

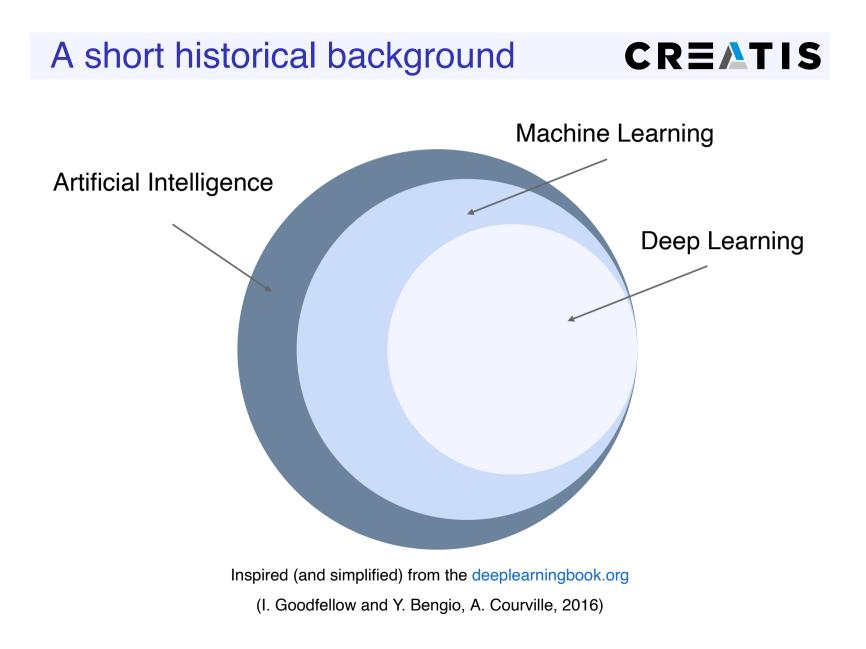
Introduction to Machine Learning

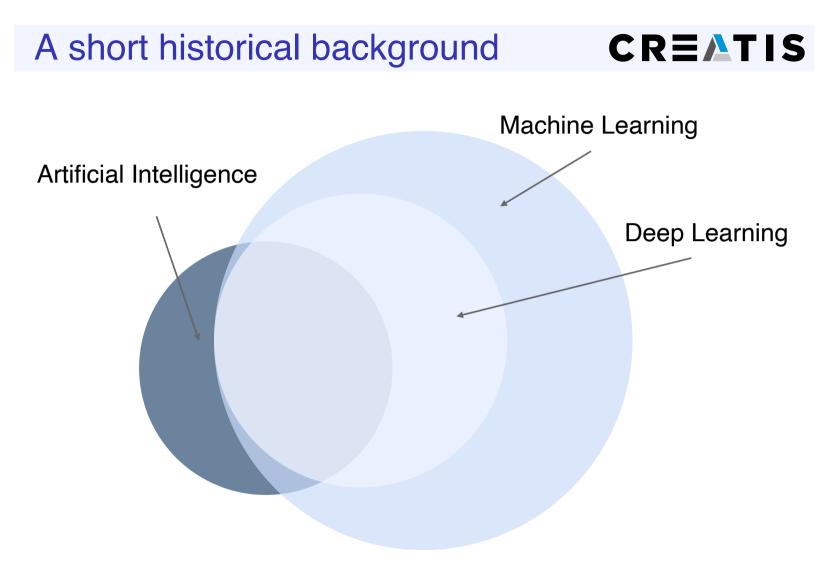
Odyssée Merveille and Emmanuel Roux CREATIS, Lyon

Content

CREATIS

- A short historical background
- Supervised Learning
- Unsupervised Learning
- Conclusion

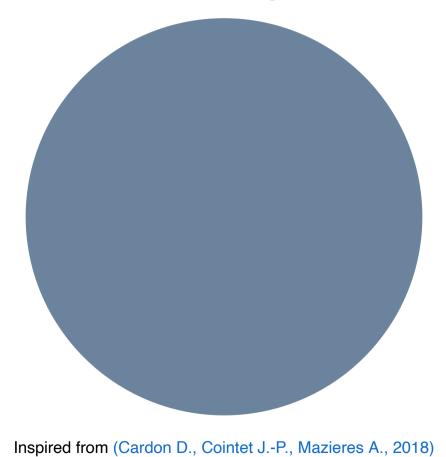




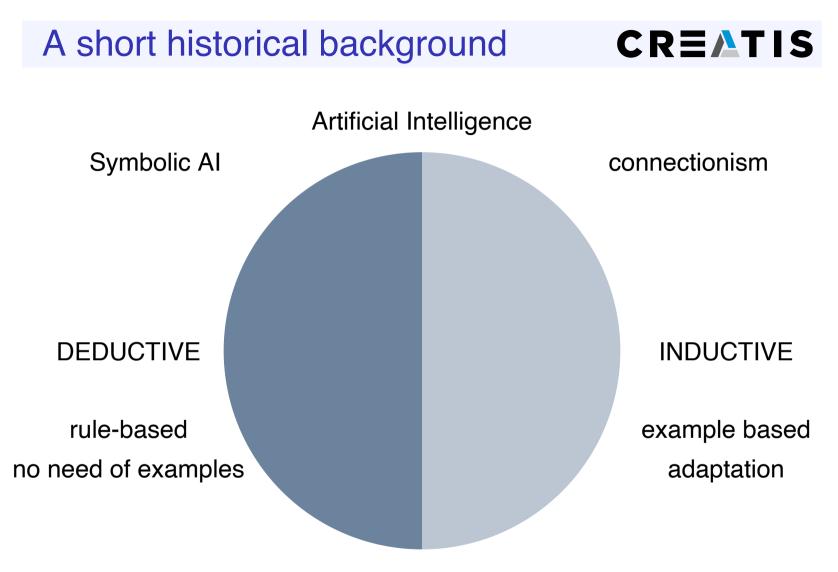
Inspired from Sebastian Raschka's deep-learning course



Artificial Intelligence



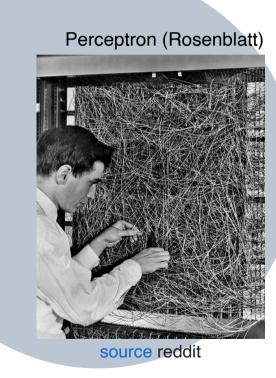
5





Cybernetics (40's to 60's)

Symbolic Al



connexionism

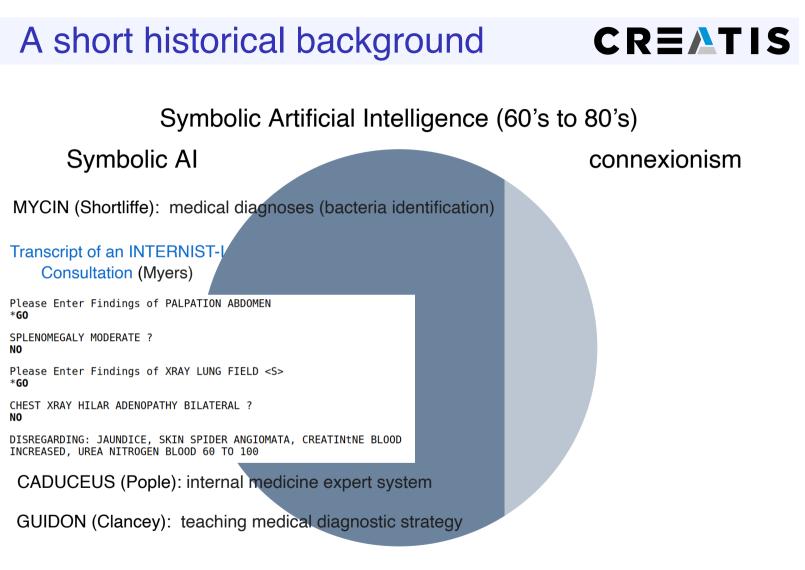


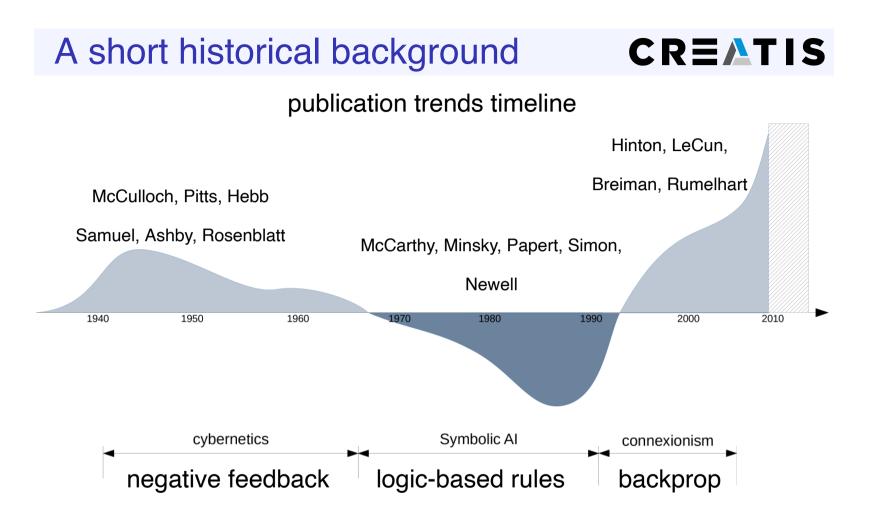
https://isl.stanford.edu/~widrow/ papers/t1960anadaptive.pdf

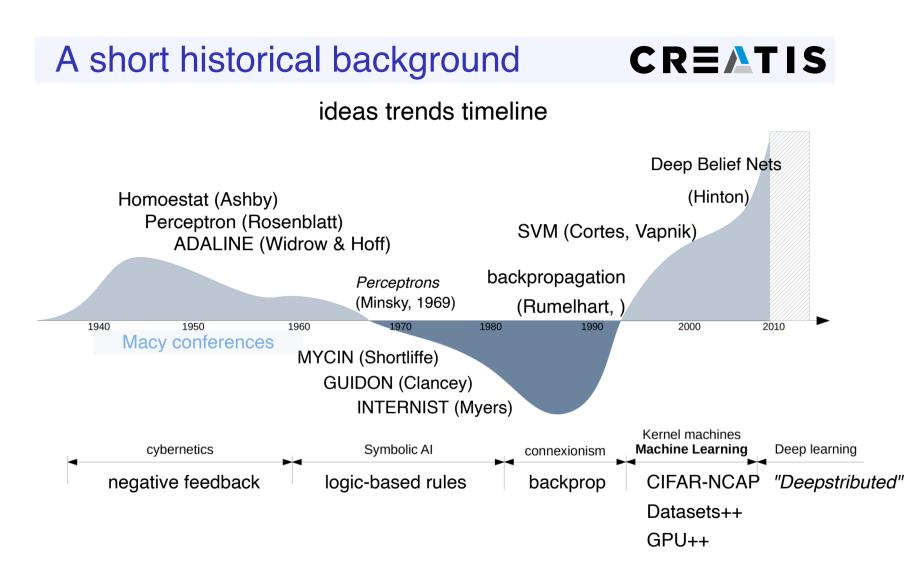


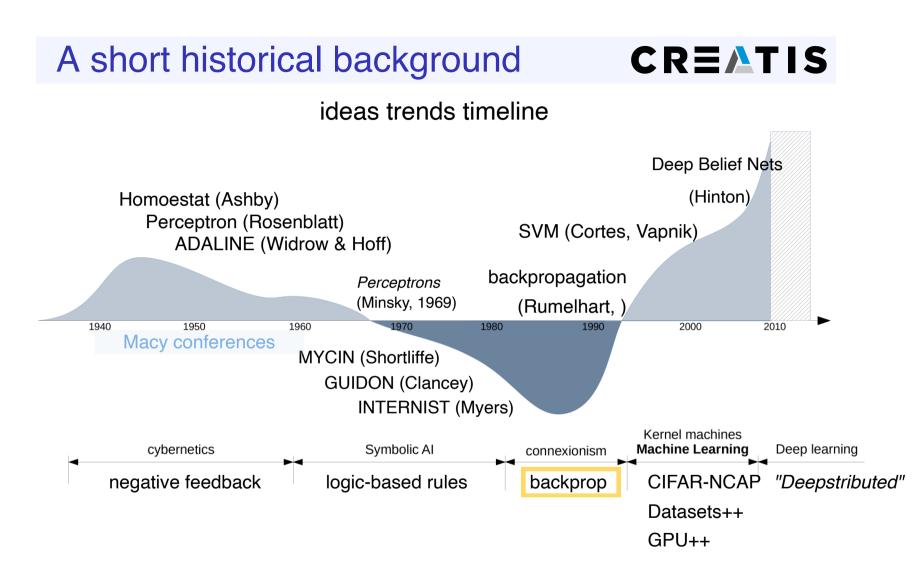
Homeostat, 1948 (W. Ross Ashby)

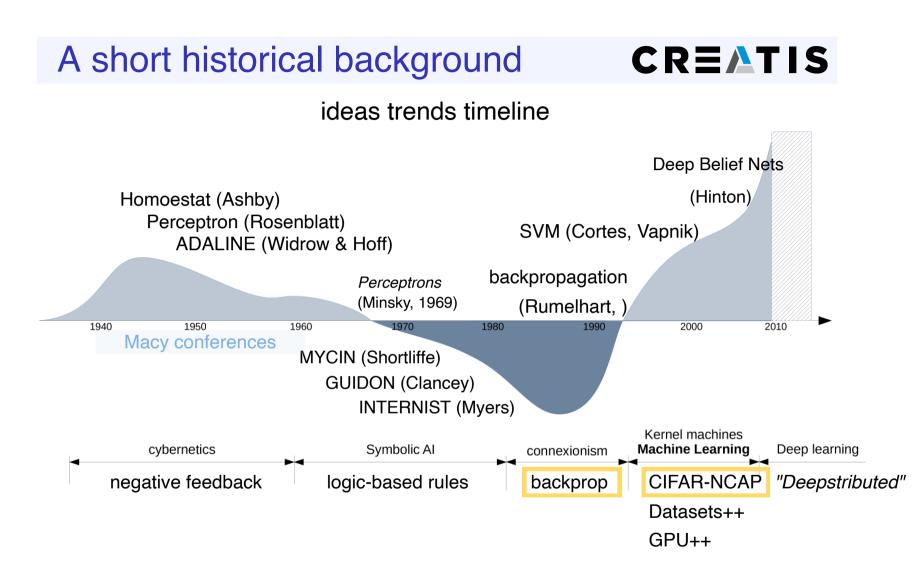
source wikipedia

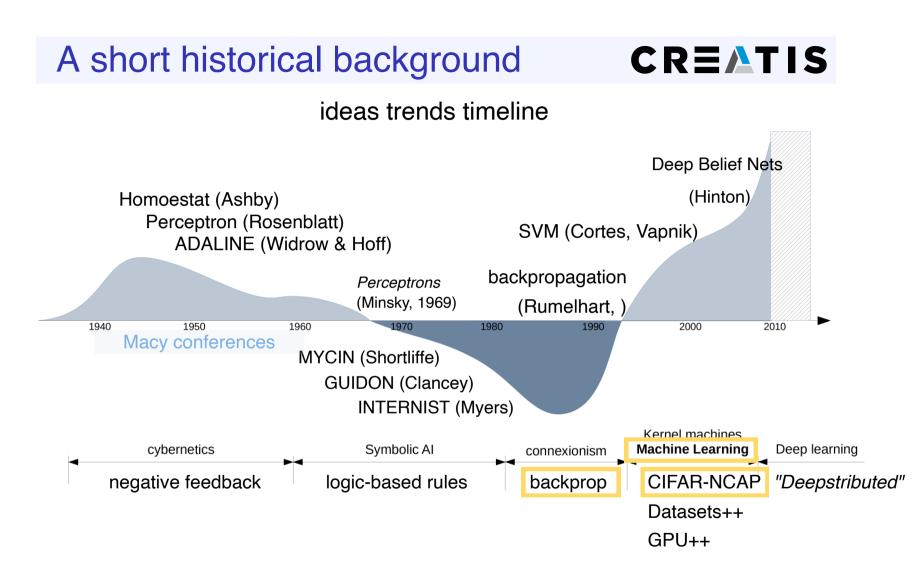














Machine Learning

" A computer program is said to learn [...] if



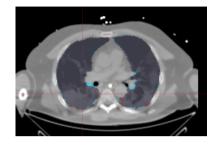
 Machine learning is the field of study that <u>gives computers the ability to learn</u> without being explicitly programmed.
 Arthur L. Samuel, Al pionneer, 1959

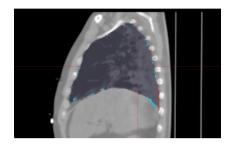


" A computer program is said to learn […] if its performance at tasks in T, as measured by a performance indicator P, improves with experience E.

