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0,
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0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 1,
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0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0,
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1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0,
0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0,
0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0,
```

```

1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 1,
1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 0,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1,
1, 0, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 0,
1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1,
1, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1]], 'frame': None,
'target_names': array(['malignant', 'benign'], dtype='<U9'), 'DESCR': '..
_breast_cancer_dataset:\n\nBreast cancer wisconsin (diagnostic)
dataset\n-----\n\n**Data Set
Characteristics:**\n\n      :Number of Instances: 569\n\n      :Number of
Attributes: 30 numeric, predictive attributes and the class\n\n      :Attribute
Information:\n          - radius (mean of distances from center to points on the
perimeter)\n          - texture (standard deviation of gray-scale values)\n
- perimeter\n          - area\n          - smoothness (local variation in radius
lengths)\n          - compactness (perimeter2 / area - 1.0)\n          - concavity
(severity of concave portions of the contour)\n          - concave points (number
of concave portions of the contour)\n          - symmetry\n          - fractal
dimension ("coastline approximation" - 1)\n\n      The mean, standard error,
and "worst" or largest (mean of the three\n      worst/largest values) of
these features were computed for each image,\n      resulting in 30 features.
For instance, field 0 is Mean Radius, field\n      10 is Radius SE, field 20
is Worst Radius.\n\n      - class:\n          - WDBC-Malignant\n
- WDBC-Benign\n\n      :Summary Statistics:\n\n
===== \n
Min      Max\n
radius
(mean):          6.981 28.11\n
texture (mean):          43.79 188.5\n
area
(mean):          143.5 2501.0\n
smoothness (mean):          0.019 0.345\n
compactness (mean):          0.053 0.163\n
concavity (mean):          0.0 0.427\n
concave points (mean):          0.106 0.304\n
symmetry (mean):          0.0 0.201\n
fractal dimension (mean):          0.05 0.097\n
radius (standard error):          0.112 2.873\n
texture (standard error):          0.36 4.885\n
perimeter (standard error):          0.757 21.98\n
area (standard error):          6.802 542.2\n
smoothness (standard error):          0.002 0.031\n
concavity (standard
error):          0.0 0.396\n
concave points (standard error):          0.0
0.053\n
symmetry (standard error):          0.008 0.079\n
fractal
dimension (standard error):          0.001 0.03\n
radius (worst):          7.93 36.04\n
texture (worst):          50.41 251.2\n
area (worst):          185.2 4254.0\n
smoothness (worst):          0.071 0.223\n
concavity (worst):          0.027 1.058\n
concave points (worst):          0.0 1.252\n
symmetry (worst):          0.156 0.664\n
fractal dimension

```

```
(worst):          0.055  0.208\n      =====
===== \n\n      :Missing Attribute Values: None\n\n      :Class Distribution:
212 - Malignant, 357 - Benign\n\n      :Creator:  Dr. William H. Wolberg, W. Nick
Street, Olvi L. Mangasarian\n\n      :Donor: Nick Street\n\n      :Date: November,
1995\n\nThis is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic)
datasets.\nhttps://goo.gl/U2Uwz2\n\nFeatures are computed from a digitized image
of a fine needle\naspirate (FNA) of a breast mass.  They
describe\ncharacteristics of the cell nuclei present in the image.\n\nSeparating
plane described above was obtained using\nMultisurface Method-Tree (MSM-T) [K.
P. Bennett, "Decision Tree\nConstruction Via Linear Programming." Proceedings of
the 4th\nMidwest Artificial Intelligence and Cognitive Science Society,\npp.
97-101, 1992], a classification method which uses linear\nprogramming to
construct a decision tree.  Relevant features\nwere selected using an exhaustive
search in the space of 1-4\nfeatures and 1-3 separating planes.\n\nThe actual
linear program used to obtain the separating plane\nin the 3-dimensional space
is that described in:\n[K. P. Bennett and O. L. Mangasarian: "Robust
Linear\nProgramming Discrimination of Two Linearly Inseparable
Sets",\nOptimization Methods and Software 1, 1992, 23-34].\n\nThis database is
also available through the UW CS ftp server:\n\nftp ftp.cs.wisc.edu\ncd math-
prog/cpo-dataset/machine-learn/WDBC/\n\n.. topic:: References\n\n      - W.N.
Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction \n      for
breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on \n
Electronic Imaging: Science and Technology, volume 1905, pages 861-870,\n
San Jose, CA, 1993.\n      - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast
cancer diagnosis and \n      prognosis via linear programming. Operations
Research, 43(4), pages 570-577, \n      July-August 1995.\n      - W.H. Wolberg,
W.N. Street, and O.L. Mangasarian. Machine learning techniques\n      to diagnose
breast cancer from fine-needle aspirates. Cancer Letters 77 (1994) \n
163-171.', 'feature_names': array(['mean radius', 'mean texture', 'mean
perimeter', 'mean area',
      'mean smoothness', 'mean compactness', 'mean concavity',
      'mean concave points', 'mean symmetry', 'mean fractal dimension',
      'radius error', 'texture error', 'perimeter error', 'area error',
      'smoothness error', 'compactness error', 'concavity error',
      'concave points error', 'symmetry error',
      'fractal dimension error', 'worst radius', 'worst texture',
      'worst perimeter', 'worst area', 'worst smoothness',
      'worst compactness', 'worst concavity', 'worst concave points',
      'worst symmetry', 'worst fractal dimension'], dtype='<U23'), 'filename':
'breast_cancer.csv', 'data_module': 'sklearn.datasets.data'}
```

Loading the dataset to our pandas dataframe

