- Noise filtering
- Visualization
- Feature Extraction
- Stock market predictions
- Gene data analysis

- Identify patterns in data
- Detect the correlation between variables

Reduce the dimensions of a d-dimensional dataset by projecting it onto a (k)-dimensional subspace (where k<d)

- Standardize the data.
- Obtain the Eigenvectors and Eigenvalues from the covariance matrix or correlation matrix, or perform Singular Vector Decomposition.
- Sort eigenvalues in descending order and choose the k eigenvectors that correspond to the k largest eigenvalues where k is the number of dimensions of the new feature subspace $(k \le d)/$.
- Construct the projection matrix W from the selected k eigenvectors.
- Transform the original dataset X via W to obtain a k-dimensional feature subspace Y

https://plot.ly/ipython-notebooks/principal-component-analysis/

- Used as a dimensionality reduction technique
- Used in the pre-processing step for pattern classification
- Has the goal to project a dataset onto a lower-dimensional space

• Sounds similar to PCA right?

LDA differs because in addition to finding the component axises with LDA we Are interested in the axes that maximize the separation between multiple classes.

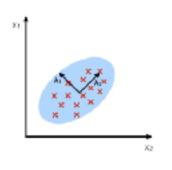
Breaking it down further:

The goal of LDA is to project a feature space (a dataset n-dimensional samples) onto a small subspace subspace $k(where k \le n-1)$ while maintaining the class-discriminatory information.

Both PCA and LDA are linear transformation techniques used for dimensional reduction. PCA is described as unsupervised but LDA is supervised because of the relation to the dependent variable.

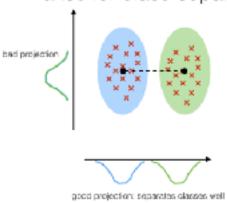
PCA:

component axes that maximize the variance



LDA:

maximizing the component axes for class-separation

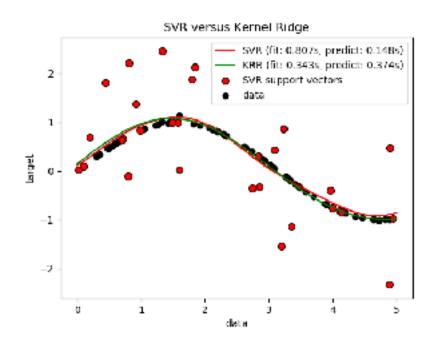


LDA: https://sebastianraschka.com/Articles/2014_python_lda.html

- 1. Compute the d-dimensional mean vectors for the different classes from the dataset.
- 2. Compute the scatter matrices (in-between-class and within-class scatter matrix).
- 3. Compute the eigenvectors (e_1 , e_2 , ..., e_d) and corresponding eigenvalues (λ_1 , λ_2 , ..., λ_d) for the scatter matrices.
- 4. Sort the eigenvectors by decreasing eigenvalues and choose k eigenvectors with the largest eigenvalues to form a $d \times k$ dimensional matrix W (where every column represents an eigenvector).
- 5. Use this $d \times k$ eigenvector matrix to transform the samples onto the new subspace. This can be summarized by the matrix multiplication: $\mathbf{Y} = \mathbf{X} \times \mathbf{W}$ (where \mathbf{X} is a $n \times d$ -dimensional matrix representing the n samples, and \mathbf{y} are the transformed $n \times k$ -dimensional samples in the new subspace).

https://sebastianraschka.com/Articles/2014_python_lda.html

How does it work?



Building a SVR

- 1. Collect a training set $\tau = \{\overrightarrow{X}, \overrightarrow{Y}\}$
- 2. Choose a kernel and it's parameters as well as any regularization needed.
- 3. Form the correlation matrix, \vec{K}
- 4. Train your machine, exactly or approximately, to get contraction coefficients $\vec{\alpha} = \{\alpha_i\}$
- 5. Use those coefficients, create your estimator $f(\vec{X}, \vec{\alpha}, x^*) = y^*$

Next step is to choose a kernel

Gaussian

Regularization

Noise

Correlation Matrix

$$K_{i,j} = \exp\left(\sum_{k} \theta_{k} |x_{k}^{i} - x_{k}^{j}|^{2}\right) + \epsilon \delta_{i,j}$$