Tom Mitchel, 1978 (tweaked citation)

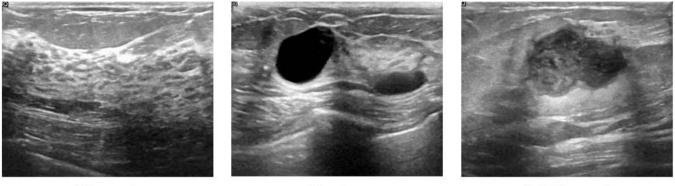
CREATIS





| <pre>1 ~ while epoch < max_epochs: 2 # run an epoch on data 3 data iter = iter(data)</pre> | Experiment |
|---|--|
| 4 v while True: 5 x, y = next(data iter) | Images from PhD student Ludmilla Penarrubia |
| 6 y_pred = model(x) ← 7 loss = loss_fn(y_pred, y) | |
| <pre>8 loss.backward() 9 optimizer.step()</pre> | Learn |
| <pre>10 iter_counter += 1</pre> | |
| <pre>11 ~ if iter_counter == epoch_le</pre> | ength: |
| 12 break | |

supervised learning

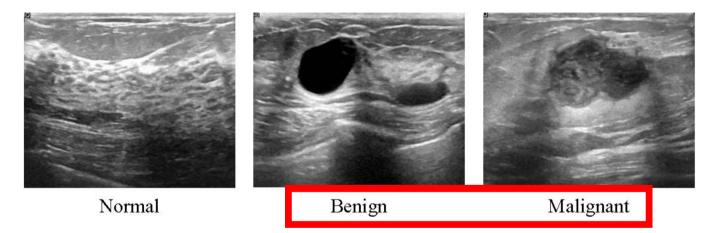


Normal



Benign

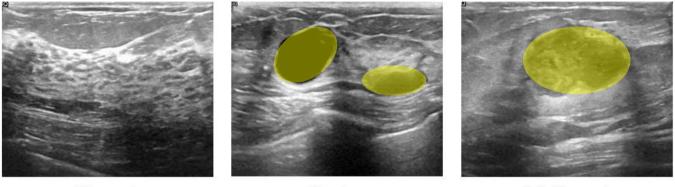
supervised learning



supervised learning



supervised learning



Normal



Benign

supervised learning

unsupervised learning

- detection (lesions)
- classification (benign/malign)
- segmentation (organs)
- prediction (prognostic)
- ...

supervised learning unsupervised learning

- detection (lesions)
- classification (benign/malign)
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- clustering
- dimension reduction
- representation
- density estimation
- ...

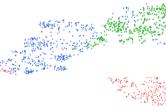
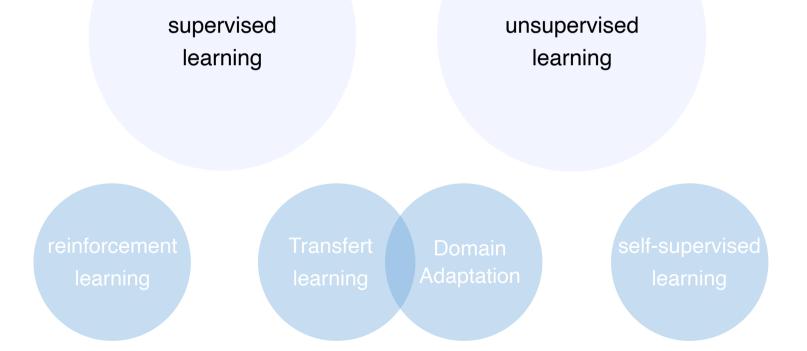
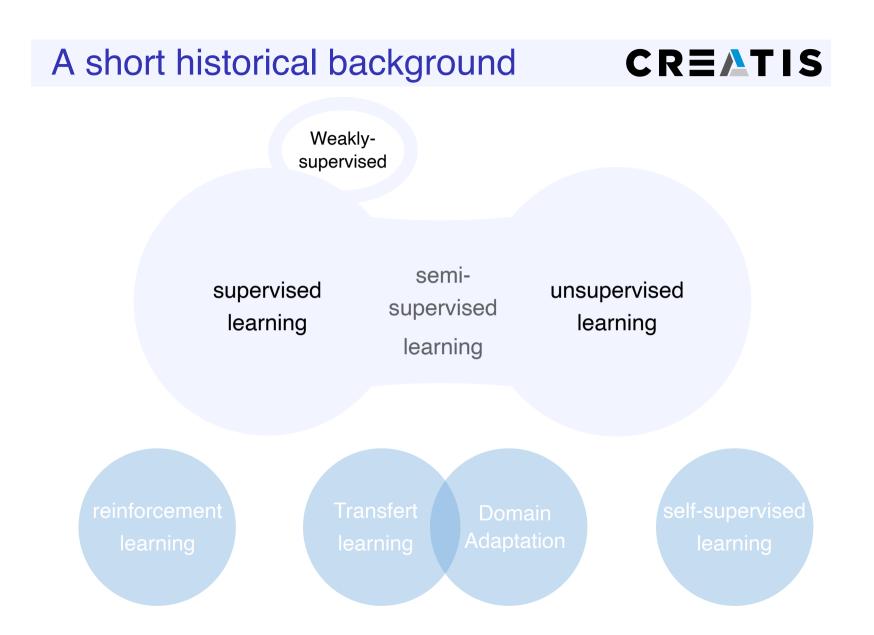


Image from PhD student Yamil Vindas









supervised learning

Supervised Learning

Supervised machine learning

A. Introduction

B. Choice of machine learning algorithm

C. Machine learning pipeline

- 1. Training
- **2. Evaluation**
- 3. Model selection

D. Special considerations in medical applications

Supervised machine learning

A. Introduction

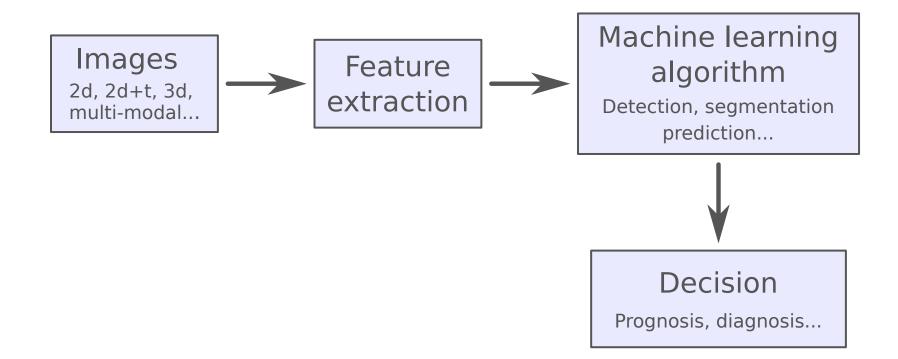
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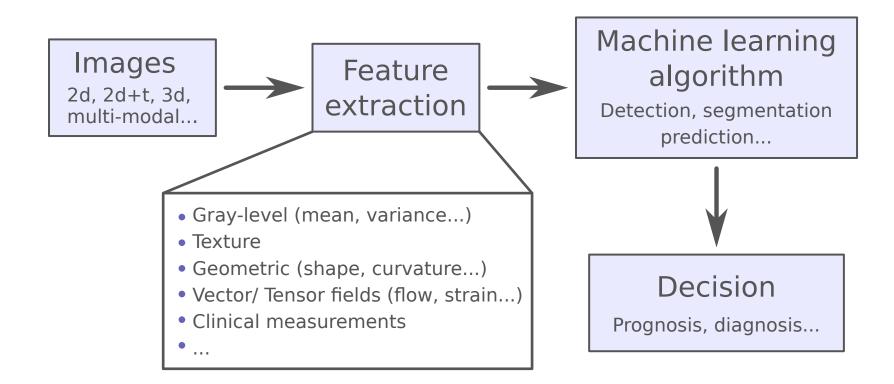
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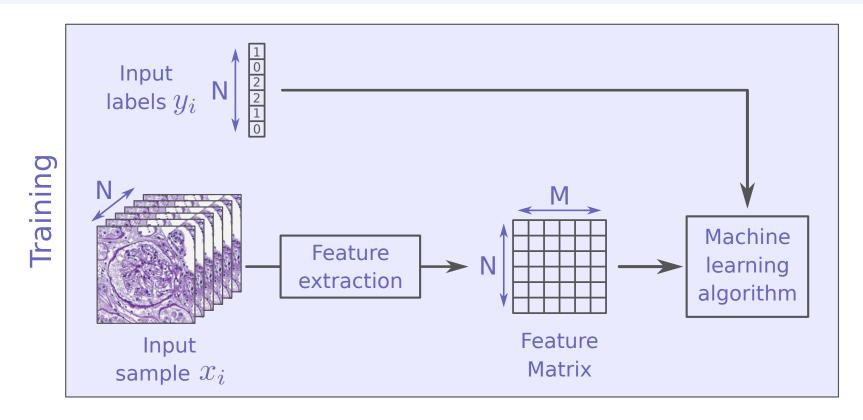
Introduction



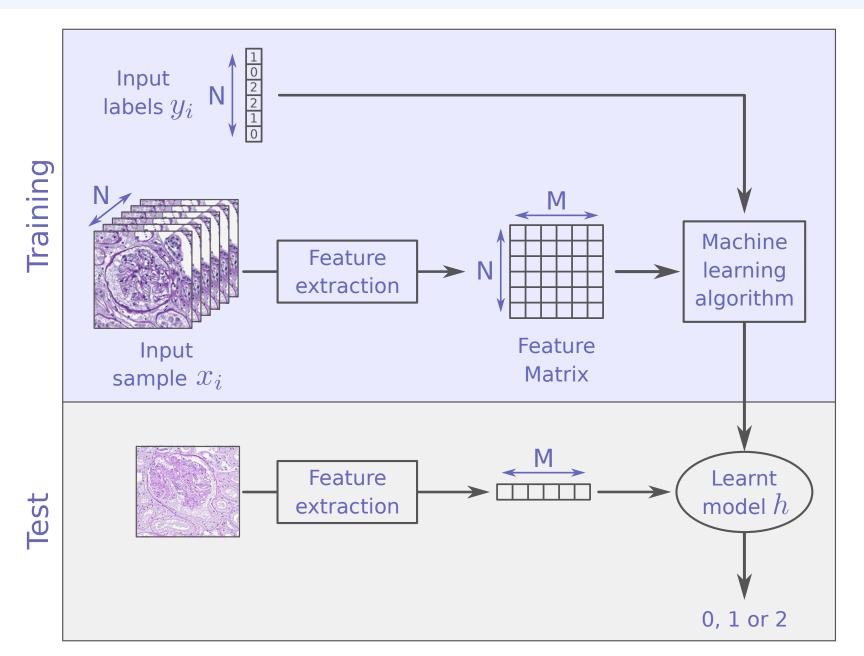
Introduction



Supervised machine learning pipeline



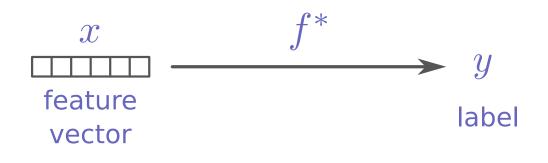
Supervised machine learning pipeline



What is supervised learning ?

Let $f^* : X \mapsto Y$ be an unknown function such as $\forall x \in X$ and $\forall y \in Y$:

 $y = f^*(x)$



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Definition

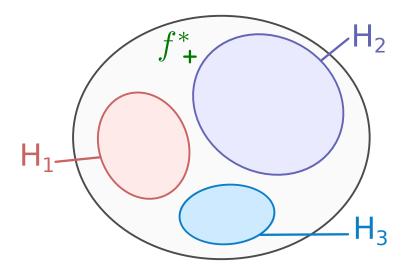
Supervised learning is the task of learning a function $h_L \in H$ $(h_L : X \mapsto Y)$, called a **hypothesis** that best approximates f^* based on a **dataset** \mathcal{D} of N input/output pairs $(\mathcal{D} = \{x_i, y_i\}_{1 \leq i \leq N})$



- *H* is called the hypothesis space
- *h*₁ may also be called a **predictor** or a **model**

How to learn from data ?

Choose the type of algorithm (*i.e.* the hypothesis space H)

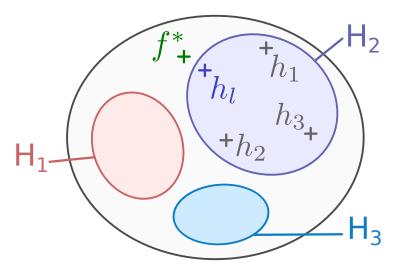


How to learn from data ?

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Train a model (*i.e.* find the best $h_l \in H$)

What is a good model ?



How to learn from data ?

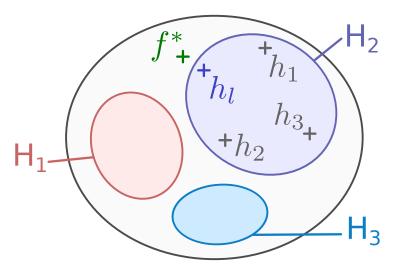
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What is a good model ?

Evaluate the model

Evaluation metrics



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Classification vs Regression

<u>Task</u>: Learn $h: X \mapsto Y$ based on a dataset $\mathcal{D} = \{x_i, y_i\}_{1 \leq i \leq N}$

Two different tasks depending on the type of label y_i :

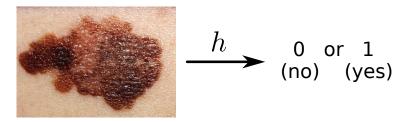
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Two different tasks depending on the type of label y_i :

Classification: $y_i \in \mathbb{N}$

Example: Does the image contain a malignant melanoma ?



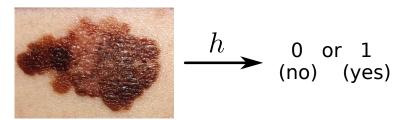
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Classification: $y_i \in \mathbb{N}$

Example: Does the image contain a malignant melanoma ?



Regression: $y_i \in \mathbb{R}$

Example: FFR (Fractional Flow Reserve) prediction from a coronary angiography.



Various types of models

Choose a type of model (*i.e.* the hypothesis space H):

Linear models

- Naive Bayes
- Logistic regression
- Perceptron
- Linear Discriminant Analysis (LDA)

Support Vector Machine (SVM)

K Nearest Neighbors

Decision Tree

Neural networks

How to make the choice ?

There is no "best" algorithm that will work on any dataset \rightarrow "No free lunch" theorems [1]

How to make the choice ?

There is no "best" algorithm that will work on any dataset \rightarrow "No free lunch" theorems [1]

The choice of a "good" machine learning algorithm depends on:

The complexity of the unknown targeted function f^*

- The amount of labeled data
- The dimension of the input space X
- The amount of noise in the data and labels

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Parameters vs hyperparameters

Once *H* is chosen, learning a model *h* consists in finding the best $h \in H$ given a dataset. A model *h* is defined by:

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A set of parameters Θ_1

The parameters of a model are learnt from the data.

Examples:

- The weight values in neural networks
- The support vectors in SVM
- The split values in decision trees

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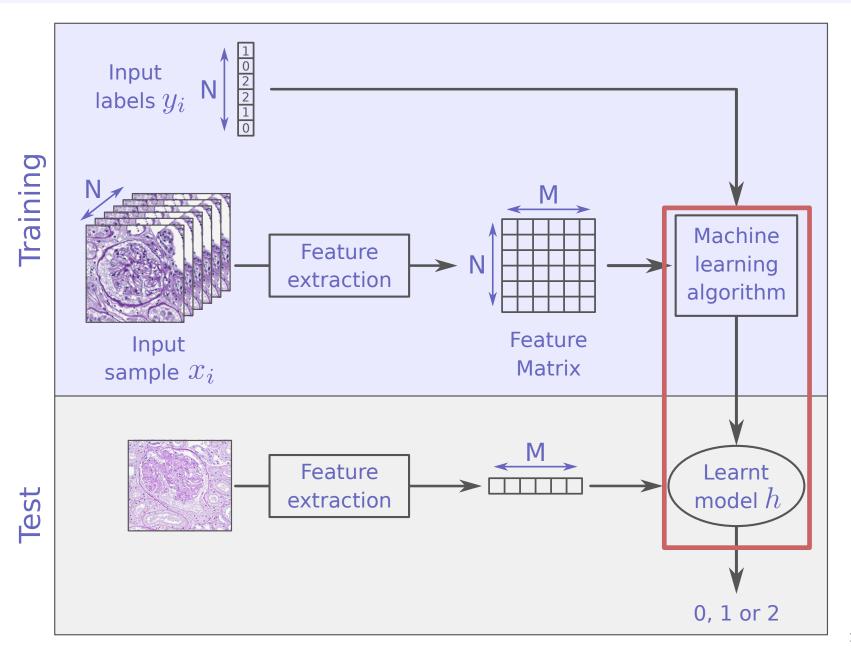
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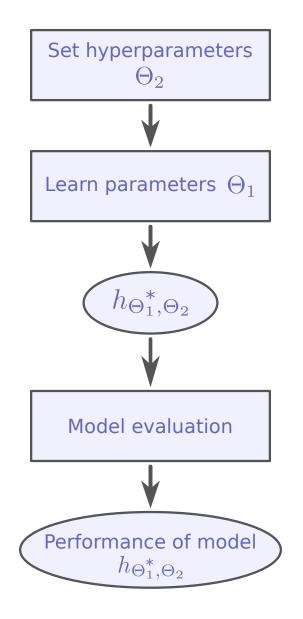
A set of hyperparameters Θ_2

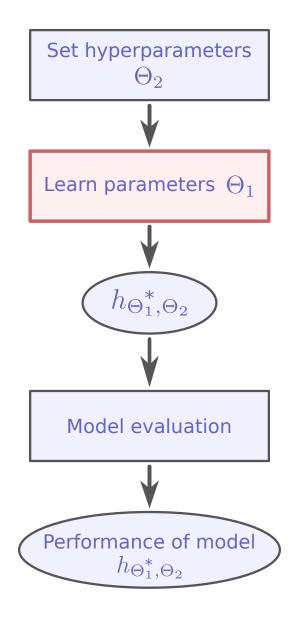
The hyperparameters cannot be learnt from the data. They have to be set before training the model.

