



**UNIVERSITÀ  
DEGLI STUDI  
DI BERGAMO**

Dipartimento  
di Ingegneria Gestionale,  
dell'Informazione e della Produzione

# Lesson 6.

# Performance metrics

**DYNAMIC SYSTEMS  
IDENTIFICATION COURSE**

**MASTER DEGREE  
ENGINEERING AND  
MANAGEMENT FOR HEALTH**

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# Outline

1. Metrics
2. Precision and recall
3. Receiver Operating Characteristic (ROC) curves
4. Worked example



# Outline

## 1. Metrics

2. Precision and recall

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# Metrics

It is extremely important to use **quantitative metrics** for evaluating a machine learning model

- Until now, we relied on the **cost function value** for regression and classification
- Other metrics can be used to **better evaluate** and understand the model
- **For classification**
  - ✓ Accuracy/Precision/Recall/F1-score, ROC curves,...
- **For regression**
  - ✓ Normalized RMSE, Normalized Mean Absolute Error (NMAE),...



# Classification case: metrics for skewed classes

## Disease dichotomic classification example

Train logistic regression model  $h(x)$ , with  $y = 1$  if disease,  $y = 0$  otherwise.

Find that you got 1% error on test set (99% correct diagnoses)

Only 0.5% of patients **actually have** disease

The  $y = 1$  class has very few examples with respect to the  $y = 0$  class

If I use a classifier that **always classifies** the observations to the **0 class**, I get 99.5% of accuracy!!

For **skewed classes**, the accuracy metric can be deceptive



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# Precision and recall

Suppose that  $y = 1$  in presence of a **rare class** that we want to detect

**Precision** (How much we are precise in the detection)

*Of all patients where we classified  $y = 1$ , what fraction actually has the disease?*

$$\frac{\text{True Positive}}{\# \text{ Estimated Positive}} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Positive}}$$

**Recall** (How much we are good at detecting)

*Of all patients that actually have the disease, what fraction did we correctly detect as having the disease?*

$$\frac{\text{True Positive}}{\# \text{ Actual Positive}} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}}$$

## Confusion matrix

		Actual class	
		1 (p)	0 (n)
Estiamted class	1 (Y)	True positive (TP)	False positive (FP)
	0 (N)	False negative (FN)	True negative (TN)



# Trading off precision and recall

Logistic regression:  $0 \leq s(\boldsymbol{\varphi}^\top \boldsymbol{\theta}) \leq 1$

- Classify 1 if  $s(\boldsymbol{\varphi}^\top \boldsymbol{\theta}) \geq 0.5$
  - Classify 0 if  $s(\boldsymbol{\varphi}^\top \boldsymbol{\theta}) < 0.5$
- These thresholds can be different from 0.5!



*At different thresholds, correspond different confusion matrices!*

Suppose we want to classify  $y = 1$  (disease) only if very confident

- Increase threshold  $\rightarrow$  Higher precision, lower recall

Suppose we want to avoid missing too many cases of disease (avoid false negatives)

- Decrease threshold  $\rightarrow$  Higher recall, lower precision



# F1-score

It is usually better to compare models by means of one number only. The **F1 – score** can be used to **combine precision and recall**

	Precision(P)	Recall (R)	Average	F <sub>1</sub> Score
Algorithm 1	0.5	0.4	0.45	0.444
Algorithm 2	0.7	0.1	0.4	0.175
Algorithm 3	0.02	1.0	0.51	0.0392

Algorithm 3 classifies always 1

Average says not correctly that Algorithm 3 is the best

The best is Algorithm 1

$$\text{Average} = \frac{P + R}{2}$$

$$\text{F}_1 \text{ score} = 2 \frac{P \cdot R}{P + R}$$

- $P = 0$  or  $R = 0 \Rightarrow \text{F}_1 \text{ score} = 0$
- $P = 1$  and  $R = 1 \Rightarrow \text{F}_1 \text{ score} = 1$

# Summaries of the confusion matrix

Different metrics can be computed from the confusion matrix, depending on the class of interest ([https://en.wikipedia.org/wiki/Precision\\_and\\_recall](https://en.wikipedia.org/wiki/Precision_and_recall))

