

# Lecture 16: Summary and outlook

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**MSA220/MVE440** Statistical Learning for Big Data

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# The big topics

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1. Statistical Learning
2. Supervised learning
  - ▶ Classification
  - ▶ Regression
3. Unsupervised learning
  - ▶ Clustering
4. Data representations and dimension reduction
5. Large scale methods

# The big data paradigms

- ▶ **Small to medium sized data**

- ▶ “Good old stats”
- ▶ Typical methods:  $k$ -nearest neighbour (kNN), linear and quadratic discriminant analysis (LDA and QDA), Gaussian mixture models, ...

- ▶ **High-dimensional data**

- ▶ big- $p$  paradigm
- ▶ Typical methods: Feature selection, penalized regression and classification (Lasso, ridge regression, shrunken centroids, ...), low-rank approximations (SVD, NMF), ...
- ▶ **Curse of dimensionality**

- ▶ **Large scale data**

- ▶ big- $n$  paradigm (sometimes in combination with big- $p$ )
- ▶ Typical methods: Random forests (with its big- $n$  extensions), subspace clustering, low-rank approximations (randomized SVD), ...

# Statistical Learning

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# What is Statistical Learning?

Learn **a model** from **data** by minimizing **expected prediction error** determined by a **loss function**.

- ▶ **Model:** Find a model that is suitable for the data
- ▶ **Data:** Data with known outcomes is needed
- ▶ **Expected prediction error:** Focus on quality of prediction (predictive modelling)
- ▶ **Loss function:** Quantifies the discrepancy between observed data and predictions

- ▶ Theoretically best regression function for squared error loss

$$\hat{f}(\mathbf{x}) = \mathbb{E}_{p(y|\mathbf{x})}[y]$$

- ▶ Approximate (1) or make model-assumptions (2)
  1. k-nearest neighbour regression

$$\mathbb{E}_{p(y|\mathbf{x})}[y] \approx \frac{1}{k} \sum_{\mathbf{x}_{i_l} \in N_k(\mathbf{x})} y_{i_l}$$

2. linear regression (viewpoint: generalized linear models (GLM))

$$\mathbb{E}_{p(y|\mathbf{x})}[y] \approx \mathbf{x}^T \boldsymbol{\beta}$$

# Statistical Learning for Classification

- ▶ Theoretically best classification rule for 0-1 loss and  $K$  possible classes (**Bayes rule**)

$$\hat{c}(\mathbf{x}) = \arg \max_{1 \leq i \leq K} p(i|\mathbf{x})$$

- ▶ Approximate (1) or make model-assumptions (2)
  1. k-nearest neighbour classification

$$p(i|\mathbf{x}) \approx \frac{1}{k} \sum_{\mathbf{x}_l \in N_k(\mathbf{x})} \mathbb{1}(i_l = i)$$

2. Multi-class logistic regression

$$p(i|\mathbf{x}) = \frac{e^{\mathbf{x}^T \boldsymbol{\beta}^{(i)}}}{1 + \sum_{l=1}^{K-1} e^{\mathbf{x}^T \boldsymbol{\beta}^{(l)}}} \quad \text{and} \quad p(K|\mathbf{x}) = \frac{1}{1 + \sum_{l=1}^{K-1} e^{\mathbf{x}^T \boldsymbol{\beta}^{(l)}}}$$

## ► Training error

$$R^{tr} = \frac{1}{n} \sum_{l=1}^n L(y_l, \hat{f}(\mathbf{x}_l | \mathcal{T}))$$

where

$$\mathcal{T} = \{(y_l, \mathbf{x}_l) : 1 \leq l \leq n\}$$

## ► Test error

$$R^{te} = \frac{1}{m} \sum_{l=1}^m L(\tilde{y}_l, \hat{f}(\tilde{\mathbf{x}}_l | \mathcal{T}))$$

where  $(\tilde{y}_l, \tilde{\mathbf{x}}_l)$  for  $1 \leq l \leq m$  are new samples from the same distribution as  $\mathcal{T}$ , i.e.  $p(\mathcal{T})$ .

## Splitting up the data

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- ▶ **Holdout method:** If we have a lot of samples, **randomly split** available data into **training set** and **test set**
- ▶  **$c$ -fold cross-validation:** If we have few samples
  1. **Randomly split** available data into  $c$  equally large subsets, so-called **folds**.
  2. By taking turns, use  $c - 1$  folds as the **training set** and the last fold as the **test set**

## Approximations of expected prediction error

- Use **test error** for hold-out method, i.e.

$$R^{te} = \frac{1}{m} \sum_{l=1}^m L(\tilde{y}_l, \hat{f}(\tilde{\mathbf{x}}_l | \mathcal{T}))$$

where  $(\tilde{y}_l, \tilde{\mathbf{x}}_l)$  for  $1 \leq l \leq m$  are the elements in the test set.

- Use average **test error** for c-fold cross-validation, i.e.

$$R^{cv} = \frac{1}{n} \sum_{j=1}^c \sum_{(y_l, \mathbf{x}_l) \in \mathcal{F}_j} L(y_l, \hat{f}(\mathbf{x}_l | \mathcal{F}_{-j}))$$

where  $\mathcal{F}_j$  is the  $j$ -th fold and  $\mathcal{F}_{-j}$  is all data except fold  $j$ .

**Note:** For  $c = 1$  this is called **leave-one-out cross validation (LOOCV)**

## Careful data splitting

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- ▶ **Note:** For the approximations to be justifiable, test and training sets need to be identically distributed
- ▶ **Splitting has to be done randomly**
- ▶ If data is unbalanced, then **stratification** is necessary.  
Examples:
  - ▶ Class imbalance
  - ▶ Continuous outcome is observed more often in some intervals than others (e.g. high values more often than low values)

# Bias-Variance Tradeoff

## Bias-Variance Decomposition

$$R = \mathbb{E}_{p(\mathcal{T}, \mathbf{x}, y)} [(y - \hat{f}(\mathbf{x}))^2]$$

$$= \sigma^2$$

$$+ \mathbb{E}_{p(\mathbf{x})} \left[ \left( f(\mathbf{x}) - \mathbb{E}_{p(\mathcal{T})} [\hat{f}(\mathbf{x})] \right)^2 \right]$$