Examples:

- The number of trees in a random forest
- The learning rate in neural networks
- The number of neighbors "k" in KNN







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Loss function

Loss function

The loss function $L(L: Y \times Y \mapsto \mathbb{R}^+)$ associates a cost to the prediction $\tilde{y}_i = h(x_i)$ of a model h compared to its true label $y_i = f^*(x_i)$.

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Examples:

Binary loss for classification

$$L(y_i, ilde{y}_i) = \left\{egin{array}{cc} 1 & ext{if} \; y_i
eq ilde{y}_i \ 0 \; ext{otherwise} \end{array}
ight.$$

Quadratic loss for regression

$$L(y_i, \tilde{y}_i) = (y_i - \tilde{y}_i)^2$$

Real risk and model error

Real Risk

Let assume that $\{x_i, y_i\}_{1 \le i \le N}$ is drawn from a joint probability distribution P(x, y) over X and Y.

The **Real risk** R(h) of a hypothesis h is:

$$R(h) = \mathbb{E}[L(h(x), y)] = \int_{X \times Y} L(h(x), y) \, \mathrm{d}P(x, y)$$

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Model error

- f*: the unknown function we want to learn
- \blacktriangleright h_l : the model we learn from dataset $\mathcal D$

The **model error** is defined as:

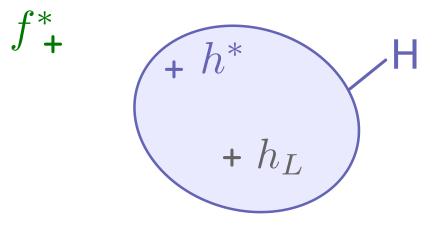
$$Error = R(h_l) - R(f^*)$$

<u>Remark</u>: We usually assume that $R(f^*) = 0$ (deterministic model)

Error decomposition

- f^* : the unknown function we want to learn
- h^{*}: the optimal model in H
- \blacktriangleright h_l : the model we learn from dataset \mathcal{D}

$$\underbrace{\frac{R(h_l) - R(f^*)}{\mathsf{Error}}}_{\mathsf{Error}}$$

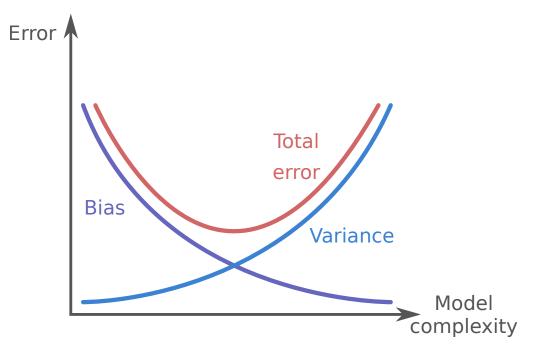


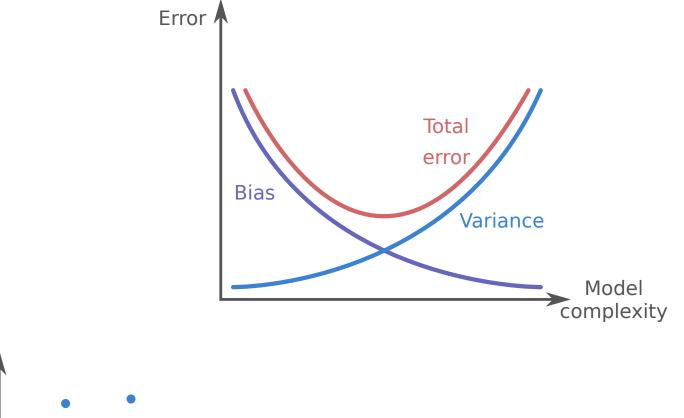
Error decomposition

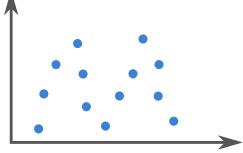
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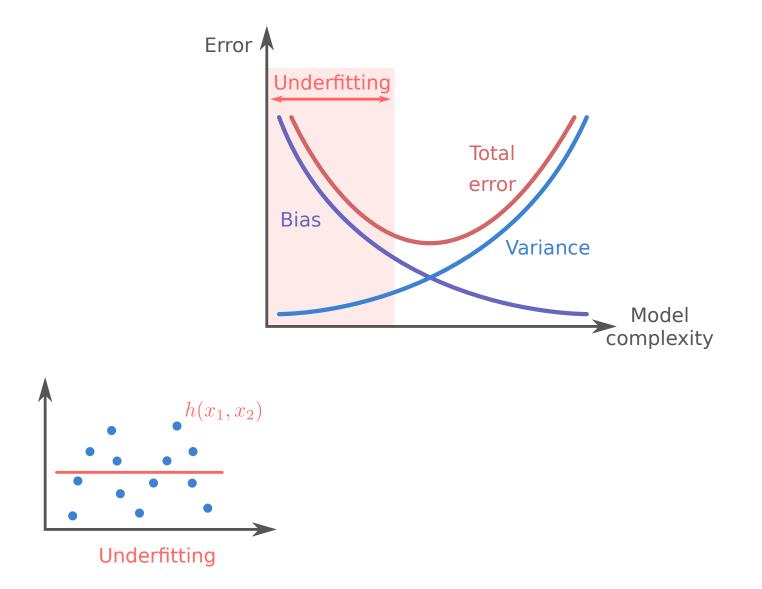
$$\underbrace{R(h_{l}) - R(f^{*})}_{\text{Error}} = \underbrace{R(h_{l}) - R(h^{*})}_{\text{Variance}} + \underbrace{R(h^{*}) - R(f^{*})}_{\text{Bias}}$$

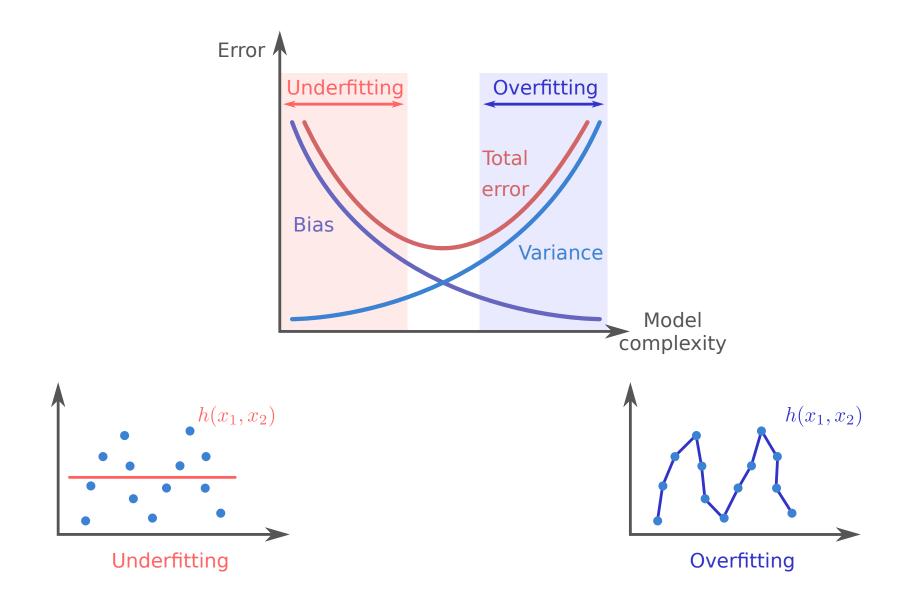
$$f^* \xrightarrow{\text{Bias}} h^* \xrightarrow{\text{H}} H$$
Error
Variance
+ h_L

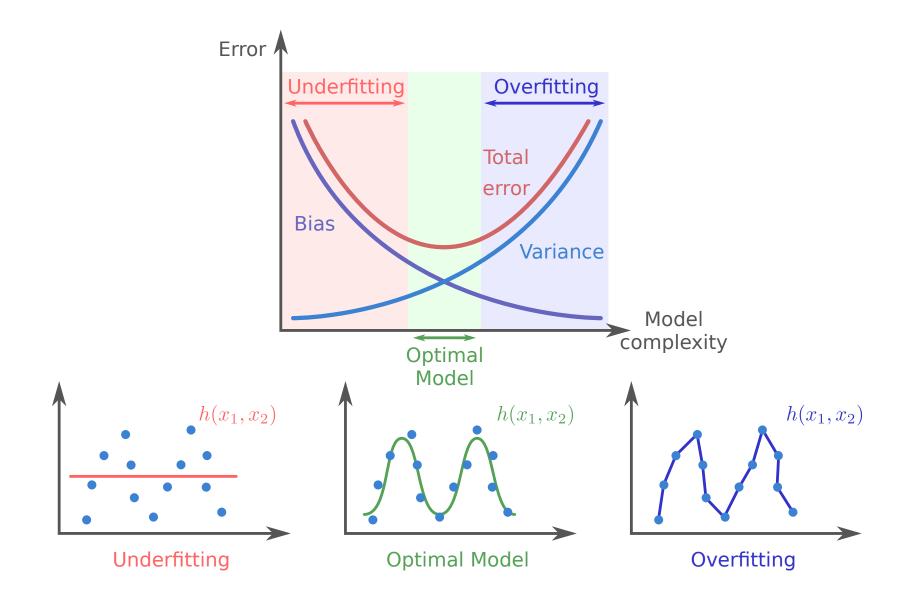












Learning a model is finding its best set of parameters Θ_1 , which is done by minimizing the model error (= Real Risk)

Real Risk

$$R(h) = \int_{X \times Y} L(h(x), y) \, \mathrm{d}P(x, y)$$

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Real Risk

$$R(h) = \int_{X \times Y} L(h(x), y) \, \mathrm{d}P(x, y)$$

 \longrightarrow In practice P(x, y) is not known.

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Real Risk

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Empirical Risk

Approximation of the real risk over a dataset $\mathcal{D} = \{x_i, y_i\}_{1 \leq i \leq N}$

$$R_{\rm emp}(h) = \frac{1}{|N|} \sum_{x,y \in \mathcal{D}} L(h(x), y)$$

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Real Risk

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Empirical Risk

Approximation of the real risk over a dataset $\mathcal{D} = \{x_i, y_i\}_{1 \leq i \leq N}$

$$R_{\rm emp}(h) = \frac{1}{|N|} \sum_{x,y \in \mathcal{D}} L(h(x), y)$$

$$R_{\mathrm{emp}}(h_l) \underset{N \to +\infty}{\longrightarrow} R(h_l)$$

Empirical Risk Minimization

In theory, learning a model is minimizing the error $R(h_l)$

In practice, we cannot compute $R(h_l)$ so we minimize $R_{emp}(h_l)$

 $\longrightarrow \mbox{This}$ is called $\mbox{Empirical Risk Minimization}$

Empirical Risk Minimization (ERM)

$$h_I = \operatorname*{arg\,min}_{h\in H} \frac{1}{|N|} \sum_{x,y\in \mathcal{D}} L(h(x),y)$$

where $\mathcal{D} = \{x_i, y_i\}_{1 \leq i \leq N}$ is the **training dataset**

Supervised machine learning

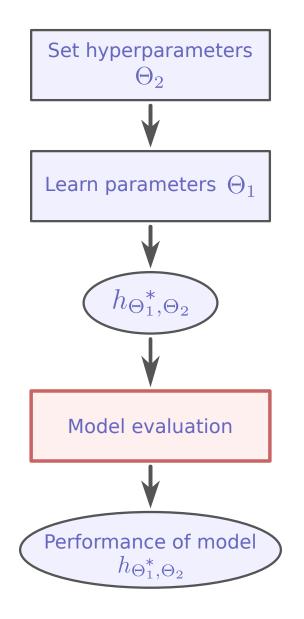
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A good model is a model exhibiting:

High performance

- A good **generalization** power when seeing new data
 - **Stable** performance for small dataset variations

To select a good model, we need to validate its performance according to these 3 criteria

 \longrightarrow Choose a validation strategy

Validation strategies

Several validation strategies were developed:

Hold out

K-fold cross validation

Leave-one-out cross validation

Bootstrapping

Validation strategies

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 \longrightarrow They all require to split the dataset

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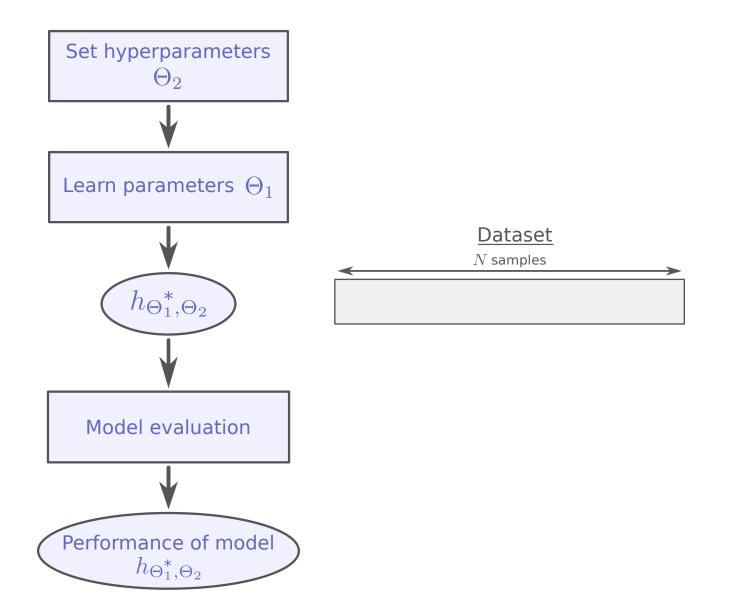
K-fold cross validation

Leave-one-out cross validation

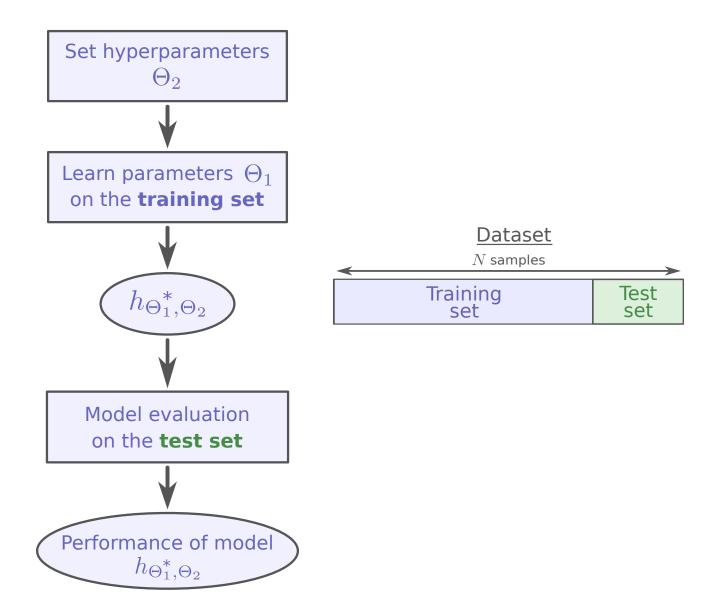
Bootstrapping

 \longrightarrow They all require to split the dataset

Dataset splitting



Dataset splitting



<u>Goal</u>: Evaluation of the model **mean performance**, **generalization** and **stability**.

Split the dataset in k folds

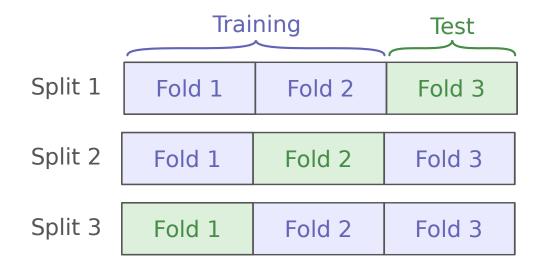
| Fold 1 | Fold 2 | Fold 3 |
|--------|--------|--------|
|--------|--------|--------|

Objective: Evaluation of the model **mean performance**, **generalization** and **stability**.

