EPL448: Data Mining on the Web – Lab 6

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Γραφείο: B109, ΘΕΕ01

Prepare data for machine learning

- Data preparation is the process of gathering, combining, structuring and organizing data so it can be used in Exploratory Data Analysis (statistical analysis and visualization) and Predictive Modelling
  - **Gather/combine data**: Finding the right data. This can come from databases, files (.csv, .json, .txt, .xml) or Rest APIs (web-based apps).
  - **Preprocess data**: Organize your selected data by formatting, cleaning, encoding and (re-)sampling.
    - Cleaning data is the fixing/deleting/filling in missing data
    - Encoding is the conversion of labeled/categorical data into numerical data
    - Resampling is about changing the frequency of observations
  - **Transform data**: Transform preprocessed data by engineering features using scaling, unskewing, feature selection and feature extraction (next lab) for achieving better performance of predictive modelling methods
    - Scaling is the process of rescaling or standardizing or normalizing features
    - Unskewing is making features' distribution symmetrical

Cleaning data

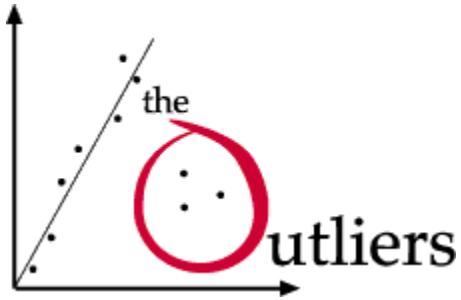
- Fixing up formats
  - Often when data is coming from various international sources may (a) involve mixed formats, and/or (b) not follow the expected numeric syntax
    - decimal separator is dot (need to be replaced if comma)
    - there is no thousands separator (need to be removed if any)
    - monetary symbols before or after numbers (need to be removed if any)
  - Data may not follow the default (expected by Python plots or functions) formats
    - e.g. dates as integers 20090609231247 instead of the expected format 2009-06-09 23:12:47 (ISO 8601 format) need to be transformed

Cleaning data

- Deleting missing values
  - may delete rows if the number of these rows is relatively small compared to the dataset
    - e.g. do not account for more than 10% of all lines
  - may delete rows if rows to be deleted are not important
    - e.g. do not contain info about a specific category in dataset
      - missing ages in some rows may correspond to older and more privacy or conscious users and are important in the decision-making process, so cannot be removed
  - action can be performed with Pandas dropna(), see next slides

Cleaning data

- Filling in missing values
  - For categorical data (e.g. device type, countries) makes sense to create a new category ‘unknown’
  - For numerical values (e.g. age) makes sense to use:
    - Statistical aggregations such as mean or median of either (a) all rows of the column or (b) take into account rows belonging to the same category of that of the missing value
    - Interpolation: applied on time-series data, see slides about sampling
  - Build a predictors to predict a missing value based on columns that do have data
- Correcting erroneous values
  - For some columns, some values can be identified as obviously incorrect
    - E.g. find a number in a gender column
    - an age column with values below 0 or well over 100 (**outliers**)



Cleaning data

- Standardizing categories
  - When data collected directly from users, especially from text fields → spelling mistakes, language differences → a given answer may be provided in multiple ways
    - E.g. country: USA, United States, U.S
    - E.g. dates: 1982-10-01, 1/10/1982
  - Goal: standardize values to ensure that there is only one version of each value

Missing values manipulation

- Missing values are marked as NaN

In [ ]:
```
# Read a dataset with missing values (download zipped dataset from here)
nfl_data = pd.read_csv('NFL Play by Play 2009-2016 (v3).csv', dtype='unicode')
nfl_data.head()
```

Out[ ]:

	Date	GameID	...	yacWPA	Season
0	2009-09-10	2009091000	...	**NaN**	2009
1	2009-09-10	2009091000	...	0.0368989644153847 6	2009
2	2009-09-10	2009091000	...	**NaN**	2009
3	2009-09-10	2009091000	...	-0.156238531986491 3	2009
4	2009-09-10	2009091000	...	**NaN**	2009

In [ ]:
```
nfl_data.isnull().head()
```

Out[ ]:

	Date	GameID	Drive	qtr	down	...	Win_Prob	WPA	airWPA	yacWPA	Season
0	False	False	False	False	True	...	False	False	True	**True**	False
1	False	False	False	False	False	...	False	False	False	False	False
2	False	False	False	False	False	...	False	False	True	**True**	False
3	False	False	False	False	False	...	False	False	False	False	False
4	False	False	False	False	False	...	False	False	True	**True**	False

Missing values manipulation

- There is a number of methods to deal with missing values in the data frame:

df.method()	description
dropna()	**Drop observations (rows) with at least one missing value**
dropna(how='all')	Drop observations (rows) where all cells is NA
dropna(axis=1)	**Drop the columns where at least one value is missing**
dropna(thresh = 5)	Drop rows that contain less than 5 non-missing values
fillna(0)	**Replace missing values with a specified value**
isnull()	returns True if the value is missing
notnull()	Returns True for non-missing values

Missing values manipulation

In [ ]:
```
# get the number of missing data points per column; sum True values
missing_values_count = nfl_data.isnull().sum()

# look at the # of missing points in the first ten columns
missing_values_count[0:10]
```

Out[ ]:
```
Date                0
GameID              0
Drive               0
qtr                 0
down            54218
time              188
TimeUnder           0
TimeSecs          188
PlayTimeDiff      374
SideofField       450
dtype: int64
```

Drop rows with missing values

```
In [ ]: # remove all the rows that contain a missing value
        nfl_data.dropna()
```

Out[ ]:

Date	GameID	Drive	qtr	down	time	TimeUnder	TimeSecs	PlayTimeDiff	SideofField	...	yacl

0 rows × 102 columns

It looks like that's removed all our data! This is because every row in our dataset had at least one missing value.

Drop columns with missing values

In [ ]:
```
# remove all columns with at least one missing value
columns_cleaned = nfl_data.dropna(axis=1)
columns_cleaned.head()
```

Out[ ]:

	Date	GameID	Drive	...	ExPoint_Prob	TwoPoint_Prob	Season
0	2009-09-10	2009091000	1	...	0	0	2009
1	2009-09-10	2009091000	1	...	0	0	2009
2	2009-09-10	2009091000	1	...	0	0	2009
3	2009-09-10	2009091000	1	...	0	0	2009
4	2009-09-10	2009091000	1	...	0	0	2009

[5 rows x 41 columns]

In [ ]:
```
# just how much data did we lose?
print("Columns in original dataset: %d" % nfl_data.shape[1])
print("Columns with na's dropped: %d" % columns_cleaned.shape[1])
```

Out[ ]:
```
Columns in original dataset: 102
Columns with na's dropped: 41
```

Fill in missing values

- One option we have is to specify what we want the NaN values to be replaced with

```
In [ ]: # replace all NA's with 0
        nfl_data.fillna(0)
```

- Another option is to replace missing values with whatever value comes directly after it in the same column
  - This makes a lot of sense for datasets where the observations have some sort of logical order to them

```
In [ ]: # replace all NA's the value that comes directly after it in the same
        column, then replace all the remaining na's with 0
        nfl_data.fillna(method = 'bfill', axis=0).fillna(0)
```

Fill in missing values with imputation

- Imputation fills in the missing value with some number
- Imputed value won't be exactly right in most cases, but it usually gives more accurate models than dropping the column entirely

```
In [ ]: # Using Sklearn's simple imputer
from sklearn.impute import SimpleImputer
import numpy as np
my_imputer = SimpleImputer(missing_values=np.NaN, strategy='mean')
nfl_data['yacWPA'] = my_imputer.fit_transform(nfl_data[['yacWPA']])
```