The main part of the algorithm

$$\vec{K}\vec{\alpha} = \vec{y}$$

y is the vector of values corresponding to your training set,

 \overline{K} is your correlation matrix

 $\vec{\alpha}$ is a set of unknowns we need to solve for.

$$\vec{\alpha} = \vec{K}^{-1} \vec{y}$$

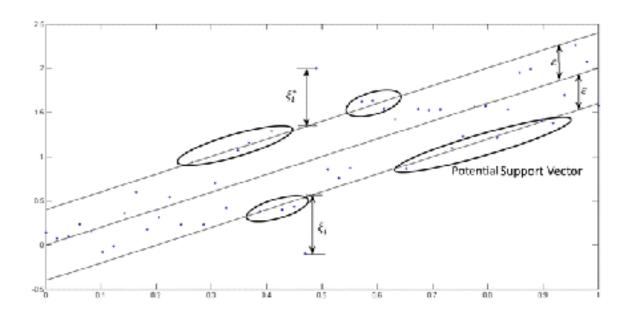
- Once $\vec{\alpha}$ parameters known form the estimator
- we use the coefficients we found during the optimization step and the kernel we started off with.

- To estimate the value y^* for a test point, x^* compute the correlation vector k,
- $y^* = \overrightarrow{a} \cdot \overrightarrow{k}$

$$k_i = \exp\left(\sum_k \theta_k |x_k^i - x_k^{\star}|^2\right)$$

Let's try to simplify everything:

SVR has a different regression goal compared to linear regression. In linear regression we are trying to minimize the error between the prediction and data. In SVR our goal is to make sure that errors do not exceed the threshold.



https://link.springer.com/chapter/10.1007/978-1-4302-5990-9 4

Notes: SVR is very useful for:

Since you are able to generate training points you then know what the "right" is. But it may be expensive to compute the answer for every new point needed.

SVR and in particular gaussian processes are a very good method to use for
efficient computations, by pre-computing a training set and then using a SVR
machine to interpolate the results.

In a classification problem, the vectors \vec{X} are used to define a hyperplane that separates the two different classes in your solution.

These vectors are used to perform linear regression. The vectors closest to the test point are referred to as support vectors. We can evaluate our function anywhere so any vectors could be closest to our test evaluation location.

Gaussian processes are a particular form of SVM. The difference between the two lies in choice of kernel and loss function. The functional form of the kernel determines which vectors in your training set most strongly influence the regression and the form of your estimator. The loss function choice determines the coefficients used in regression. Together these two pieces totally determine the form and accuracy of your estimator. Although this makes it sound like the two are totally different, the spirit of the two are identical.

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Kernel Principal Component Analysis

PCA Recap

- PCA finds the directions of maximal variance in the data.
- The goal of PCA is to look to identify patterns in the data by finding the directions of maximal variance and high dimensional data and project it into a smaller dimensional subspace.

What is Kernel PCA and what does it do?

- Kernel PCA just performs PCA but in a new space.
- It uses Kernel trick to find principal components in a different space (higher dimensional space)
- PCA finds new directions based on covariance matrix of original variables. It can extract maximum P (number of features) eigen values.
- KPCA finds new directions based on kernel matrix. It can extract n (number of observations) eigenvalues.
- Kernel PCA does take more time compared to PCA

Kernel functions and the kernel trick

The basic idea to deal with linearly inseparable data is to project it onto a higher dimensional space where it becomes linearly separable. Let us call this nonlinear mapping function ϕ so that the mapping of a sample x can be written as $x \mapsto \phi(x)$, which is called "wirnel function."