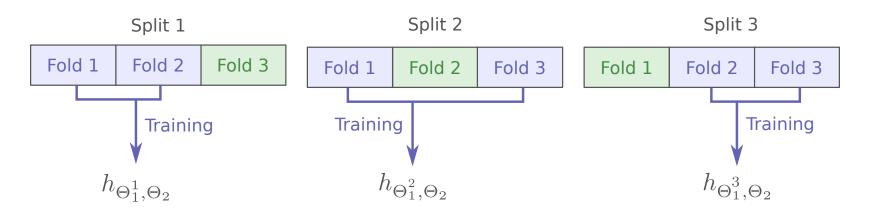
Split the dataset in k folds

| Fold 1 | Fold 2 | Fold 3 |
|--------|--------|--------|
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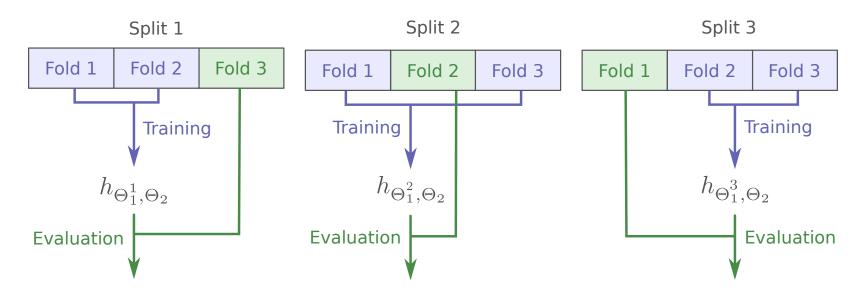
Generate the k combinations of 1 test fold and the remaining k - 1 training folds



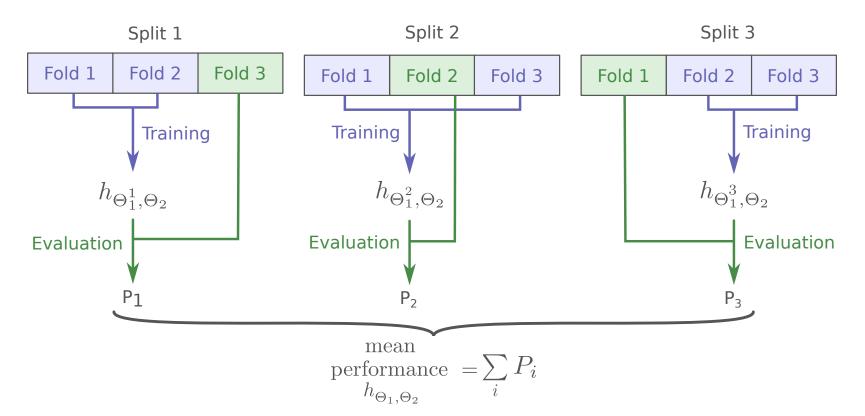
For each split, use the training folds to learn a model $h_{\Theta_1^i,\Theta_2}$ and evaluate the model on the remaining test fold.



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Compute the mean and standard deviation of the performance of the model.

What is the performance of a model ?

The performance of a model is assessed based on one or several metrics

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Examples of popular metrics:

Regression metrics

- Mean Square Error (MSE)
- Root Mean Square Error (RMSE)
- Peak Signal-to-Noise Ratio (PSNR)
- Structural Similarity (SSIM)

What is the performance of a model?

The performance of a model is assessed based on one or several metrics

Examples of classic metrics:

Regression metrics

- Mean Square Error (MSE)
- Root Mean Square Error (RMSE)
- Peak Signal-to-Noise Ratio (PSNR)
- Structural Similarity (SSIM)

Classification metrics

- Accuracy
- Dice / F1
- Intersection over union (IoU)Sensitivity
- Sensitivity
- Specificity
- Precision

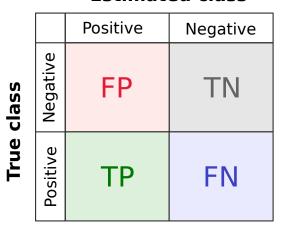
Based on the Confusion Matrix

| | | Positive | Negative |
|------------|----------|----------|----------|
| True class | Negative | FP | ΤN |
| True | Positive | TP | FN |

Estimated class

FP: false positive

- **TN**: true negative
- **TP**: true positive
- **FN**: false negative

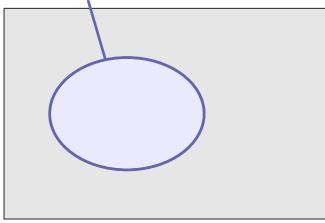


Estimated class

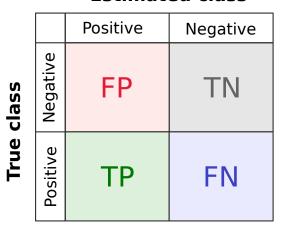
- **FP**: false positive
- **TN**: true negative
- **TP**: true positive
- **FN**: false negative

Example for segmentation:

Ground truth



$$\begin{aligned} \mathsf{Accuracy} &= \frac{TP + TN}{TP + TN + FP + FN} \\ \mathsf{Sensitivity} &= \frac{TP}{TP + FN} \\ \mathsf{Specificity} &= \frac{TN}{TN + FP} \end{aligned}$$

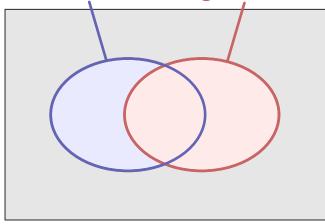


Estimated class

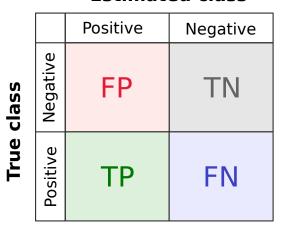
- **FP**: false positive
- **TN**: true negative
- **TP**: true positive
- **FN**: false negative

Example for segmentation:

Ground truth Segmentation



$$\begin{aligned} \mathsf{Accuracy} &= \frac{TP + TN}{TP + TN + FP + FN} \\ \mathsf{Sensitivity} &= \frac{TP}{TP + FN} \\ \mathsf{Specificity} &= \frac{TN}{TN + FP} \end{aligned}$$

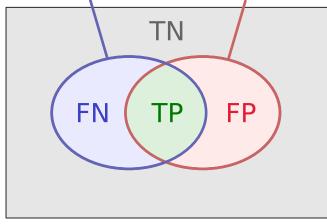


Estimated class

- **FP**: false positive
- **TN**: true negative
- **TP**: true positive
- **FN**: false negative

Example for segmentation:

Ground truth Segmentation



$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$
$$Sensitivity = \frac{TP}{TP + FN}$$
$$Specificity = \frac{TN}{TN + FP}$$

Choice of metric

The metrics should be chosen depending on the application.
— For the same task, the notion of performance may be very different depending on the application.

Choice of metric

The metrics should be chosen depending on the application.
— For the same task, the notion of performance may be very different depending on the application.

Example: Detection of a rare disease.

- Test used to select people that should be immediately hospitalized or may die
 - \longrightarrow Missing a case is very bad (false negative)
 - \longrightarrow We want a test with a high **sensitivity**
- Test used to select people that will receive a very effective treatment. However giving the treatment to someone who is not sick is deadly.
 Detecting a person that is not sick is very bad (false positive)
 We want a test with a high **specificity**

Supervised machine learning

A. Introduction

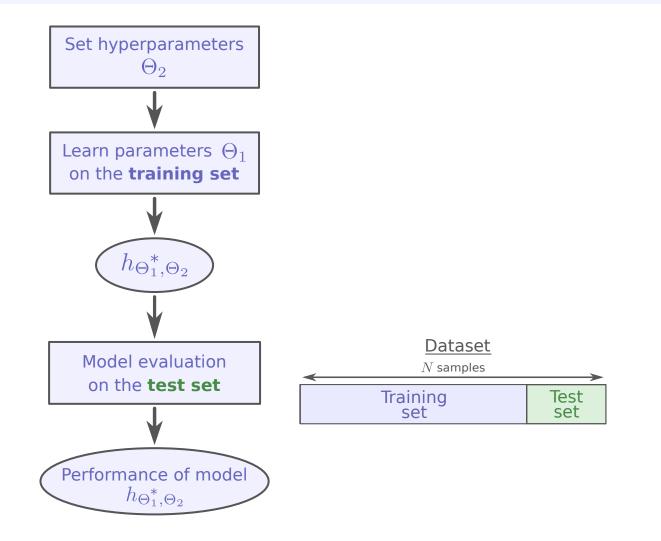
B. Choice of machine learning algorithm

C. Machine learning pipeline

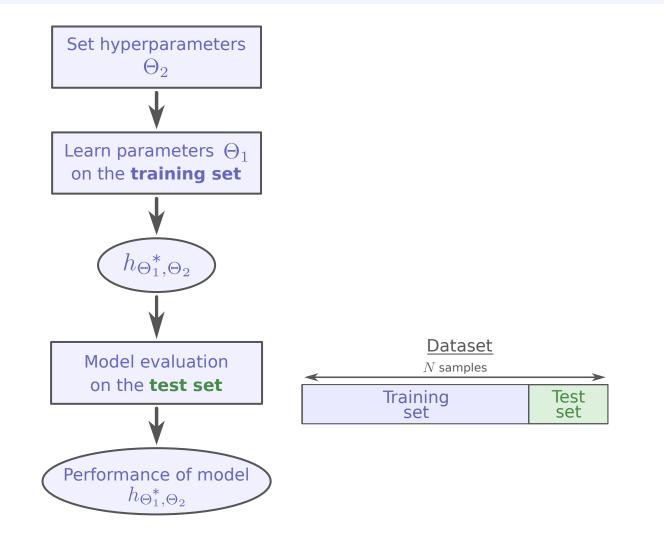
- 1. Training
- **2. Evaluation**
- 3. Model selection

D. Special considerations in medical applications

How to choose the model hyperparameters ?

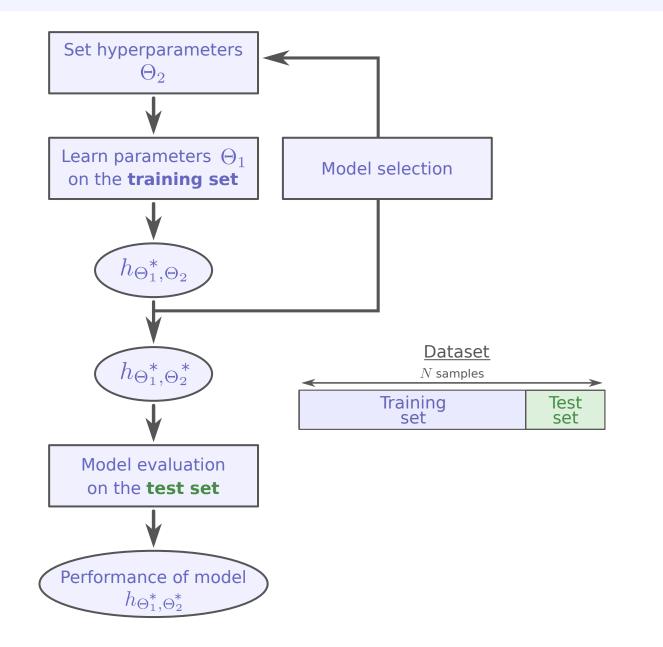


How to choose the model hyperparameters ?

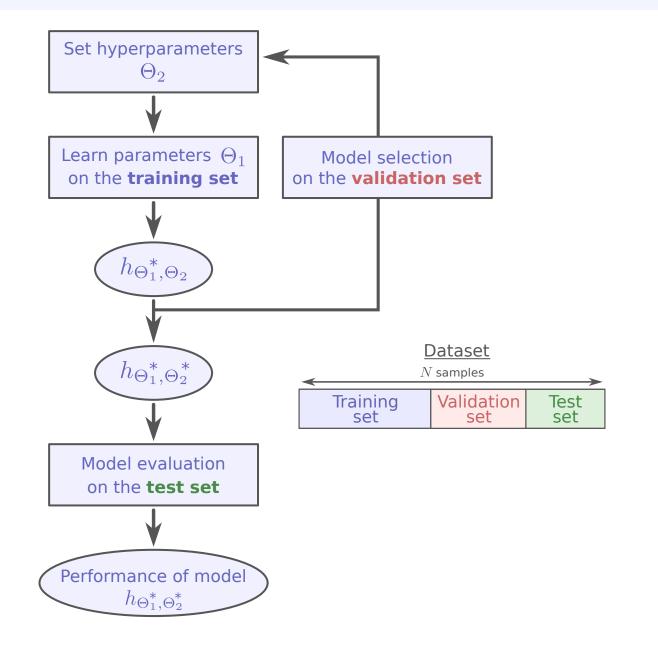


 \longrightarrow Model selection

Model selection

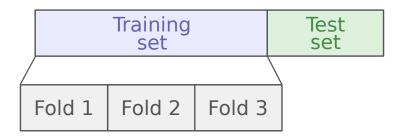


Model selection



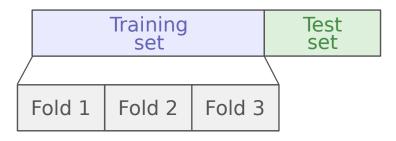
Objective: Selection of the best set of hyperparameters Θ_2^* .

Split the dataset in two: a training and a test set. Keep the test set aside and split the training set in k folds

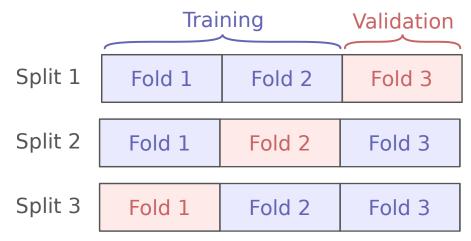


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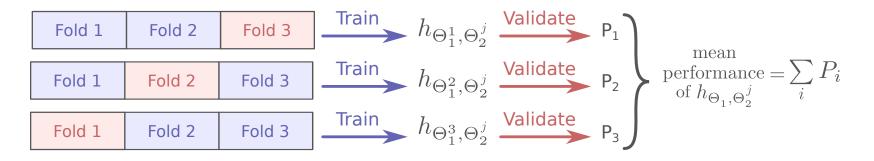


Generate the k combinations of 1 validation fold and the remaining k-1 training folds from the training set



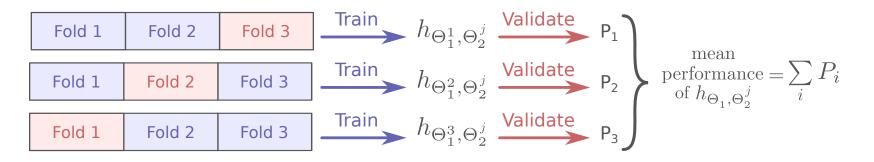
For each set of hyperparameters Θ_2^j , perform a k-fold cross validation evaluation.

Compute the mean performance of the model for fixed Θ_2^j .

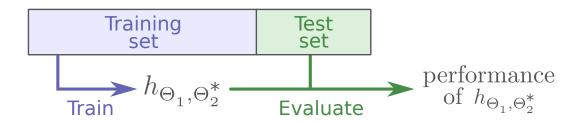


For each set of hyperparameters Θ_2^j , perform a k-fold cross validation evaluation.

Compute the mean performance of the model for fixed Θ_2^j .



- Choose the set of hyperparameters Θ_2^* providing the best mean performance and train a new model on the full training set.
- Evaluate the performance of this model on the test set.



Problems with k-fold cross validation for model selection

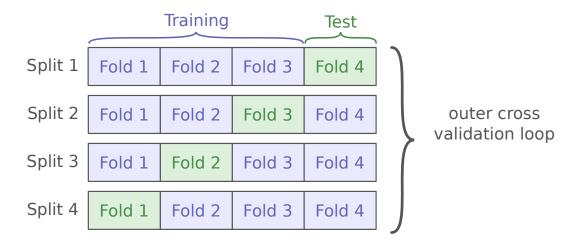
The choice of the best model is done based on the average performance on training set and not on an independent dataset.
Introduction of a model selection bias

The performance of the selected model is evaluated on a single test set

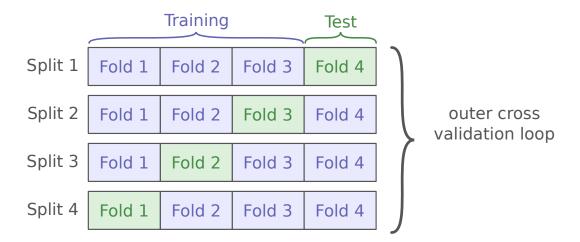
 \longrightarrow No estimation of the variance due to the test set choice.

 \longrightarrow Use **nested k-fold cross validation**

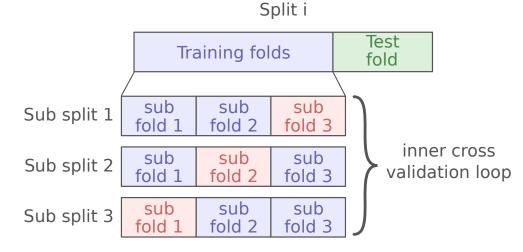
Split the dataset in k-folds and generate the classic k combinations.



Split the dataset in k-folds and generate the classic k combinations.



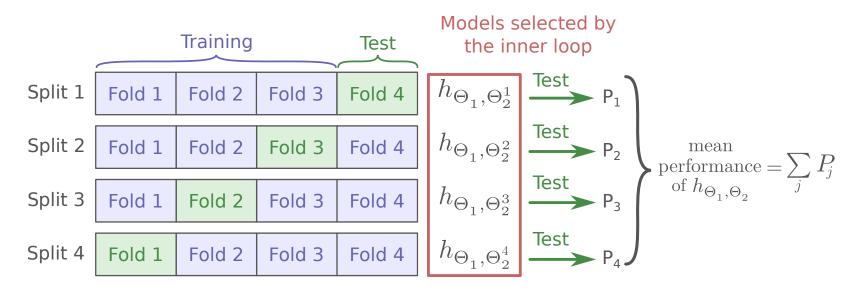
For each split, perform a k-fold cross validation on the training folds to select the best model.



For each split *j*, test the best inner loop model on the test fold

Compute the mean and standard deviation of the performance of the models

 \longrightarrow Provides an estimate of the generalization and stability of the learnt models



Remarks:

- The inner loop does the model selection and the outer loop does the evaluation of the selected model
- The model selection is included in the learning where the hyperparameters are learnt from the data.
 - Two common strategies to obtain the final model:
 - Run the inner loop one more time on the complete dataset and choose the hyperparameters yielding the best mean performance
 - Use the k models selected by the inner loops to do ensembling.

How to learn a "good" model

Keep in mind the bias/variance tradeoff when learning a model.