  - SimpleImputer takes two arguments such as missing_values and strategy
    - Strategy can be set to mean, median, most_frequent, constant (with fill_value argument)
      - Numerical missing values: mean, median, most frequent, constant
      - Categorical missing values: most frequent, constant
  - fit_transform method is invoked on the instance of SimpleImputer to impute the missing values

Fill in missing values with imputation

- Strategy = mean

	Date	GameID	...	yacWPA	Season
0	2009-09-10	2009091000	...	**NaN**	2009
1	2009-09-10	2009091000	...	0.0368989644153847 6	2009
2	2009-09-10	2009091000	...	**NaN**	2009
3	2009-09-10	2009091000	...	-0.156238531986491 3	2009
4	2009-09-10	2009091000	...	**NaN**	2009

Before imputation

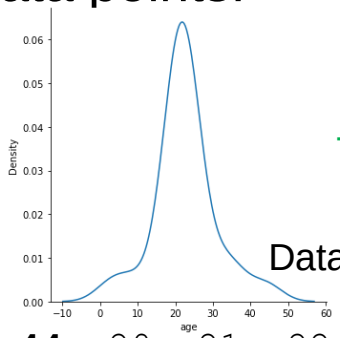
`nfl_data.head()`

	Date	GameID	...	yacWPA	Season
0	2009-09-10	2009091000	...	**-0.010492**	2009
1	2009-09-10	2009091000	...	0.0368989644153847 6	2009
2	2009-09-10	2009091000	...	**-0.010492**	2009
3	2009-09-10	2009091000	...	-0.156238531986491 3	2009
4	2009-09-10	2009091000	...	**-0.010492**	2009

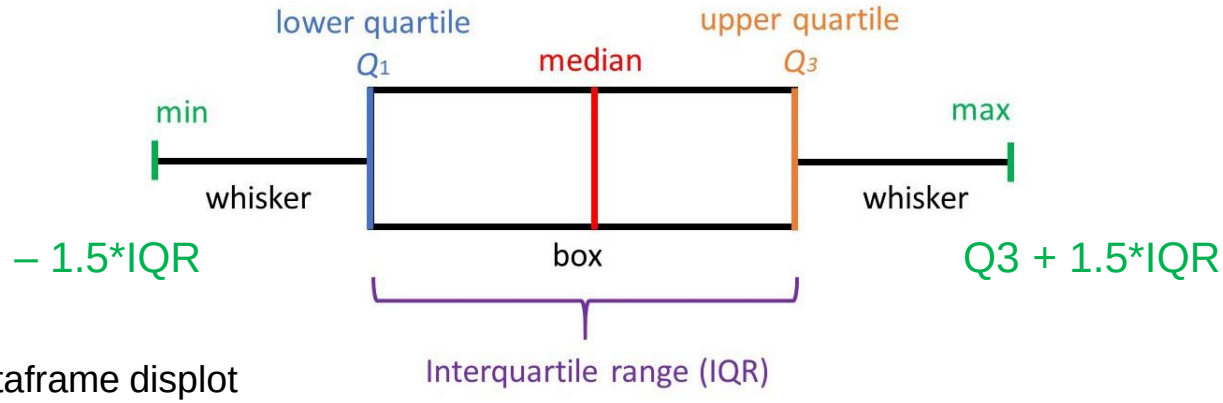
After imputation

Removing outliers

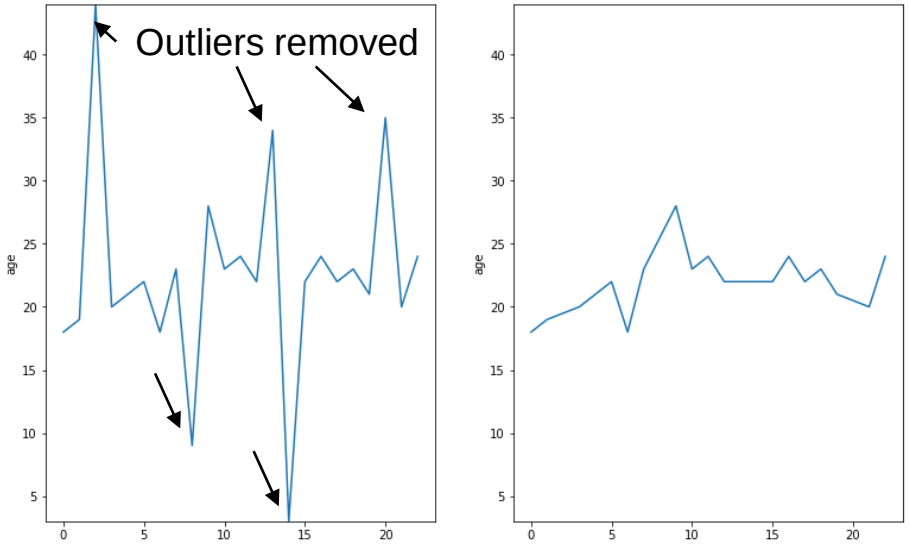
- Methods for removing outliers on each feature independently:
  - Interquartile Range (IQR) method
    - Outliers are considered data points:
      - below Q1 – 1.5*IQR
      - above Q3 + 1.5*IQR



Dataframe displot




```
import seaborn as sns
import matplotlib.pyplot as plt
df2 = pd.DataFrame({'age': [18, 19, 44, 20, 21, 22, 18, 23, 9, 28, 23, 24, 22, 34, 3, 22, 24, 22, 23,
21, 35, 20, 24]})
plt.subplot(1,2,1)
sns.lineplot(data=df2, y=df2['age'], x=df2.index)
plt.ylim([df2['age'].min(), df2['age'].max()])
Q1 = df2['age'].quantile(0.25)
Q3 = df2['age'].quantile(0.75)
IQR = Q3-Q1
maximum = Q3 + 1.5*IQR
minimum = Q1 - 1.5*IQR
df3 = df2[ (df2['age'] > minimum) & (df2['age'] < maximum) ]
plt.subplot(1,2,2)
sns.lineplot(data=df3, y=df3['age'], x=df3.index)
plt.ylim([df2['age'].min(), df2['age'].max()])
```