		True condition			
		Condition positive	Condition negative		
Predicted condition	Total population			Prevalence = $\frac{\sum \text{Condition positive}}{\sum \text{Total population}}$	Accuracy (ACC) = $\frac{\sum \text{True positive} + \sum \text{True negative}}{\sum \text{Total population}}$
	Predicted condition positive	<b>True positive</b> , Power	<b>False positive</b> , Type I error	Positive predictive value (PPV), Precision = $\frac{\sum \text{True positive}}{\sum \text{Predicted condition positive}}$	False discovery rate (FDR) = $\frac{\sum \text{False positive}}{\sum \text{Predicted condition positive}}$
	Predicted condition negative	<b>False negative</b> , Type II error	<b>True negative</b>	False omission rate (FOR) = $\frac{\sum \text{False negative}}{\sum \text{Predicted condition negative}}$	Negative predictive value (NPV) = $\frac{\sum \text{True negative}}{\sum \text{Predicted condition negative}}$
		True positive rate (TPR), Recall, Sensitivity, probability of detection = $\frac{\sum \text{True positive}}{\sum \text{Condition positive}}$	False positive rate (FPR), Fall-out, probability of false alarm = $\frac{\sum \text{False positive}}{\sum \text{Condition negative}}$	Positive likelihood ratio (LR+) = $\frac{\text{TPR}}{\text{FPR}}$	Diagnostic odds ratio (DOR) = $\frac{\text{LR+}}{\text{LR-}}$
		False negative rate (FNR), Miss rate = $\frac{\sum \text{False negative}}{\sum \text{Condition positive}}$	Specificity (SPC), Selectivity, True negative rate (TNR) = $\frac{\sum \text{True negative}}{\sum \text{Condition negative}}$	Negative likelihood ratio (LR-) = $\frac{\text{FNR}}{\text{TNR}}$	

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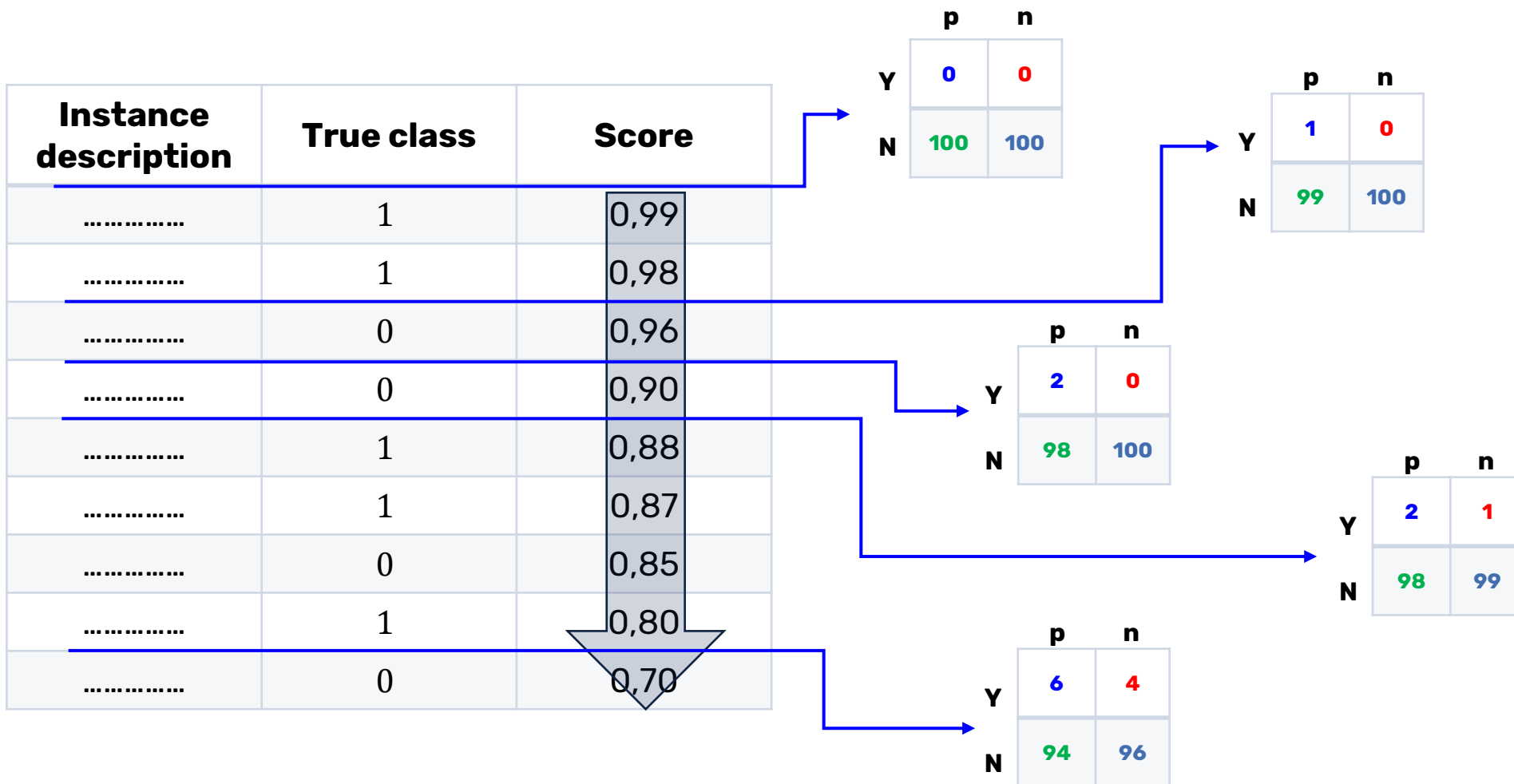
# Ranking instead of classifying