- How to reduce the bias (avoid underfitting)
 - Increase the complexity of your model
 - Add more features
- How to reduce the variance (avoid overfitting)
 - Use a validation strategy
 - Reduce the complexity of the model
 - Add more training data
 - Reduce the number of features (dimensionality reduction)
 - Use regularization
 - Perform ensembling

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Carefully chose your metrics and evaluation strategy

Supervised machine learning

A. Introduction

B. Choice of machine learning algorithm

C. Machine learning pipeline

- 1. Training
- **2. Evaluation**
- 3. Model selection

D. Special considerations in medical applications

Imbalanced classification

In medical applications the datasets are often imbalanced (number of healthy cases ≫ number of pathological cases)

Imbalanced classification

In medical applications the datasets are often imbalanced (number of healthy cases ≫ number of pathological cases)

Specific strategies should be used:

Resampling methods

oversampling of the rare class, downsampling of the majority class, data augmentation...

Cost-sensitive training

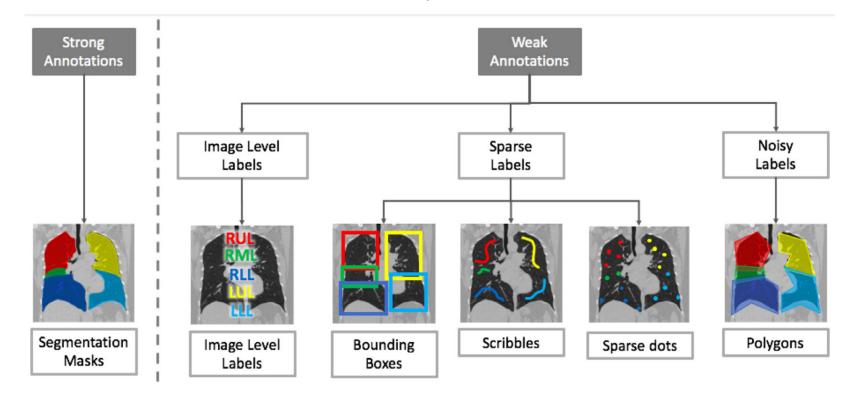
Add weight in the loss to penalize misclassifications of the rare class more.

Adapt the metrics

Dice or MCC over Accuracy, Precision/Recall over Sensitivity/Specificity...

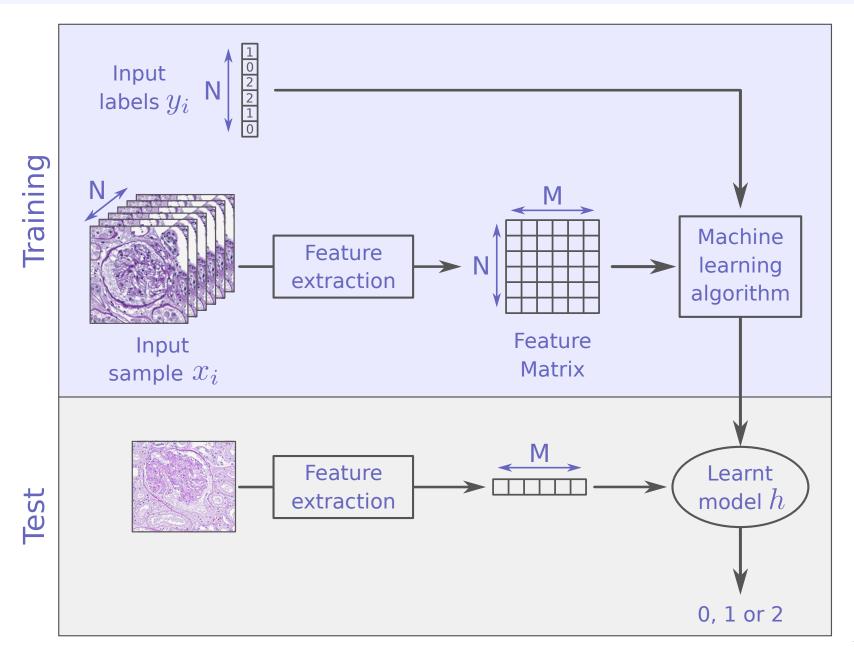
Annotation scarcity and weak supervision

Annotations are very expensive in medical applications. \longrightarrow Weak annotations, semi-supervision

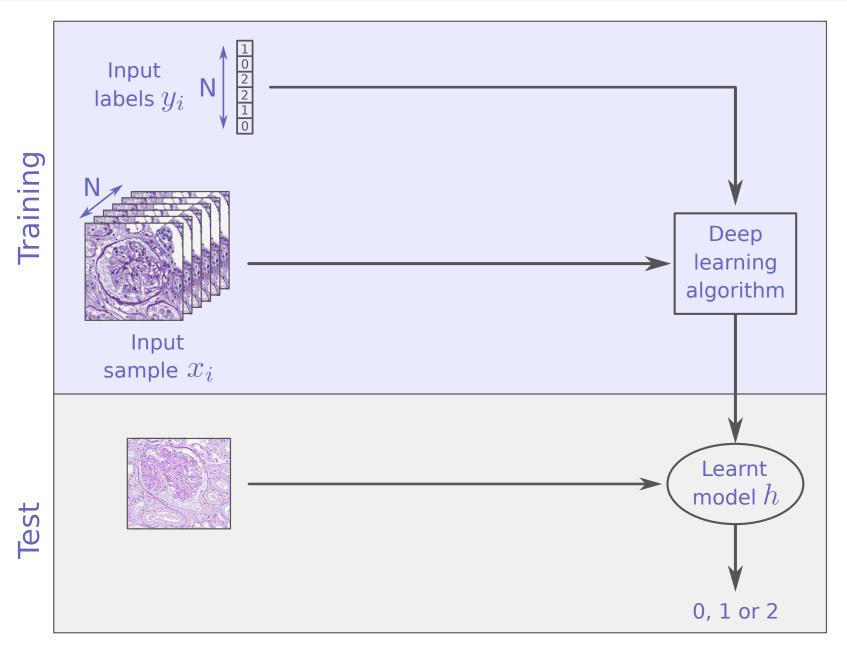


Tajbakhsh *et al.*, "Embracing imperfect datasets: A review of deep learning solutions for medical image segmentation", MedIA, 2020 Karimi *et al.*, "Deep learning with noisy labels: Exploring techniques and remedies in medical image analysis", MedIA, 2020

Classical supervised machine learning pipeline

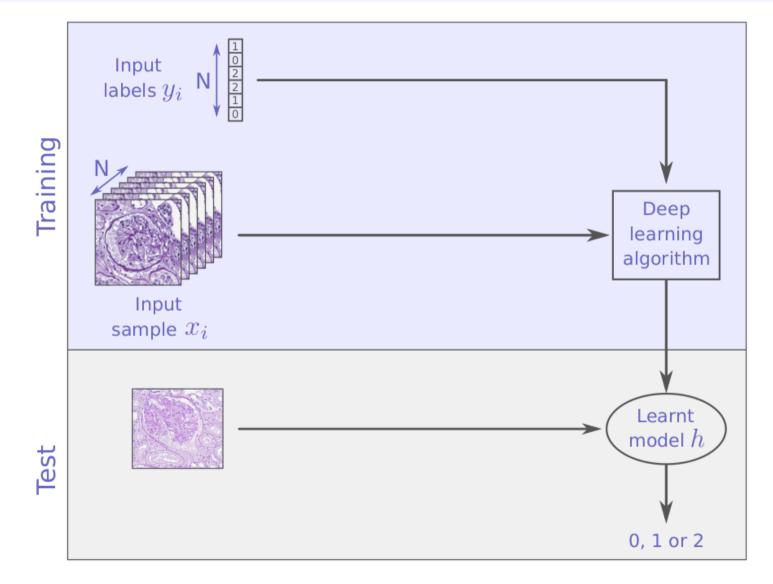


Supervised deep learning pipeline

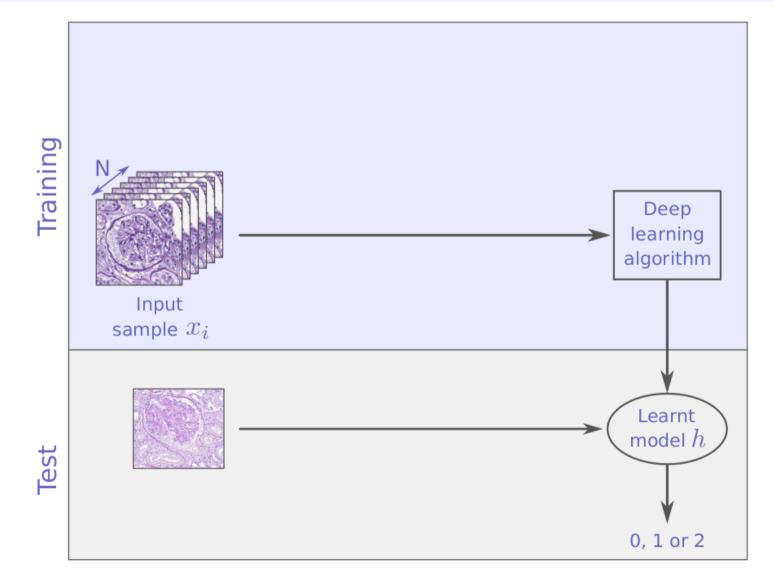


from supervised learning ...











supervised learning

 $\mathcal{D} = \{x_i, y_i\}_{1 \leq i \leq N}$



unsupervised learning

 $\mathcal{D} = \{x_i\}_{1 \leq i \leq N}$

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unsupervised learning

 $\mathcal{D} = \{x_i\}_{1 \leq i \leq N}$

CREATIS

unsupervised learning

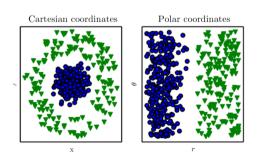
with unsupervised learning you can find

... efficient representations (embedding, interpret) ... estimations of your data distribution (generate new samples)



with unsupervised learning you can find

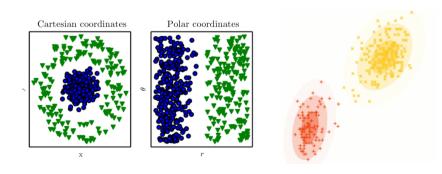
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with unsupervised learning you can find

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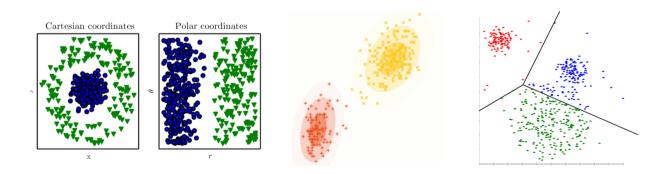


CREATIS

unsupervised learning

with unsupervised learning you can find

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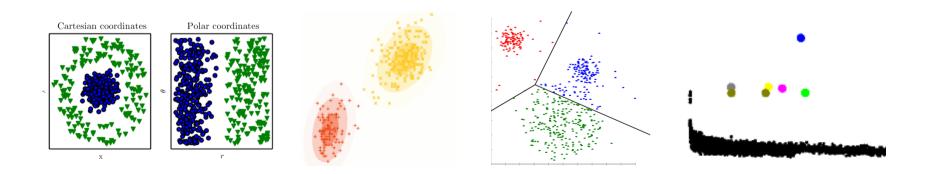


CREATIS

unsupervised learning

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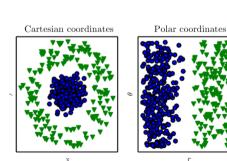




How to ?

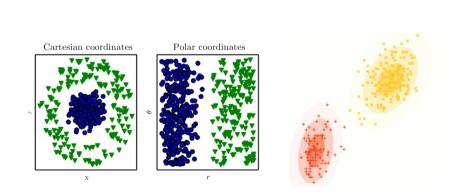


How to ?



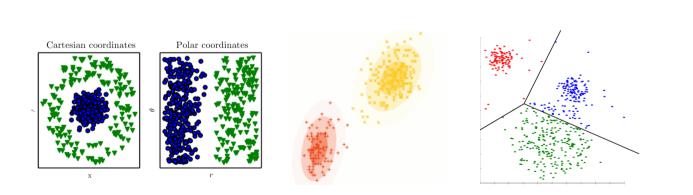


How to ?



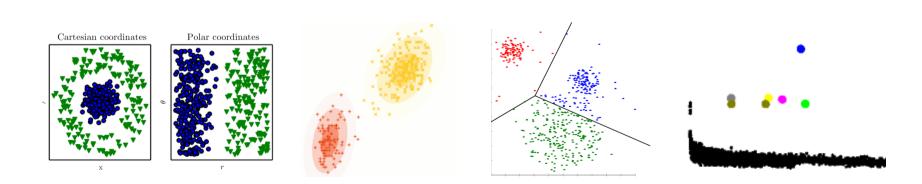


How to ?





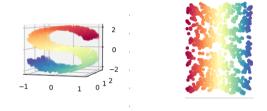
How to ?





Dimension reduction

"the curse of dimensionality"



To avoid redundancy and unnecessary computational load

To visualize the data

To improve data representation

(supervised task pre-processing: semi-supervised learning)





Dimension reduction

Feature selection

Feature extraction



Feature selection

$$\mathcal{D} = \{x_i\}_{1 \leq i \leq N}$$

| | feat1 | feat2 | feat3 | feat4 | feat5 |
|----|-------|-------|-------|-------|-------|
| x1 | 1 | 2 | 2 | 6 | 3 |
| x2 | 2 | 4 | 4 | 12 | 7 |
| x3 | 3 | 6 | 8 | 24 | 9 |
| | | | | | |
| xn | 4 | 8 | 16 | 48 | 11 |



Feature selection

M

 $\mathcal{D}=\{x_i\}_{1\leq i\leq N}$

feat1 feat2 feat3 feat4 feat5 x1 1 2 2 3 6 x2 2 7 12 4 4 NDхЗ 3 6 8 9 24 . . . 8 16 11 4 48 xn

11



Feature selection

| | Ļ | \star ×2 | Ļ | ×3 | |
|----|-------|------------|-------|-------|-------|
| | feat1 | feat2 | feat3 | feat4 | feat5 |
| x1 | 1 | 2 | 2 | 6 | 3 |
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Feature selection

| | feat1 | feat3 | feat5 |
|----|-------|-------|-------|
| x1 | 1 | 2 | 3 |
| x2 | 2 | 4 | 7 |
| x3 | 3 | 8 | 9 |
| | | | |
| xn | 4 | 16 | 11 |

N = 569



Feature selection example with the Breast Cancer dataset

| 4 | | > |
|---------------|---------------|-----------------|
| # texture_m = | # perimeter = | # area_mean = |
| 14.36 | 87.46 | 566.3 |
| 15.71 | 85.63 | 520 |
| 12.44 | 60.34 | 273.9 |
| 18.42 | 82.61 | 523.8 |
| 16.84 | 51.71 | 201.9 |
| 14.63 | 78.04 | 449.3 |
| 22.3 | 86.91 | 561 |
| 21.6 | 74.72 | 427.9 |
| 19.98 | 119.6 | 1040 |
| 20.83 | 90.2 | 577.9 |
| 21.82 | 87.5 | 519.8 |
| 24.04 | 83.97 | 475.9 |
| 23.24 | 102.7 | 797.8 |
| 17.89 | 103.6 | 781 |
| 24.8 | 132.4 | 1123 (K. P. Ben |

M = 10 (only 3 here)

malignant breast fine needle aspirates

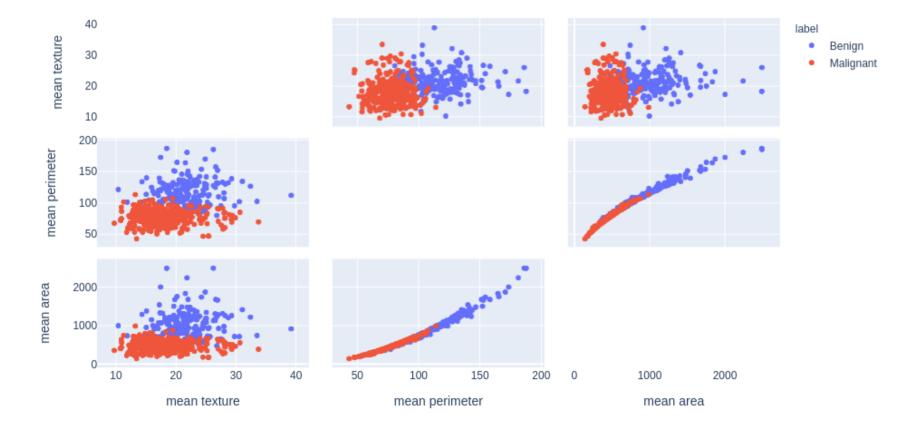


(K. P. Bennett and O. L. Mangasarian, 1994)