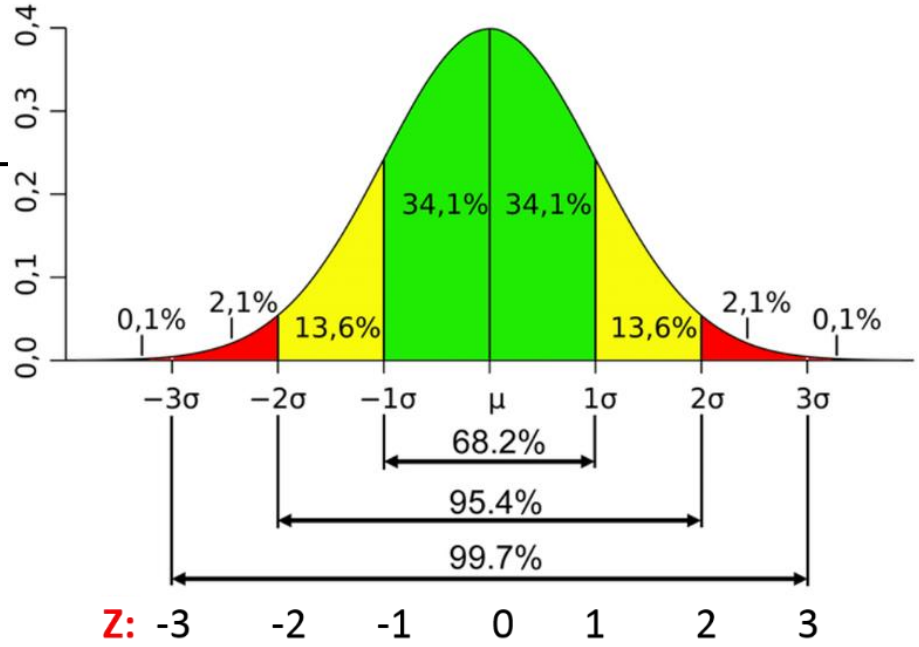


Initial dataframe

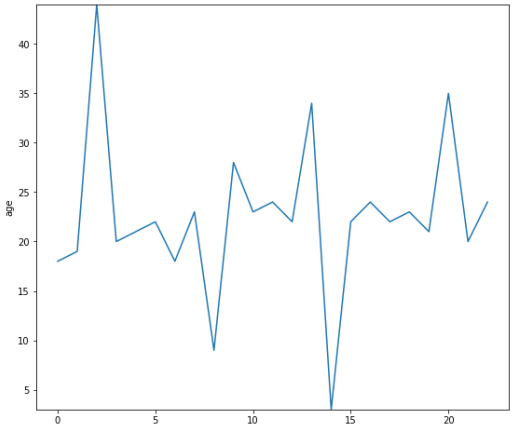
After outlier removal

Removing outliers

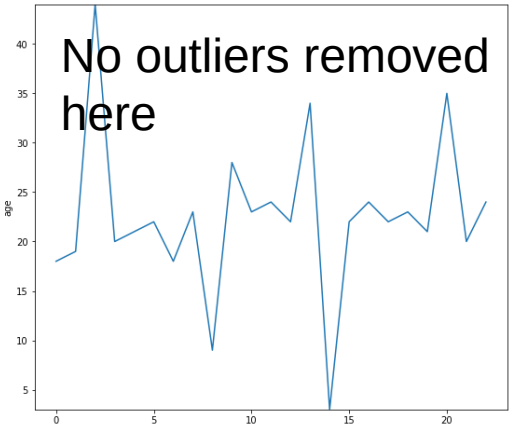
- Mean (μ) and Standard Deviation (σ) method
  - **For features that follow the normal distribution**
  - Outliers are considered data points:
    - below μ – 3*σ
    - above μ + 3*σ




```
mean = df2['age'].mean()
std = df2['age'].std()
maximum = mean + 3*std
minimum = mean - 3*std
df4 = df2[ (df2['age'] > minimum) & (df2['age'] < maximum) ]
plt.subplot(1,2,2)
sns.lineplot(data=df4, y=df4['age'], x=df4.index)
plt.ylim([df2['age'].min(), df2['age'].max()])
```



Initial dataframe



After outlier removal

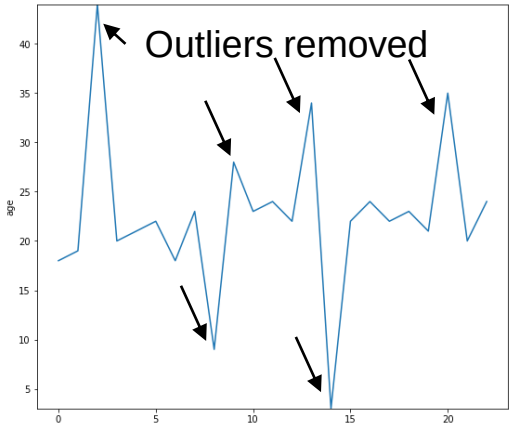
Removing outliers

- Median and Median Absolute Deviation (mad) method
  - Replaces the mean and standard deviation with more robust statistics such as the median and median absolute deviation
  - Outliers are considered data points:
    - below median – 3*mad
    - above median + 3*mad

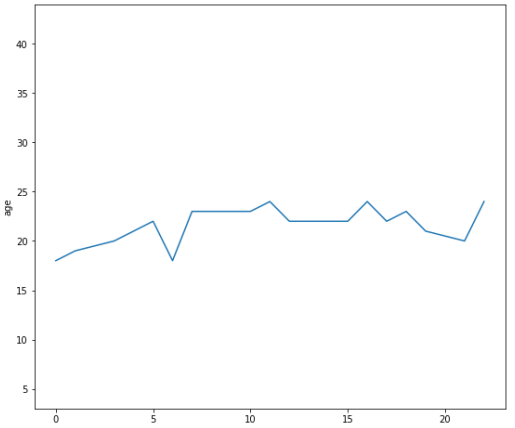
$$MAD = Median(|X_i - median|)$$

Step 1: Find the median.
Step 2: Subtract the median from each x-value using the formula $|x_i - median|$.
Step 3: find the median of the absolute differences.

```
import scipy as sp
median = df2['age'].median()
mad = sp.stats.median_abs_deviation(df2['age'])
maximum = median + 3*mad
minimum = median - 3*mad
df4 = df2[ (df2['age'] > minimum) & (df2['age'] < maximum) ]
plt.subplot(1,2,2)
sns.lineplot(data=df4, y=df4['age'], x=df4.index)
plt.ylim([df2['age'].min(), df2['age'].max()])
```



Initial dataframe



After outlier removal

Mean/std vs Median/mad

- Mean and std are highly affected by outliers
  - All values (including outliers) are used to calculate the mean and std
- Median and MAD are not highly affected by outliers
  - Outlier changes only center value(s) which are used to calculate the median
- Example:
  - dataset: {2,3,5,6,9}
    - mean = 5, std = 2.738, median = 5, mad = 2
  - Add outlier value 1000 to dataset
  - dataset: {2, 3, 5, 6, 9, 1000}
    - mean = 170.83, std = 406.21, median = (5+6)/2 = 5.5, mad = 3
  - The outlier
    - increases mean by 165.83 and std by 403.472
    - increases median by 0.5 and mad by 1

Encoding categorical data

- Machine learning models require all input and output variables to be numerical
- Categorical data must be encoded to numbers
- Popular techniques:
  - Label Encoding or Ordinal Encoding
  - One-Hot Encoding
  - Dummy Variable Encoding
  - Effect Encoding
  - Bin counting
  - Feature Hashing
- Scikit-learn lib involves a few encoders but category_encoders lib has more with useful properties

```
conda install -c conda-forge category_encoders
```

(website: http://contrib.scikit-learn.org/category_encoders)

Label or Ordinal Encoding

- We use this categorical data encoding technique **when the categorical feature is ordinal** (with natural, ordered values)
- In this case, **retaining the order is important**.
- Encoding should reflect the sequence
- Therefore, each label (or category value) is converted into an integer value

	Degree
0	High school
1	Masters
2	Diploma
3	Bachelors
4	Bachelors
5	Masters
6	Phd
7	High school
8	High school

```
Natural order:
'High school':1
'Diploma':2
'Bachelors':3
'Masters':4
'Phd':5
```

Label or Ordinal Encoding

```
import category_encoders as ce
import pandas as pd
df=pd.DataFrame(
{'Degree':['High school', 'Masters', 'Diploma',
'Bachelors', 'Bachelors', 'Masters', 'Phd', 'High
school', 'High school']})

#Original data
df
```

	Degree
0	High school
1	Masters
2	Diploma
3	Bachelors
4	Bachelors
5	Masters
6	Phd
7	High school
8	High school

```
# create object of Ordinal encoding
ordinal_encoder= ce.OrdinalEncoder(return_df=True,
mapping=[{'col':'Degree','mapping':{'None':0,'High
school':1,'Diploma':2,'Bachelors':3,'Masters':4,
'Phd':5}}])

#fit and transform data
df['Ordinal'] =
ordinal_encoder.fit_transform(df['Degree'])
df
```

	Degree	Ordinal
0	High school	1
1	Masters	4
2	Diploma	2
3	Bachelors	3
4	Bachelors	3
5	Masters	4
6	Phd	5
7	High school	1
8	High school	1

