# **CSI5180.** Machine Learning for Bioinformatics Applications

**Deep learning** — architectures

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# Preamble

#### Deep learning — architectures

In this lecture, we focus our attention on the **architecture** of deep learning networks. On the back cover of their book "Deep Learning", Goodfellow, Bengio and Courville present deep learning as a form of machine learning that enables computers to "**understand the world in terms of a hierarchy of concepts**". This idea was implicit when we looked at the model behind feed forward networks:  $h_{W,b}(X) = f_k(\ldots f_2(f_1(X))\ldots)$ , where  $f_l(Z) = \phi(W_l Z + b_l)$  for  $l = 1 \ldots k$ . This idea becomes much more concrete when examining the various architectures; namely, convolution neural networks and recurrent neural networks.

#### General objective :

**Discuss** the relationships between the nature of the problems to be solved and the architecture of deep networks.

# Learning objectives

- Discuss the relationships between the nature of the problems to be solved and the architecture of deep networks.
- **Explain** convolution neural networks (CNN).
- **Describe** recurrent neural networks (RNN).

#### Reading:

- Vanessa Isabell Jurtz, Alexander Rosenberg Johansen, Morten Nielsen, Jose Juan Almagro Armenteros, Henrik Nielsen, Casper Kaae Sønderby, Ole Winther, and Søren Kaae Sønderby, An introduction to deep learning on biological sequence data: examples and solutions, *Bioinformatics* 33:22, 36853690, 2017.
- Seonwoo Min, Byunghan Lee, and Sungroh Yoon, Deep learning in bioinformatics, *Brief Bioinform* 18:5, 851869, 2017.

# Reading

- Vanessa Isabell Jurtz, Alexander Rosenberg Johansen, Morten Nielsen, Jose Juan Almagro Armenteros, Henrik Nielsen, Casper Kaae Sønderby, Ole Winther, and Søren Kaae Sønderby, An introduction to deep learning on biological sequence data: examples and solutions, *Bioinformatics* 33:22, 36853690, 2017.
  - The authors solve three (3) bioinformatics problems using deep networks:
    - Subcellular localization
    - Protein secondary structure
    - Peptide binding to MHCII molecules
  - For each problem, they discuss the pros and cons of convolutional networks and recurrent networks.
  - https://github.com/vanessajurtz/lasagne4bio

## Plan

## 1. Preamble

#### 2. Introduction

- 3. Convolutional Neural Network
- 4. Pooling
- 5. Recurrent Neural Network

#### 6. Dropout

7. Further considerations

### 8. Prologue

# Introduction

## **Hierarchy of concepts**



Yann LeCun, Yoshua Bengio, and Geoffrey Hinton, Deep learning, Nature 521:7553, 43644, 2015.

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  - Analyzing an image, the networks first detect simple patterns, such as **vertical**, **horizontal**, **diagonal** lines, **arcs**, etc.
  - These are then combined to form **corners**, **crosses**, etc.
- This explains how transfer learning works and why selecting the bottom layers only.

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"An MLP with just **one hidden layer** can theoretically model even the most **complex functions**, provided it **has enough neurons**. But for complex problems, **deep networks** have a much **higher parameter efficiency** than shallow ones: they can model complex functions **using exponentially fewer neurons** than shallow nets, allowing them to reach much **better performance** with the same amount of training data." [4] §10

- Start with one layer, then increase the number of layers until the model starts overfitting the training data.
- **Finetune** the model adding regularization (dropout layers, regularization terms, etc.).

The number of neurons and other hyperparameters are determined using a grid search.

## Remarks

Consider a **feed-forward network** (FFN) and its model:

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where

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Two layers 1,000-unit implies 1,000,000 parameters!

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**Convolutional networks** come from the field of **machine vision**. Hence their close connection to **grid-like inputs**.

# **CNN** - receptive field



Source: [4] Figure 14.2

- Each unit is connected to neurons in its **receptive fields**.
  - Unit *i*, *j* in layer *l* is connected to the units *i* to *i* + *f<sub>h</sub>* − 1, *j* to *j* + *f<sub>w</sub>* − 1 of the layer *l* − 1, where *f<sub>h</sub>* and *f<sub>w</sub>* are respectively the **height** and **width** of the **receptive field**.