D

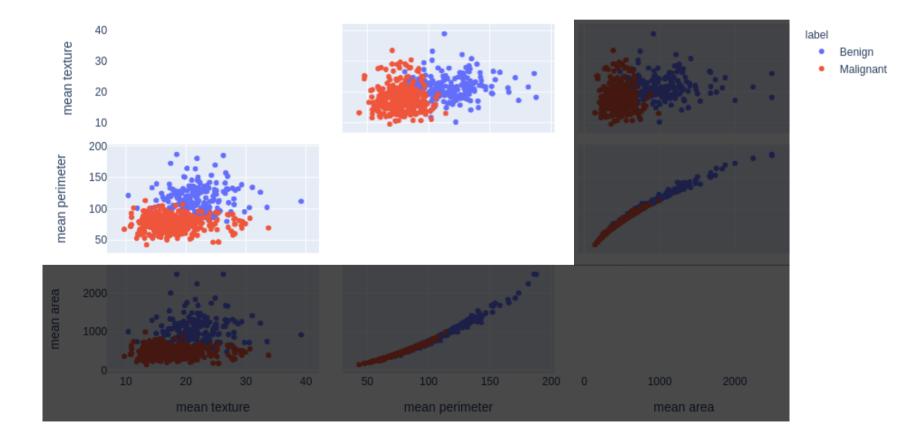


Feature selection example with the Breast Cancer dataset





Feature selection example with the Breast Cancer dataset





Feature extraction

e.g. Principal Component Analysis (PCA)

| # texture_m = | # perimeter = | ⋕ area_mean 🖃 |
|---------------|---------------|---------------|
| 14.36 | 87.46 | 566.3 |
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Feature extraction e.g. Principal Component Analysis (PCA)

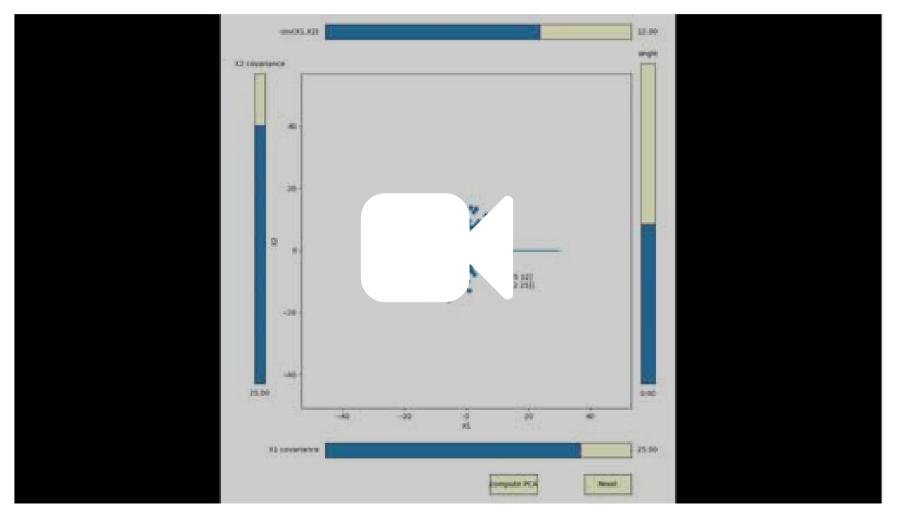
linearly combine features to find mutually orthogonal components

the (principal) components are ranked from the most "significant" to least "significant" projecting the data on the first components maximize its spread (variance)

dimension reduction: select the *d* first components

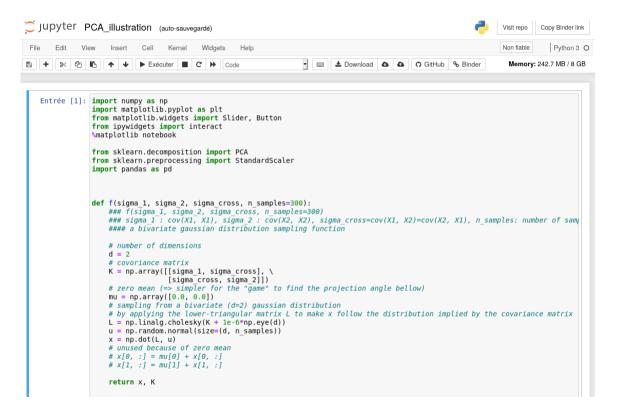


Feature extraction demo with PCA

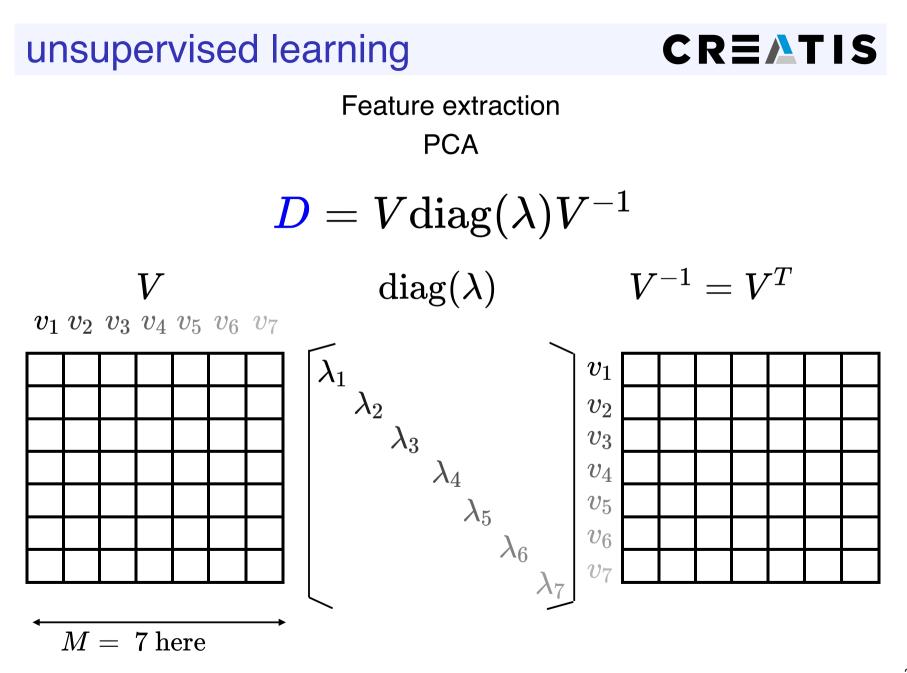


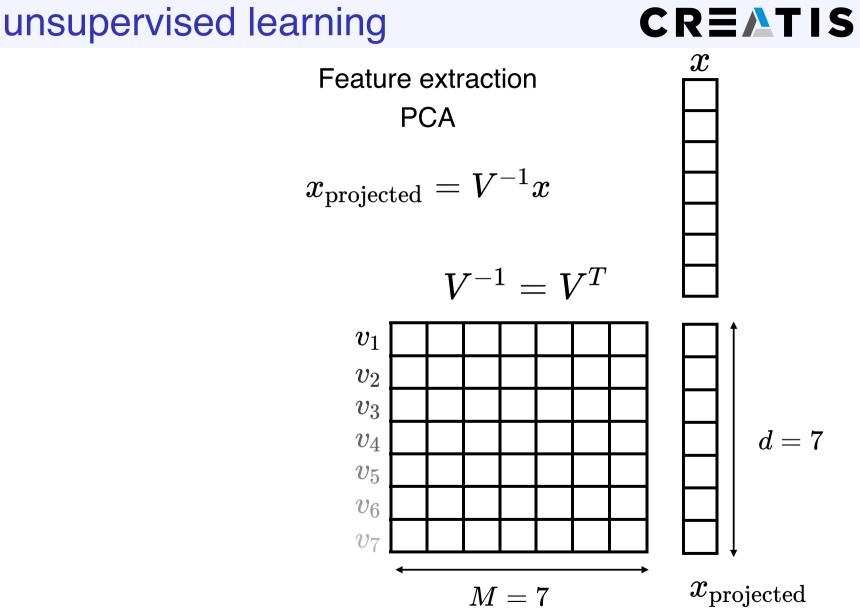


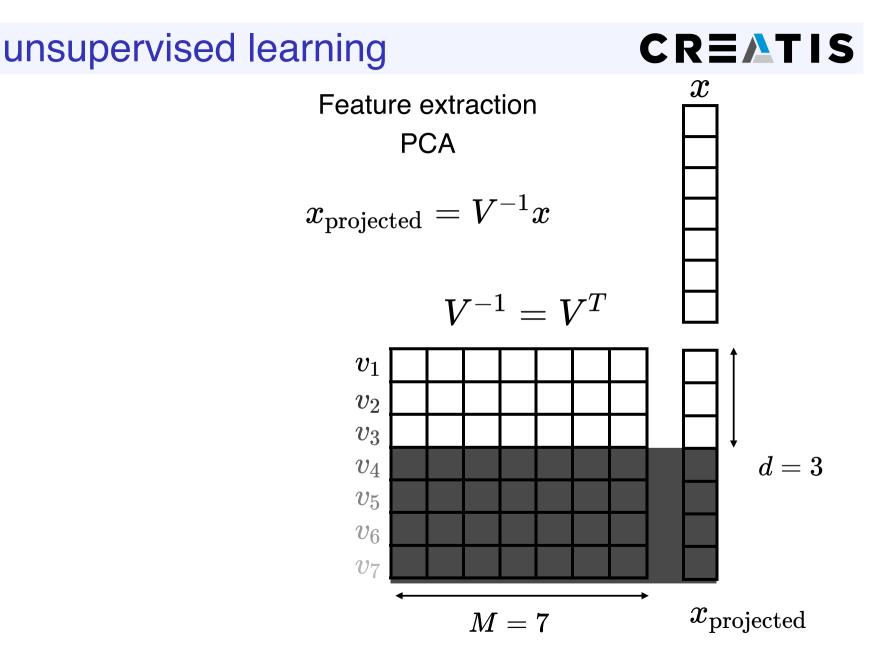
Feature extraction demo with PCA



https://github.com/emmanuelrouxfr/PCA_illustration

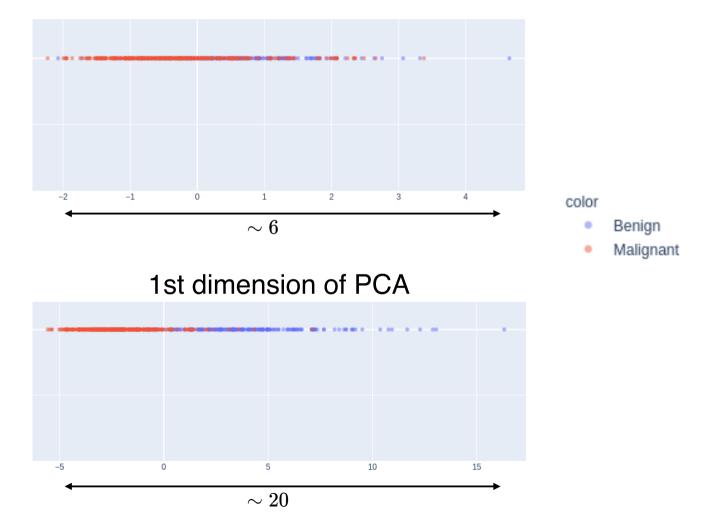






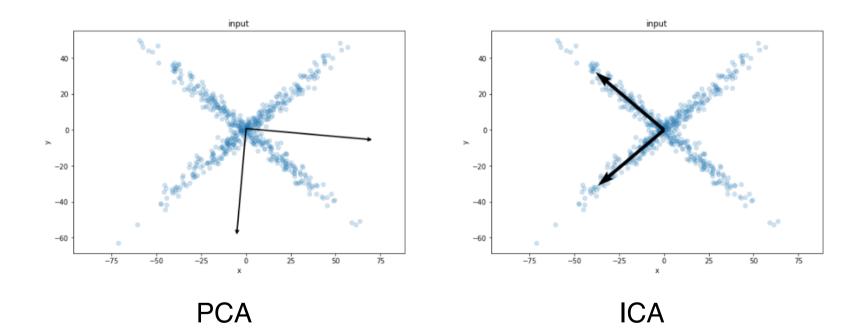


selection of the "mean texture" feature (normalized)





Dimension reduction (linear) ICA



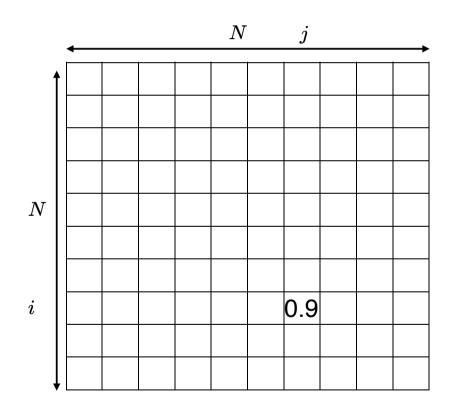


non-linear dimension reduction

ISOMAP Locally Linear Embedding Hessian Eigenmapping Local Tangent Space Alignment t-distributed Stochastic Neighbor Embedding (t-SNE) UMAP (deep) auto-encoders...



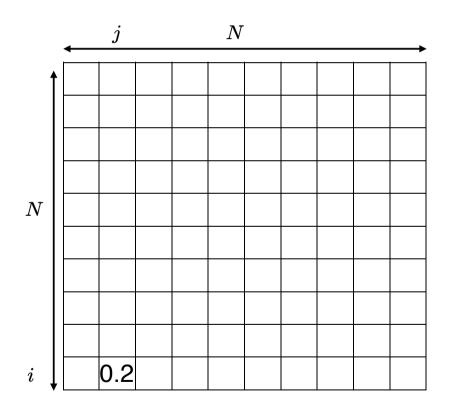
Dimension reduction (non-linear) t-distributed Stochastic Neighbor Embedding (t-SNE)



similarity matrix in input space



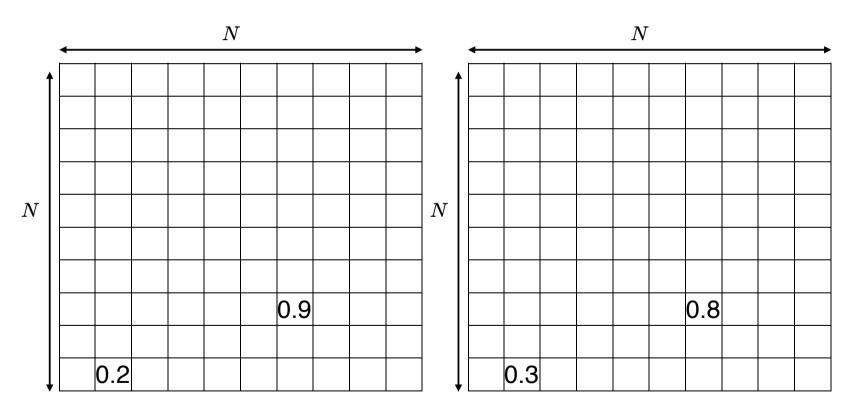
Dimension reduction (non-linear) t-distributed Stochastic Neighbor Embedding (t-SNE)



similarity matrix in input space



Dimension reduction (non-linear) t-distributed Stochastic Neighbor Embedding (t-SNE)

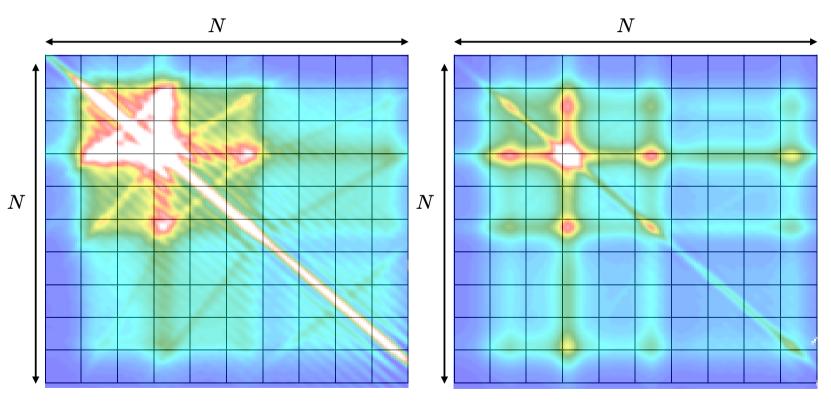


similarity matrix in input space

similarity matrix in lower space



Dimension reduction (non-linear) t-distributed Stochastic Neighbor Embedding (t-SNE)



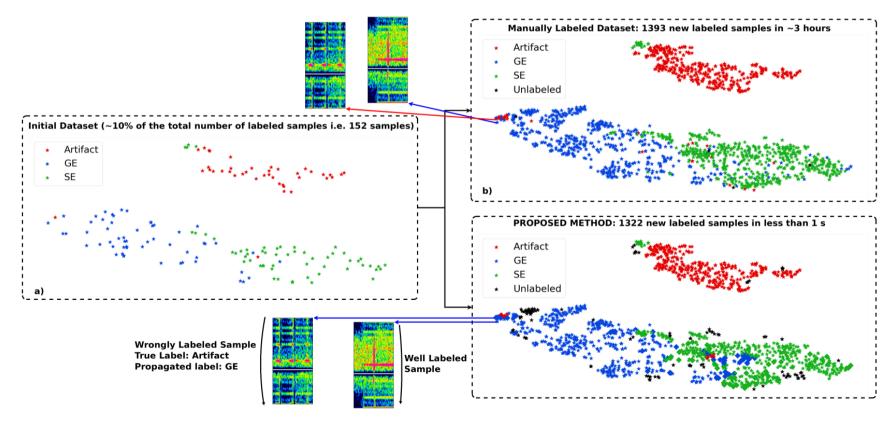
similarity matrix in input space

similarity matrix in lower space



example of t-SNE application

accelerating the annotation of a Transcranial Doppler ultrasound micro-embolic dataset

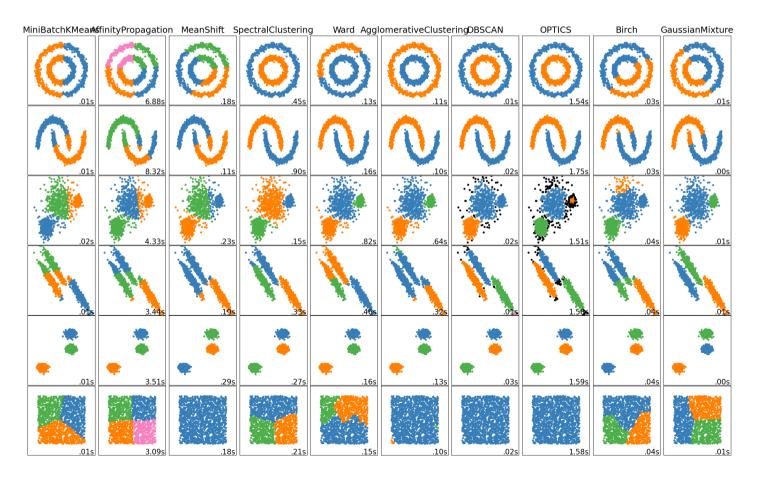


(Vindas et al. 2021, IEEE IUS 2021 submitted)



clustering

Find groups of similar examples (clusters)







what is a cluster ?