```
[17]: df = pd.DataFrame(dataset.data, columns=dataset.feature_names)
```

```
[18]: df.head()
```

```

[18]: mean radius mean texture mean perimeter mean area mean smoothness \
0      17.99      10.38      122.80      1001.0      0.11840
1      20.57      17.77      132.90      1326.0      0.08474
2      19.69      21.25      130.00      1203.0      0.10960
3      11.42      20.38       77.58       386.1      0.14250
4      20.29      14.34      135.10      1297.0      0.10030

      mean compactness mean concavity mean concave points mean symmetry \
0          0.27760          0.3001          0.14710          0.2419
1          0.07864          0.0869          0.07017          0.1812
2          0.15990          0.1974          0.12790          0.2069
3          0.28390          0.2414          0.10520          0.2597
4          0.13280          0.1980          0.10430          0.1809

      mean fractal dimension ... worst radius worst texture worst perimeter \
0          0.07871 ...          25.38          17.33          184.60
1          0.05667 ...          24.99          23.41          158.80
2          0.05999 ...          23.57          25.53          152.50
3          0.09744 ...          14.91          26.50           98.87
4          0.05883 ...          22.54          16.67          152.20

      worst area worst smoothness worst compactness worst concavity \
0          2019.0          0.1622          0.6656          0.7119
1          1956.0          0.1238          0.1866          0.2416
2          1709.0          0.1444          0.4245          0.4504
3           567.7          0.2098          0.8663          0.6869
4          1575.0          0.1374          0.2050          0.4000

      worst concave points worst symmetry worst fractal dimension
0          0.2654          0.4601          0.11890
1          0.1860          0.2750          0.08902
2          0.2430          0.3613          0.08758
3          0.2575          0.6638          0.17300
4          0.1625          0.2364          0.07678

```

[5 rows x 30 columns]

```
[19]: df.shape
```

```
[19]: (569, 30)
```

x= features which are the dataset values and analyzing the featureswe get the target. y = the target

```
[27]: x = df
      y =dataset.target
```

```
[25]: print(x)
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	\
0	17.99	10.38	122.80	1001.0	0.11840	
1	20.57	17.77	132.90	1326.0	0.08474	
2	19.69	21.25	130.00	1203.0	0.10960	
3	11.42	20.38	77.58	386.1	0.14250	
4	20.29	14.34	135.10	1297.0	0.10030	
..	
564	21.56	22.39	142.00	1479.0	0.11100	
565	20.13	28.25	131.20	1261.0	0.09780	
566	16.60	28.08	108.30	858.1	0.08455	
567	20.60	29.33	140.10	1265.0	0.11780	
568	7.76	24.54	47.92	181.0	0.05263	

	mean compactness	mean concavity	mean concave points	mean symmetry	\
0	0.27760	0.30010	0.14710	0.2419	
1	0.07864	0.08690	0.07017	0.1812	
2	0.15990	0.19740	0.12790	0.2069	
3	0.28390	0.24140	0.10520	0.2597	
4	0.13280	0.19800	0.10430	0.1809	
..	
564	0.11590	0.24390	0.13890	0.1726	
565	0.10340	0.14400	0.09791	0.1752	
566	0.10230	0.09251	0.05302	0.1590	
567	0.27700	0.35140	0.15200	0.2397	
568	0.04362	0.00000	0.00000	0.1587	