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# **CNN** - filters





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- For each location, it calculates the product between the extracted patch and a matrix of the same size, called a convolution kernel or filter. The sum of the values of the resulting matrix is the output for that location.

# CNN - model



Source: [4] Figure 14.6

$$z_{i,j,k} = b_k + \sum_{u=0}^{f_h-1} + \sum_{v=0}^{f_w-1} + \sum_{k'=0}^{f_{n'}-1} x_{i',j',k'} \cdot w_{u,v,k',k}$$

where  $i' = i \times s_h + u$  and  $j' = j \times s_w + v$ ; see [4] §14.
## **CNN** - convolutional layer

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- "(...) and the layers above will learn to combine them into more complex patterns."
- "The fact that all neurons in a feature map share the same parameters dramatically reduces the number of parameters in the model."

# **CNN** - convolution (ressources)

#### A guide to convolution arithmetic for deep learning

- Vincent Dumoulin and Francesco Visin
- Last revised 11 Jan 2018
  - https://arxiv.org/abs/1603.07285
  - https://github.com/vdumoulin/conv\_arithmetic/



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- This (subsampling) has the effect of **shrinking the network**, each window of size  $f_h \times f_w$  is reduced to a single value, **max** or **mean** of that window.
- "[A] max pooling layer also introduces some level of invariance to small translations." [4] §14

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- Each unit stores information about its own state.
  - Let  $h_{u,l}$  be the state of the unit u in layer l.
- Each unit has two inputs, as before the output of the units from the previous layer (*l* 1), but also the vector of states for this layer (*l*) at the previous time step.





$$Y^{(t)} = \phi(X^{(t)}W_X + Y^{(t-1)}W_Y + b)$$

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- Long Short-Term Memory (LSTM) are networks with long-term memory.

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model = keras.models.Sequential([
    keras.layers.LSTM(20,return_sequences=True,input_shape=[None,1])
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Bidirectional LSTM cells also exist.



#### Dropout

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- Hinton and colleagues say that they are "preventing co-adaptation".
- Dropout layers can make the network converging more slowly. However, the resulting network is expected to make fewer generalization errors.



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  - **Pooling** makes the network less sensitive to small translations.
  - In bioinformatics, CNN networks are ideally suited to detect local (sequence) motifs, independent of their position within the input (sequence).
- Recurrent networks (RNN) and LSTM can input sequences of varying length.

#### Keras

```
model = keras.models.Sequential([
    keras.layers.Conv2D(64, 7, ..., input_shape=[28, 28, 1]),
    keras.layers.MaxPooling2D(2),
    keras.layers.Conv2D(128, 3, activation="relu", padding="same"),
    keras.layers.Conv2D(128, 3, activation="relu", padding="same"),
    keras.layers.MaxPooling2D(2),
    keras.layers.Conv2D(256, 3, activation="relu", padding="same"),
    keras.layers.Conv2D(256, 3, activation="relu", padding="same"),
    keras.layers.MaxPooling2D(2),
    keras.layers.Flatten(),
    keras.layers.Dense(128, activation="relu"),
    keras.layers.Dropout(0.5),
    keras.layers.Dense(64, activation="relu"),
    keras.layers.Dropout(0.5),
    keras.layers.Dense(10, activation="softmax")
])
```

[4] §14:

# **Further considerations**

We obviously barely scratched the surface of deep learning. Here are some important concept that we did not consider:

- The vanishing and exploding gradient.
- Initialization.
- Data augmentation.
- Attention layer.
- Understanding what the network has learnt.





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- **CNN** is able to detect patterns in a positon independent manner.
- **RNN** and **LSTM** handle sequence information, where the input sequences can be of different lengths. They can detect patterns along the sequence.
- **Dropout** layers are an effective regularization mechanism.

**Concept**- and **rule**-based

#### References

Vanessa Isabell Jurtz, Alexander Rosenberg Johansen, Morten Nielsen, Jose Juan Almagro Armenteros, Henrik Nielsen, Casper Kaae Sønderby, Ole Winther, and Søren Kaae Sønderby.

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