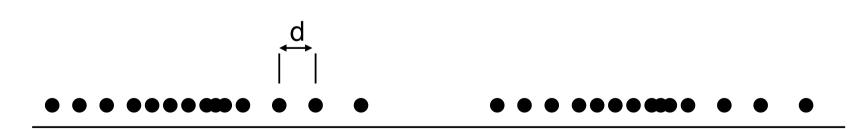
33



clustering

what is a cluster ?

• distance-based definition





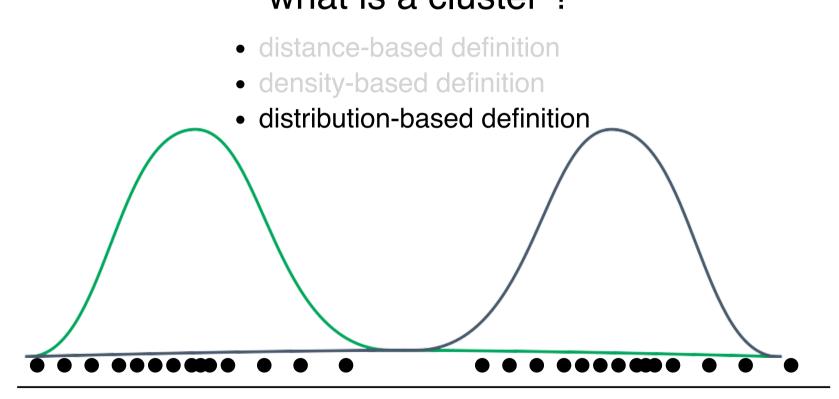
clustering

what is a cluster ?

- distance-based definition
- density-based definition



unsupervised learning clustering what is a cluster ?



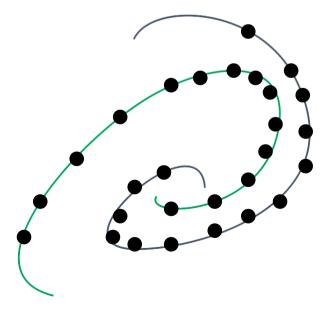
CREATIS



clustering

what is a cluster ?

- distance-based definition
- density-based definition
- distribution-based definition
- path-based distribution (graphs)





clustering

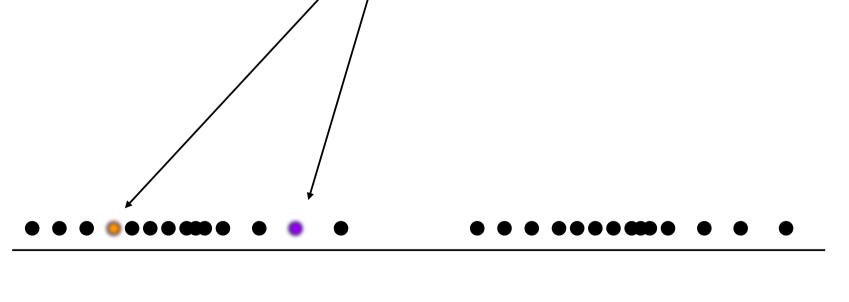
K-means (distance-based method)

38





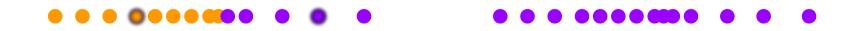






clustering

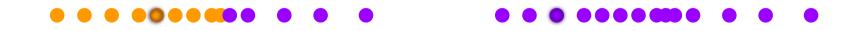
- 1. initialize k samples as centers
- 2. for each sample associate the label of its **closest center**





clustering

- 1. initialize k samples as centers *
- 2. for each sample associate the label of its **closest center**
- 3. update the centers (mean position of its group)





clustering

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- 4. repeat steps 2. and 3. until no update in the clusters



clustering

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clustering

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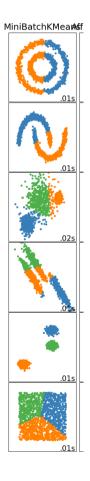
clustering

K-means (distance-based method)

+ fast (O(n))

- need to know / find k (number of clusters)
- can detect only circular clusters

alt. k-median (more computation because need to sort...)





clustering

hierarchical clustering (distance-based method)

agglomerative (bottom up) or divisive (top-down)

use of an appropriate metric *d* (between samples *a* and *b*)

and

a linkage criterion (dissimilarity between sets) example: single-linkage clustering

 $\min\{d(a,b):a\in A,b\in B\}$





hierarchical clustering (distance-based method)

50











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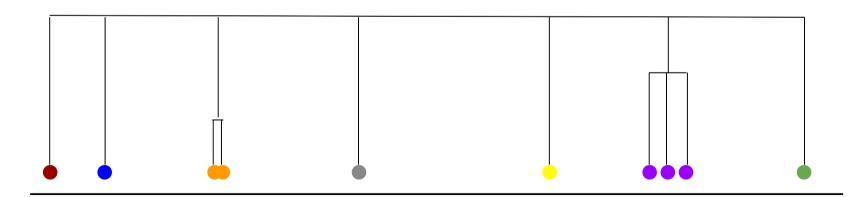






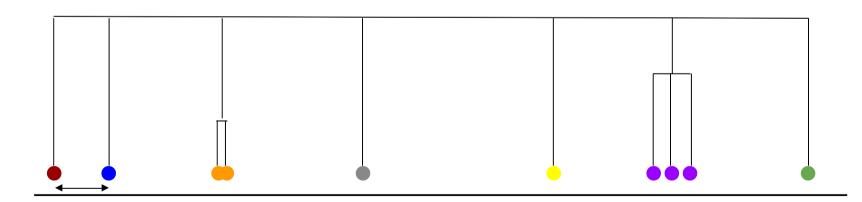






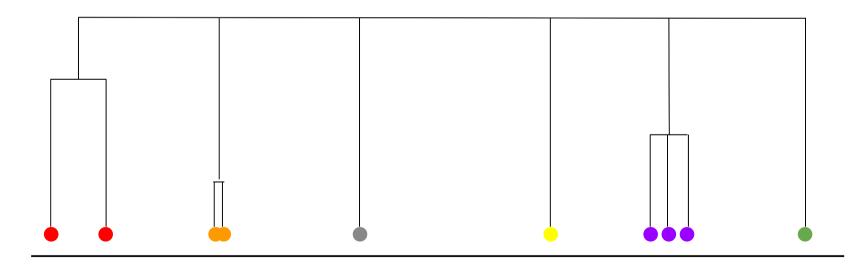






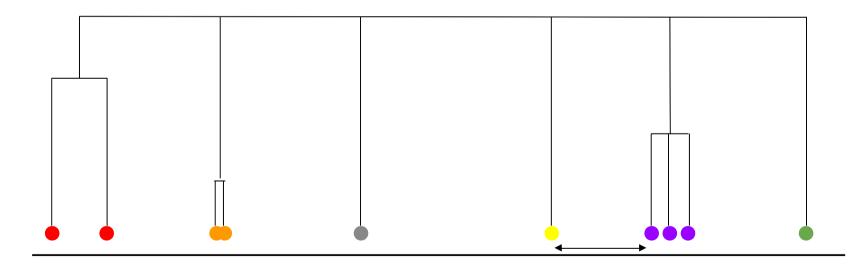






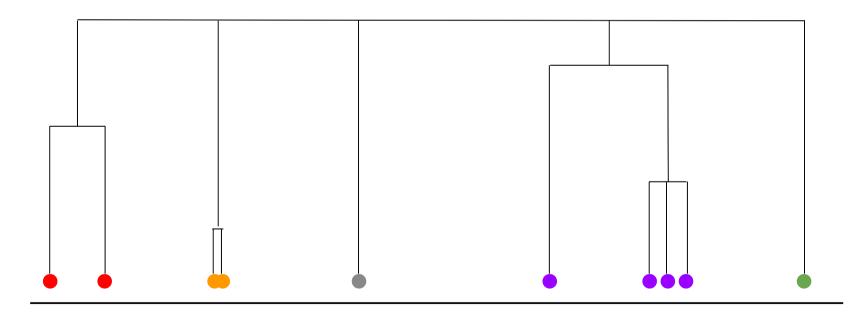






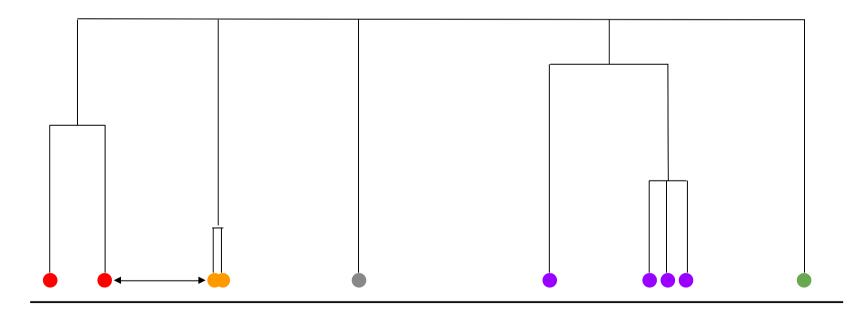






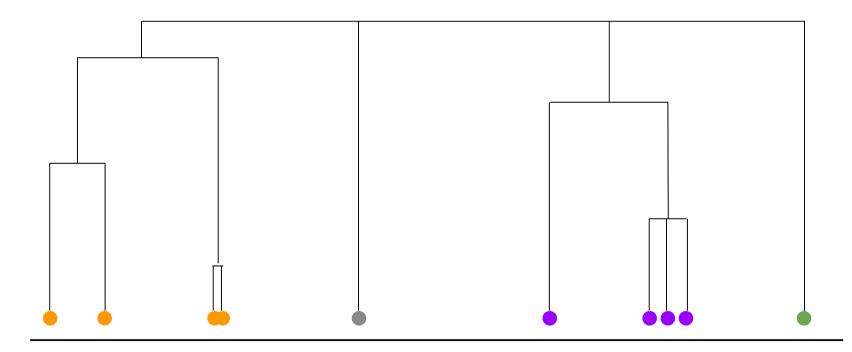






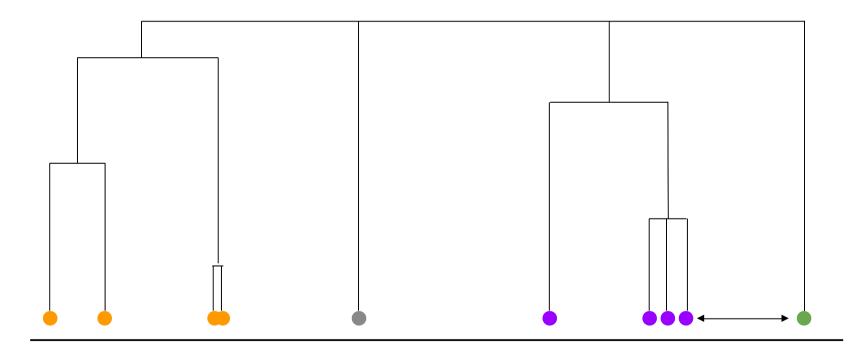






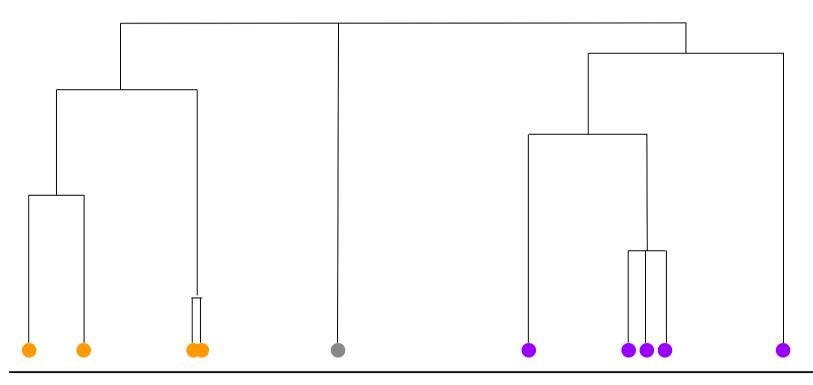






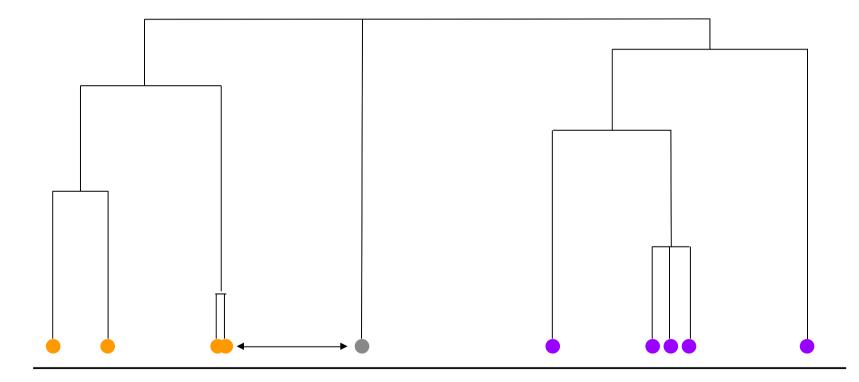






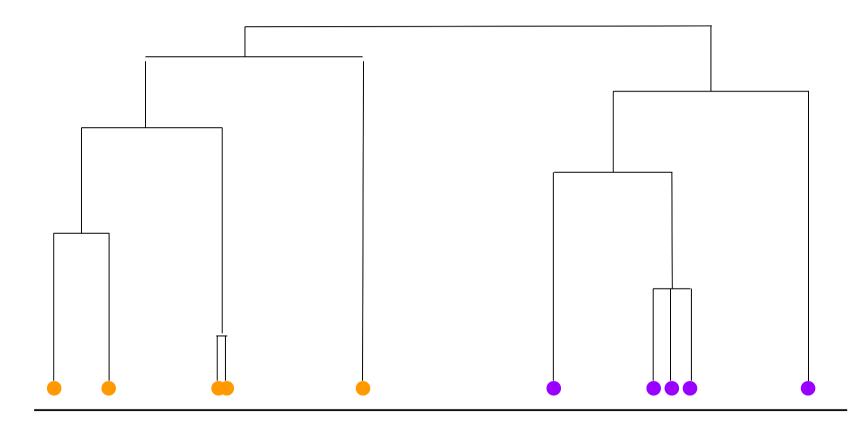


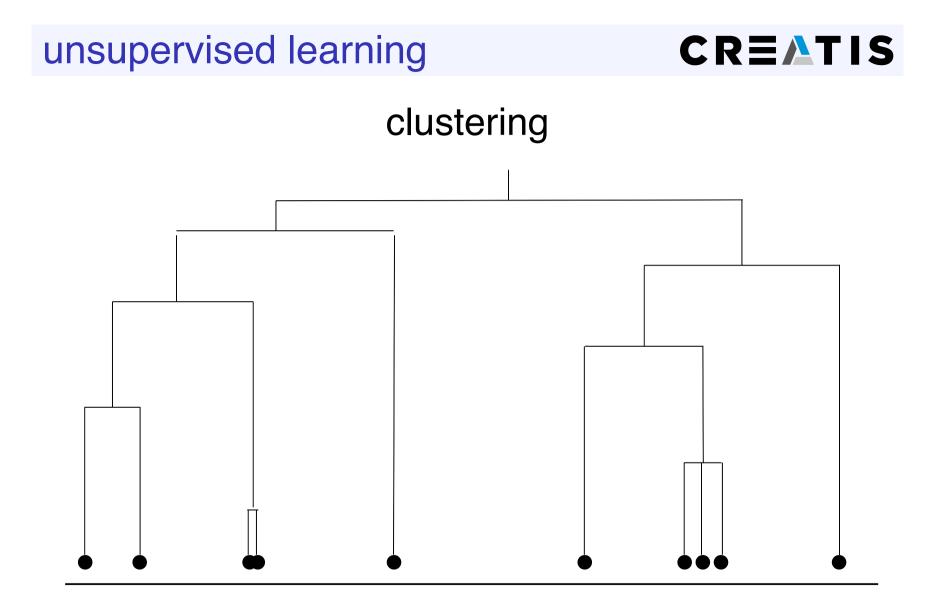






clustering





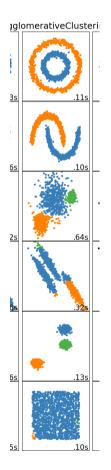


clustering

hierarchical clustering (distance-based method)

+ does not need to know the number of clusters before.
+ does not depend on the chosen distance metric (source?)