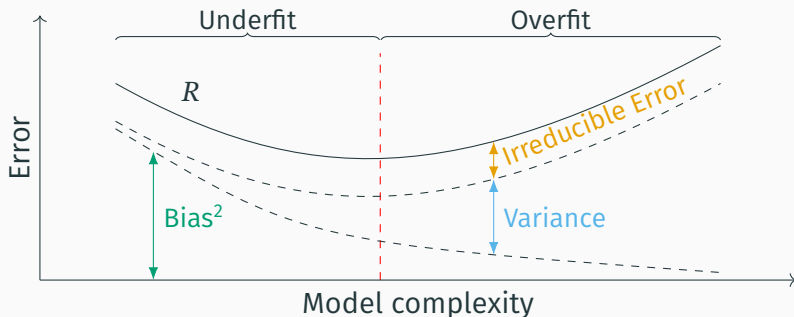
$$+ \mathbb{E}_{p(\mathbf{x})} \left[ \text{Var}_{p(\mathcal{T})} [\hat{f}(\mathbf{x})] \right]$$

Total expected prediction error

Irreducible Error

Bias<sup>2</sup> averaged over  $\mathbf{x}$

Variance of  $\hat{f}$  averaged over  $\mathbf{x}$



# Classification

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# Overview

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1.  $k$ -nearest neighbours (Lecture 1)
2. 0-1 regression (Lecture 2)
  - ▶ just an academic example - **do not use in practice**
3. Logistic regression (Lecture 2, both binary and multi-class; Lecture 11 for sparse case)
4. Nearest Centroids (Lecture 2) and shrunken centroids (Lecture 10)
5. Discriminant analysis (Lecture 2)
  - ▶ Many variants: linear (LDA), quadratic (QDA), diagonal/Naive Bayes, regularized (RDA; Lecture 5), Fisher's LDA/reduced-rank LDA (Lecture 6), mixture DA (Lecture 8)
6. Classification and Regression trees (CART) (Lecture 4)
7. Random Forests (Lecture 5 & 15)

## Multiple angles on the same problem

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1. **Bayes rule:** Approximate  $p(i|\mathbf{x})$  and choose largest
  - ▶ e.g. kNN or logistic regression
2. **Model of the feature space:** Assume models for  $p(\mathbf{x}|i)$  and  $p(i)$  separately
  - ▶ e.g. discriminant analysis
3. **Partitioning methods:** Create explicit partitions of the feature space and assign each a class
  - ▶ e.g. CART or Random Forests

## Finding the parameters of DA

- ▶ Notation: Write  $p(i) = \pi_i$  and consider them as unknown parameters
- ▶ Given data  $(i_l, \mathbf{x}_l)$  the likelihood maximization problem is

$$\arg \max_{\mu, \Sigma, \pi} \prod_{l=1}^n N(\mathbf{x}_l | \mu_{i_l}, \Sigma_{i_l}) \pi_{i_l} \quad \text{subject to} \quad \sum_{i=1}^K \pi_i = 1.$$

- ▶ Can be solved using a Lagrange multiplier (try it!) and leads to

$$\hat{\pi}_i = \frac{n_i}{n}, \quad \text{with} \quad n_i = \sum_{l=1}^n \mathbb{1}(i_l = i)$$

$$\hat{\mu}_i = \frac{1}{n_i} \sum_{i_l=i} x_l$$

$$\hat{\Sigma}_i = \frac{1}{n_i - 1} \sum_{i_l=i} (x_l - \hat{\mu}_i)(x_l - \hat{\mu}_i)^T$$

## Performing classification in DA

Bayes' rule implies the classification rule

$$c(\mathbf{x}) = \arg \max_{1 \leq i \leq K} N(\mathbf{x} | \boldsymbol{\mu}_i, \boldsymbol{\Sigma}_i) \pi_i$$

Note that since  $\log$  is strictly increasing this is equivalent to

$$c(\mathbf{x}) = \arg \max_{1 \leq i \leq K} \delta_i(\mathbf{x})$$

where

$$\begin{aligned} \delta_i(\mathbf{x}) &= \log N(\mathbf{x} | \boldsymbol{\mu}_i, \boldsymbol{\Sigma}_i) + \log \pi_i \\ &= \log \pi_i - \frac{1}{2}(\mathbf{x} - \boldsymbol{\mu}_i)^T \boldsymbol{\Sigma}_i^{-1}(\mathbf{x} - \boldsymbol{\mu}_i) - \frac{1}{2} \log |\boldsymbol{\Sigma}_i| \quad (+ C) \end{aligned}$$

This is a quadratic function in  $\mathbf{x}$ .

## Different levels of complexity

- ▶ This method is called **Quadratic Discriminant Analysis (QDA)**
- ▶ **Problem:** Many parameters that grow quickly with dimension
  - ▶  $K - 1$  for all  $\pi_i$
  - ▶  $p \cdot K$  for all  $\mu_i$
  - ▶  $p(p + 1)/2 \cdot K$  for all  $\Sigma_i$  (most costly)
- ▶ **Solution:** Replace covariance matrices  $\Sigma_i$  by a pooled estimate

$$\hat{\Sigma} = \sum_{i=1}^K \hat{\Sigma}_i \frac{n_i - 1}{n - K} = \frac{1}{n - K} \sum_{i=1}^K \sum_{l_l=i} (x_l - \hat{\mu}_i)(x_l - \hat{\mu}_i)^T$$

- ▶ **Simpler correlation and variance structure:** All classes are assumed to have the same correlation structure between features

## Performing classification in the simplified case

As before, consider

$$c(\mathbf{x}) = \arg \max_{1 \leq i \leq K} \delta_i(\mathbf{x})$$

where

$$\delta_i(\mathbf{x}) = \log \pi_i + \mathbf{x}^T \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu}_i - \frac{1}{2} \boldsymbol{\mu}_i^T \boldsymbol{\Sigma}^{-1} \boldsymbol{\mu}_i \quad (+ C)$$

This is a linear function in  $\mathbf{x}$ . The method is therefore called **Linear Discriminant Analysis (LDA)**.

