### Modify the weight values

to obtain better predictions

## We need a way to measure the difference between the predictions and the true species (the cross-entropy error)

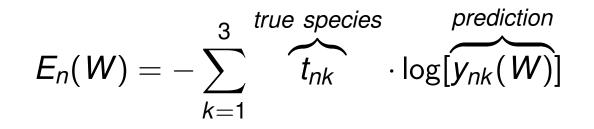
## And our goal is to find the weights that minimizes that error function (using gradient descent)

## Notation

## The matrices $W^{(1)}$ and $W^{(2)}$ are combined as W

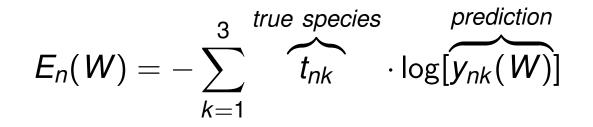
row	features				true species			predictions		
n	S.L.	S.W.	P.L.	P.W.	t <sub>n1</sub>	t <sub>n2</sub>	t <sub>n3</sub>	y <sub>n1</sub>	y <sub>n2</sub>	y <sub>n3</sub>
4	4.6	3.1	1.5	0.2	1	0	0	1	0	0
5	5.0	3.6	1.4	0.2	1	0	0	0.94	0.05	0.01

The cross-entropy error/loss function for the *n*th row:



row	features				true species			predictions		
n	S.L.	S.W.	P.L.	P.W.	t <sub>n1</sub>	t <sub>n2</sub>	t <sub>n3</sub>	y <sub>n1</sub>	y <sub>n2</sub>	y <sub>n3</sub>
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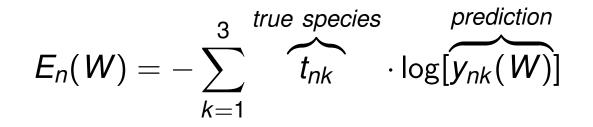


Example:

$$E_4(W) = -t_{n1} \cdot \log[y_{n1}(W)] = -\log(1) = 0$$

row	features				true species			predictions		
n	S.L.	S.W.	P.L.	P.W.	t <sub>n1</sub>	t <sub>n2</sub>	t <sub>n3</sub>	y <sub>n1</sub>	y <sub>n2</sub>	y <sub>n3</sub>
4	4.6	3.1	1.5	0.2	1	0	0	1	0	0
5	5.0	3.6	1.4	0.2	1	0	0	0.94	0.05	0.01

The cross-entropy error/loss function for the *n*th row:



Example:

$$E_5(W) = -t_{n1} \cdot \log[y_{n1}(W)] = -\log(0.94) = 0.06$$

# Find the weights *W* that minimize the total cross-entropy error:

$$E(W) = \sum_{n=1}^{N} E_n(W)$$

# How to derive the cross-entropy formula ?

#### The maximum likelihood method

Data:

$$X_1,\ldots,X_N\sim\mathcal{N}(\mu,\sigma^2)$$

Point estimate of  $\mu$ :

$$\hat{\mu} = \operatorname{argmax}_{\mu} \mathcal{L}(\mu | X) = \operatorname{argmax}_{\mu} \prod_{i=1}^{N} \mathcal{N}_{i}(\mu, \sigma^{2}) = \frac{1}{N} \sum_{i=1}^{N} X_{i}$$

Equivalently:

$$\hat{\mu} = {\sf argmin}_{\mu} \left[ - \log \mathcal{L}(\mu | oldsymbol{X}) 
ight]$$

## The total cross-entropy error is defined as the negative log-likelihood

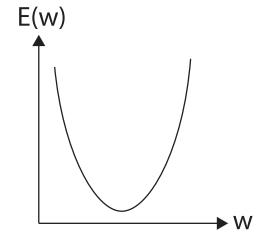
$$E(W) = -\log \mathcal{L}(W|T);$$
  $\hat{W} = \operatorname{argmin}_W E(W)$ 

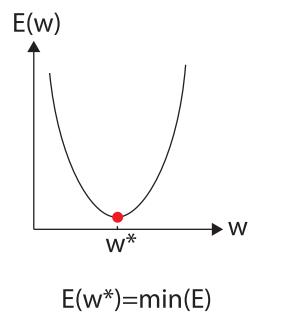
where

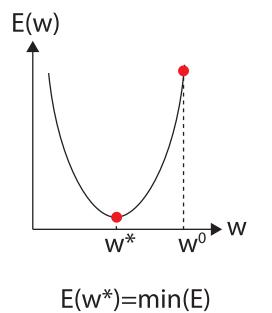
$$\mathcal{L}(W|T) = \prod_{n=1}^{N} \prod_{k=1}^{K} y_{nk}^{t_{nk}}(W)$$

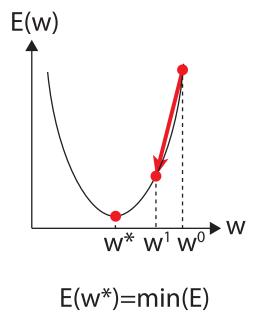
In RED: the probability for the correct class

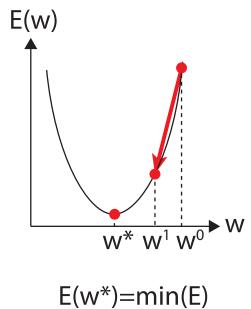
# How does gradient descent work ?