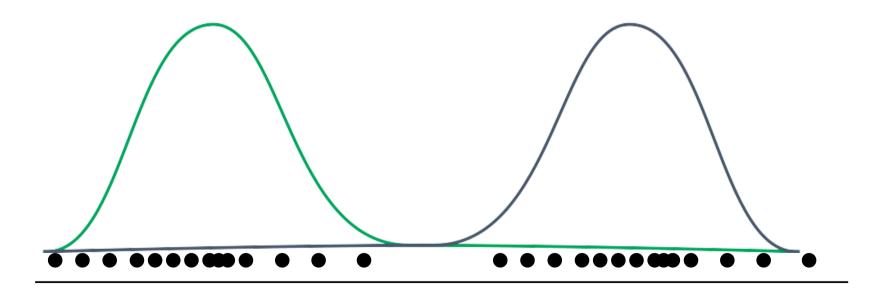
- + sub-groups discovery
- lower efficiency, O(n^3)





Gaussian Mixture Model with Expected-Maximization (distribution-based method)

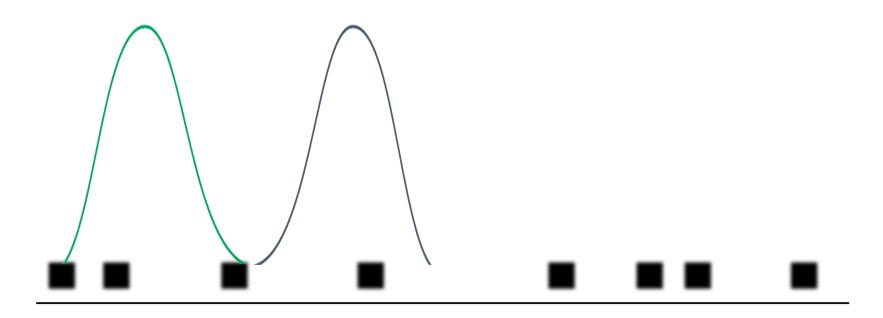
k-means with probability of assignment (instead of closest point assignment)





Gaussian Mixture Model with Expected-Maximization (distribution-based method)

initialize the k = 2 distribution (*several strategies)

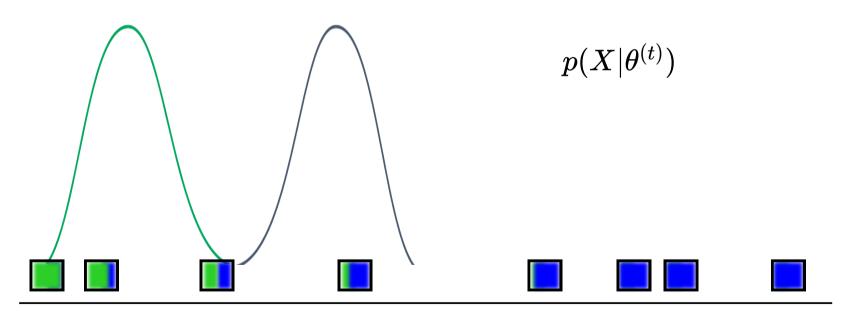




Gaussian Mixture Model with Expected-Maximization (distribution-based method)

Expectation (E) step

find the probability for each point to be generated by each mixture

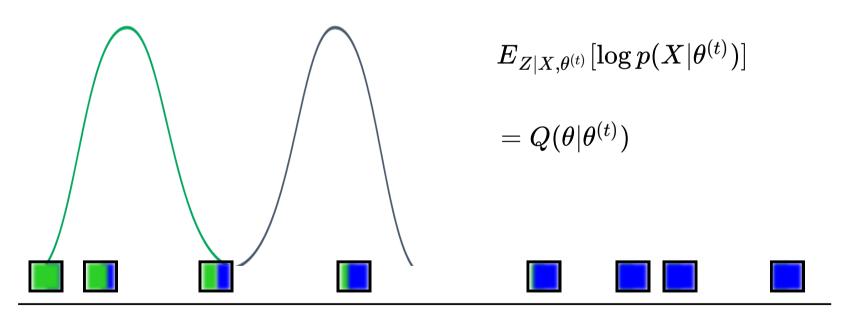




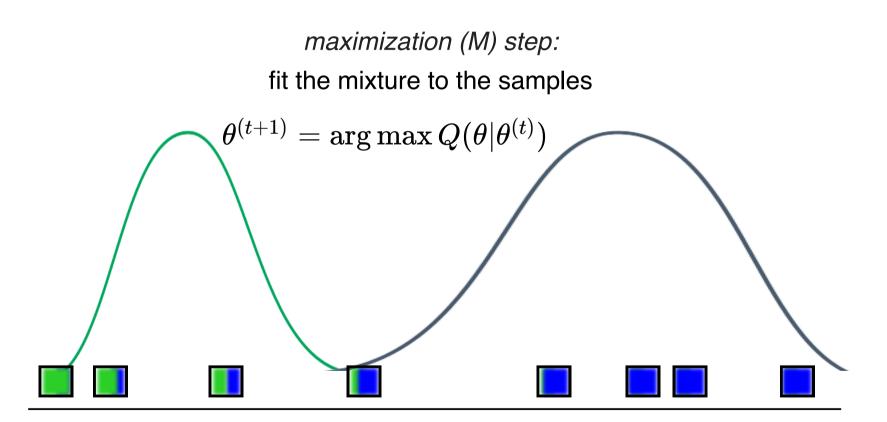
Gaussian Mixture Model with Expected-Maximization (distribution-based method)

Expectation (E) step

find the probability for each point to be generated by each mixture



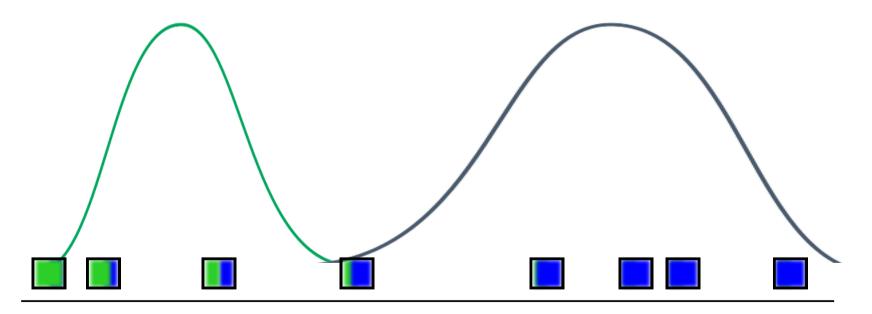




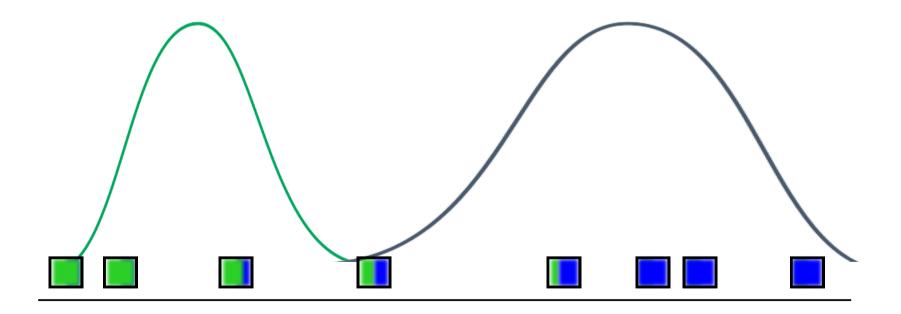


Gaussian Mixture Model with Expected-Maximization (distribution-based method)

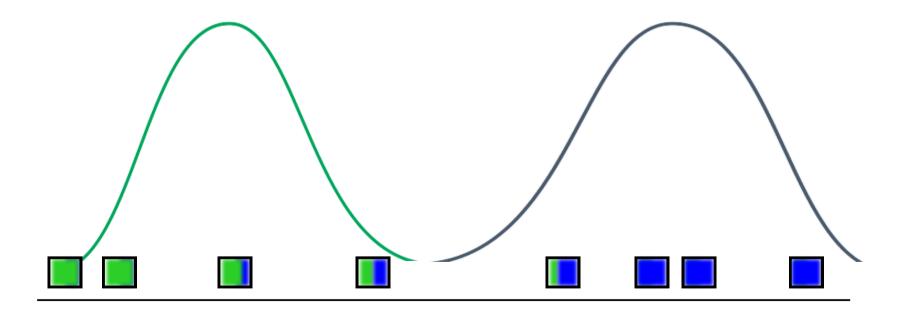
ready for a new E step ? check the colors in the squares...



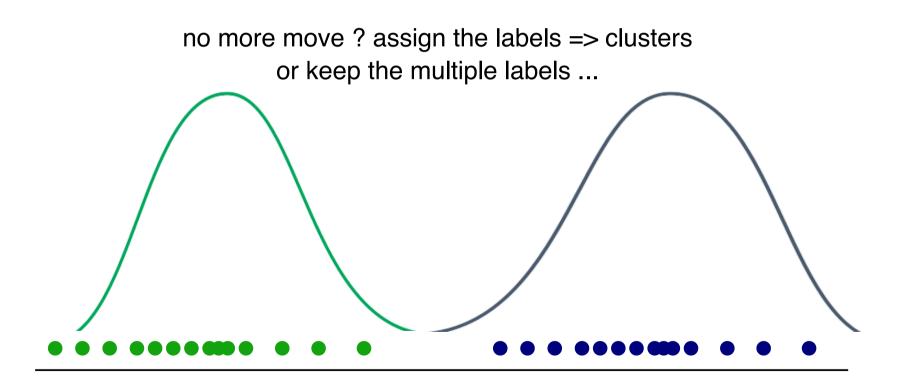














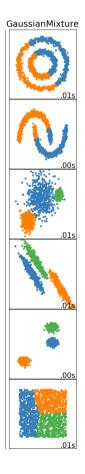
clustering

Gaussian Mixture Model with Expected-Maximization (distribution-based method)

+ not restricted to circular clusters... possibly ellipses !+ support mixed membership labeling

- + you can generate new samples (probabilistic model)

- need to fix the number of Gaussians (expected number of clusters) as in k-means







DBSCAN (density-based method)

All points within the cluster are mutually density-connected

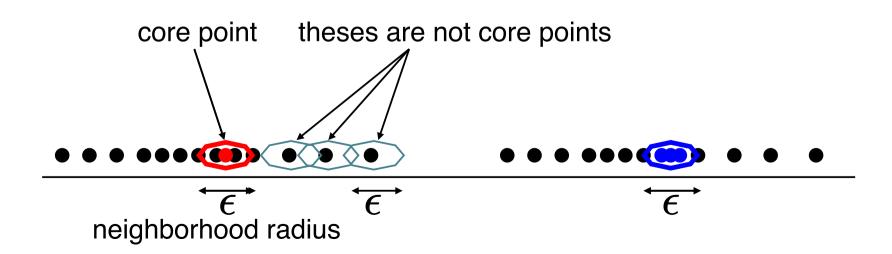
If a point is "density-reachable" from some point of the cluster, it is also part of the cluster

 $\boldsymbol{\epsilon}$: neighborhood radius minPts: minimum number of neighbors to be a **core point**



DBSCAN (density-based method)

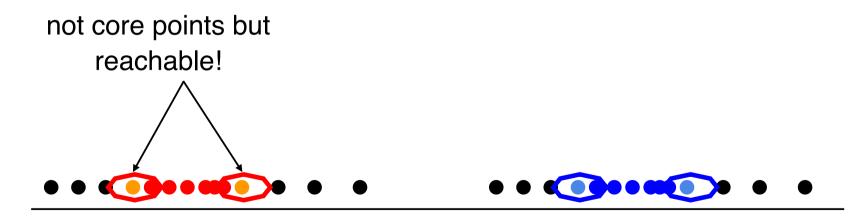
minPts = 2





DBSCAN (density-based method)

minPts = 2

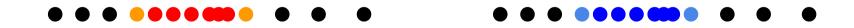




DBSCAN (density-based method)

minPts = 2

the rest is "noise"





DBSCAN (density-based method)

minPts = 2

different results with smaller epsilon ...





DBSCAN (density-based method)

minPts = 2

different results with greater epsilon ...





clustering

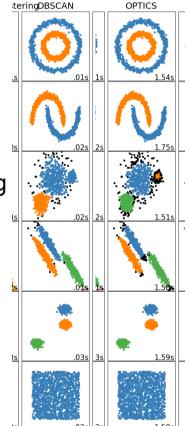
DBSCAN (density-based method)

+ Does not assume any predefined shape on data clusters

- data defined by set of coordinates (not capable of handling arbitrary feature spaces)

- computationally costly... (...)
- not robust to clusters of varying density

=> OPTICS (density-based method)





clustering

Performance Metrics ?

Silhouette coefficient Calinski-Harabaz index Davies-Bouldin Index Rand index Mutual Information based scores Homogeneity, completeness and V-measure Fowlkes-Mallows scores Contingency Matrix Pair Confusion Matrix



clustering

Silhouette coefficient (between -1 and 1) for each sample

the higher its value, the more similar the sample is within its cluster (and not to neighboring clusters).

If most samples have a low or negative value, then the clustering configuration is not appropriate.

 $rac{b-a}{\max(a,b)}$

with a the mean distance between a sample and all other points in the same cluster with b the mean distance between a sample and all other points in the next nearest cluster



clustering

Performance Metrics ?

Calinski-Harabaz index

The higher the Calinski-Harabaz index s(k) the more dense and well separated the k-thcluster is.

$$rac{{
m Tr}(B_k)}{{
m Tr}(W_k)}\,rac{N{-}k}{k{-}1}$$

with B_k the inter-cluster dispersion matrix and W_k the intra-cluster dispersion matrix



unsupervised learning

Dimension reduction Clustering



- A machine learning expert must make assumptions on the data distribution and the task
 - Metrics should be chosen in relation with the application
 - Issues specific to medical imaging should be addressed
 - Imbalanced dataset
 - Annotation scarcity
 - High dimensionality

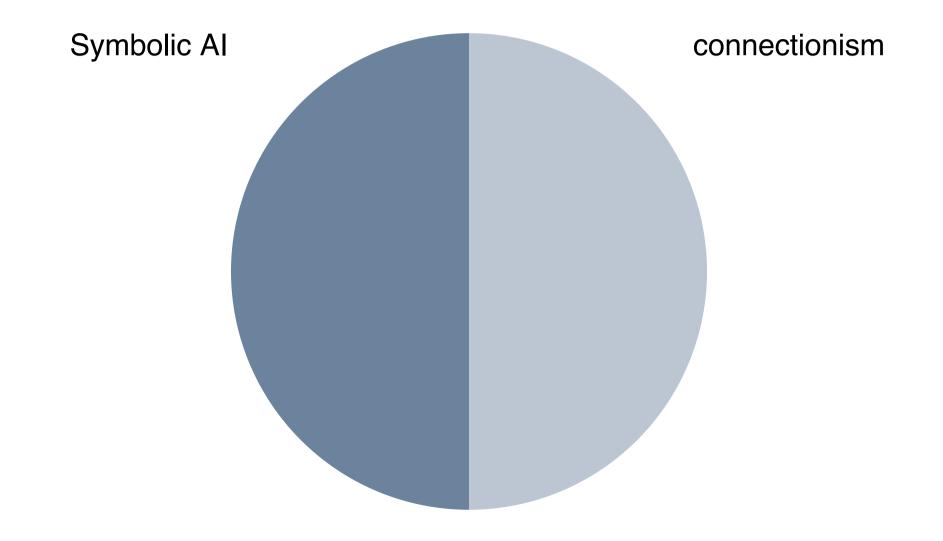
CREATIS

Weaklysupervised Talk by Ismail Ben Ayed and Jose Dolz Friday April 23 4 pm - Paris time

supervised learning semisupervised learning

unsupervised learning

CREATIS



#responsibleAl (biases, ethics)

« a priori » within learning Hands-on session 2.x



explanable AI (xAI)

Talk by Narine Kokhlikyan

Tuesday April 20 4.20 pm - Paris time

- Book "Artificial Intelligence: A Modern approach" Russell Norvig
- Book "Understanding Machine Learning: From Theory to Algorithms" by Shai Shalev-Shwartz and Shai Ben-David
- Lecture notes "Machine Learning" Central Supélec by Jérémy Fix, Hervé Frezza-Buet, Matthieu Geist, Frédéric Pennerath
- Lectures "Machine Learning for Intelligent Systems", Cornell University by Kilian Weinberger Youtube link
 - Model evaluation and selection https://arxiv.org/abs/1811.12808



deeplearningbook.org Goodfellow-et-al-2016

Cardon, D., Cointet, J. P., & Mazières, A. (2018). La revanche des neurones: L'invention des machines inductives et la controverse de l'intelligence artificielle. *Réseaux*, *211*(5), 173-220.

Shervine Amidi (lecture notes) https://stanford.edu/~shervine/teaching/cs-229

Sebastian Raschka (lecture notes) https://github.com/rasbt/stat453-deep-learning-ss20/blob/master/L01-intro/L01-intro_slides.pdf

Nando de Freitas (lecture notes)

https://www.cs.ubc.ca/~nando/540-2013/lectures/l1.pdf

Stephane Canu (lecture notes)

http://asi.insa-rouen.fr/enseignants/~scanu/

https://scikit-learn.org/

https://en.wikipedia.org/