

Introduction to Machine Learning with Scikit-Learn

District Data Labs



Feature Engineering

Getting the most out of data for predictive models

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"Feature engineering is the process of transforming raw data into features that better represent the underlying problem to the predictive models, resulting in improved model accuracy on unseen data."

- [Jason Brownlee](#)

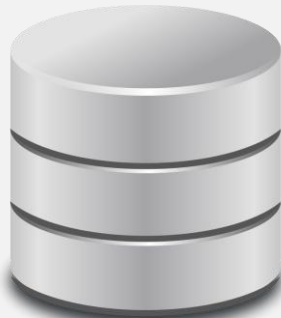
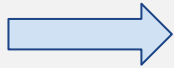
“Coming up with features is difficult,
time-consuming,
requires expert knowledge.
'Applied machine learning' is basically
feature engineering.”

- Andrew Ng

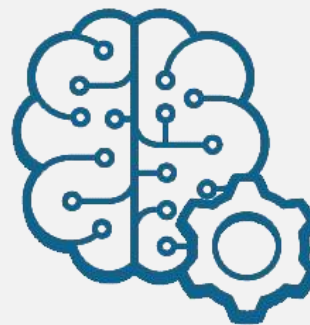
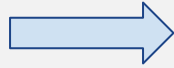
The Dream...