## Even more simplifications

Other simplifications of the correlation structure are possible

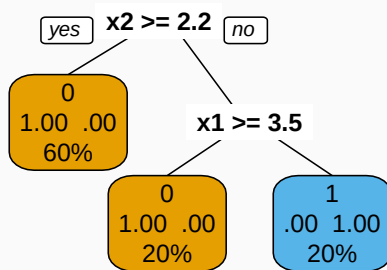
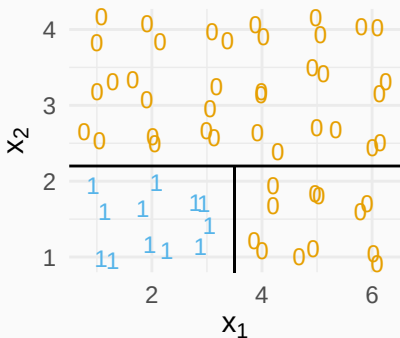
- ▶ Ignore all correlations between features but allow different variances, i.e.  $\Sigma_i = \Lambda_i$  for a diagonal matrix  $\Lambda_i$  (**Diagonal QDA** or **Naive Bayes' Classifier**)
- ▶ Ignore all correlations and make feature variances equal, i.e.  $\Sigma_i = \Lambda$  for a diagonal matrix  $\Lambda$  (**Diagonal LDA**)
- ▶ Ignore correlations and variances, i.e.  $\Sigma_i = \sigma^2 \mathbf{I}_{p \times p}$  (**Nearest Centroids adjusted for class frequencies  $\pi_i$** )

# Classification and Regression Trees (CART)

- **Complexity of partitioning:**

Arbitrary Partition  $>$  Rectangular Partition  $>$  Partition from a sequence of binary splits

- Classification and Regression Trees create a **sequence of binary axis-parallel splits** in order to **reduce variability** of values/classes in each region



## Bootstrap aggregation (bagging)

1. Given a training sample  $(y_l, \mathbf{x}_l)$  or  $(i_l, \mathbf{x}_l)$ , we want to fit a predictive model  $\hat{f}(\mathbf{x})$
2. For  $b = 1, \dots, B$ , form bootstrap samples of the training data and fit the model, resulting in  $\hat{f}_b(\mathbf{x})$
3. Define

$$\hat{f}_{\text{bag}}(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \hat{f}_b(\mathbf{x})$$

where  $\hat{f}_b(\mathbf{x})$  is a continuous value for a regression problem or a vector of class probabilities for a classification problem

**Majority vote** can be used for classification problems instead of averaging

# Random Forests

## Computational procedure

1. Given a training sample with  $p$  features, do for  $b = 1, \dots, B$ 
  - 1.1 Draw a bootstrap sample of size  $n$  from training data (with replacement)
  - 1.2 Grow a tree  $T_b$  until each node reaches minimal node size  $n_{\min}$ 
    - 1.2.1 Randomly select  $m$  variables from the  $p$  available
    - 1.2.2 Find best splitting variable among these  $m$
    - 1.2.3 Split the node
2. For a new  $\mathbf{x}$  predict

$$\text{Regression: } \hat{f}_{rb}(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B T_b(\mathbf{x})$$

Classification: Majority vote at  $\mathbf{x}$  across trees

**Note:** Step 1.2.1 leads to less correlation between trees built on bootstrapped data.

# Regression and feature selection

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# Overview

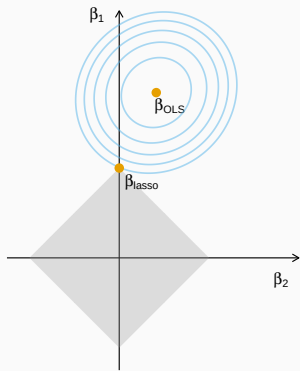
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1.  $k$ -nearest neighbours ([Lecture 1](#))
2. Linear regression ([Lecture 1](#))
3. Filtering ([Lecture 9](#))
  - ▶ F-score, mutual information, RF variable importance, ...
4. Wrapping ([Lecture 9](#))
  - ▶ Forward-, backward-, and best subset selection
5. Penalized regression and variable selection
  - ▶ Ridge regression and lasso ([Lecture 9](#)), group lasso and elastic net ([Lecture 10](#)), adaptive lasso and SCAD ([Lecture 11](#))
6. Computation of the lasso ([Lecture 10](#))
7. Applications of penalisation
  - ▶ For Discriminant Analysis: Shrunken centroids ([Lecture 10](#))
  - ▶ For GLM: sparse multi-class logistic regression ([Lecture 11](#))
  - ▶ For networks: Graphical lasso ([Lecture 14](#))

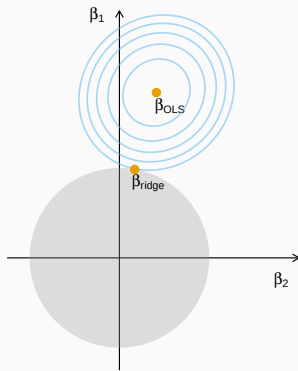
# Intuition for the penalties

The least squares RSS is minimized for  $\beta_{OLS}$ . If a constraint is added ( $\|\beta\|_q \leq t$ ) then the RSS is minimized by the closest  $\beta$  possible that fulfills the constraint.

Lasso



Ridge

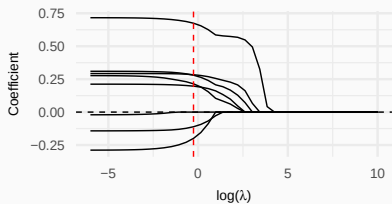
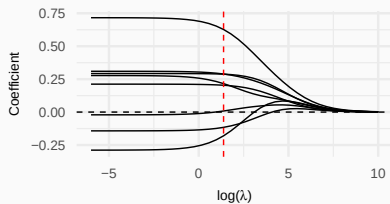
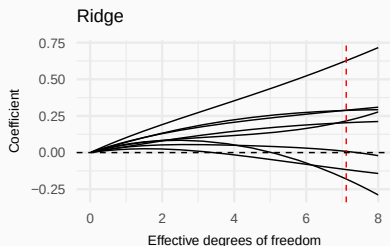


The blue lines are the contour lines for the RSS.