Note: labels with high ordinal values possess higher “weight” and may be considered of higher importance

Note: If no mapping is given, order is automatically chosen by the encoder

One-Hot Encoding

- We use this categorical data encoding technique when the features are nominal (do not have any order)
- For each label of a categorical feature, we create a new feature
- Each label is mapped with a binary feature containing either 0 or 1
  - 0 represents the absence, and 1 represents the presence of that category value
- These newly created binary features are known as Dummy variables
- The number of dummy variables depends on the labels (categories) present in the categorical variable

One-Hot Encoding

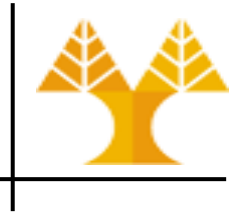
```
# Create object for One-hot encoding
onehot_encoder=ce.OneHotEncoder(cols=['Degree'],handle_unknown='return_nan', return_df=True,
use_cat_names=True)
#fit and transform data
df_onehot = onehot_encoder.fit_transform(df)
df_onehot
```

Dummy variables

	Degree	Ordinal
0	High school	1
1	Masters	4
2	Diploma	2
3	Bachelors	3
4	Bachelors	3
5	Masters	4
6	Phd	5
7	High school	1
8	High school	1

	Degree_High school	Degree_Masters	Degree_Diploma	Degree_Bachelors	Degree_Phd	Ordinal
0	1.0	0.0	0.0	0.0	0.0	1
1	0.0	1.0	0.0	0.0	0.0	4
2	0.0	0.0	1.0	0.0	0.0	2
3	0.0	0.0	0.0	1.0	0.0	3
4	0.0	0.0	0.0	1.0	0.0	3
5	0.0	1.0	0.0	0.0	0.0	4
6	0.0	0.0	0.0	0.0	1.0	5
7	1.0	0.0	0.0	0.0	0.0	1
8	1.0	0.0	0.0	0.0	0.0	1

Dummy Variable Encoding



- The one-hot encoding creates one binary feature for each category
  ➔ this representation includes redundancy
  - For example, if we know that [1, 0, 0] represents “blue” and [0, 1, 0] represents “green” we don’t need another binary variable to represent “red“, instead we could use 0 values for both “blue” and “green” alone, e.g. [0, 0] to represent “red”.

- This is called a dummy variable encoding, and always represents N labels (categories) with N-1 binary variables.

Dummy Variable Encoding

```
df_dummy = pd.get_dummies(df, drop_first=True)
df_dummy
```

	Degree	Ordinal
0	High school	1
1	Masters	4
2	Diploma	2
3	Bachelors	3
4	Bachelors	3
5	Masters	4
6	Phd	5
7	High school	1
8	High school	1

Dummy variables

	Ordinal	Degree_Diploma	Degree_High school	Degree_Masters	Degree_Phd
0	1	0	1	0	0
1	4	0	0	1	0
2	2	1	0	0	0
3	3	0	0	0	0
4	3	0	0	0	0
5	4	0	0	1	0
6	5	0	0	0	1
7	1	0	1	0	0
8	1	0	1	0	0

Drawbacks of One-Hot & Dummy Encoding

- If there are multiple labels (categories) in a feature ➔ we need a similar number of dummy variables to encode the data
  - For example, a feature with 30 different values will require 29-30 new dummy variables for coding
- If there are multiple categorical features in the dataset we will end with a high number of binary features
- Due to the massive increase in the dataset, coding slows down the learning of the model along with deteriorating the overall performance that ultimately makes the model computationally expensive.

Cyclical feature encoding

- When dealing with time-dependent data (e.g. months, days, hours) it's important to encode the properties of time properly
  - For example, if you're building a model to predict road traffic, the time of day is an important factor
  - One approach might be to encode the time of day as a number between zero and one, where midnight is zero and 11:59 PM is 1. Unfortunately, that distorts the proximity of 11:59 PM and midnight
  - A better way is to represent time of day as a point on the unit circle, using sine and cosine transformation

	datetime	temperature	hour
9	2012-10-01 21:00:00	12.776627	21
10	2012-10-01 22:00:00	12.789767	22
11	2012-10-01 23:00:00	12.802906	23
12	2012-10-02 00:00:00	12.816046	0
13	2012-10-02 01:00:00	12.829185	1

```
data['hour_sin'] = np.sin(2 * np.pi * data['hour']/23.0)
data['hour_cos'] = np.cos(2 * np.pi * data['hour']/23.0)
```

	datetime	temperature	hour	hour_sin	hour_cos
10	2012-10-01 22:00:00	12.789767	22	-2.697968e-01	0.962917
11	2012-10-01 23:00:00	12.802906	23	-2.449294e-16	1.000000
12	2012-10-02 00:00:00	12.816046	0	0.000000e+00	1.000000
13	2012-10-02 01:00:00	12.829185	1	2.697968e-01	0.962917

– 11 PM is close to 12 midnight in terms of sin and cos

Data Transformation: Scaling data

- Feature rescaling
  - Majority of clustering / classification algorithms use the notion of distance (e.g. Euclidean) between 2 points
  - Example
    - Classify houses with 2 features
    - $x_1 = size\ (0 - 2000m^2)$
    - $x_2 = number\ of\ bedrooms\ (1 - 5)$
    - $Euclidean\ distance(X_1, X_2) = \sqrt{(523 - 127)^2 + (4 - 2)^2}$
    - Distance is governed by features having boarder range of values

$$X = \begin{bmatrix} 523 & 4 \\ 127 & 2 \\ 25 & 1 \end{bmatrix}$$

Feature x1 with high magnitudes weights a lot more in the distance calculations than feature x2 with low magnitudes

  - When distance is used by algorithms **make sure features are on a similar scale**
  - Target value (to be predicted) is not necessary to be scaled

Data Transformation: Scaling data

- Feature rescaling
  - Some examples of algorithms where feature scaling matters are:
    - k-nearest neighbors using Euclidean distance – classification algorithm
    - k-means using Euclidean distance – clustering algorithm
    - logistic regression, SVMs, perceptrons, neural networks etc.
      - if you are using gradient descent/ascent-based optimization, otherwise some weights will update much faster than others
    - linear discriminant analysis (LDA), principal component analysis (PCA)
      - you want to find directions of maximizing the variance (under the constraints that those directions/eigenvectors/principal components are orthogonal)

Data Transformation: Scaling data

- Feature rescaling
  - Rescale **each feature** individually into a given range, e.g. [0, 1]

$$x = \begin{bmatrix} 4 & 13 \\ 3 & 2 \\ 7 & 8 \end{bmatrix}, x_{i,j,resc} = \frac{x_{i,j} - min(x_j)}{\max(x_j) - \min(x_j)} \Rightarrow x_{resc} = \begin{bmatrix} 0.25 & 1 \\ 0 & 0 \\ 1 & 0.55 \end{bmatrix}$$