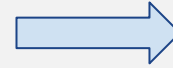
Raw data



Dataset

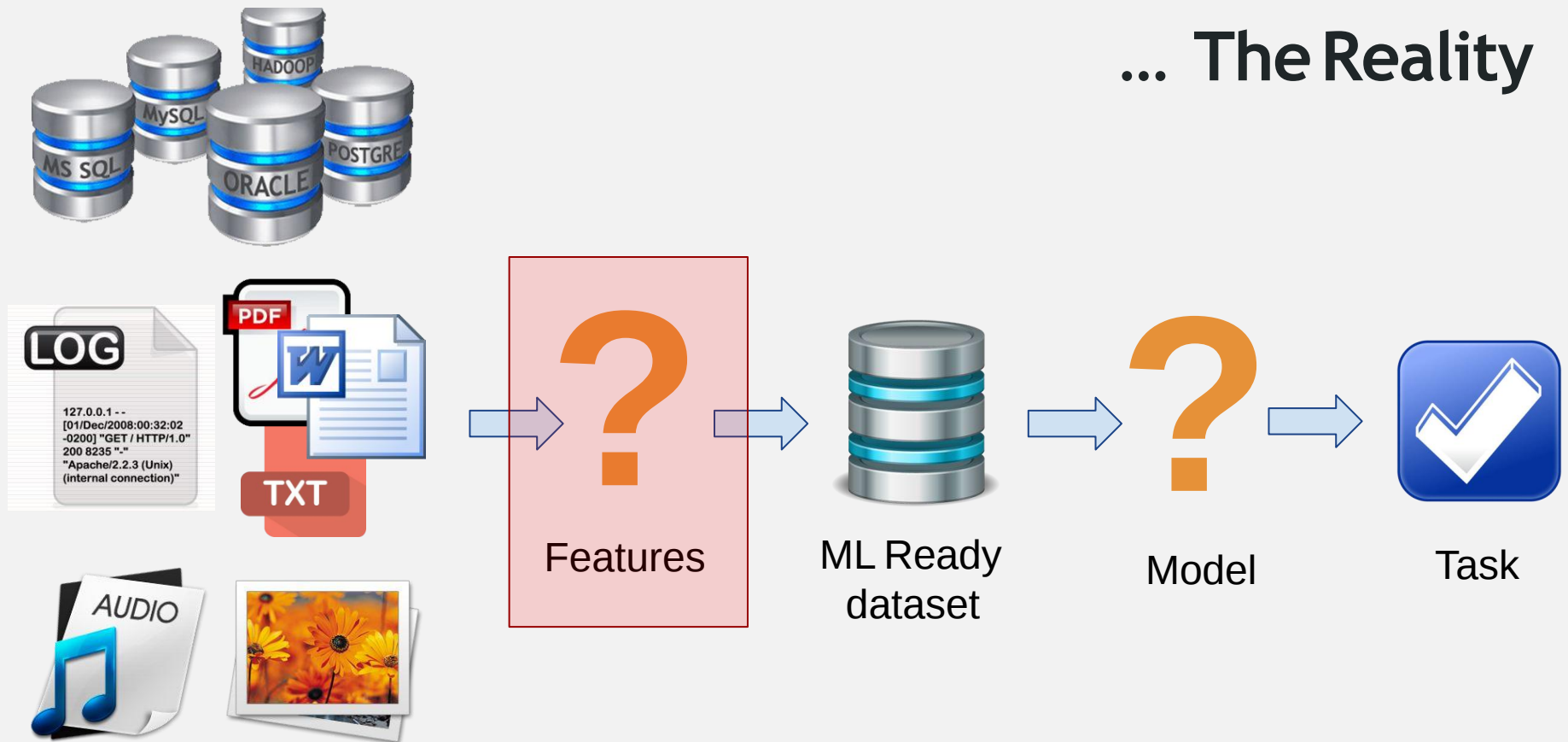


Model



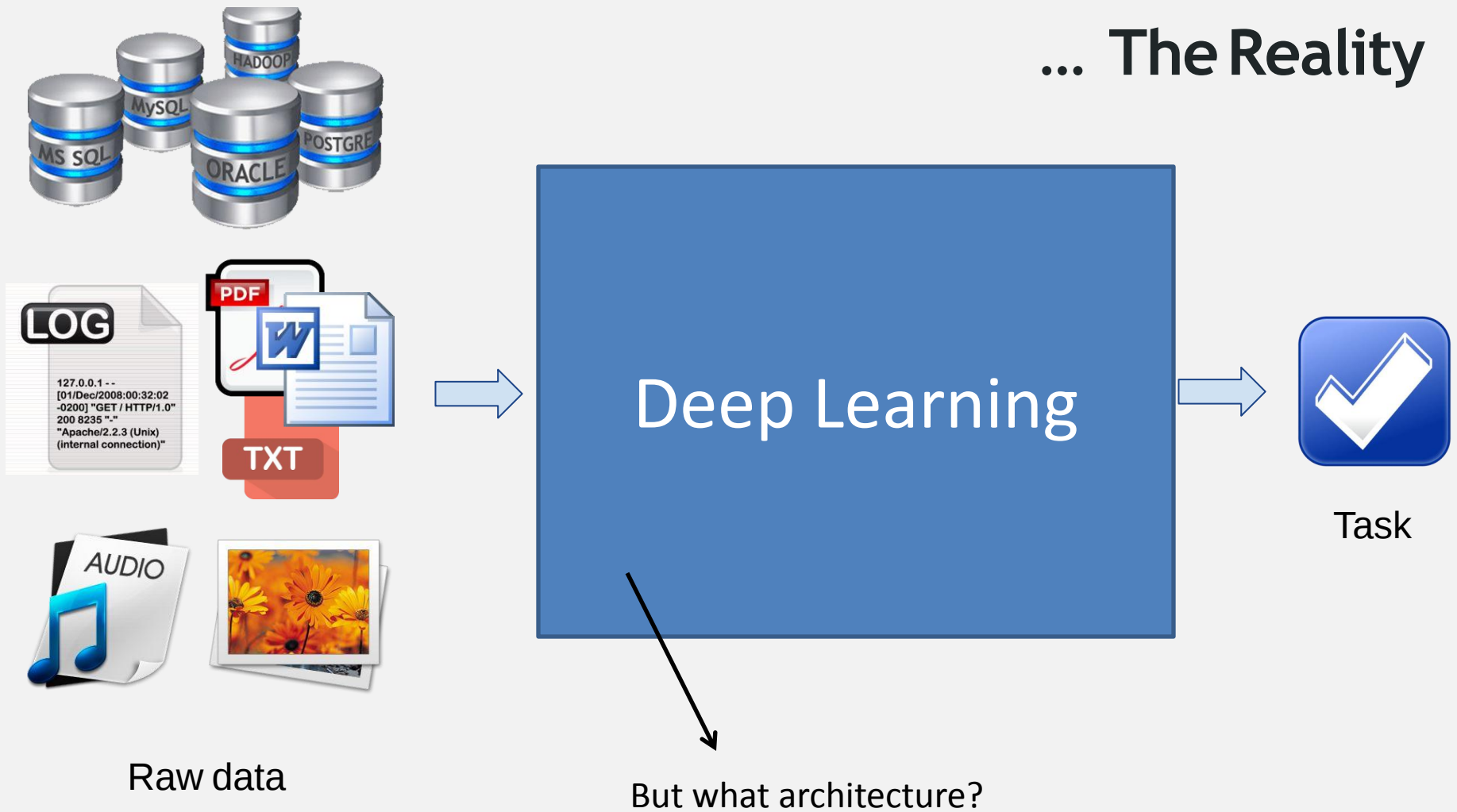
Task

... The Reality



Raw data

... The Reality



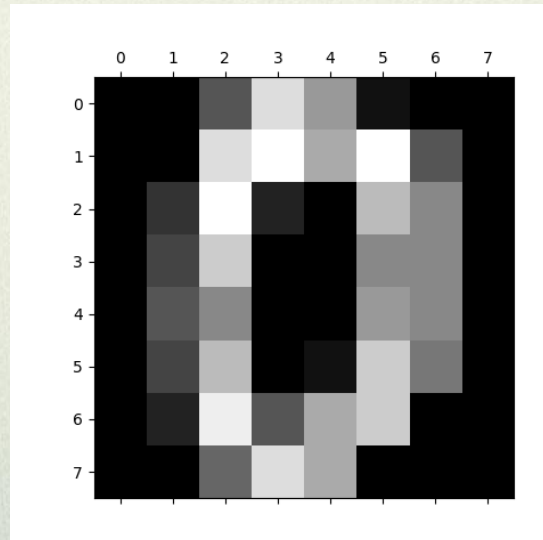
More on scikit-learn

- Data loading and pre-processing
- Feature engineering
- Hyperparameter tuning and Model evaluation
- Pipelines

Load dataset

- sklearn.datasets
 - Some „toy examples“ ready to use
 - datasets.load_iris()
 - datasets.load_wine()
 - Generate artificial data

```
>>> from sklearn.datasets import load_digits
>>> digits = load_digits()
>>> digits.data.shape
(1797, 64)
>>> digits.target_names
[0 1 2 3 4 5 6 7 8 9]
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.matshow(digits.images[0])
>>> plt.show()
```



Data pre-processing and transformation

- Inputing for NaNs
- Normalization / standardization
- Transform nominals
- Transform numeric
- Data Aggregation
- Feature extraction / combination

sklearn.preprocessing
sklearn.feature_extraction
sklearn.feature_selection

Exploratory Data Analysis (EDA)

- Get the knowledge about your data
 - What does the data model look like?
 - What is the features distribution?
 - What are the features with missing or inconsistent values?
 - What are the most predictive features?

Exploratory Data Analysis (EDA)

- Get the knowledge about your data
 - get a basic description of the data
 - visualize it
 - identify patterns in it
 - identify challenges of using the data
 - form hypothesis about the data
 - ...

Exploratory Data Analysis (EDA)

Basic knowledge

- Describe data (quantiles, med, mean, max, min...)
- head(), tail()
- Pd.Query(), sorting,

Challenges

- NaNs, outliers, numeric -> nominal and vice versa

Patterns

- correlation, covariation, linear dependence, dimensionality reduction...

Visualization

- boxplots, histograms, cumulative distribution, scatter plots, corr matrices, ...