Now, the term "Fernel" describes a function that calculates the dot product of the images of the samples X under &.

$$u(\mathbf{x}_i,\mathbf{x}_j) = \phi(\mathbf{x}_i)\phi(\mathbf{x}_j)^T$$

More details about the damation of this equation are provided in this excellent review article by Quan. Wantz Kernel Principal Component Analysis and its Applications in Face Recognition and Active Shape Modes.[1]

In other words, the function gives poster original define retired leadures into a larger, k-dimensional teature space by exeating nononlinear combinations of the original features. For example, if **x** consists of 2 leafures:

$$\mathbf{x} = \begin{bmatrix} x_1 & x_2 \end{bmatrix}^T \qquad \mathbf{x} \in \mathbb{R}^d$$

$$\label{eq:def_x} \psi \ \phi$$

$$\mathbf{x}' = \begin{bmatrix} x_1 & x_2 & x_1x_2 & x_1^2 & x_1x_2^2 & \dots \end{bmatrix}^T \qquad \mathbf{x} \in \mathbb{R}^d(k >> d)$$

Often, the matteral definition of the RSF kernel is written and implemented as

$$\kappa(x_i, x_j) = \exp \left(-\gamma \| x_i - x_j \|_2^2 \right)$$

where $\gamma = \frac{1}{2\sigma^2}$ is a free parameter that is to be optimized.

http://sebastianraschka.com/Articles/2014_kernel_pca.html#kernel-functions-and-the-kernel-trick

Pick a kernel

Construct the normalized kernel matrix of the data (dimension $m \times m$):

$$\widetilde{K} = K - 21_{1/n}K + 1_{1/n}K1_{1/n}$$

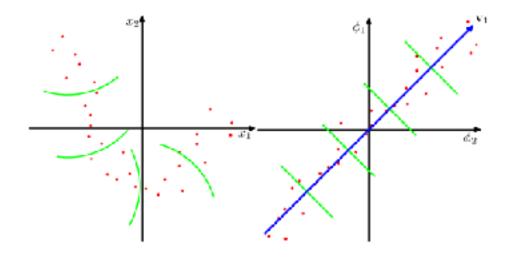
Solve an eigenvalue problem:

$$\widetilde{K}\alpha_i = \lambda_i \alpha_i$$

For any data point (new or old), we can represent it as

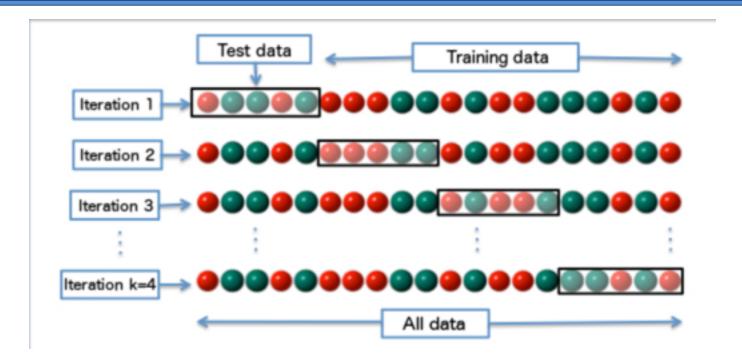
$$y_j = \sum_{i=1}^n \alpha_{ji} K(x, x_i), j = 1,...,d$$

http://www.cs.haifa.ac.il/~rita/uml_course/lectures/KPCA.pdf



K-FOLD CROSS-VALIDATION

- How to split training and testing data?
- Maximize the learning to obtain the best validation
- Cross-Validation
- K-Fold



https://upload.wikimedia.org/wikipedia/commons/1/1c/K-fold_cross_validation_EN.jpg

- The advantage of this method over repeated sub-sampling is that all observations are used for both training and validation
- Each observation is used for validation exactly once
- 10-fold is commonly used

- K = 2
- Two sets d0 and d1
- Train on d0 and validate on d1
- Train on d1 and validate on d0
- When K = n (number of observations), the k-fold cross validation is exactly the leave one out cross-validation.

https://en.wikipedia.org/wiki/Cross-validation_(statistics)