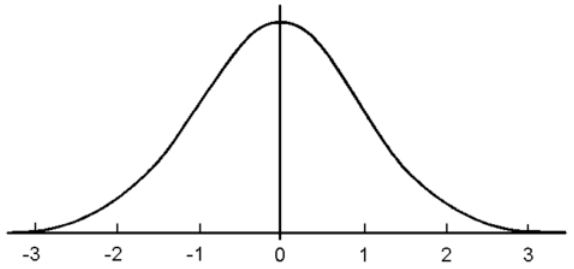
  - Scikit-learn module: MinMaxScaler or MaxAbsScaler
    - MinMaxScaler: Transforms features by scaling each feature to a given range (x_{min} → x_{max}).

```
from sklearn.preprocessing import MinMaxScaler
df = pd.DataFrame({'A': [4, 3, 7], 'B': [13, 2, 8] })
# create the scaler object
scaler = MinMaxScaler(feature_range=(0, 1))
# train the scaler (find min and max)
scaler.fit(df)
# scale the dataset (apply the transformation)
minMaxRescaledX = scaler.transform(df)
print(minMaxRescaledX)
```

```
minMaxRescaledX =
scaler.fit_transform(df)
```

http://scikit-learn.org/stable/modules/classes.html#module-sklearn.preprocessing

Data Transformation: Scaling



- Feature standardization
  - Rescale **each feature** individually to make values have zero mean ($\mu = 0$) and unit variance ($\sigma^2 = 1$)

$$x = \begin{bmatrix} 4 & 13 \\ 3 & 2 \\ 7 & 8 \end{bmatrix}, x_{i,j,std} = \frac{x_{i,j} - mean(x_j)}{\sigma} \Rightarrow x_{std} = \begin{bmatrix} -0.39 & 1.86 \\ -0.98 & -1.226 \\ 1.37 & 0.07 \end{bmatrix}$$

  - Center data around zero
    - Not recommended for sparse data: destroys sparseness
  - Useful for algorithms such as the SVM (RBF kernel)
  - Scikit-learn module: StandardScaler

```
from sklearn.preprocessing import StandardScaler
df = pd.DataFrame({'A': [4, 3, 7], 'B': [13, 2, 8] })
scaler = StandardScaler()
# train the standardizer (find mean, std) and standardize the dataset
standardRescaledX = scaler.fit_transform(df)
print(standardRescaledX)
```

Data Transformation: Scaling data

- Feature standardization
  - When data contains outliers, Standard Scaler can be often mislead since mean value and variance can be influenced by outliers – MinMaxScaler is sensitive to the presence of outliers as well
  - Rescale **each feature** individually using the median (Q2) and the interquartile range (Q3-Q1)
  - Scikit-learn module: RobustScaler

```
from sklearn.preprocessing import RobustScaler
df = pd.DataFrame({'A': [4, 3, 7], 'B': [13, 2, 8] })
rscaler = RobustScaler().fit(df)
# train the standardizer (find median, quantiles) and standardize the dataset
robustRescaledX = rscaler.fit_transform(df)
print(robustRescaledX)
```

Compare the effect of different scalers on data with outliers

Data Transformation: Scaling data

- Normalize observations
  - Normalize each observation (row) independently of other rows so that its norm (l1 or l2) equals 1

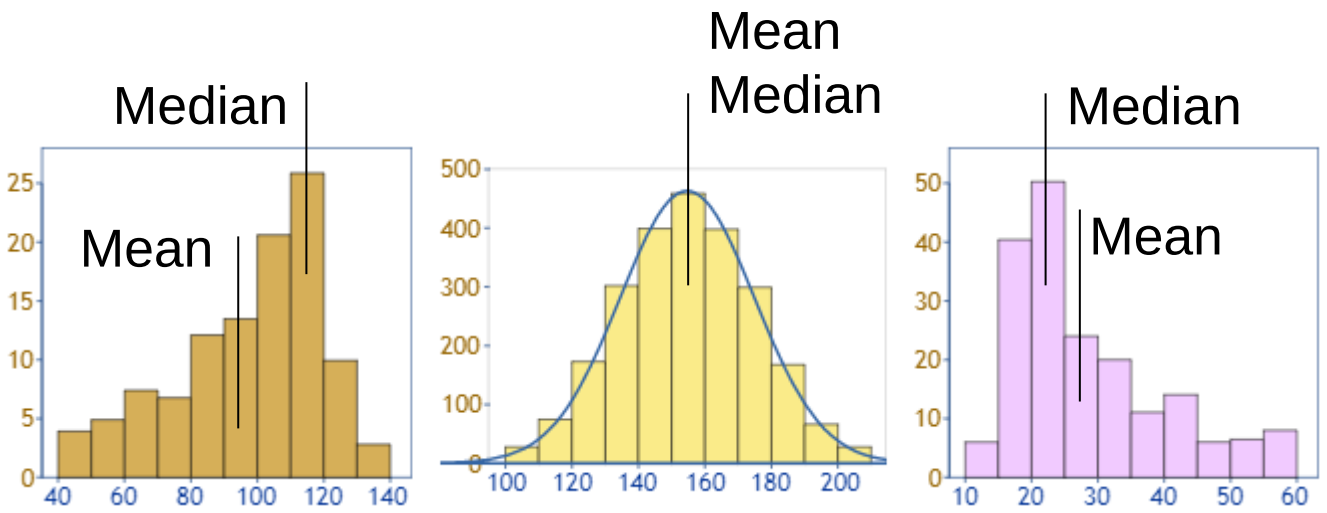
$$x = \begin{bmatrix} 4 & 13 \\ 3 & 2 \\ 7 & 8 \end{bmatrix}, x_{i,j,norm} = \frac{x_{i,j}}{\sqrt{\sum_{k=0}^{n} x_{i,k}^2}} \Rightarrow x_{norm} = \begin{bmatrix} 0.29 & 0.96 \\ 0.83 & 0.55 \\ 0.66 & 0.75 \end{bmatrix}$$

$$\sqrt{0.29^2 + 0.96^2} = 1$$

  - Useful for sparse datasets (lots of zeros)
  - Common operation for text classification or clustering
    - dot product of two l2-normalized TF-IDF vectors is the cosine similarity of the vectors and is the base similarity metric for the Vector Space Model
  - Scikit-learn module: Normalizer

Data Transformation: Unskewing data

- Data is skewed when its distribution curve is asymmetrical as compared to a normal distribution curve that is perfectly symmetrical
- *Skewness* is the measure of the asymmetry
  - The skewness for a gaussian or normal distribution is 0



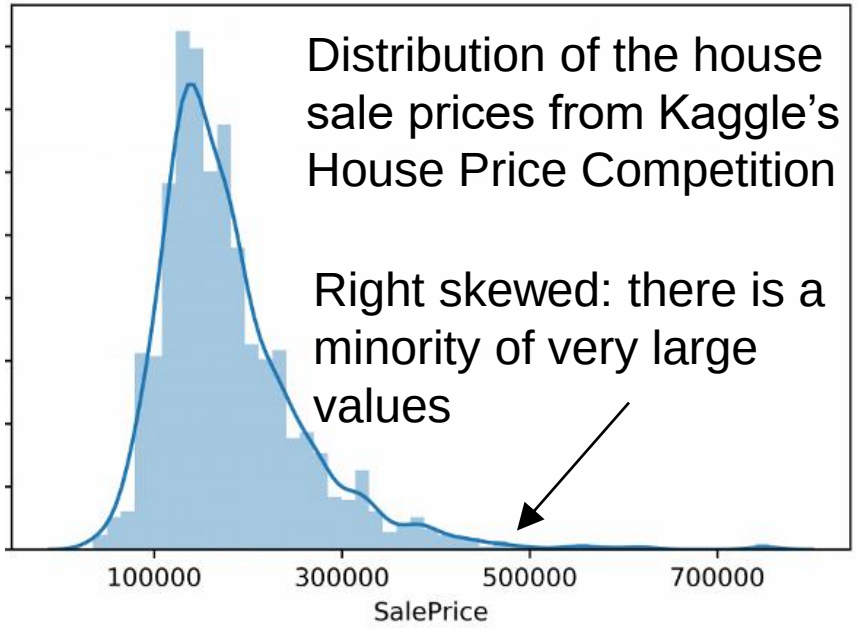
Left / **negative** skew: Long tail is on the left / negative side of the peak

No skew (symmetrical distribution)

Right / **positive** skew: Long tail is on the right / positive side of the peak

Effects of skewed data

- Skewness degrades the predictive model's ability (especially regression models) to predict values towards the long tail side



