

# Machine learning for RNA (secondary) structure prediction

Julia Wielach

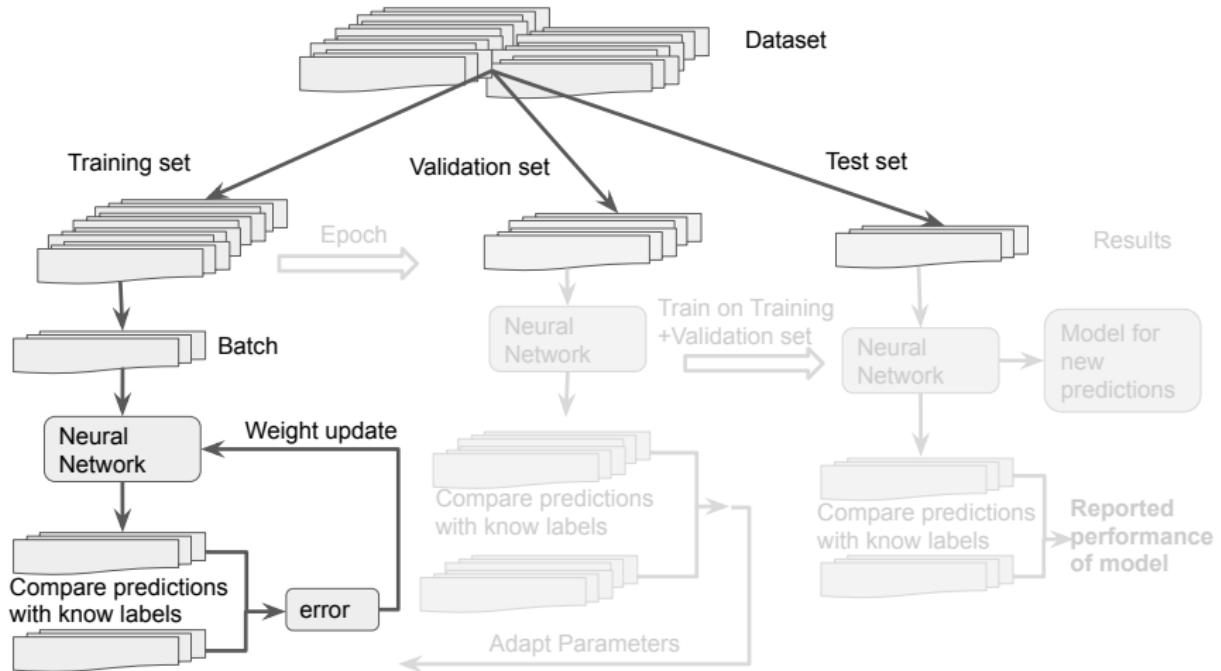


12th February 2020

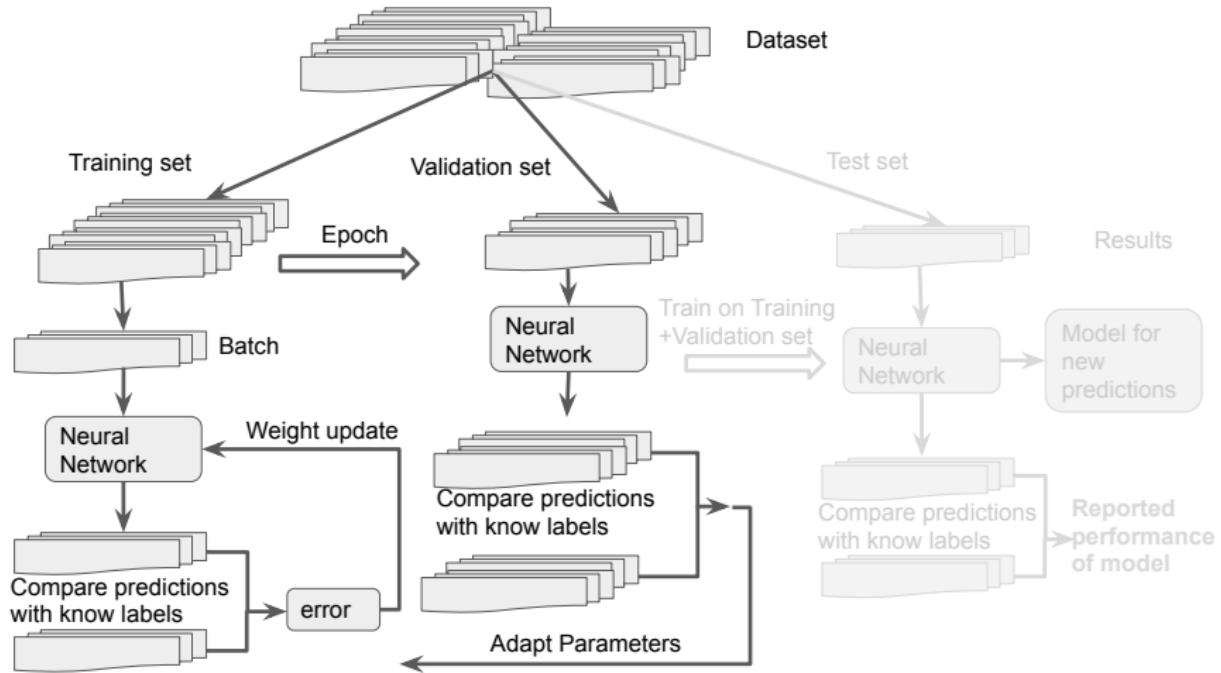
# Overview

- ▷ Machine Learning
  - Training Process
  - Network Types
- ▷ ML for RNA structure prediction
  - Introduction
  - Aim of Project
  - Input
  - Output
  - Networks