Classifiers such as logistic regression can output a **probability** of belonging to a class (or something similar)

- We can use this to **rank** the different instances and take actions on the cases at top of the list
- We may have a **budget**, so we have to target most promising individuals
- Ranking enables to use different techniques for **visualizing** model performance



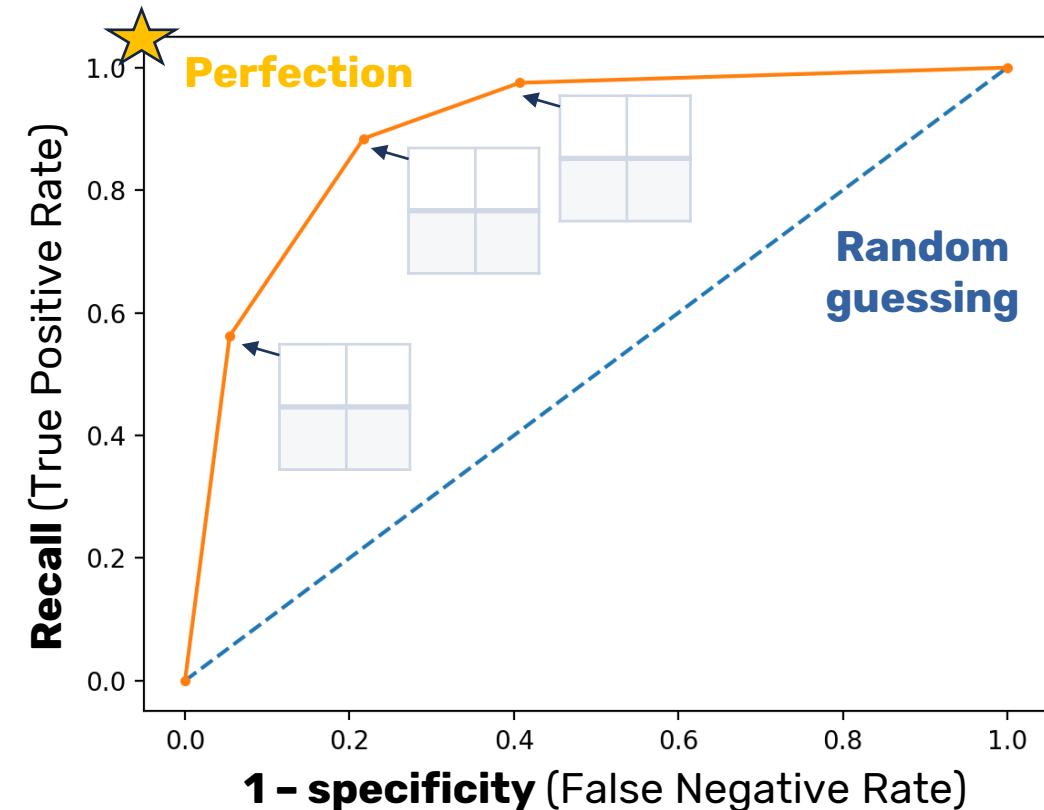
# Ranking instead of classifying



Different confusion matrices by changing the **threshold**

# Ranking instead of classifying

**ROC curves** are a very general way to **represent and compare** the performance of different models (on a binary classification task)



## Observations

- (0,0): classify always negative
- (1,1): classify always positive
- Diagonal line: random classifier