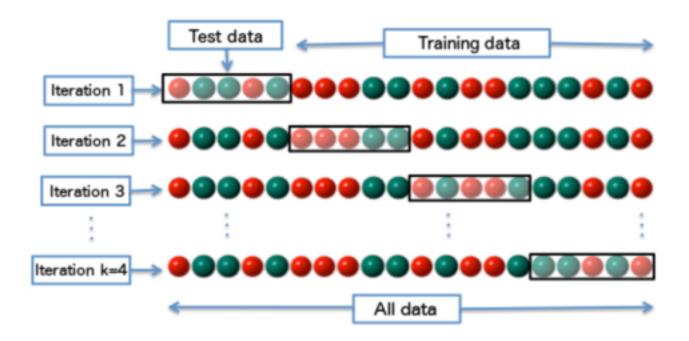
- Randomly partitioned into K equal sized subsamples
- Of the K subsamples, a single subsample is retained as the validation data for testing
- The remaining K 1 subsamples are used as training data
- Cross-validation is then repeated K times (folds)
- The K results from the folds are then averaged for a single estimation

Cross Validation:

- Reserve part of your data to use in evaluating the model
- K-Fold
- Take 80% of your data and use it for training and then you take the remaining 20% of the data and use it to evaluate the performance of the model.

Cross Validation:

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https://en.wikipedia.org/wiki/Cross-validation_(statistics)

- Grid search means that you have a set of models (that each have differing values and lie on a grid).
- You take each of the models to train and evaluate it using cross-validation.
- Then you select the one that performs the best

Example:

- You have a grid with the following values for (gamma, C): (1, 1), (0.1, 1), (1, 10), (0.1, 10).
- It's a grid because it's like a product of [1, 0.1] for gamma and [1, 10] for C.
- Grid-search would basically train for each of these four pair of (gamma, C) values.
- Then evaluate it using cross-validation, and select the one that did best.

https://stackoverflow.com/questions/19335165/cross-validation-and-grid-search

Recap:

- Applied across machine learning to calculate the best parameters to use for any given model.
- Can be extremely computationally expensive
- Grid Search will build a model on each parameter combination possible.
- It iterates through every parameter combination and stores a model for each combination.

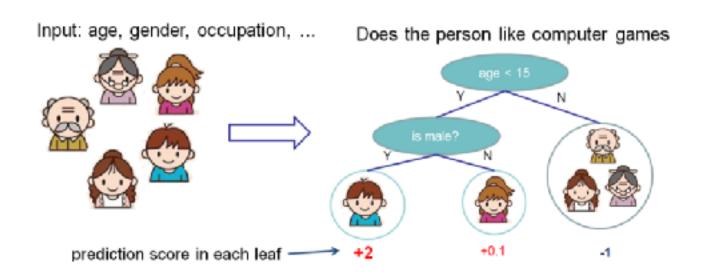
XGBoost stands for extreme Gradient Boosting

- Awesome tool and algorithm used to push the limits of computation resources for boosted tree algorithms.
- Belongs to a broad collection of tools under Distributed Machine Learning Community (DLMC) and XGBoost was created by Tianqi Chen.
- Supports many languages
- Command Line Interface
- It can run on Hadoop

- Supervised Learning
- An ensemble method that seeks to create a strong classifier (model) based on "weak" classifiers.
- XGBoost implements this algorithm for decision tree boosting with an additional custom regularization term in the objective function.

- Adds predictors and corrects previous models
- Fits the new model to new residuals of the previous prediction
- Regression and Classification

- Engineered to exploit every bit of memory and hardware resources for tree boosting algorithms.
- XGBoost offers several advanced features for model tuning, computing environments and algorithm enhancement.
- Capable of performing the three main forms of gradient boosting (Gradient Boosting (GB), Stochastic GB and Regularized GB) and it is robust enough to support fine tuning and addition of regularization parameters.

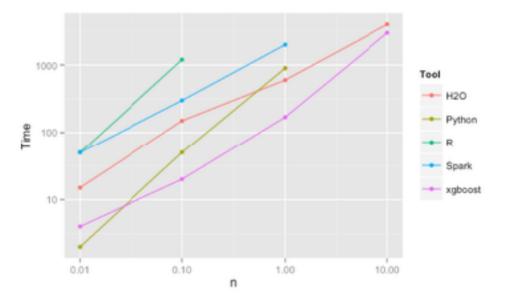


https://xgboost.readthedocs.io/en/latest/model.html



Why Choose To Use XGBoost?

Execution Speed Model Performance



https://www.kdnuggets.com/2017/10/xgboost-top-machine-learning-method-kaggle-explained.html