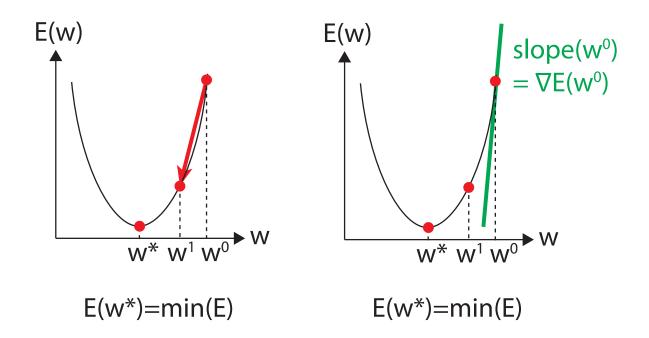


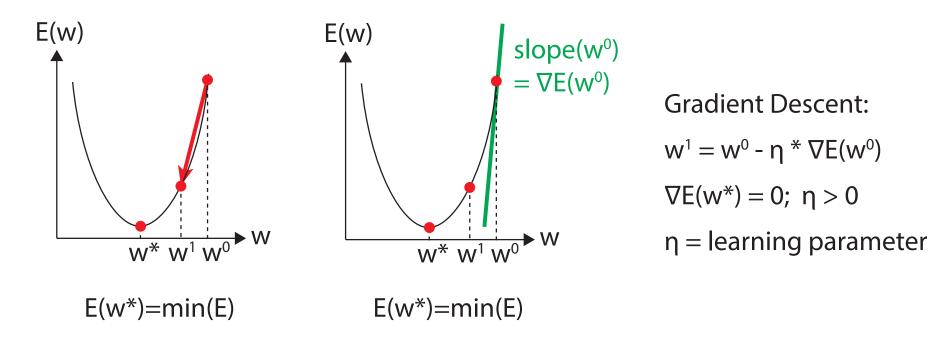




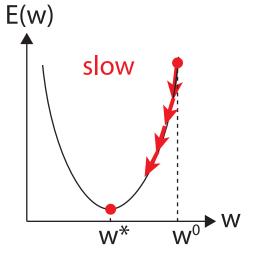
Several iterations:

 $W^0 \rightarrow W^1 \rightarrow W^2 \rightarrow W^3 \rightarrow W^*$ 

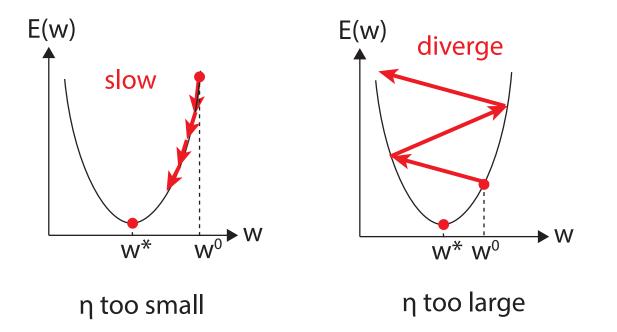


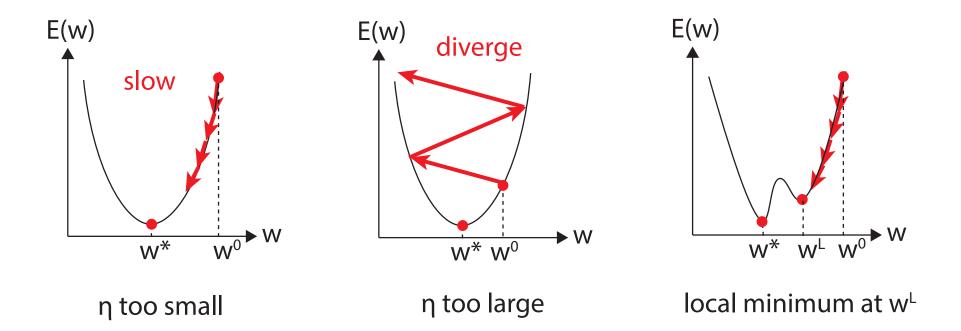


## Possible problems



η too small





Initialization  $\tau = 0$ : Choose the initial weights  $W^0$  with  $\mathcal{N}(0, \sigma^2)$ 

Initialization  $\tau = 0$ : Choose the initial weights  $W^0$  with  $\mathcal{N}(0, \sigma^2)$ 

$$W^{(1)} = \begin{pmatrix} 0.5 & 0.1 & -0.2 & -0.4 \\ -0.4 & 1.0 & 0.5 & 1.0 \\ -0.2 & -0.2 & -0.5 & -0.1 \\ 0.2 & 0.7 & 0.3 & 0.2 \\ 0.6 & 0.6 & 0.1 & -0.4 \end{pmatrix}$$

$$W^{(2)} = \begin{pmatrix} 0.6 & 0.1 & 0.9 & -0.2 & -0.5 \\ 0.3 & -0.3 & 0.3 & -0.9 & -0.9 \\ 0.3 & 0.2 & 0.4 & -1.0 & 0.6 \end{pmatrix}$$

## 3 possibilities for the next steps

## 3 possibilities for the next steps

#### Batch Gradient Descent

- Mini-batch Gradient Descent
- Stochastic Gradient Descent

## **Batch Gradient Descent**

- Apply the NN to all the train set
- Record all the errors
- **3** Update the weights:

$$\boldsymbol{W}^{\tau} = \boldsymbol{W}^{\tau-1} - \eta \cdot \nabla \boldsymbol{E}(\boldsymbol{W}^{\tau-1})$$

## Mini-batch Gradient Descent

- Apply the NN to a batch of the train set
- Record the corresponding errors
- **Output** Update the weights:

$$W^{\tau} = W^{\tau-1} - \eta \cdot \nabla \sum_{n \in batch} E_n(W^{\tau-1})$$

## Stochastic Gradient Descent

- Apply the NN to one sample of the train set
- Record the one sample error
- **3** Update the weights:

$$\boldsymbol{W}^{\tau} = \boldsymbol{W}^{\tau-1} - \eta \cdot \nabla \boldsymbol{E}_n(\boldsymbol{W}^{\tau-1})$$

## Iteration

1 iteration (or pass) is one weight update

## Epoch

#### 1 epoch is reached

## when the NN has passed through all the training data

## EXAMPLE

#### If you have 100 training samples,

#### and your batch size is 50,

then it will take 2 iterations to complete 1 epoch

## **Gradient Descent**

- Batch Gradient Descent:
   1 epoch = 1 iteration
- Mini-batch Gradient Descent:
   1 epoch = (N/batch) iterations
- Stochastic Gradient Descent:
   1 epoch = N iterations