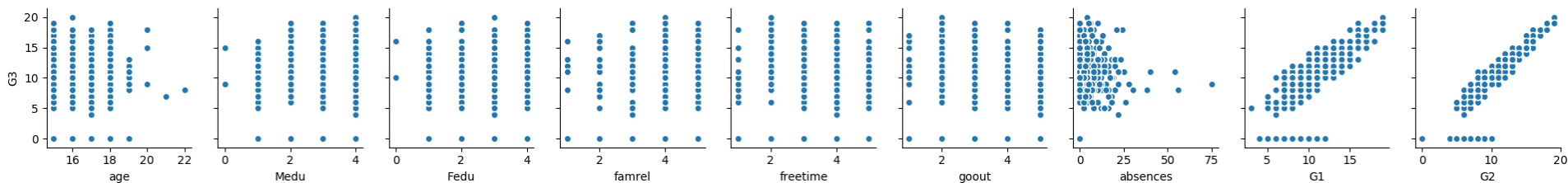
Exploratory Data Analysis (EDA) - pairplot

```
import pandas as pd
import seaborn as sns #statistical data visualization, based on matplotlib
import matplotlib.pyplot as plt

df = pd.read_csv("C:/Users/peska/Documents/uceni/2017_2018/NPRG065/cviceni/student-mat.csv", delimiter=";")

sns.pairplot(data=df,
             x_vars= ["age", "Medu", "Fedu", "famrel", "freetime", "goout", "absences", "G1", "G2"],
             y_vars= ['G3'])

plt.show()
```

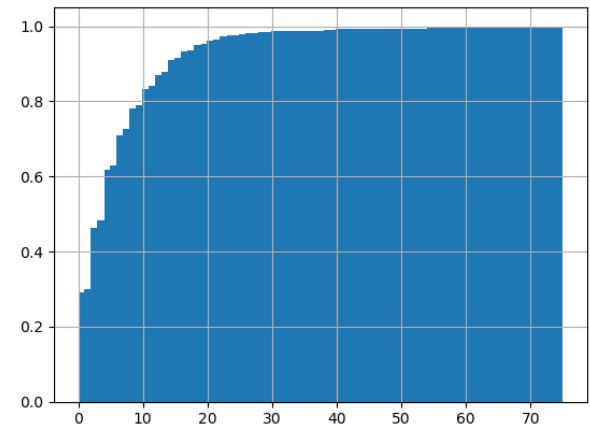
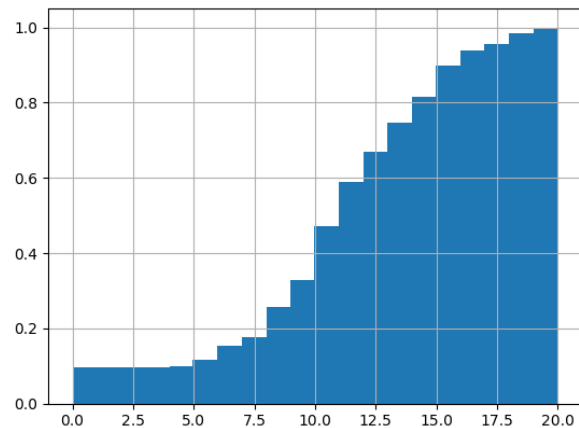


Exploratory Data Analysis (EDA) - CDF

```
import pandas as pd
import matplotlib.pyplot as plt

df = pd.read_csv("C:/Users/peska/Documents/uceni/2017_2018/NPRG065/cviceni/student-mat.csv", delimiter=";")

df.G3.hist(cumulative=True, normed=1, bins=len(df.G3))
#df.absences.hist(cumulative=True, normed=1, bins=len(df.absences))
plt.show()
```





Imputation for missing values

- Datasets contain missing values, often encoded as blanks, NaNs or other placeholders
- Ignoring rows and/or columns with missing values is possible, but at the price of losing data which might be valuable
- Better strategy is to infer them from the known part of data
- Strategies
 - **Mean:** Basic approach
 - **Median:** More robust to outliers
 - **Mode:** Most frequent value
 - **Using a model:** Can expose algorithmic bias



Imputation for missing values

```
>>> import numpy as np
>>> from sklearn.preprocessing import Imputer
>>> imp = Imputer(missing_values='NaN', strategy='mean', axis=0)
>>> imp.fit([[1, 2], [np.nan, 3], [7, 6]])
Imputer(axis=0, copy=True, missing_values='NaN', strategy='mean',
verbose=0)
>>> X = [[np.nan, 2], [6, np.nan], [7, 6]]
>>> print(imp.transform(X))
[[ 4.      2.    ]
 [ 6.      3.666...]
 [ 7.      6.    ]]
```

Missing values imputation with scikit-learn



Binarization

- Transform discrete or continuous numeric features in binary features

Example: Number of user views of the same document

document_id	uuid	views_count
25792	6d82e412aa0f0d	8
25792	571016386ffee7	6
25792	6a91157d820e37	6
25792	ad45fc764587b0	6
25792	a743b03f2b8ddc	3



document_id	uuid	viewed
25792	6d82e412aa0f0d	1
25792	571016386ffee7	1
25792	6a91157d820e37	1
25792	ad45fc764587b0	1
25792	8d87becfb35857	1
25792	abcdefg1234567	0

```
>>> from sklearn import preprocessing
>>> X = [[ 1., -1., 2.],
...      [ 2., 0., 0.],
...      [ 0., 1., -1.]]

>>> binarizer =
preprocessing.Binarizer(threshold=1.0)
>>> binarizer.transform(X)
array([[ 1., 0., 1.],
       [ 1., 0., 0.],
       [ 0., 1., 0.]])
```

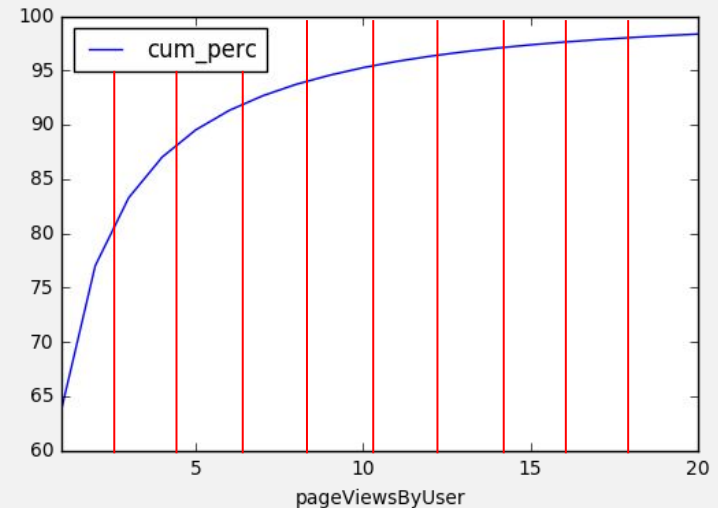
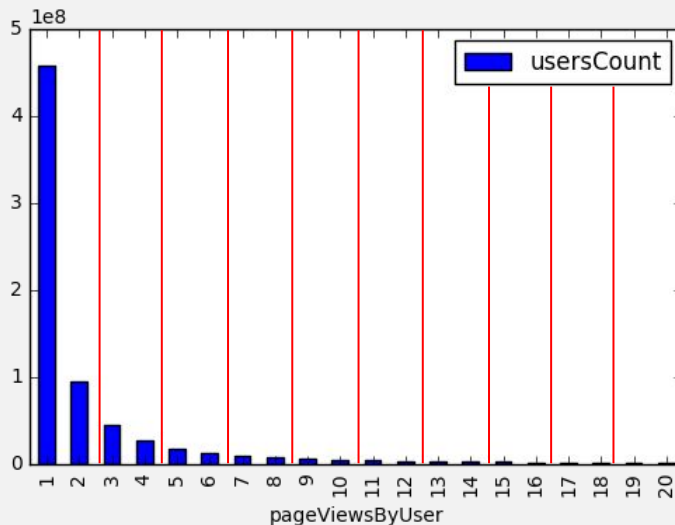
Binarization with scikit-learn