# A regularisation path

**Prostate cancer dataset** ( $n = 67, p = 8$ )

Red dashed lines indicate the  $\lambda$  selected by cross-validation



## Potential caveats of the lasso

- ▶ **Sparsity of the true model:**

- ▶ The lasso only works if the data is generated from a sparse process.
- ▶ However, a dense process with many variables and not enough data or high correlation between predictors can be unidentifiable either way

- ▶ **Correlations:** Many non-relevant variables correlated with relevant variables can lead to the selection of the wrong model, even for large  $n$

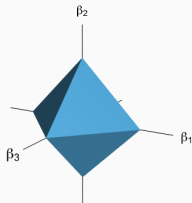
- ▶ **Irrepresentable condition:** Split  $\mathbf{X}$  such that  $\mathbf{X}_1$  contains all **relevant variables** and  $\mathbf{X}_2$  contains all **irrelevant variables**. If

$$|(\mathbf{X}_2^T \mathbf{X}_1)(\mathbf{X}_1^T \mathbf{X}_1)^{-1}| < 1 - \eta$$

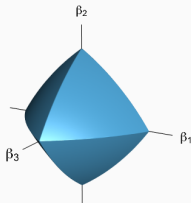
for some  $\eta > 0$  then the lasso is (almost) guaranteed to pick the true model

# Elnet and group lasso

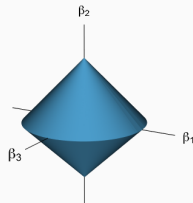
Lasso



Elastic net ( $\alpha = 0.7$ )



Group lasso ( $\{\beta_1, \beta_3\}, \{\beta_2\}$ )



- ▶ The lasso sets variables exactly to zero either on a corner (all but one) or along an edge (fewer).
- ▶ The elastic net similarly sets variables exactly to zero on a corner or along an edge. In addition, the curved edges encourage coefficients to be closer together.
- ▶ The group lasso has actual information about groups of variables. It encourages whole groups to be zero simultaneously. Within a group, it encourages the coefficients to be as similar as possible.

# Clustering

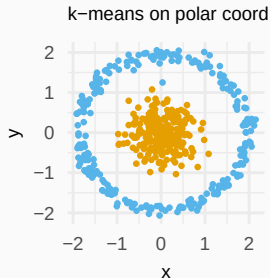
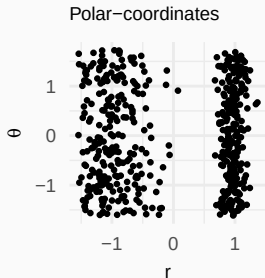
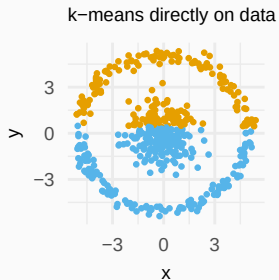
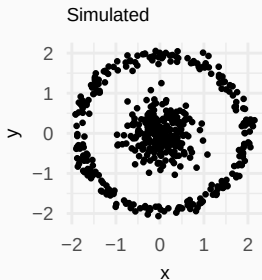
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# Overview

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1. Combinatorial Clustering ([Lecture 6](#))
2. k-means ([Lecture 6](#))
3. Partition around medoids (PAM)/k-medoids ([Lecture 7](#))
4. Cluster count selection ([Lecture 7 & 8](#))
  - ▶ Elbow heuristic, Silhouette Width, Cluster Strength Prediction, Bayesian Information Criterion (BIC) for GMM
5. Hierarchical clustering ([Lecture 7](#))
6. Gaussian Hierarchical Models (GMM; [Lecture 8](#))
7. DBSCAN ([Lecture 8](#))
8. Non-negative matrix factorisation (NMF; [Lecture 11](#))
9. Subspace clustering ([Lecture 14](#))
  - ▶ In particular, CLIQUE and ProClus
10. Spectral clustering ([Lecture 14](#))

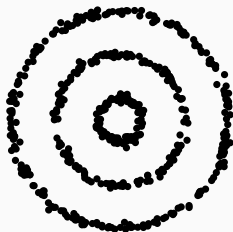
# k-means and the assumption of spherical geometry



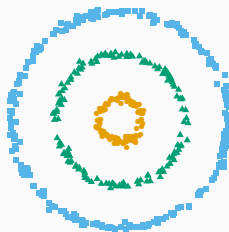
# Spectral Clustering

1. Determine the weighted adjacency matrix  $\mathbf{W}$  and the graph Laplacian  $\mathbf{L}$
2. Find the  $K$  smallest eigenvalues of  $\mathbf{L}$  that are near zero and well separated from the others
3. Find the corresponding eigenvectors  $\mathbf{U} = (\mathbf{u}_1, \dots, \mathbf{u}_K) \in \mathbb{R}^{n \times K}$  and use k-means on the rows of  $\mathbf{U}$  to determine cluster membership

Raw data (n = 500)



Spectral clustering



# Hierarchical Clustering

## Procedural idea:

1. **Initialization:** Let each observation  $\mathbf{x}_l$  be in its own cluster  $g_l^0$  for  $l = 1, \dots, n$
2. **Joining:** In step  $i$ , join the two clusters  $g_l^{i-1}$  and  $g_m^{i-1}$  that are closest to each other resulting in  $n - i$  clusters
3. After  $n - 1$  steps all observations are in one big cluster

## Subjective choices:

- ▶ How do we measure distance between observations?
- ▶ What is **closeness** for clusters?

Cluster-cluster distance is called **linkage**

**Distance between clusters  $g$  and  $h$**

1. **Average Linkage:**

$$d(g, h) = \frac{1}{|g| \cdot |h|} \sum_{\substack{x_l \in g \\ x_m \in h}} D_{l,m}$$

2. **Single Linkage**

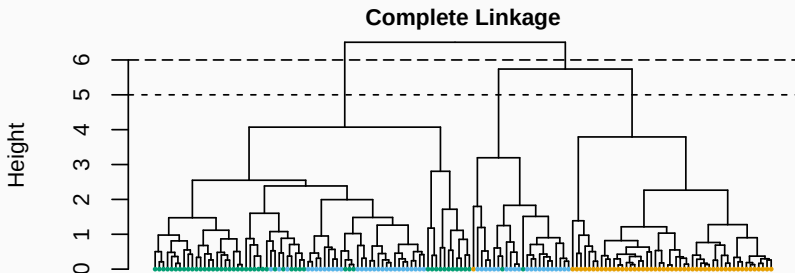
$$d(g, h) = \min_{\substack{x_l \in g \\ x_m \in h}} D_{l,m}$$