- A regression model for predicting the house sale price will be trained on a much larger number of moderately priced houses and will be less likely to successfully predict the price for the most expensive houses

Unskewing transformations

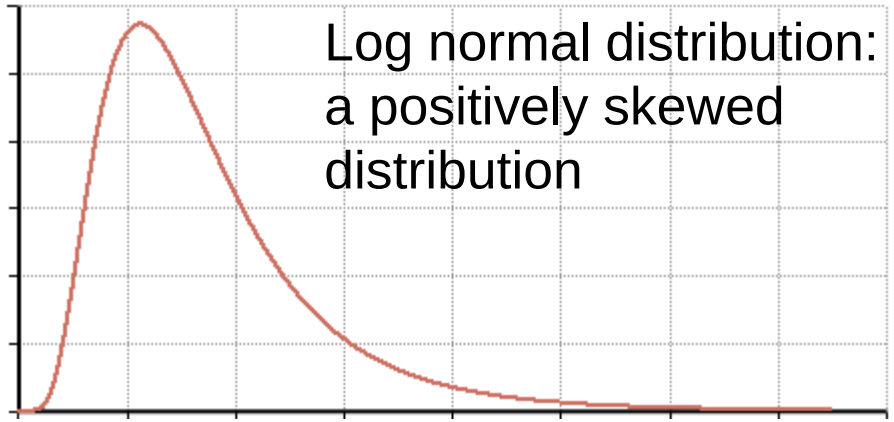
- When removing skewness, transformations are attempting to make the dataset follow the Gaussian distribution
  - The reason is simply that if the dataset can be transformed to be statistically close enough to a Gaussian dataset, then the largest set of tools and models possible are available to them to use
  - However, there are more robust models (e.g. decision tree based models) that are not affected by skewness
- To ensure that the machine learning model predicting capabilities are not affected, skewed data (both features and target value) has to be transformed to approximate to a gaussian distribution
  - The method used to transform the skewed data depends on the characteristics of the data

Unskewing transformations

- Square Root (SQRT) transformation
  - can work well on positively skewed continuous data:

```
import numpy as np
np.sqrt(df.column)
```

- Log(arithmic) transformation
  - one of the most popular transformations to deal with skewed data: `np.log(df.column)`
  - **Hint**: if the original data does not follow or approximate log-normal distribution, then log transformation does remove or reduce skewness

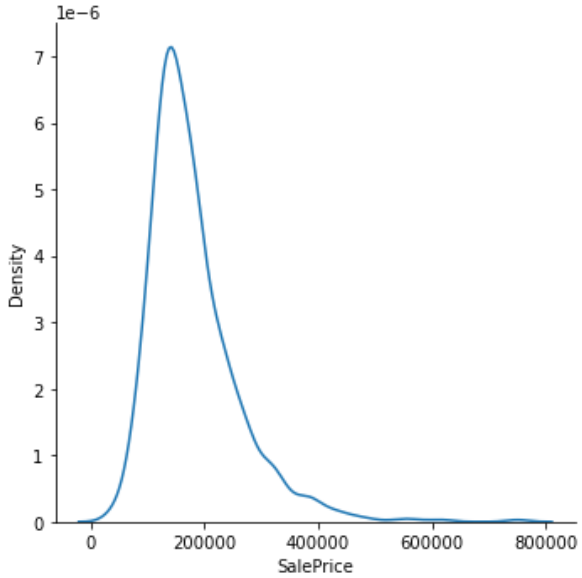


- Boxcox transformation
  - Another popular transformation:

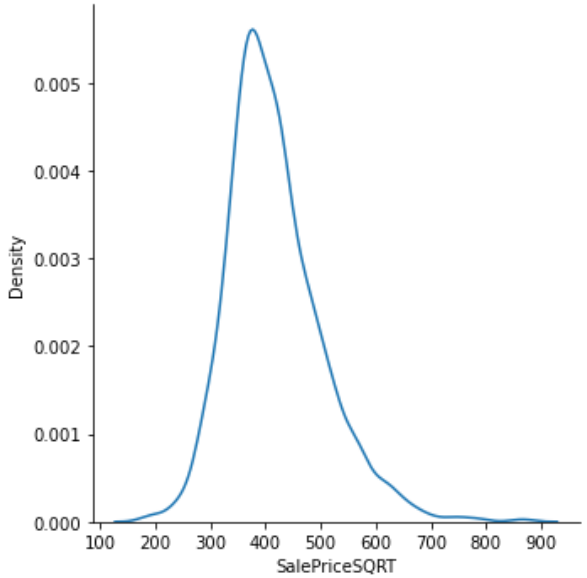
```
import scipy as sp stats
sp.stats.boxcox(df.column)
```

Unskewing transformations: Examples

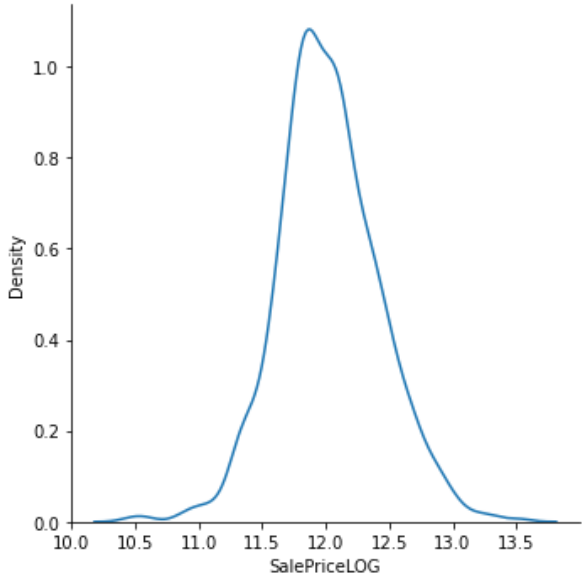
- Pandas .skew() method can be used to find the skewness of the data



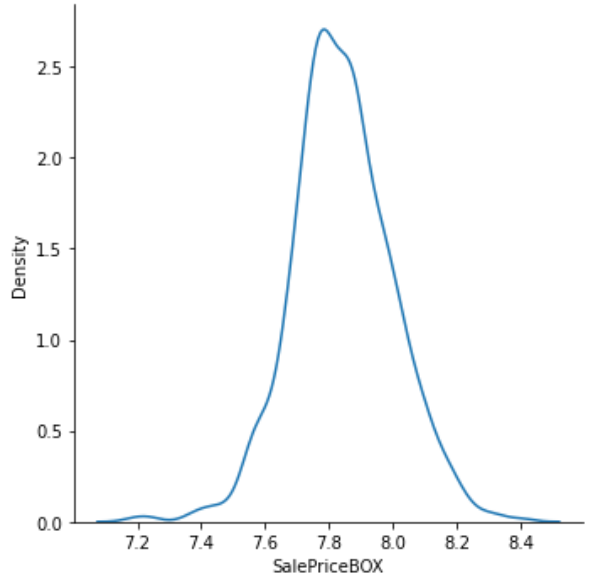
Original SalePrice column
Skewness: 1.8828757



SQRT transformation
Skewness: 0.9431527



LOG transformation
Skewness: 0.1213351



BoxCox transformation
Skewness: -0.0086529

- Source code and results are available in .ipynb file in course website
- A quite descriptive document on skewness can be found here

Resampling data

- Resampling involves changing the frequency of time series observations
- Two types of resampling are:
  - Upsampling: Where you increase the frequency of the samples, such as from minutes to seconds
  - Downsampling: Where you decrease the frequency of the samples, such as from minutes to hours
- Resampling may be required if:
  - data is not available at the same frequency that you want to make predictions
    - For example, you may have daily data and want to predict a monthly problem. So you need to downsample it to monthly data prior developing your model
  - there is an extremely high number of observations that needs to be diminished so as to speedup both EDA and ML algorithms execution time
    - Need for downsampling