Binning

- Split numerical values into bins and encode with a bin ID
- Can be set arbitrarily or based on distribution
- **Fixed-width binning**

Does fixed-width binning make sense for this long-tailed distribution?



Most users ($458,234,809 \sim 5 \times 10^8$) had only 1 pageview during the period.

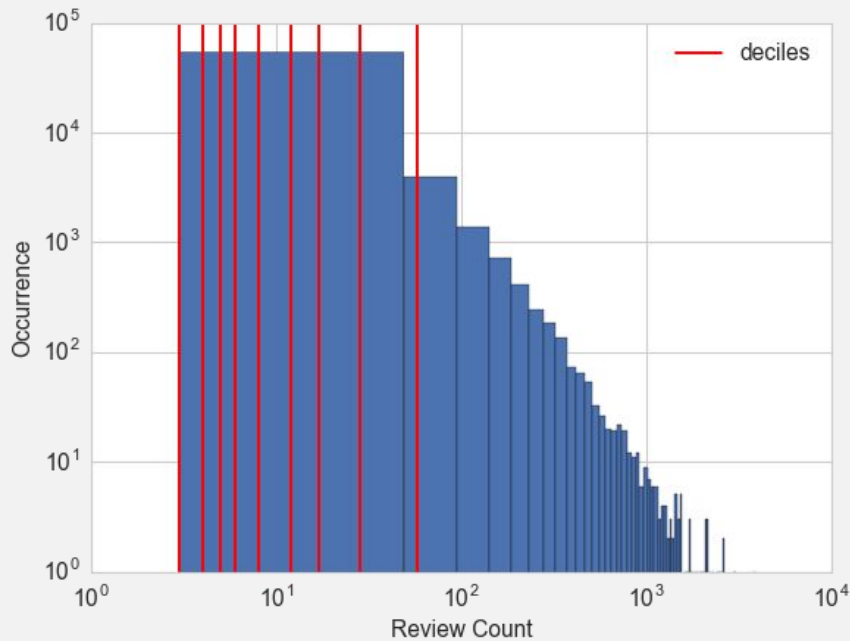
`numpy.digitize`



Binning

- **Adaptative or Quantile binning**

Divides data into equal portions (eg. by median, quartiles, deciles)



```
>>> deciles = dataframe['review_count'].quantile([.1, .2, .3, .4, .5, .6, .7,
.8, .9])
>>> deciles
0.1    3.0
0.2    4.0
0.3    5.0
0.4    6.0
0.5    8.0
0.6   12.0
0.7   17.0
0.8   28.0
0.9   58.0
```

Quantile binning with Pandas

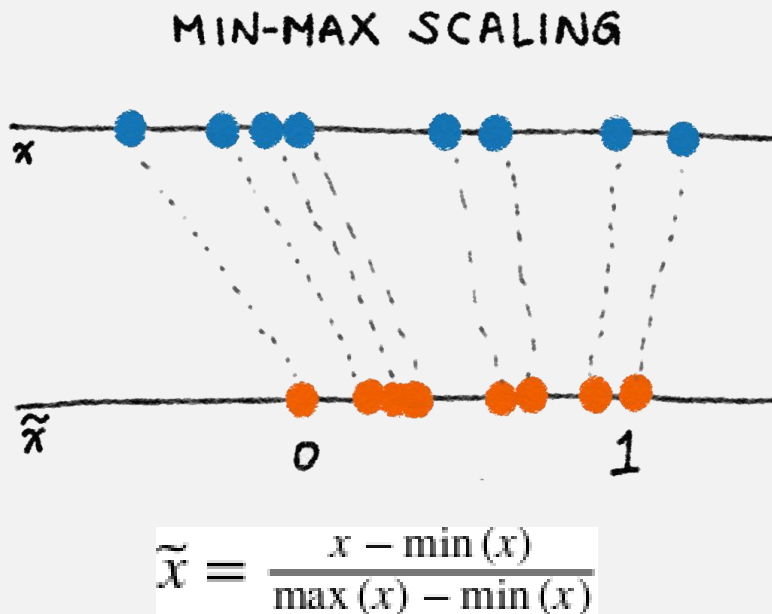
Scaling

- Models that are smooth functions of input features are sensitive to the scale of the input (eg. Linear Regression)
- Scale numerical variables into a certain range, dividing values by a normalization constant (no changes in single-feature distribution)
- Popular techniques
 - MinMax Scaling
 - Standard (Z) Scaling



Min-max scaling

- Squeezes (or stretches) all values within the range of [0, 1] to add robustness to very small standard deviations and preserving zeros for sparse data.