## What are

## the performance metrics ?

### They may be used on the training, validation and test sets

## Cross-entropy error/loss function

$$E = -\sum_{n=1}^{N} \sum_{k=1}^{3} t_{nk} \cdot \log y_{nk}$$

## Confusion matrix

predictions					
actuals	setosa	versicolor	virginica		
setosa	14	0	0		
versicolor	0	9	0		
virginica	0	2	10		

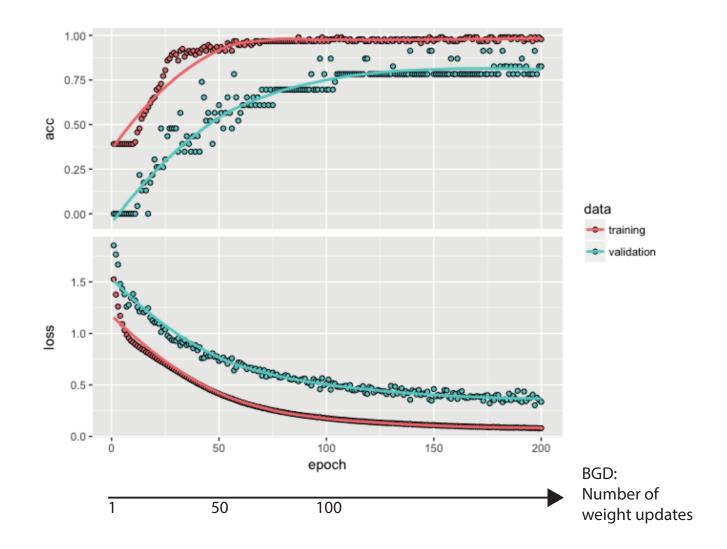
## Accuracy rate = 1 - Error rate

Accuracy rate	=	Number of correct predictions Total number of predictions	$=rac{33}{35}=94\%$
Error rate	=	Number of wrong predictions Total number of predictions	$=rac{2}{35}=6\%$

## EXAMPLES

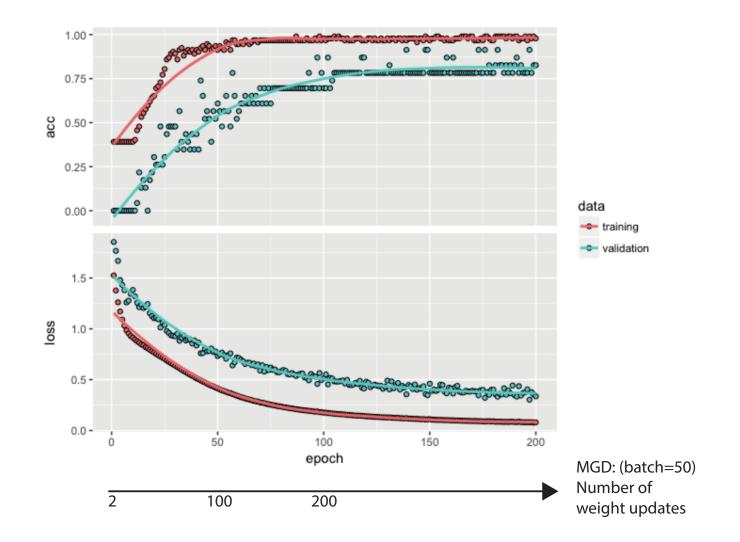
### Performance metrics

Training and validation datasets:



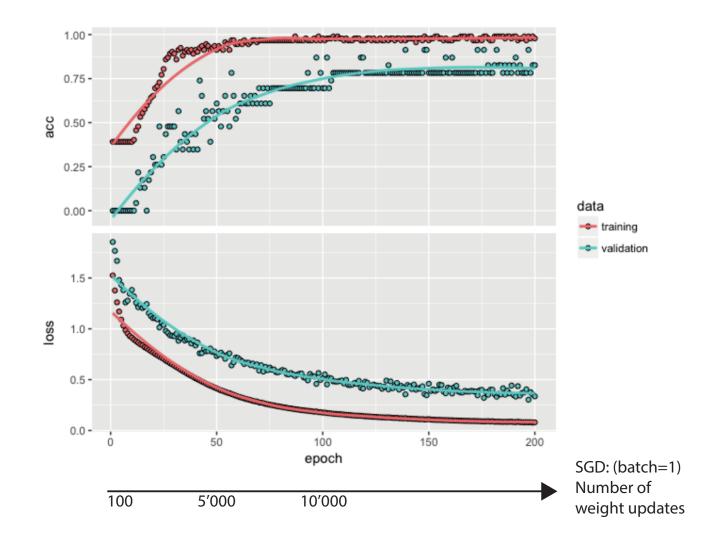
#### Performance metrics

Training and validation datasets:



#### Performance metrics

Training and validation datasets:



### Test set

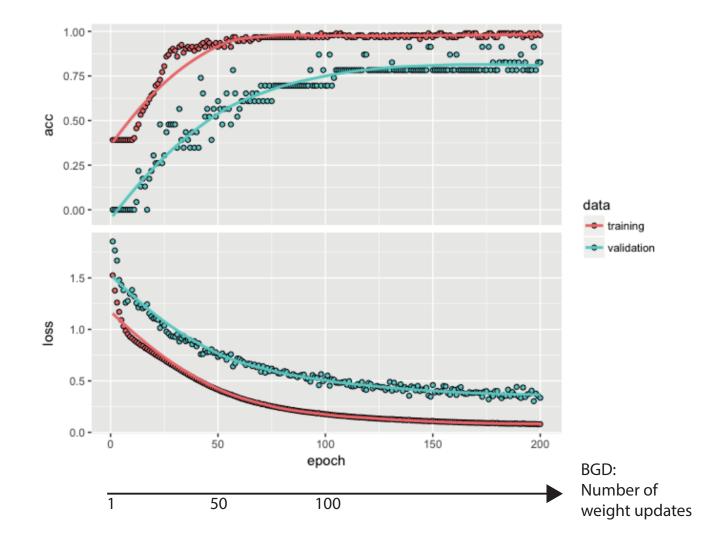
### Test set

### Accuracy=0.91 and cross-entropy loss=0.22

## Test set

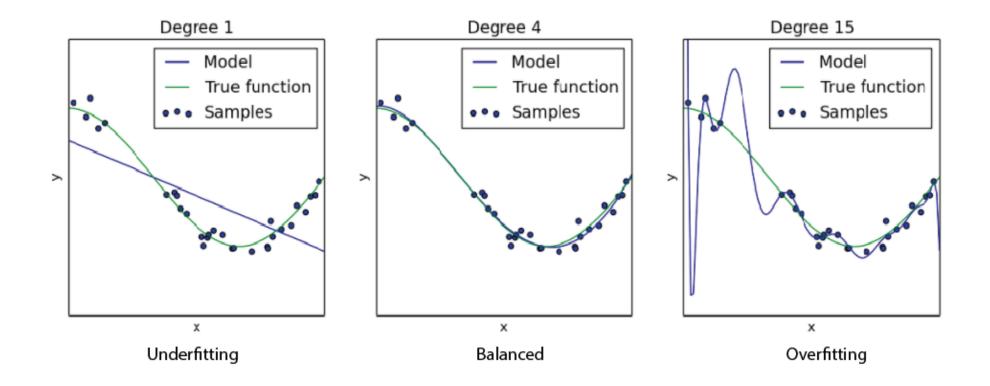
### Accuracy=0.91 and cross-entropy loss=0.22

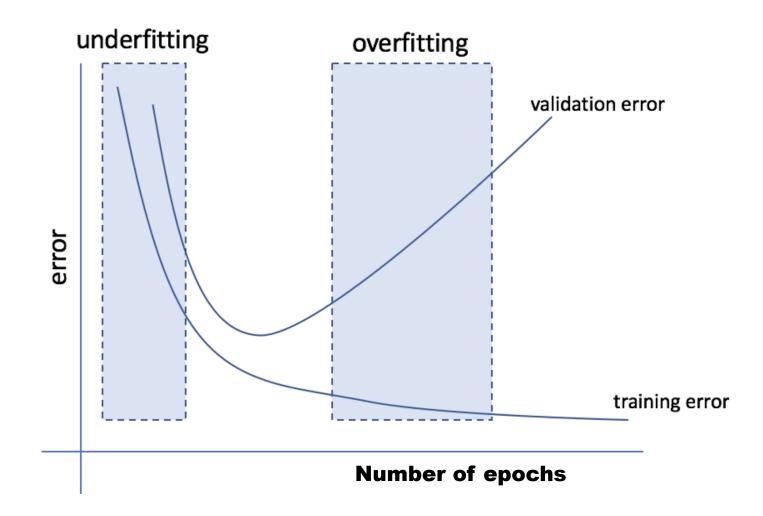
### THE END

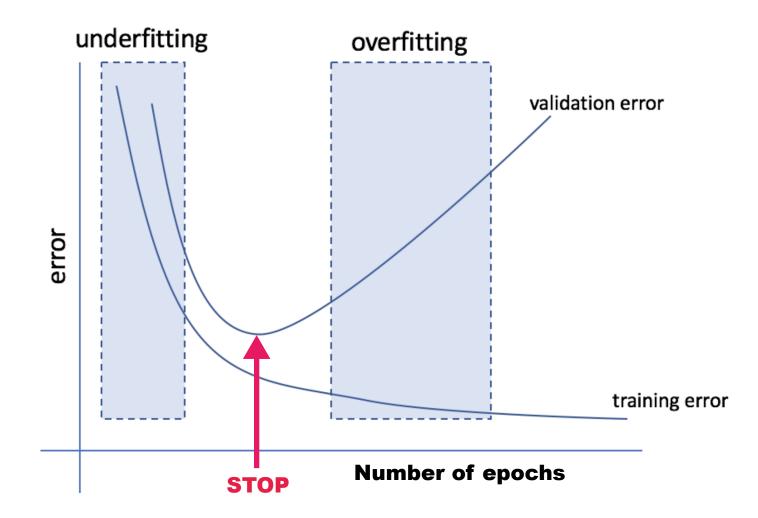


# What is the optimum number of epochs ?

## The answer is related to the problem of under-fitting and over-fitting







## Can one reach 100% accuracy ?

## Short answer

### It is possible only if

## there is enough information in the input X to predict Y uniquely

Conclusion on neural network

## EXAMPLE

If two plants have the same four attributes

$$(X_1=X_2)$$

but belong to two different species  $(Y_1 \neq Y_2),$ 

then we need additional features

to characterize uniquely the three iris species

If two people have the same gender and age

$$(X_1 = X_2)$$

## but only one has a specific disease $(Y_1 \neq Y_2),$

then we need additional features (physical activity, smoking, genetics)

to characterize uniquely the risk of this disease

## IN GENERAL

$$Y = f(X) + error$$

## Hyperparameters

Number of layers, number of nodes,

initial weight values, activation function,

error/loss function, number of epochs,

learning rate, batch size, bias node

## How to choose them ?

## Trial and Error

Select the combination that performs best

(highest validation accuracy)

## Trial and Error

The goal is to predict (and not really to explain)

Main advantage:

• Works well on a whole range of problems including image and signal recognitions.

Main advantage:

 Works well on a whole range of problems including image and signal recognitions.

Main disadvantage:

 Black box: difficult to understand what are the main features that the neural network uses to make prediction.
 Decision trees are better suited for interpretation.