Resampling data – Example

- Shampoo dataset: describes the monthly number of sales of shampoo over a 3-year period (2001 to 2003) – 36 observations
- Load dataset

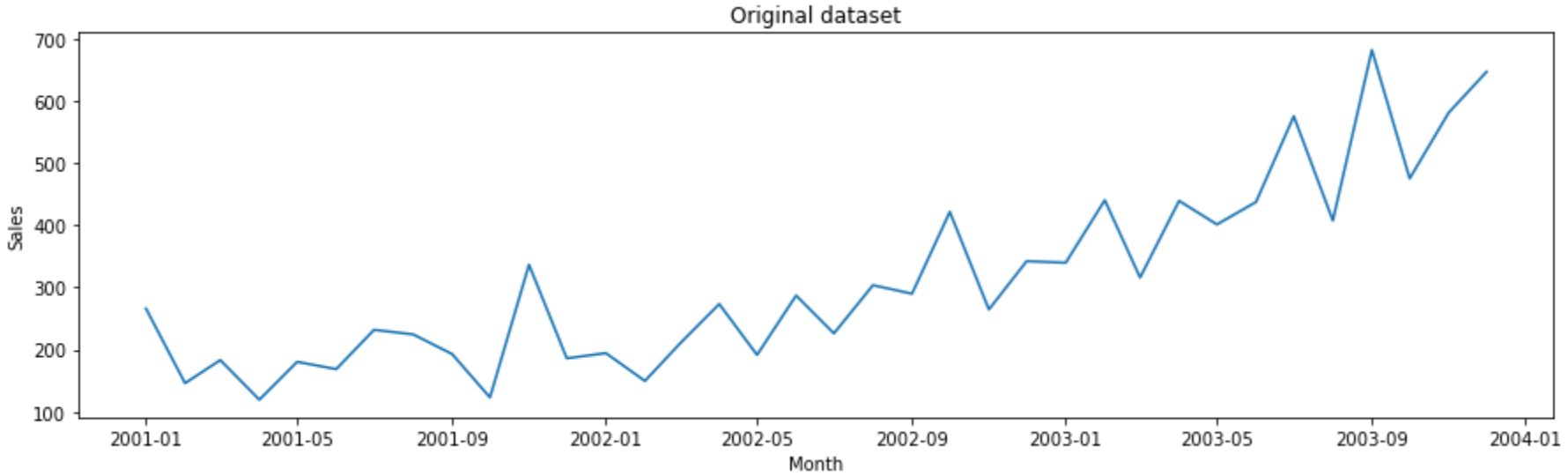
```
from pandas import read_csv
from datetime import datetime

shampoo_df = read_csv('shampoo.csv')
print(shampoo_df.head())

# convert Month feature (e.g. from 1-01 20 2001-01-01)
shampoo_df['Month'] = shampoo_df['Month'].map(lambda m: datetime.strptime('200'+m, '%Y-%m'))

# dataframe must have a datetime-like index in order to use resample function
# set Month feature as index
shampoo_df = shampoo_df.set_index('Month')
print(shampoo_df.head())
```

```
   Month  Sales
0  1-01   266.0
1  1-02   145.9
2  1-03   183.1
3  1-04   119.3
4  1-05   180.3
```

```
            Sales
Month
2001-01-01  266.0
2001-02-01  145.9
2001-03-01  183.1
2001-04-01  119.3
2001-05-01  180.3
```

Resampling data – Example

```
plt.figure(1,figsize=(15,4))
sns.lineplot(data=shampoo_df, x=shampoo_df.index, y=shampoo_df.Sales)
plt.title('Original dataset')
plt.show()
```



Resampling data – Upsampling

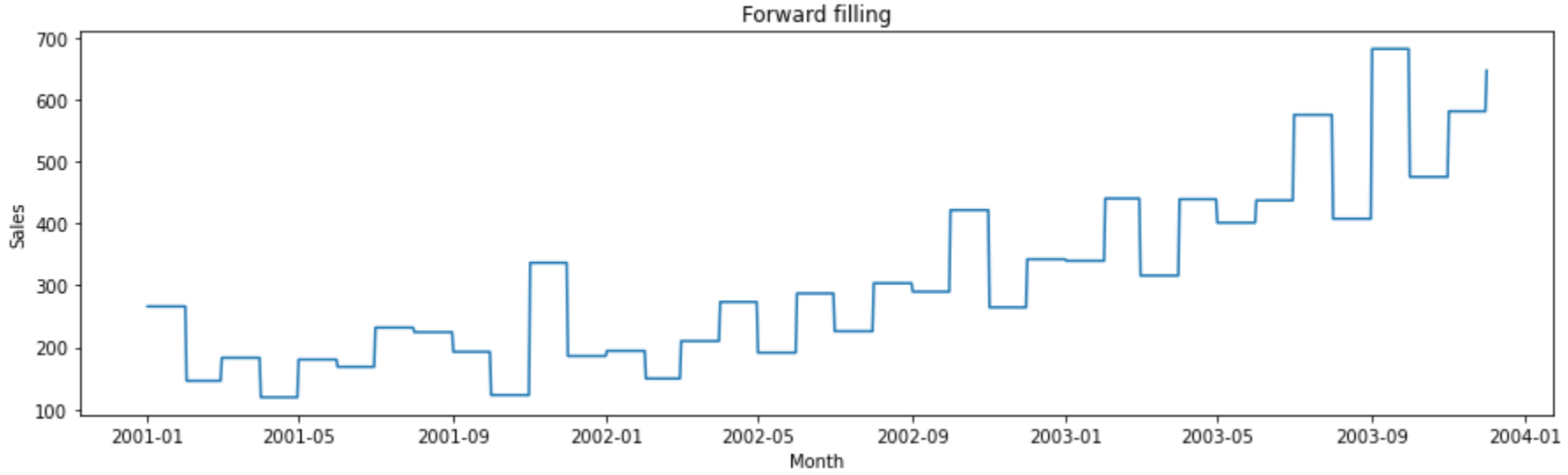
- Resample by day

```
# forward fill
daily=shampoo_df.resample('D').ffill()
plt.figure(1,figsize=(15,4))
sns.lineplot(data=daily, x=daily.index, y=daily.Sales)
plt.title('Forward filling')
plt.show()
print(daily.head())
```

Resampling can be performed by: second (‘S’), minute (‘T’), hour (‘H’), day (‘D’), week (‘W’), month (‘M’), quarter (‘Q’), year (‘Y’)

Forward-filling imputed missing values using the last observed value.