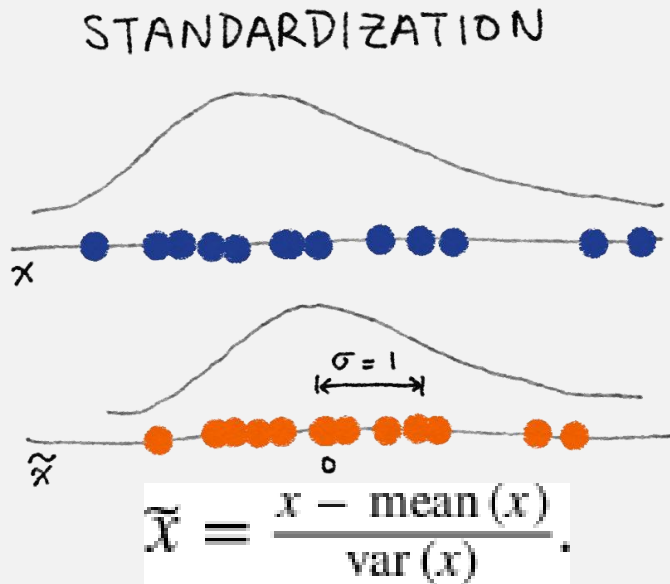
```
>>> from sklearn import preprocessing
>>> X_train = np.array([[ 1., -1., 2.],
...                      [ 2., 0., 0.],
...                      [ 0., 1., -1.]])
...
>>> min_max_scaler =
preprocessing.MinMaxScaler()
>>> X_train_minmax =
min_max_scaler.fit_transform(X_train)
>>> X_train_minmax
array([[ 0.5, 0., 1.],
       [ 1., 0.5, 0.33333333],
       [ 0., 1., 0.]])
```

Min-max scaling with scikit-learn



Standard (Z) Scaling

After Standardization, a feature has mean of 0 and variance of 1 (assumption of many learning algorithms)



```
>>> from sklearn import preprocessing
>>> import numpy as np
>>> X = np.array([[ 1., -1., 2.],
...               [ 2., 0., 0.],
...               [ 0., 1., -1.]])
>>> X_scaled = preprocessing.scale(X)
>>> X_scaled
array([[ 0. ..., -1.22..., 1.33...],
       [ 1.22..., 0. ..., -0.26...],
       [-1.22..., 1.22..., -1.06...]])
>> X_scaled.mean(axis=0)
array([ 0., 0., 0.])
>>> X_scaled.std(axis=0)
array([ 1., 1., 1.] )
```

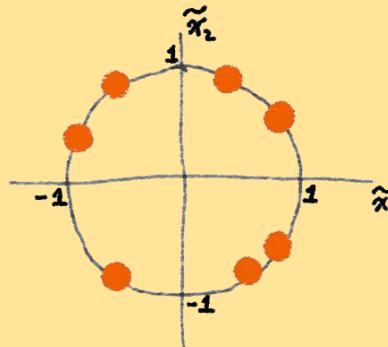
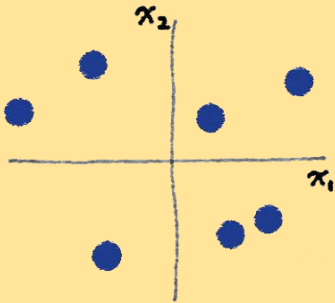
Standardization with scikit-learn



Normalization

- Scales individual samples (rows) to have [unit vector](#), dividing values by vector's L^2 norm, a.k.a. the Euclidean norm
- Useful for quadratic form (like dot-product) or any other kernel to quantify similarity of pairs of samples. This assumption is the base of the **Vector Space Model** often used in **text classification and clustering** contexts

L_2 NORMALIZATION



$$\tilde{x} = \frac{x}{\|x\|_2}$$

Normalized vector

$$\|x\|_2 = \sqrt{x_1^2 + x_2^2 + \dots + x_m^2}$$

Euclidean (L^2) norm





Normalization

```
>>> from sklearn import preprocessing
>>> X = [[ 1., -1., 2.],
...      [ 2., 0., 0.],
...      [ 0., 1., -1.]]
>>> X_normalized = preprocessing.normalize(X, norm='l2')
>>> X_normalized
array([[ 0.40..., -0.40...,  0.81...],
       [ 1. ...,  0. ...,  0. ...],
       [ 0. ...,  0.70..., -0.70...]])
```

Normalization with scikit-learn





Log transformation

Compresses the range of large numbers and expand the range of small numbers.

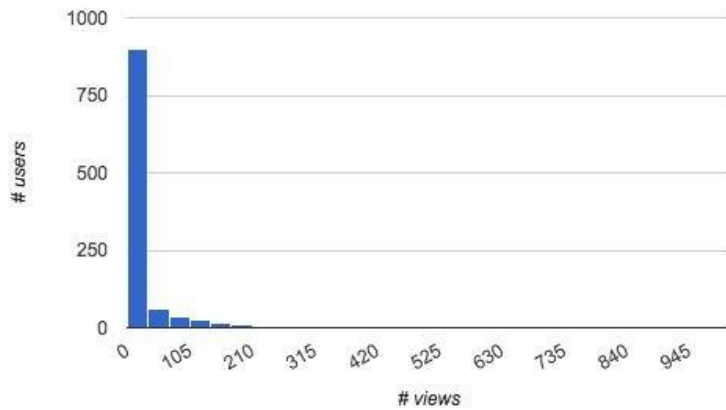
Eg. The larger x is, the slower $\log(x)$ increments.

user_id	views_count		$\log(1+\text{views_count})$
a	1000		6.91
b	500		6.22
c	300		5.71
d	200		5.30
e	150		5.02
f	100		4.62
g	70		4.26
h	50		3.93
i	30		3.43
j	20		3.04
k	10		2.40
l	5		1.79
m	1		0.69

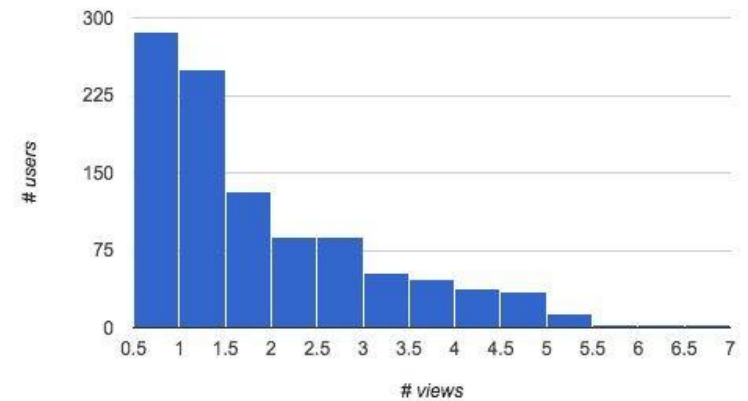


Log transformation

Smoothing long-tailed data with log



Histogram of # views by user



Histogram of # views by user
smoothed by $\log(1+x)$

Feature extraction



Interaction Features

$$(X_1, X_2) \longrightarrow (1, X_1, X_2, X_1^2, X_1X_2, X_2^2)$$

```
>>> import numpy as np
>>> from sklearn.preprocessing import PolynomialFeatures
>>> X = np.arange(6).reshape(3, 2)
>>> X
array([[0, 1],
       [2, 3],
       [4, 5]])
>>> poly = PolynomialFeatures(degree=2, interaction_only=False,
include_bias=True)
>>> poly.fit_transform(X)
array([[ 1.,  0.,  1.,  0.,  0.,  1.],
       [ 1.,  2.,  3.,  4.,  6.,  9.],
       [ 1.,  4.,  5., 16., 20., 25.]])
```