- Below diagonal line: worse than random classifier
- Different classifiers can be compared
- Area Under the Curve (AUC): probability that a randomly chosen positive instance will be ranked ahead of randomly chosen negative instance

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# Disclaimer

This example is **ONLY** for **educational purposes**, in order to see how to train and use a convolutional neural network in practice with real data.

I am **NOT**, by any means, trying to say that this should be an accurate or valid system from a medical point of view.

Artificial intelligence tools show **ALWAYS be supported** by domain knowledge from humans.

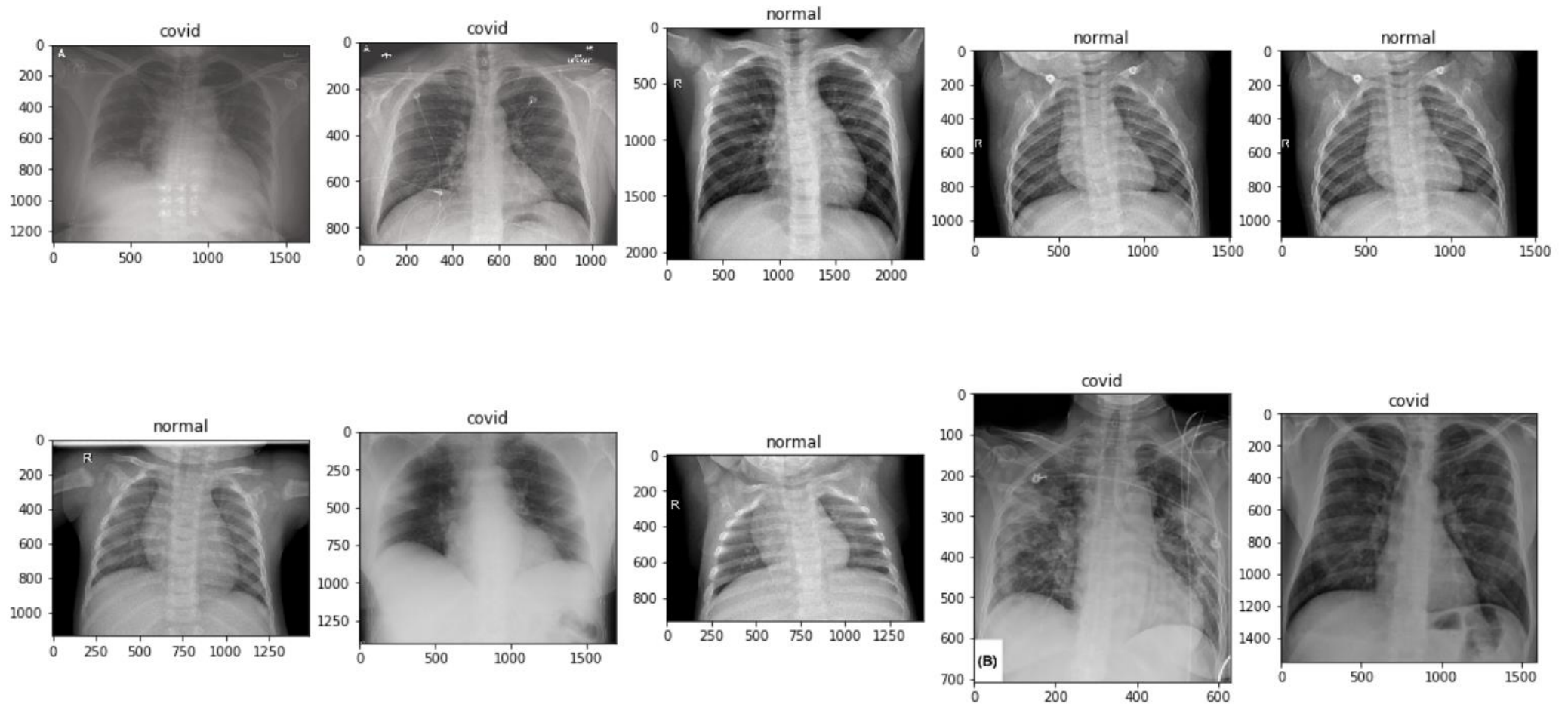
**Again, this example does not claim to solve COVID-19 detection.**