3. **Complete Linkage**

$$d(g, h) = \max_{\substack{x_l \in g \\ x_m \in h}} D_{l,m}$$

# Dendrograms

Hierarchical clustering applied to **iris dataset**



- ▶ Leaf colours represent iris type: **setosa**, **versicolor** and **virginica**
- ▶ **Height** is the distance between clusters
- ▶ The tree can be **cut** at a certain height to achieve a final clustering. Long branches mean large increase in within cluster scatter at join

## Remember QDA

In Quadratic Discriminant Analysis (QDA) we assumed

$$p(\mathbf{x}|i) = N(\mathbf{x}|\boldsymbol{\mu}_i, \boldsymbol{\Sigma}_i) \quad \text{and} \quad p(i) = \pi_i$$

This is known as a **Gaussian Mixture Model (GMM)** for  $\mathbf{x}$  where

$$p(\mathbf{x}) = \sum_{i=1}^K p(i)p(\mathbf{x}|i) = \sum_{i=1}^K \pi_i N(\mathbf{x}|\boldsymbol{\mu}_i, \boldsymbol{\Sigma}_i)$$

QDA used that the classes  $i_l$  and feature vectors  $\mathbf{x}_l$  of the observations were known to calculate  $\pi_i$ ,  $\boldsymbol{\mu}_i$  and  $\boldsymbol{\Sigma}_i$ .

**What if we only know the features  $\mathbf{x}_l$ ?**

# Expectation-Maximization for GMMs

Finding the MLE for parameters  $\theta$  in GMMs results in an iterative process called **Expectation-Maximization (EM)**

1. Initialize  $\theta$
2. **E-Step:** Update

$$\eta_{li} = \frac{\pi_i N(\mathbf{x}_l | \boldsymbol{\mu}_i, \boldsymbol{\Sigma}_i)}{\sum_{j=1}^K \pi_j N(\mathbf{x}_l | \boldsymbol{\mu}_j, \boldsymbol{\Sigma}_j)}$$

3. **M-Step:** Update

$$\boldsymbol{\mu}_i = \frac{\sum_{l=1}^n \eta_{li} \mathbf{x}_l}{\sum_{l=1}^n \eta_{li}} \quad \pi_i = \frac{\sum_{l=1}^n \eta_{li}}{n}$$

$$\boldsymbol{\Sigma}_i = \frac{1}{\sum_{l=1}^n \eta_{li}} \sum_{l=1}^n \eta_{li} (\mathbf{x}_l - \boldsymbol{\mu}_i)(\mathbf{x}_l - \boldsymbol{\mu}_i)^T$$

4. Repeat steps 2 and 3 until convergence

## Density-based clusters

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A **cluster**  $C$  is a set of points in  $D$  s.th.

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1. If  $p \in C$  and  $q$  is density-reachable from  $p$  then  $q \in C$   
(**maximality**)

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(**maximality**)
2. For all  $p, q \in C$ :  $p$  and  $q$  are density-connected  
(**connectivity**)

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This leads to **three types of points**

1. **Core points:** Part of a cluster and at least  $n_{\min}$  points in neighbourhood
2. **Border points:** Part of a cluster but not core points
3. **Noise:** Not part of any cluster

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3. **Noise:** Not part of any cluster

**Note:** Border points can have **non-unique cluster assignments**

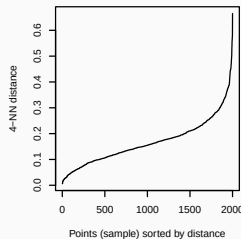
## Computational procedure:

1. Go through each point  $p$  in the dataset  $D$
2. If it has already been processed take the next one
3. Else determine its  $\varepsilon$ -neighbourhood. If less than  $n_{\min}$  points in neighbourhood, label as noise. Otherwise, start a new cluster.
4. Find all points that are density-reachable from  $p$  and add them to the cluster.

- ▶ Controls how easy it is to connect components in a cluster
  - ▶ Too small and most points are core points, creating many small clusters
  - ▶ Too large and few points are core points, leading to many noise labelled observations
- ▶ A cluster has by definition at least  $n_{\min}$  points
- ▶ Choice of  $n_{\min}$  is very dataset dependent
- ▶ Tricky in high-dimensional data (**curse of dimensionality**, everything is far apart)

## Dependence on $\varepsilon$

- ▶ Controls how much of the data will be clustered
  - ▶ Too small and small gaps in clusters cannot be bridged, leading to isolated islands in the data
  - ▶ Too large and everything is connected
- ▶ Choice of  $\varepsilon$  is also dataset dependent but there is a **decision tool**
  - ▶ Determine distance to the  $k$  nearest neighbours for each point in the dataset
  - ▶ Inside clusters, increasing  $k$  should not lead to a large increase of  $d$
  - ▶ The optimal  $\varepsilon$  is supposed to be roughly at the knee



# **Dimension reduction and data representation**

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# Overview

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1. Principal Component Analysis (PCA; [Lecture 5](#))
2. Singular Value Decomposition (SVD; [Lecture 5, 11 & 15](#))
3. Factor Analysis ([Lecture 11](#))
4. Non-negative matrix factorization (NMF; [Lecture 11 & 12](#))
5. Kernel-PCA (kPCA; [Lecture 12](#))
6. Multi-dimensional scaling (MDS; [Lecture 13](#))
  - ▶ Classical scaling and metric MDS for general distance matrices
7. Isomap ([Lecture 13](#))
8. t-distributed Stochastic Neighbour Embedding (tSNE; [Lecture 13](#))
9. Laplacian Eigenmaps ([Lecture 14](#))

# Principal Component Analysis (PCA)

## Computational Procedure:

1. **Centre** and **standardize** the columns of the data matrix  $\mathbf{X} \in \mathbb{R}^{n \times p}$
2. Calculate the **empirical covariance matrix**  $\hat{\Sigma} = \frac{1}{n-1} \mathbf{X}^T \mathbf{X}$
3. Determine the **eigenvalues**  $\lambda_j$  and corresponding orthonormal **eigenvectors**  $\mathbf{r}_j$  of  $\hat{\Sigma}$  for  $j = 1, \dots, p$  and order them such that

$$\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_p \geq 0$$

4. The vectors  $\mathbf{r}_j$  give the direction of the **principal components (PC)**  $\mathbf{r}_j^T \mathbf{x}$  and the eigenvalues  $\lambda_j$  are the **variances along the PC directions**