## QUESTIONS ?

## Applications

### Predict the 1-year mortality rate

### of elderly patients

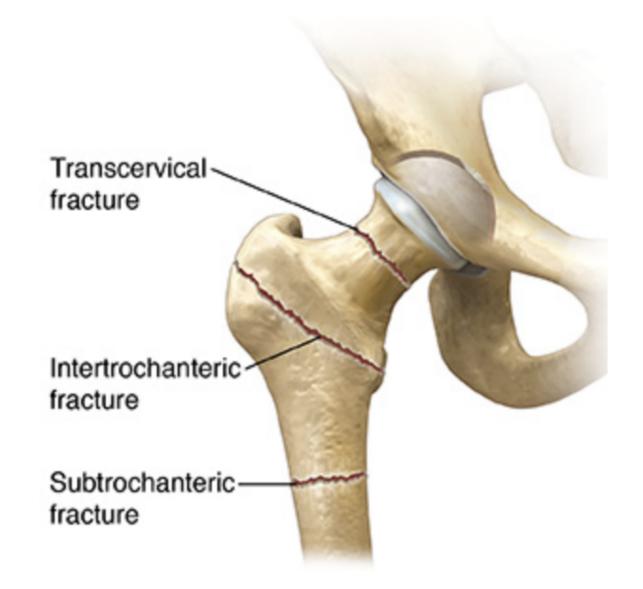
### with intertrochanteric fractures

Ref: Artificial neural network models for predicting 1-year mortality in elderly patients with intertrochanteric fractures in China, L. Shi, X.C. Wang and Y.S. Wang, Brazilian Journal of Medical and Biological Research (2013)

## Some older people fall and break one of their hips

## 50% of hip fractures are intertrochanteric fractures

### Application 1



## There is an increase of death after intertrochanteric fractures (because of reduced mobility)



## 1-year mortality rate = D/N

D = number of deaths occurring within 1 year

N = the size of the population (all patients with intertrochanteric fractures)



## Data

2150 patients with intertrochanteric fractures:

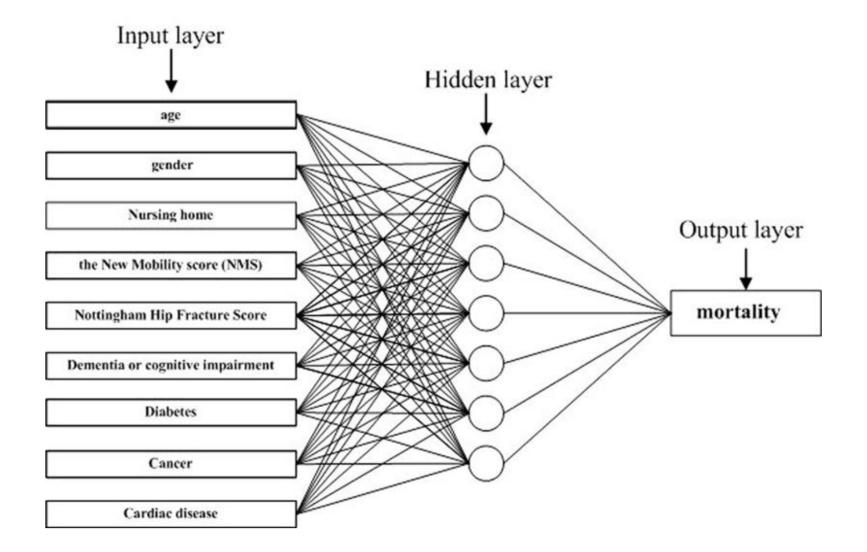
70% in the training group 30% patients in the testing group

## After some trial and error

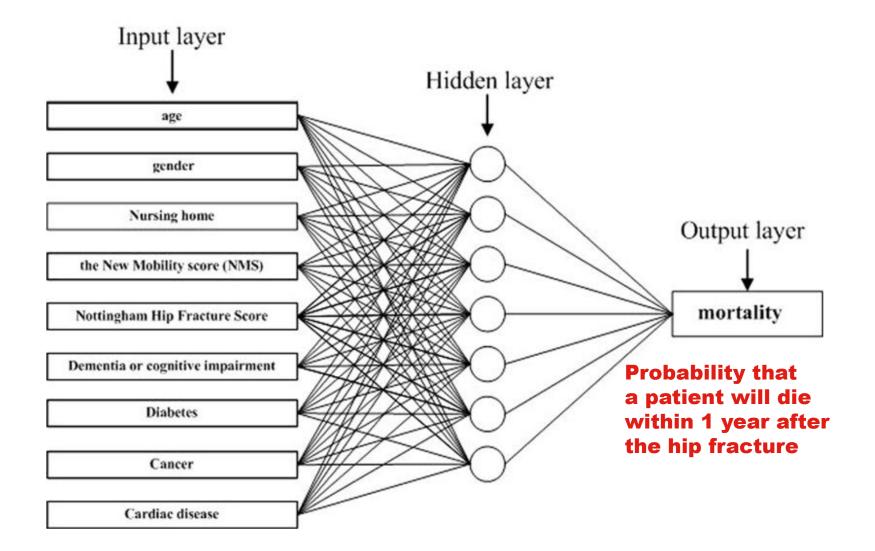
## with different hyperparameters

## (number of layers and nodes)

they end up with the following neural network



**Figure 2** Schematic representation showing the structure of the artificial neural network models, which have 8 input nodes, 6 nodes in hidden layer, and 1 output node, which represents 1-year mortality in elderly patients with intertrochanteric fracture.