Polynomial features with scikit-learn



One-Hot Encoding (OHE)

- Transform a categorical feature with m possible values into m binary features.
- If the variable cannot be multiple categories at once, then only one bit in the group can be on.

platform		platform=desktop	platform=mobile	platform=tablet
desktop	→	1	0	0
mobile		0	1	0
tablet		0	0	1

- Sparse format is memory-friendly
- `sklearn.feature_extraction.DictVectorizer`

Large Categorical Variables

- Common in applications like targeted advertising and fraud detection
- Example:

categorical_feature	unique_values
landing_page_document_id	636482
ad_id	418295
ad_document_id	143856
content_entities	52439
advertiser	2052
publisher	830
country_state	1892

Some large categorical features from Outbrain Click Prediction competition



Feature hashing

- Hashes categorical values into vectors with fixed-length.
- Lower sparsity and higher compression compared to OHE
- Deals with new and rare categorical values (eg: new user-agents)
- May introduce collisions

100 hashed columns

country	country_hashed_1	country_hashed_2	country_hashed_3	country_hashed_4	...
brazil	1	0	0	0	...
chile	0	0	0	1	...
venezuela	0	0	1	0	...
colombia	0	0	1	0	...
... 222 countries	...	...	...	...	...



Bin-counting

- Instead of using the actual categorical value, use a global statistic of this category on historical data.
- Useful for both linear and non-linear algorithms
- May give collisions (same encoding for different categories)
- Be careful about leakage
- Strategies
 - Count
 - Average CTR



Bin-counting

ad_id
423654
123646
68655
54345



ad_views
18339
335
1244
35387

or

ad_clicks
1355
12
132
1244

or

ad_CTR
0.074
0.036
0.106
0.035



Counts



Click-Through Rate

$$P(\text{click} \mid \text{ad}) = \text{ad_clicks} / \text{ad_views}$$



Textual features

- `sklearn.feature_extraction.text`
- Count, Tf-IDF,



Image features

- `sklearn.feature_extraction.image`
- Patches, img to graph,...

Feature selection

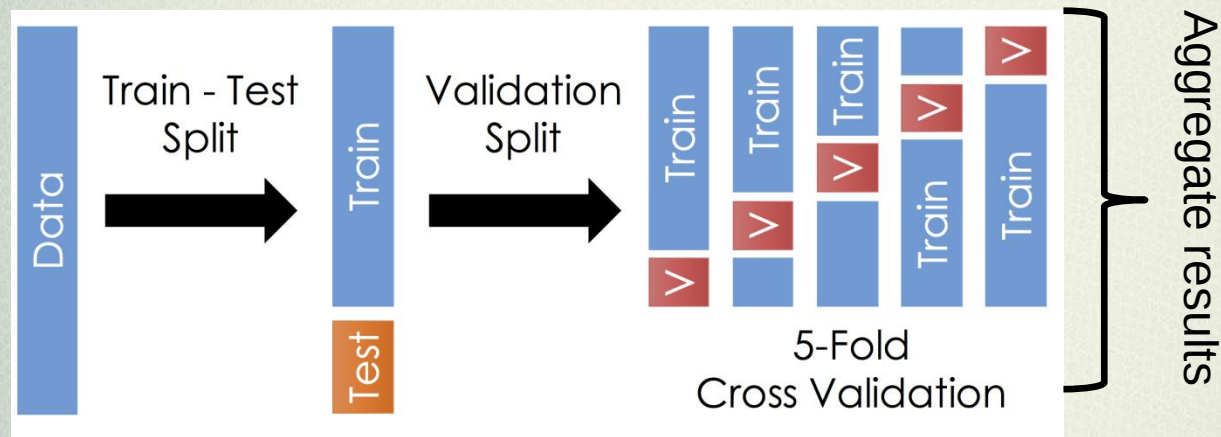
Feature selection

- Decrease complexity of model
- Remove redundant and irrelevant features
- `sklearn.feature_selection.SelectKBest`
 - Scoring function
 - K features
 - Threshold
 - ...

Model Fitting & Evaluation

Model Fitting Protocol

How to learn model's hyperparameters: grid search & cross-validation



Instead of Train – Test split, you may use additional „outer“ cross-validation

Get results from all parts of the dataset

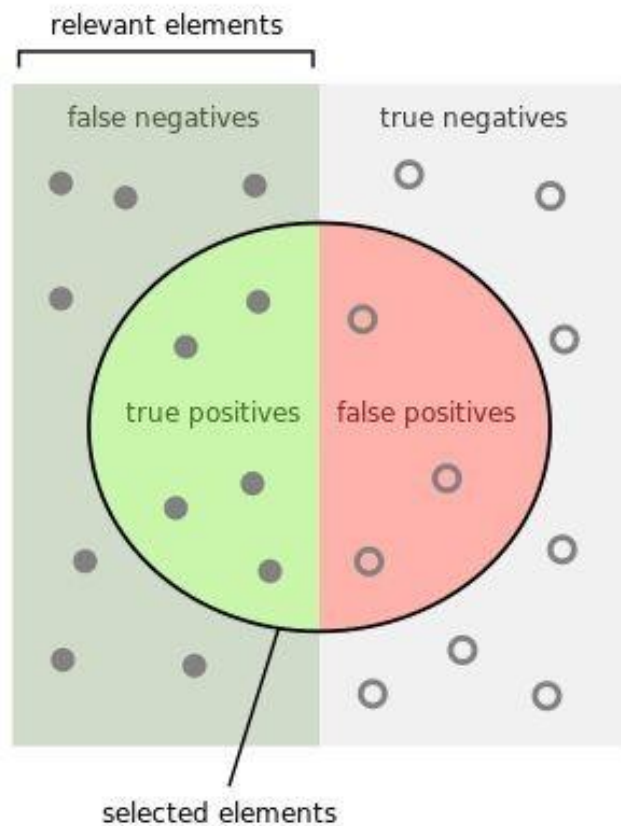
Never use any knowledge of the test set data