**Note:** Set  $\mathbf{R} = (\mathbf{r}_1, \dots, \mathbf{r}_p)$  and  $\mathbf{D} = \text{diag}(\lambda_1, \dots, \lambda_p)$  then

$$\hat{\Sigma} = \mathbf{R} \mathbf{D} \mathbf{R}^T \quad \text{and} \quad \mathbf{R}^T \mathbf{R} = \mathbf{R} \mathbf{R}^T = \mathbf{I}_p$$

## PCA and Dimension Reduction

**Recall:** For a matrix  $\mathbf{A} \in \mathbb{R}^{k \times k}$  with eigenvalues  $\lambda_1, \dots, \lambda_k$  it holds that

$$\text{tr}(\mathbf{A}) = \sum_{j=1}^k \lambda_j$$

For the empirical covariance matrix  $\hat{\Sigma}$  and the variance of the  $j$ -th feature  $\text{Var}[x_j]$

$$\text{tr}(\hat{\Sigma}) = \sum_{j=1}^p \text{Var}[x_j] = \sum_{j=1}^p \lambda_j$$

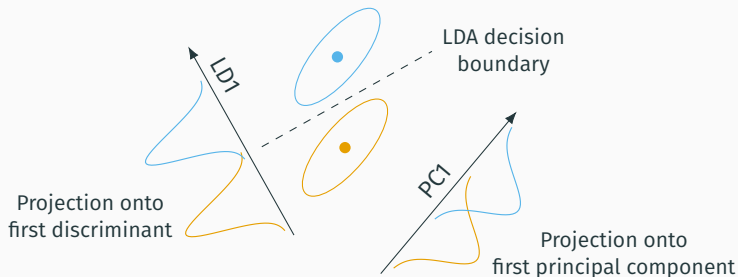
is called the **total variation**.

Using only the first  $m < p$  principal components leads to

$$\frac{\lambda_1 + \dots + \lambda_m}{\lambda_1 + \dots + \lambda_p} \cdot 100\% \quad \text{of } \mathbf{explained\ variance}$$

## Better data projection for classification?

**Idea:** Find directions along which projections result in minimal within-class scatter and maximal between-class separation.



# Non-negative matrix factorization (NMF)

A **non-negative matrix factorisation** of  $\mathbf{X}$  with rank  $q$  solves

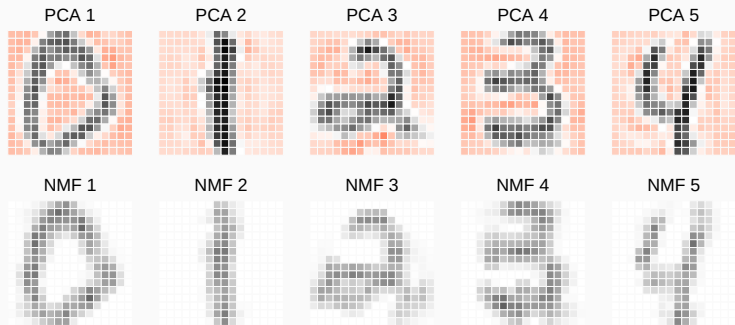
$$\arg \min_{\mathbf{W} \in \mathbb{R}^{p \times q}, \mathbf{H} \in \mathbb{R}^{q \times n}} \|\mathbf{X} - \mathbf{WH}\|_F^2 \quad \text{such that} \quad \mathbf{W} \geq 0, \mathbf{H} \geq 0$$

- ▶ **Sum of positive layers:**  $\mathbf{X} \approx \sum_{j=1}^q \mathbf{W}_{\cdot j} \mathbf{H}_{\cdot j}^T$
- ▶ Non-negativity constraint leads to **sparsity in basis** (in  $\mathbf{W}$ ) and **coefficients** (in  $\mathbf{H}$ ) [example on next slides]
- ▶ NP-hard problem, i.e. no general algorithm exists

## SVD vs NMF – Example: Reconstruction

**MNIST-derived zip code digits** ( $n = 1000$ ,  $p = 256$ )

100 samples are drawn randomly from each class to keep the problem balanced.

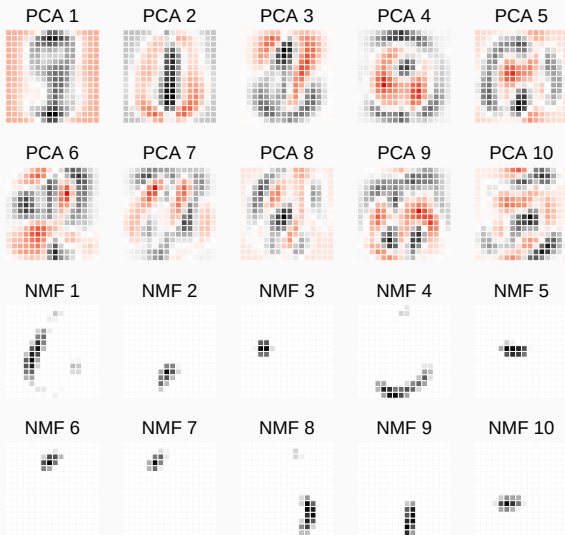


**Red-ish** colours are for negative values, white is around zero and dark stands for positive values

# SVD vs NMF – Example: Basis Components

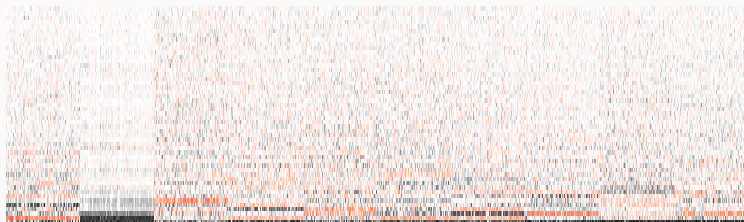
Large difference between  
SVD/PCA and NMF basis  
components

NMF captures **sparse**  
**characteristic parts** while  
PCA components capture  
more global features.



# SVD vs NMF – Example: Coefficients

## SVD coefficients



## NMF coefficients



Note the additional **sparsity** in the NMF coefficients.