# Pneumonia detection

Suppose to have at disposal X-ray images of lungs: **Healthy** people - **Covid-19 disease** patients



# Acknowledgments

- The COVID-19 X-ray image is curated by Dr. Joseph Cohen, a postdoctoral fellow at the University of Montreal, see <https://josephpcohen.com/w/public-covid19-dataset/>
- The previous data contain only X-ray images of people with a disease. To collect images of healthy people, we can download another X-ray dataset on the platform Kaggle <https://www.kaggle.com/paultimothymooney/chest-xray-pneumonia>
- The analysis is inspired from a tutorial by Adrian Rosebrock: <https://www.pyimagesearch.com/2020/03/16/detecting-covid-19-in-x-ray-images-with-keras-tensorflow-and-deep-learning/>



# Acknowledgments

We want to use a classifier to perform classification:

- **Healthy** patients: class 0
- Patients with a **disease**: class 1

The input data are directly the X-ray **images**

For these computer vision tasks, the state of the art algorithm are the **Convolutional Neural Networks**:

- we can use them to classify the images into **healthy** and **disease**

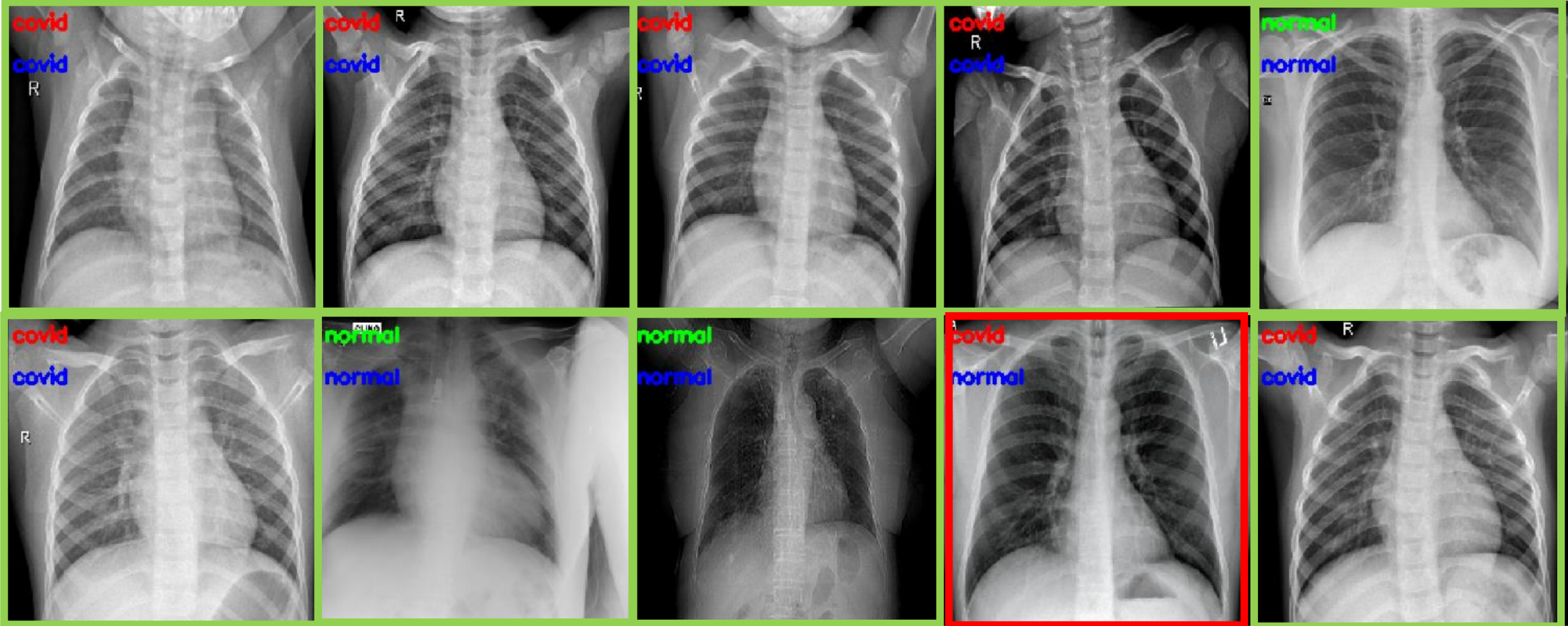


# Pneumonia detection

True label

Estimated covid label

Estimated healthy label



# Pneumonia detection

## Classification results on test set

**Sensitivity** (recall, true positive rate)

$$\frac{\text{True Positive}}{\# \text{ Actual Positive}} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}} = 0.92$$

**Specificity** (true negative rate)

$$\frac{\text{True Negative}}{\# \text{ Actual Negative}} = \frac{\text{True Negative}}{\text{False Positive} + \text{True Negative}} = 1$$

		Actual class	
		1 (p)	0 (n)
Estimated class	1 (Y)	<b>True positive</b> 11	<b>False positive</b> 0
	0 (N)	<b>False negative</b> 1	<b>True negative</b> 11

- **Accuracy:**  $\approx 96\%$