	mean fractal dimension	...	worst radius	worst texture	\
0	0.07871	...	25.380	17.33	
1	0.05667	...	24.990	23.41	
2	0.05999	...	23.570	25.53	
3	0.09744	...	14.910	26.50	
4	0.05883	...	22.540	16.67	
..	
564	0.05623	...	25.450	26.40	
565	0.05533	...	23.690	38.25	
566	0.05648	...	18.980	34.12	
567	0.07016	...	25.740	39.42	
568	0.05884	...	9.456	30.37	

	worst perimeter	worst area	worst smoothness	worst compactness	\
0	184.60	2019.0	0.16220	0.66560	
1	158.80	1956.0	0.12380	0.18660	
2	152.50	1709.0	0.14440	0.42450	
3	98.87	567.7	0.20980	0.86630	
4	152.20	1575.0	0.13740	0.20500	
..	
564	166.10	2027.0	0.14100	0.21130	
565	155.00	1731.0	0.11660	0.19220	

	worst concavity	worst concave	points	worst symmetry	\
0	0.7119		0.2654	0.4601	
1	0.2416		0.1860	0.2750	
2	0.4504		0.2430	0.3613	
3	0.6869		0.2575	0.6638	
4	0.4000		0.1625	0.2364	
..	
564	0.4107		0.2216	0.2060	
565	0.3215		0.1628	0.2572	
566	0.3403		0.1418	0.2218	
567	0.9387		0.2650	0.4087	
568	0.0000		0.0000	0.2871	

```
[569 rows x 30 columns]
```

[illegible]

```
1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1 1 1 1 1 1 0 0 0 0 0 0 1]
```

Splitting the data into training data and testing data before standardizing. And train test split function was imported already and the function is used below. test_size is how much data we want in our test size, usually 10-20% for test data random state is to reproduce the code = 3 depending on what you want. Is an identity for splitting the data in a specific way.

In most cases it is better to standardize the data before splitting it.

```
[32]: x_train, x_test, y_train, y_test = train_test_split(x, y, test_size =0.2,
↳random_state=3)
```

```
[33]: print(x.shape, x_train.shape, x_test.shape)
```

```
(569, 30) (455, 30) (114, 30)
```

Data Standardization; to do this I print the standard deviation of the whole dataset by calling the data 'dataset' because it contains all the data. The data I will call is from 'dataset = sklearn.datasets.load_breast_cancer()'

And find the standard deviation.

If our data contains all the value in the same range the standard deviation should be 1.

And my dataset below is 228.29 so the dataset are not in the same range and they varies alot

```
[35]: print(dataset.data.std())
```

```
228.29740508276657
```

Using StandardScaler since it was imported already

```
[37]: scaler = StandardScaler()
```

```
[38]: scaler.fit(x_train)
```

```
[38]: StandardScaler()
```

```
[39]: x_train_standardized = scaler.transform(x_train)
```

```
[40]: print(x_train_standardized)
```

```
[[ 1.40381088  1.79283426  1.37960065 ...  1.044121    0.52295995
  0.64990763]
 [ 1.16565505 -0.14461158  1.07121375 ...  0.5940779   0.44153782
 -0.85281516]
 [-0.0307278  -0.77271123 -0.09822185 ... -0.64047556 -0.31161687
 -0.69292805]
 ...
 [ 1.06478904  0.20084323  0.89267396 ...  0.01694621  3.06583565
 -1.29952679]
 [ 1.51308238  2.3170559   1.67987211 ...  1.14728703 -0.16599653
```



```
0.82816016]
[-0.73678981 -1.02636686 -0.74380549 ... -0.31826862 -0.40713129
-0.38233653]]
```

For x test

```
[41]: x_test_standardized = scaler.transform(x_test)
```

Now looking at the standard deviation of our x_train data it shows that our std is 1 And for x test is 0.87 and it is close to 1 This means that the data are in similar range

```
[42]: print(x_train_standardized.std())
```

```
1.0
```

```
[43]: print(x_test_standardized.std())
```

```
0.8654541077212674
```

```
[ ]:
```

```
[ ]:
```

```
[ ]:
```

```
[ ]:
```

```
[ ]:
```