E.g. For mean ratings, object similarities etc

Model Fitting Protocol

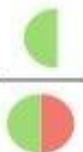
Further variants:

- Monte-Carlo cross validation:
 - random splits, arbitrary size (cold start problems)
- Bootstrap validation:
 - only one split (if you have abundant data)
- Temporal splits:
 - if domain changes over time



How many selected items are relevant?

Precision =



How many relevant items are selected?

Recall =



accuracy =

true positives + true negatives / total

precision =

true positives / (true positives + false positives)

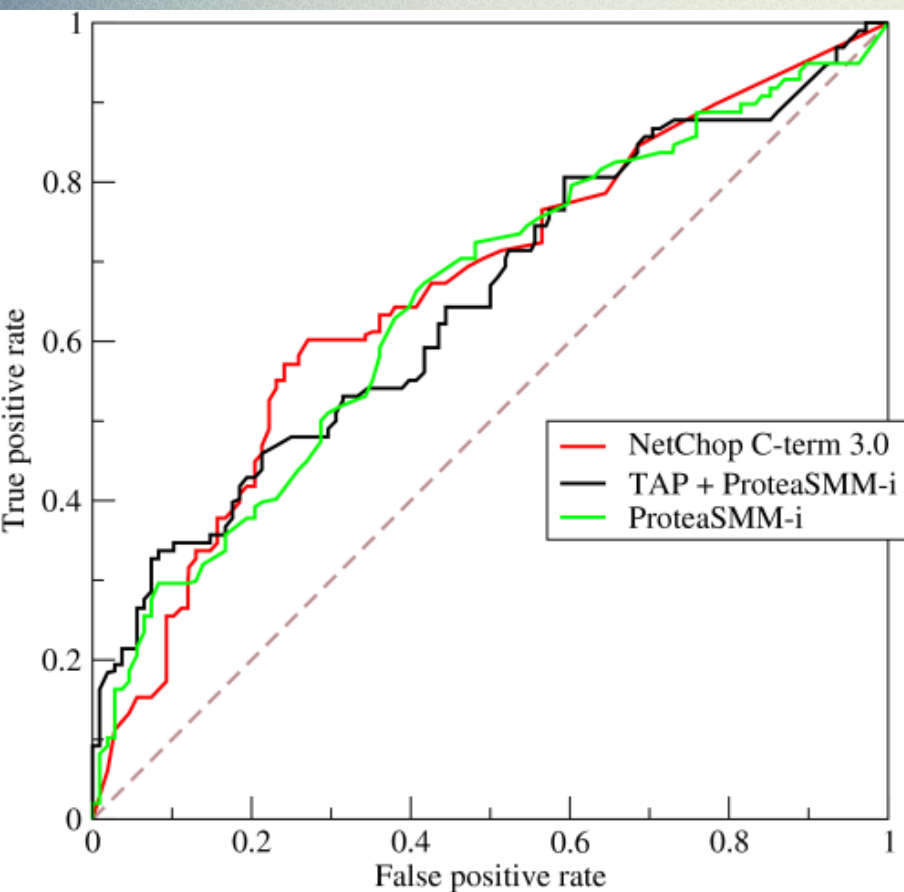
recall =

true positives / (false negatives + true positives)

F1 score =

$2 * ((\text{precision} * \text{recall}) / (\text{precision} + \text{recall}))$

https://en.wikipedia.org/wiki/Precision_and_recall



ROC (reciever-operator curve)

True Positive Rate /
False Positive Rate

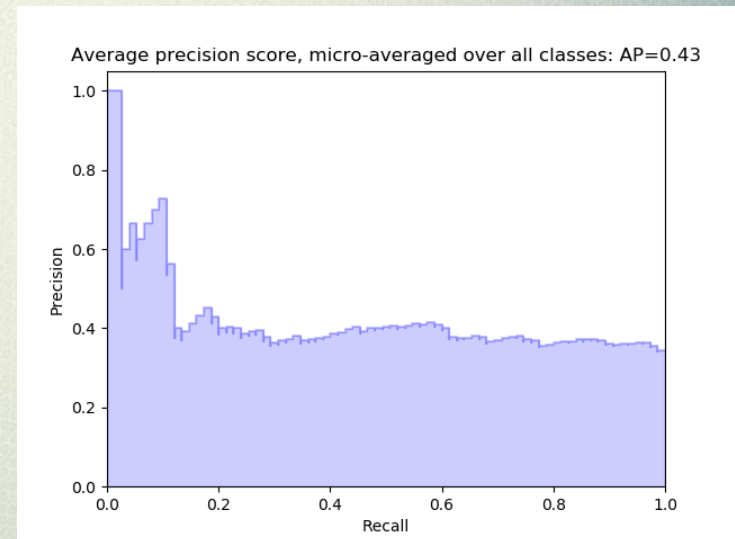
AUC (AUROC) = area under ROC

- *probability that random positive example will be ranked higher than random negative*

- calculate empirically from test results

AUPR (area under precision-recall curve)

https://en.wikipedia.org/wiki/Receiver_operating_characteristic
<http://scikit-learn.org/stable/modules/generated/sklearn.metrics.auc.html#sklearn.metrics.auc>



MSE & Coefficient of Determination

MAE / MSE / RMSE

`MSE = np.mean((predicted-expected)**2)`

Coefficient of determination

R^2 is a predictor of “goodness of fit” and is a value $\in [0,1]$ where 1 is perfect fit.