# Pneumonia detection

## Classification results on test set

**Sensitivity** (recall, true positive rate)

$$\frac{\text{True Positive}}{\# \text{ Actual Positive}} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}} = 0.92$$

**Specificity** (true negative rate)

$$\frac{\text{True Negative}}{\# \text{ Actual Negative}} = \frac{\text{True Negative}}{\text{False Positive} + \text{True Negative}} = 1$$

- **Sensitivity**: of patients that **do have** COVID-19 (i.e., *true positives*), we could accurately identify them as “COVID-19 positive” 92% of the time using our model
- **Specificity**: of patients that **do not have** COVID-19 (i.e., *true negatives*), we could accurately identify them as “COVID-19 negative” 100% of the time using our model.



# Pneumonia detection

## Classification results on test set

**Sensitivity** (recall, true positive rate)

$$\frac{\text{True Positive}}{\# \text{ Actual Positive}} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}} = 0.92$$

**Specificity** (true negative rate)

$$\frac{\text{True Negative}}{\# \text{ Actual Negative}} = \frac{\text{True Negative}}{\text{False Positive} + \text{True Negative}} = 1$$

- Being able to **accurately detect healthy patients** with 100% accuracy is great. We do not want to quarantine someone for nothing
- ...but **we don't want to classify someone as «healthy» when they are «COVID-19 positive»**, since it could infect other people without knowing



# Summary

**Balancing sensitivity and specificity** is incredibly challenging when it comes to medical applications

The results should **always be validated** with another pool of people

Furthermore, we need to be **concerned of what the model is actually learning:**

- Does the results align with the medical knowledge?
- Was the dataset well representative of the population or there was selection bias?
- Do we accounted for all external factors (confounding) that could interfere with the response?







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