Month	Sales
2001-01-01	266.0
2001-01-02	266.0
2001-01-03	266.0
2001-01-04	266.0
2001-01-05	266.0



Resampling data – Upsampling filling strategies

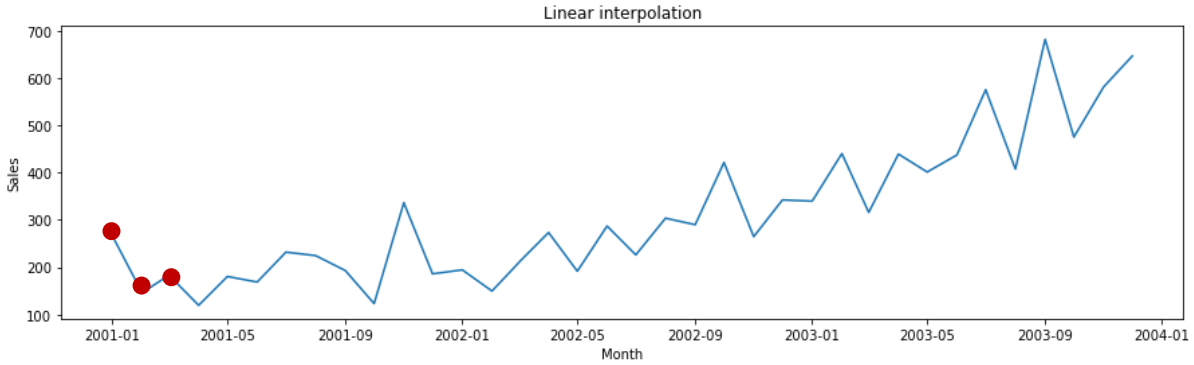
`.ffill([limit])`	Forward fill the values.
`.backfill([limit])`	Backward fill the new missing values in the resampled data.
`.bfill([limit])`	Backward fill the new missing values in the resampled data.
`.pad([limit])`	Forward fill the values.
`.nearest([limit])`	Resample by using the nearest value.
`.fillna(method[, limit])`	Fill missing values introduced by upsampling.
`.asfreq([fill_value])`	Return the values at the new freq, essentially a reindex.
`.interpolate([method, axis, limit, ...])`	Interpolate values according to different methods.

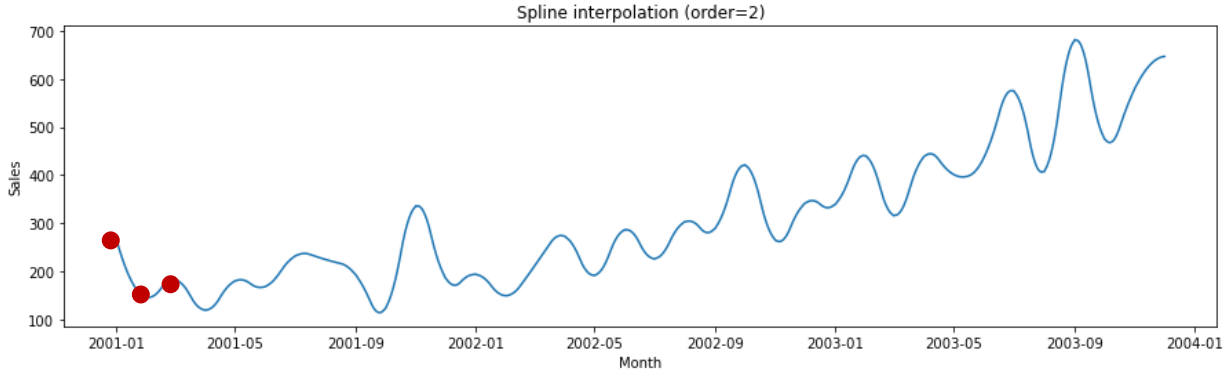
Resampling data – Upsampling

- Resample by day, filling by interpolation

```
# linear interpolation
daily=shampoo_df.resample('D').interpolate(method='linear')
plt.figure(1,figsize=(15,4))
sns.lineplot(data=daily, x=daily.index, y=daily.Sales)
plt.title('Linear interpolation')
plt.show()
```

```
# spline interpolation
daily=shampoo_df.resample('D').interpolate(method='spline', order=2)
plt.figure(1,figsize=(15,4))
sns.lineplot(data=daily, x=daily.index, y=daily.Sales)
plt.title('Spline interpolation (order=2)')
plt.show()
```



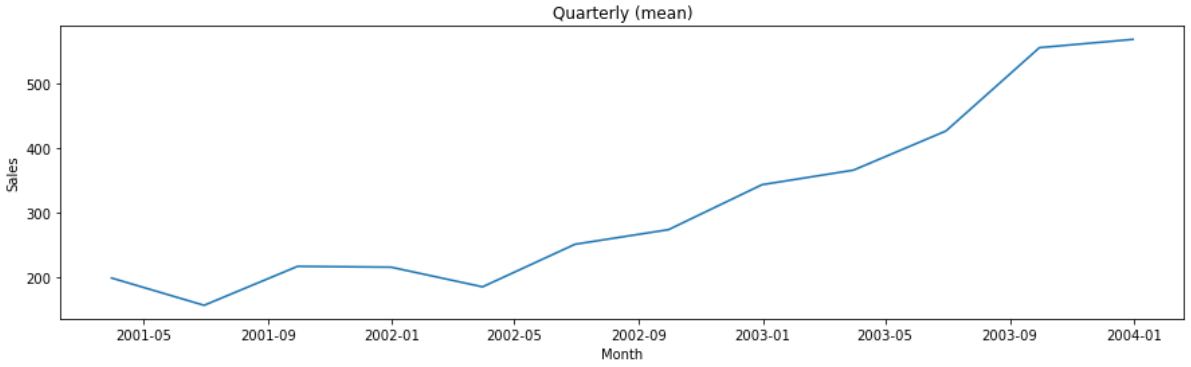


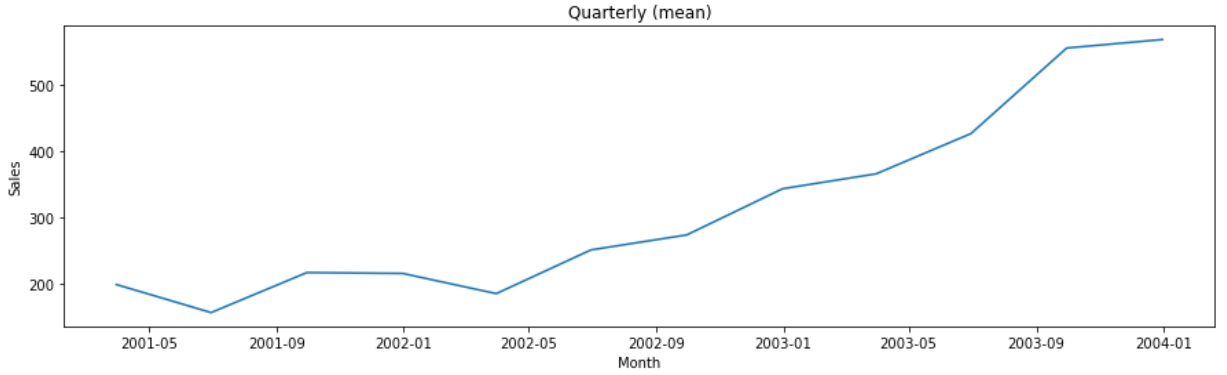
Resampling data – Downsampling

- Resample by quarter, aggregate by sum and mean

```
# sum aggregation
quarterly=shampoo_df.resample('Q').sum()
plt.figure(1,figsize=(15,4))
sns.lineplot(data=quarterly, x=quarterly.index,
y=quarterly.Sales)
plt.title('Quarterly (sum)')
plt.show()
```

```
# mean aggregation
quarterly=shampoo_df.resample('Q').mean()
plt.figure(1,figsize=(15,4))
sns.lineplot(data=quarterly, x=quarterly.index, y=quarterly.Sales)
plt.title('Quarterly (mean)')
plt.show()
```





Resampling data – Downsampling aggregation strategies

`.first([_method, min_count])`	Compute first of group values.
`.last([_method, min_count])`	Compute last of group values.
`.max([_method, min_count])`	Compute max of group values.
`.mean([_method])`	Compute mean of groups, excluding missing values.
`.median([_method])`	Compute median of groups, excluding missing values.
`.min([_method, min_count])`	Compute min of group values.
`.prod([_method, min_count])`	Compute prod of group values.
`.std([ddof])`	Compute standard deviation of groups, excluding missing values.
`.sum([_method, min_count])`	Compute sum of group values.
`.var([ddof])`	Compute variance of groups, excluding missing values.