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# Accuracy

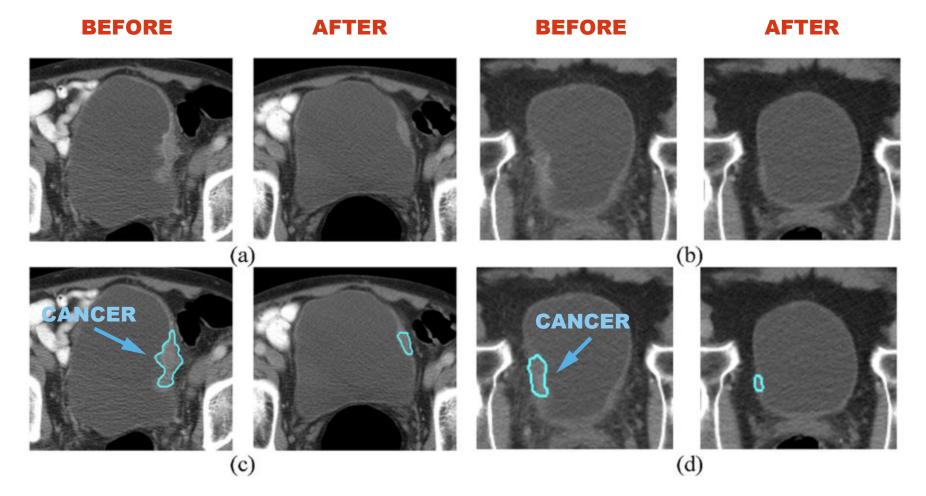
# 92% for the training group 86% for the testing group

# Predict if there is a residual tumor

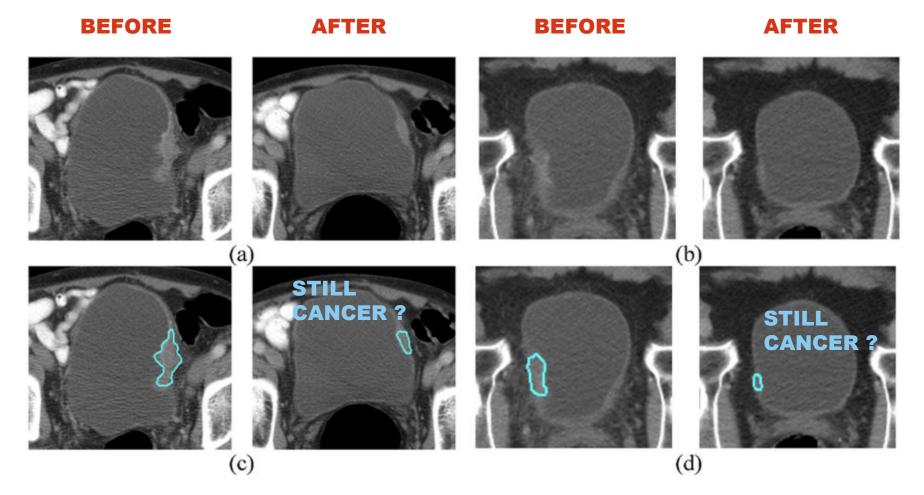
## after bladder cancer treatment

Ref: Bladder Cancer Treatment Response Assessment in CT using Radiomics with Deep-Learning, Kenny H. Cha, Lubomir Hadjiiski, Heang-Ping Chan, Alon Z. Weizer, Ajjai Alva, Richard H. Cohan, Elaine M. Caoili, Chintana Paramagul and Ravi K. Samala, Scientific Reports volume 7, Article number: 8738 (2017)

# They take X-ray images of the bladder and use an algorithm to localise the cancer region before and after treatment



Bladder lesion segmentations. Two segmented bladder cancers are illustrated. The lesions in the pre- and post-treatment scan pairs shown in (**a**,**b**) are segmented using AI-CALS, as shown in (**c**,**d**), respectively. The pre-treatment scan is on the left and the post-treatment scan is located on the right of each pair.



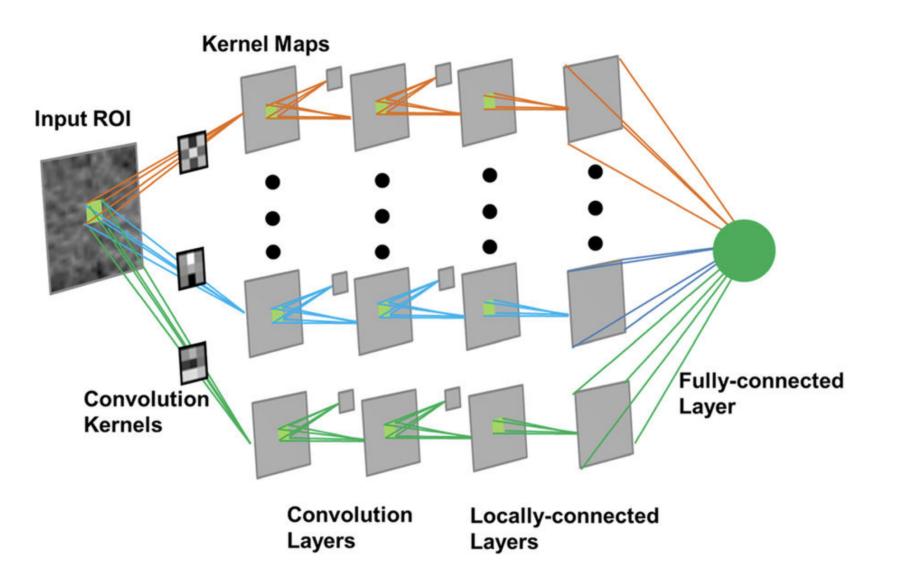
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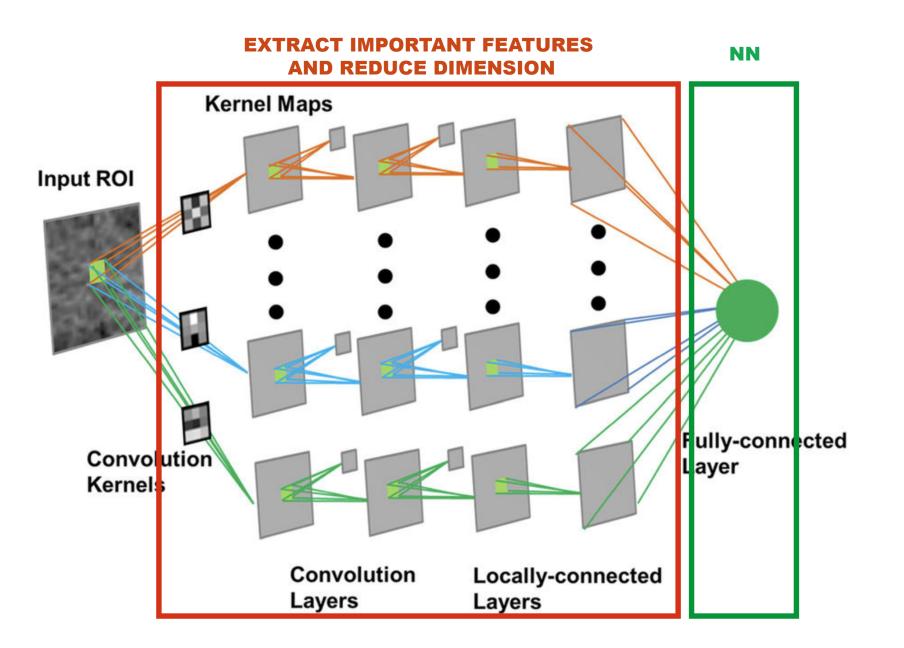
# Data