-the proportion of the variance in the dependent variable that is predictable from the independent variable(s)

-independent from the scale of the output feature

$$SS_{\text{tot}} = \sum_i (y_i - \bar{y})^2,$$

$$SS_{\text{res}} = \sum_i (y_i - f_i)^2 = \sum_i e_i^2$$

$$R^2 \equiv 1 - \frac{SS_{\text{res}}}{SS_{\text{tot}}}.$$

Evaluation - sklearn

sklearn.model_selection

-GridSearchCV

-train_test_split()

-LeaveOneOut (predict for each example separately)

- Split data / Learn hyperparameters / Validate metrics

Evaluation - sklearn

sklearn.metrics: metric(true, predicted/rank,...)

Classification

- classification_report()**
- precision, recall, auc, f1_score, jaccard,...**
- confusion matrix**

Regression

- r2_score(), MAE, MSE**

Clustering

Pairwise

- cosine / euclidean distance, ...**

...

-<http://scikit-learn.org/stable/modules/classes.html#module-sklearn.metrics>

```
from sklearn import svm, datasets
from sklearn.model_selection import GridSearchCV, train_test_split
from sklearn.metrics import classification_report

iris = datasets.load_iris()
parameters = {'kernel':('linear', 'rbf'), 'C':[1, 10]}
svc = svm.SVC()
X = iris.data
y = iris.target
X_train, X_test, y_train, y_test = train test split(X, y,
test_size=0.3, random_state=0)

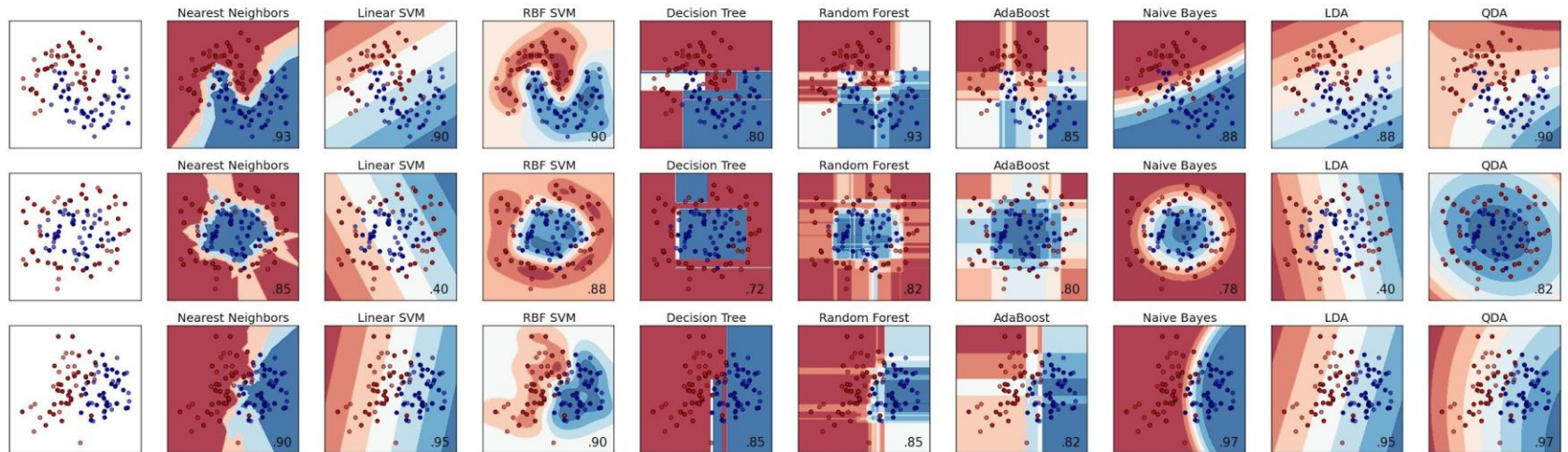
clf = GridSearchCV(svc, parameters)
clf.fit(X,y)
print(clf.cv_results_['mean_test_score'])
print(clf.cv_results_['params'])
print(clf.best_params_)

y_pred = clf.predict(X_test)
print(classification_report(y_test, y_pred))
```

Other Evaluation

How to evaluate clusters?

Visualization (but only in 2D)



Unpredictable Future

Machine learning models attempt to predict the future as new inputs come in - but human systems and processes are subject to change.



Solution: Precision/Recall tracking over time

Pipelines

Pipelines

`sklearn.pipeline.Pipeline(steps)`

- Sequentially apply *repeatable* transformations to final estimator that can be validated at every step.
- Each step (except for the last) must implement `Transformer`, e.g. `fit` and `transform` methods.
- Pipeline itself implements both methods of `Transformer` and `Estimator` interfaces.



```
>>> from sklearn.preprocessing import PolynomialFeatures
>>> from sklearn.pipeline import make_pipeline
>>> model = make_pipeline(PolynomialFeatures(2), linear_model.
Ridge())
>>> model.fit(X_train, y_train)

>>> mean_squared_error(y_test, model.predict(X_test))
3.1498887586451594

>>> model.score(X_test, y_test)
0.97090576345108104
```

Pipelined Model

Task 7

Select dataset (wines / student performance)

- Run `train_test_split()` @ 20% test set
- Select learning method
 - Select best hyperparameters based on cross-validation

Return R^2 , MAE and RMSE based on scipy methods

- visualize CDF and independent/dependent vars
- try, e.g. `StandardScaler()` and `PolynomialFeatures()` for extraction

Semestrální projekt – varianta 3

- Identifikace / autentizace osob dle keystroke dynamics
 - Vzdělávací server / online výuka atp.
 - Soutěž na <http://biointelligence.hu/typing-challenge/index.php>
 - dataset není v současné době veřejný (GDPR), zájemcům bude předán
 - malý dataset (12 osob, 5 trénovacích a 50 testovacích vzorků / osobu)
 - JavaScript events keyup/down/press, keycode, timestamp
 - Autentizace (potvrzení očekávané osoby)
 - Identifikace (která z osob odpovídá danému vzorku)
 - Evaluate:
 - Odeslat řešení v daném formátu na web soutěže
 - Accuracy (TP+TN)/ALL
 - „Rozumné“ výsledky alespoň okolo ECKNN
 - Typické algoritmy:
 - Dynamic Time Warping (https://en.wikipedia.org/wiki/Dynamic_time_warping)
 - Rychlosti lokálních přechodů / dimensionality reduction
 - RNN? asi příliš malý dataset. Možná document2vec.
 - <http://biointelligence.hu/typing.html>