# t-distributed Stochastic Neighbour Embedding (tSNE)

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**t-distributed stochastic neighbour embedding (tSNE)** follows a similar strategy as Isomap, in the sense that it **measures distances locally**.

**Idea:** Measure distance of feature  $\mathbf{x}_l$  to another feature  $\mathbf{x}_i$  proportional to the likelihood of  $\mathbf{x}_i$  under a Gaussian distribution centred at  $\mathbf{x}_l$  with an isotropic covariance matrix.

# Computation of tSNE

For feature vectors  $\mathbf{x}_1, \dots, \mathbf{x}_n$ , set

$$p_{i|l} = \frac{\exp(-\|\mathbf{x}_l - \mathbf{x}_i\|_2^2 / (2\sigma_l^2))}{\sum_{k \neq l} \exp(-\|\mathbf{x}_l - \mathbf{x}_k\|_2^2 / (2\sigma_l^2))} \quad \text{and} \quad p_{il} = \frac{p_{i|l} + p_{l|i}}{2n}, \quad p_{ll} = 0$$

The variances  $\sigma_l^2$  are chosen such that the **perplexity** (here: **approximate number of close neighbours**) of each marginal distribution (the  $p_{i|l}$  for fixed  $l$ ) is constant.

In the lower-dimensional embedding distance between  $\mathbf{y}_1, \dots, \mathbf{y}_n$  is measured with a **t-distribution with one degree of freedom** or **Cauchy distribution**

$$q_{il} = \frac{(1 + \|\mathbf{y}_i - \mathbf{y}_l\|_2^2)^{-1}}{\sum_{k \neq j} (1 + \|\mathbf{y}_k - \mathbf{y}_j\|_2^2)^{-1}} \quad \text{and} \quad q_{ll} = 0$$

To determine the  $\mathbf{y}_l$  the KL divergence between the distributions  $P = (p_{il})_{il}$  and  $Q = (q_{il})_{il}$  is minimized with gradient descent

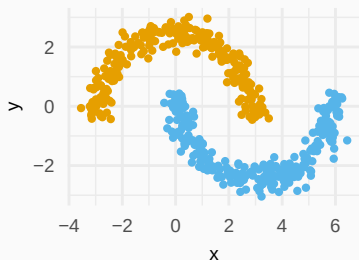
$$\text{KL}(P||Q) = \sum_{i \neq l} p_{il} \log \frac{p_{il}}{q_{il}}$$

## Caveats of tSNE

tSNE is a powerful method but comes with some difficulties as well

- ▶ Convergence to local minimum (i.e. repeated runs can give different results)
- ▶ Perplexity is hard to tune (as with any tuning parameter)

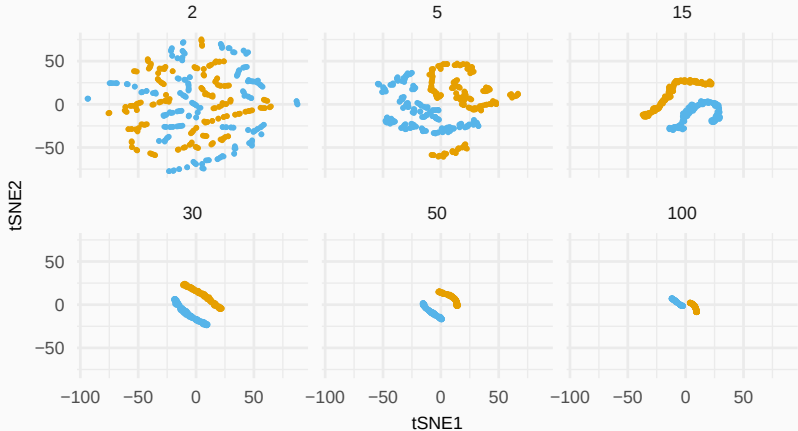
Let's see what tSNE does to our old friend, the moons dataset.



# Influence of perplexity on tSNE

Transformed with tSNE

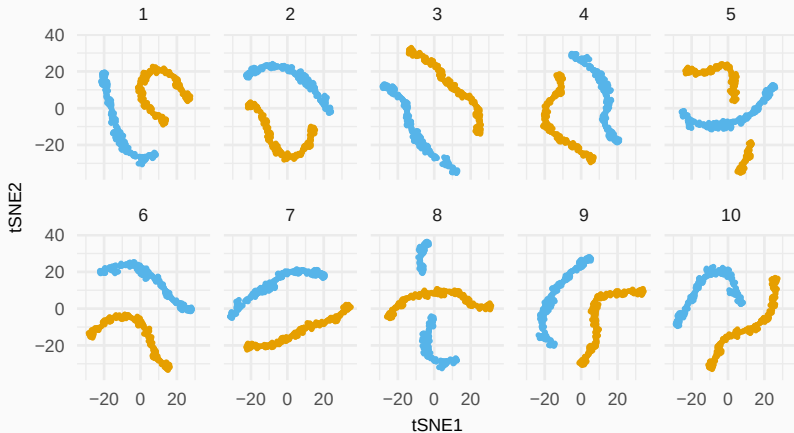
Varying perplexity



# tSNE multiple runs

Transformed with tSNE

Perplexity = 20, multiple runs



# Large scale methods

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- ▶ Randomised low-rank SVD ([Lecture 15](#))
- ▶ Divide and Conquer ([Lecture 15](#))
- ▶ Random Forests with big- $n$  extensions ([Lecture 15](#))
- ▶ Leveraging ([Lecture 15](#))

## Random projection

There are multiple possibilities how the map  $f$  in the **Johnson-Lindenstrauss theorem** can be found.

Let  $\mathbf{X} \in \mathbb{R}^{n \times p}$  be a data matrix and  $q$  the target dimension.

- **Gaussian random projection:** Set

$$\Omega_{ij} \sim N\left(0, \frac{1}{q}\right) \quad \text{for } i = 1, \dots, p, j = 1, \dots, q$$

- **Sparse random projection:** For a given  $s > 0$  set

$$\Omega_{ij} = \sqrt{\frac{s}{q}} \begin{cases} -1 & 1/(2s) \\ 0 & \text{with probability } 1 - 1/s \\ 1 & 1/(2s) \end{cases}$$

for  $i = 1, \dots, p, j = 1, \dots, q$  where often  $s = 3$   
(Achlioptas, 2003) or  $s = \sqrt{p}$  (Li et al., 2006)

then  $\mathbf{Y} = \mathbf{X}\mathbf{\Omega} \in \mathbb{R}^{n \times q}$  is a **random projection** for  $\mathbf{X}$ .