# 6700 pre-post-treatment paired images with located cancer region

# Data

# They combined the paired images into Region Of Interest (ROI) images





#### Table 2 Number of correctly predicted bladder cancer treatment response assessment of the test set at an operating point determined using the training set.

From: Bladder Cancer Treatment Response Assessment in CT using Radiomics with Deep-Learning

	DL-CNN	RF-SL	RF-ROI	Radiologist 1	Radiologist 2			
Complete Response (Sensitivity)	6/12 (50%)	6/12 (50%)	8/12 (66.7%)	11/12 (91.7%)	11/12 (91.7%)			
Non-complete Response (Specificity)	34/42 (81.0%)	33/42 (78.6%)	23/42 (54.8%)	18/42 (42.9%)	16/42 (38.1%)			
DL-CNN: Deep-learning convolution neural network. RF-SL: Radiomics features extracted from segmented lesions. RF-								

ROI: Radiomics features extracted from pre- and post-treatment paired ROIs.

#### Complete response = No residual cancer

Non-complete response = Residual cancer

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Non-complete response = Residual cancer

# Diagnose irregular heart rhythms (arrhythmias) from single-lead electrocardiography signals

Ref: Cardiologist-Level Arrhythmia Detection With Convolutional Neural Networks, Pranav Rajpurkar, Awni Hannun,

Masoumeh Haghpanahi, Codie Bourn, and Andrew Ng, arXiv:1707.01836

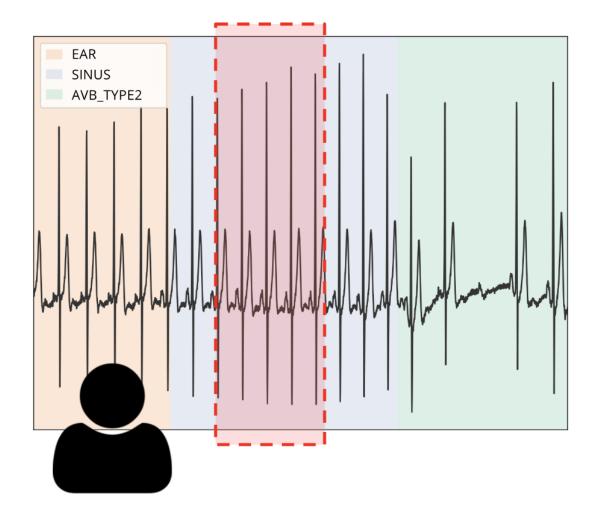
# Data

## 60'000 electrocardiography records

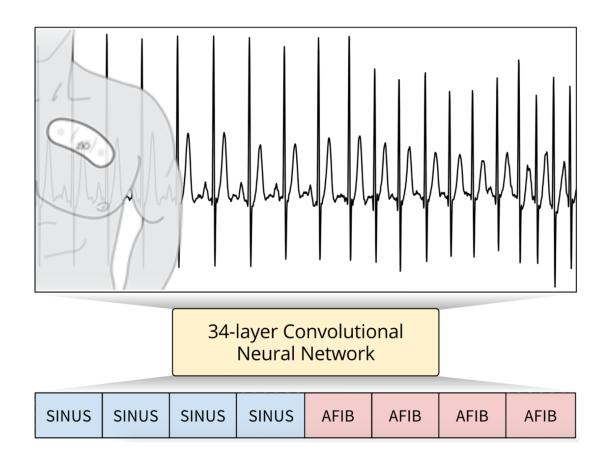
# (annotated by experts with 14 classes) from 30'000 patients

Class	Description	Example	Train + Val Patients	Test Patients	Class	Description	Example	Train + Val Patients	Test Patients
AFIB	Atrial Fibrilla- tion		4638	44	JUNCTIONAL	Junctional Rhythm		2030	36
AFL	Atrial Flutter	hand hand have have a for the second s	3805	20	NOISE	Noise		9940	41
AVB_TYPE2	Second degree AV Block Type 2 (Mobitz II)	www.www.www.www.www.www.	1905	28	SINUS	Sinus Rhythm		22156	215
BIGEMINY	Ventricular Bigeminy	nlplplplplp	2855	22	SVT	Supraventricular Tachycardia	44444	6301	34
СНВ	Complete Heart Block	a palpalpadra	843	26	TRIGEMINY	Ventricular Trigeminy	-MMp-MMp-MMp-4	2864	21
EAR	Ectopic Atrial Rhythm		2623	22	VT	Ventricular Tachycardia		4827	17
IVR	Idioventricular Rhythm		1962	34	WENCKEBACH	Wenckebach (Mobitz I)	Wann Auguru Auguru	2051	29