## Randomized low-rank SVD

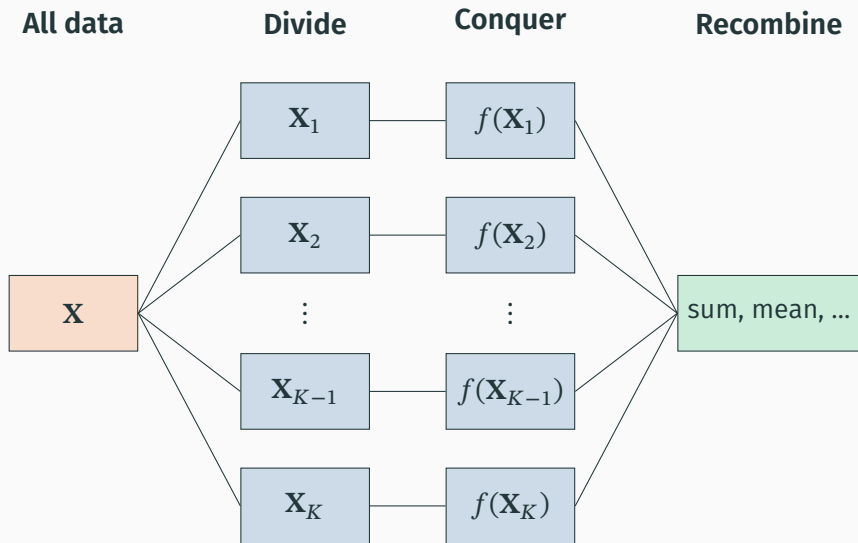
**Original goal:** Apply SVD in cases where both  $n$  and  $p$  are large.

**Idea:** Determine an approximate low-dimensional basis for the range of  $\mathbf{X}$  and perform the matrix-factorisation in the low-dimensional space.

- ▶ Using a random projection  $\mathbf{X} \approx \mathbf{Q}\mathbf{Q}^T\mathbf{X} = \mathbf{Q}\mathbf{T}$
- ▶ Note that  $\mathbf{T} \in \mathbb{R}^{q \times p}$
- ▶ Calculate the SVD of  $\mathbf{T} = \underset{q \times q}{\mathbf{U}_0} \cdot \underset{q \times q}{\mathbf{D}} \cdot \underset{q \times p}{\mathbf{V}^T}$
- ▶ Set  $\mathbf{U} = \mathbf{Q}\mathbf{U}_0 \in \mathbb{R}^{n \times q}$ , then  $\mathbf{X} \approx \mathbf{U}\mathbf{D}\mathbf{V}^T$

The SVD of  $\mathbf{X}$  can therefore be found by **random projection** into a  $q$ -dimensional subspace of the range of  $\mathbf{X}$ , performing **SVD in the lower-dimensional subspace** and subsequent **reconstruction** of the vectors into the original space.

# Divide and conquer



## Random forests for big- $n$

Instead of the standard RF with normal bootstrapping, multiple strategies can be taken

- ▶ **Subsampling (once):** Take a subsample of size  $m$  and grow RF from there. Very simple to implement, but difficult to ensure that the subsample is representative.
- ▶  **$m$ -out-of- $n$  sampling:** Instead of standard bootstrapping, draw repeatedly  $m$  samples and grow a tree on each subsample. Recombine trees in the usual fashion.
- ▶ **BLB sampling:** Grow a forest on each subset by repeatedly oversampling to  $n$  samples.
- ▶ **Divide and Conquer:** Split original data in  $K$  parts and grow a random forest on each.

## Problem: Representativeness

How can we ensure that a subsample is still representative?

We need **additional information** about the samples. Consider the special case of linear regression and  $n \gg p$ .

**Recall:** For least squares predictions it holds that

$$\hat{\mathbf{y}} = \mathbf{X}\hat{\boldsymbol{\beta}} = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{y} = \mathbf{H}\mathbf{y}$$

with the **hat-matrix**  $\mathbf{H} = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T$ .

Specifically  $\hat{y}_i = \sum_{j=1}^n H_{ij}y_j$ , which means that  $H_{ii}$  influences its own fitted values.

Element  $H_{ii}$  is called the **leverage** of the observation.

Leverage captures if the observation  $i$  is close or far from the centre of the data in feature space.

**Goal:** Subsample the data, but make the **more influential** data points, those with **high leverage**, more likely to be sampled.

## Computational approach

- ▶ Weight sample  $i$  by

$$\pi_i = \frac{H_{ii}}{\sum_{j=1}^n H_{jj}}$$

- ▶ Draw a weighted subsample of size  $m \ll n$
- ▶ Use the subsample to solve the regression problem

This procedure is called **Leveraging** (Ma and Sun, 2013).

# Outlook

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## Where to go from here?

- ▶ **Support vector machines (SVM):** Chapter 12 in ESL
- ▶ **(Gradient) Boosting:** Chapter 10 in ESL
- ▶ **Gaussian processes:** Rasmussen and Williams (2006)  
Gaussian Processes for Machine Learning<sup>1</sup>
- ▶ **Streaming/online methods**<sup>2</sup>
- ▶ **Neural networks/Deep Learning:** Bishop (2006) Pattern Recognition and Machine Learning
- ▶ **Natural Language Processing:** Course<sup>3</sup> by Richard Johansson, CSE, on this topic in the fall
- ▶ **Reinforcement Learning:** Sutton and Barto (2015)  
Reinforcement Learning: An Introduction<sup>4</sup>

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<sup>1</sup><http://www.gaussianprocess.org/gpml/chapters/RW.pdf>

<sup>2</sup>[https://en.wikipedia.org/wiki/Online\\_machine\\_learning](https://en.wikipedia.org/wiki/Online_machine_learning)

<sup>3</sup><https://chalmers.instructure.com/courses/7916>

<sup>4</sup><https://web.stanford.edu/class/psych209/Readings/SuttonBartoIPRLBook2ndEd.pdf>