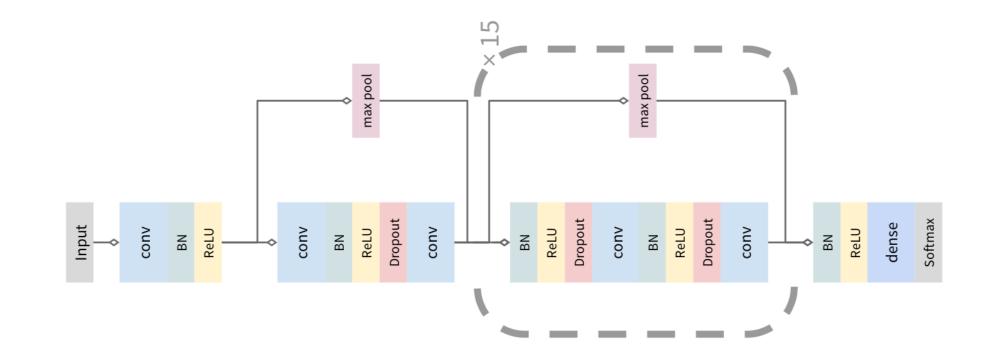
# GOAL



#### The model outputs a new prediction once every second



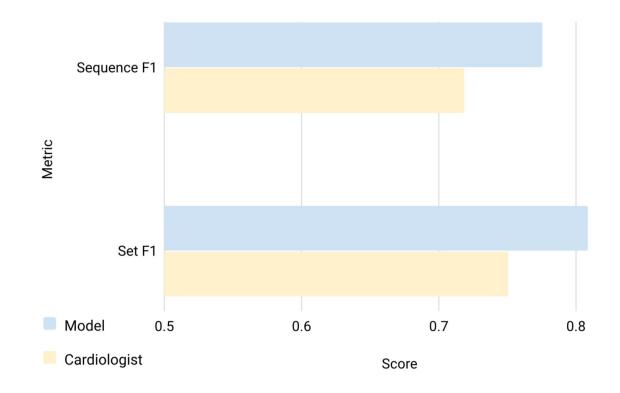
*Figure 1.* Our trained convolutional neural network correctly detecting the sinus rhythm (SINUS) and Atrial Fibrillation (AFIB) from this ECG recorded with a single-lead wearable heart monitor.



33 layers of convolution followed by a fully connected layer



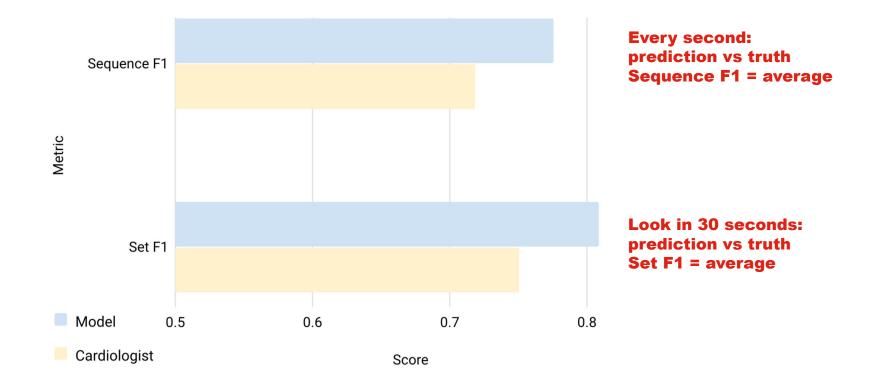
#### The model outperforms the cardiologist



*Figure 3.* Evaluated on the test set, the model outperforms the average cardiologist score on both the Sequence and the Set F1 metrics.



#### The model outperforms the cardiologist



*Figure 3.* Evaluated on the test set, the model outperforms the average cardiologist score on both the Sequence and the Set F1 metrics.

### 14 Buzz

# Algorithmes plus doués que les dermatologues

LOGICIEL <u>Une machine a</u> été capable de détecter 95% des mélanomes sur une série de photos, contre 89% pour l'humain.

Les dermatologues ont du souci à se faire. Un ordinateur a réussi à être meilleur qu'eux pour repérer les cancers de la peau sur des clichés, rapporte la revue «Annals of Oncology». Une équipe germanofranco-américaine a entraîné un système d'intelligence artificielle à distinguer des lésions de la peau et grains de beauté selon qu'ils étaient bénins ou alarmants, en lui montrant plus de 100000 images. Les performances de la machine (un réseau neuronal convolu-



Chaque année, 55000 personnes décèdent d'un mélanome malin. -ISTOCK

tif) ont ensuite été comparées à celles de 58 médecins spécialistes de 17 pays. Résultat: «La plupart des dermatologues ont

fait moins bien», écrivent les chercheurs.

Confrontés à 100 photos de cas jugés compliqués, les mé-

decins ont correctement identifié 87% des mélanomes qui leur étaient présentés. Quand ils obtenaient des images en plus gros plan et des infos plus détaillées (âge, sexe du patient, position de la lésion cutanée, par exemple), ce taux montait à 89%. Mais la machine a fait mieux, avec 95% de mélanomes détectés dès la première série de photos.

Pour les chercheurs, la question n'est pas de se passer des médecins au profit de l'intelligence artificielle, mais de faire d'elle «un outil supplémentaire». «Aujourd'hui rien ne remplace un examen clinique approfondi», ont rappelé dans l'étude deux professeurs australiens en dermatologie. -ATS

# QUESTIONS ?

# BONUS

A simple linear regression model:

$$\mathbf{y}_i = \mathbf{\alpha} + \beta \cdot \mathbf{x}_i + \varepsilon_i$$

where  $\alpha$  is called the intercept parameter

## In neural network,

the intercept parameter  $\boldsymbol{\alpha}$ 

is introduced via the bias node