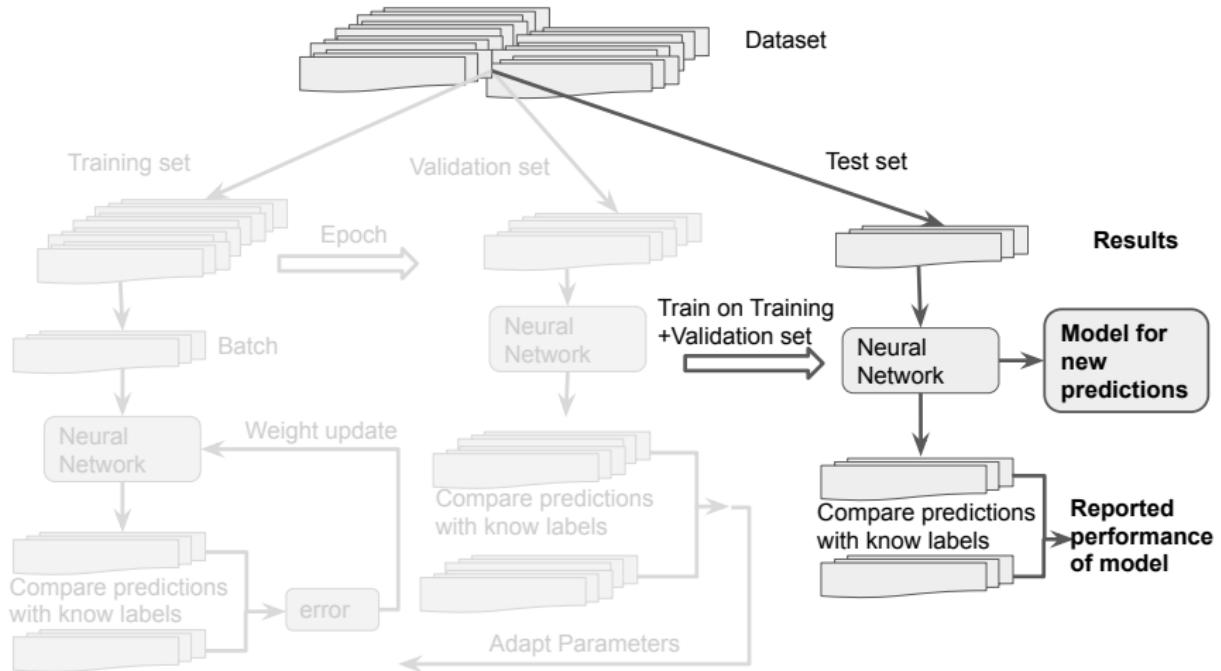
# Training



# Validation



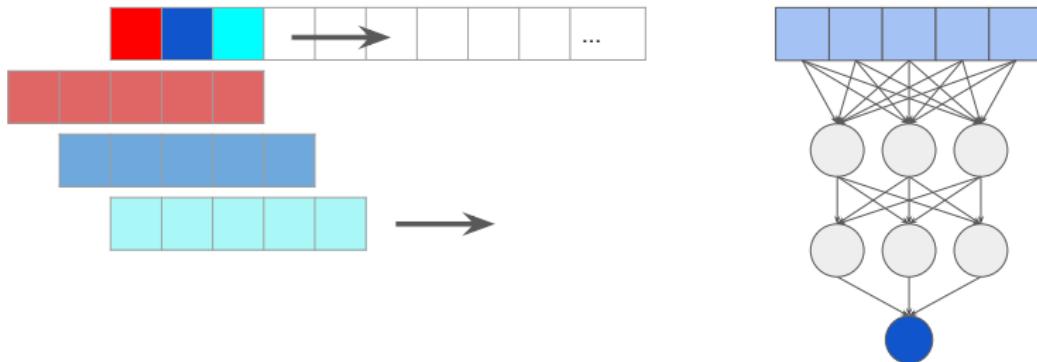
# Testing



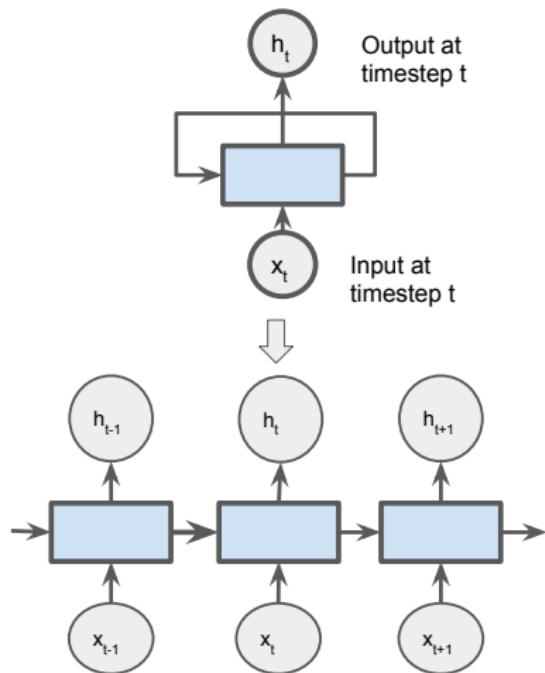
# Sliding Window

Benchmark

Only local dependencies (within window)

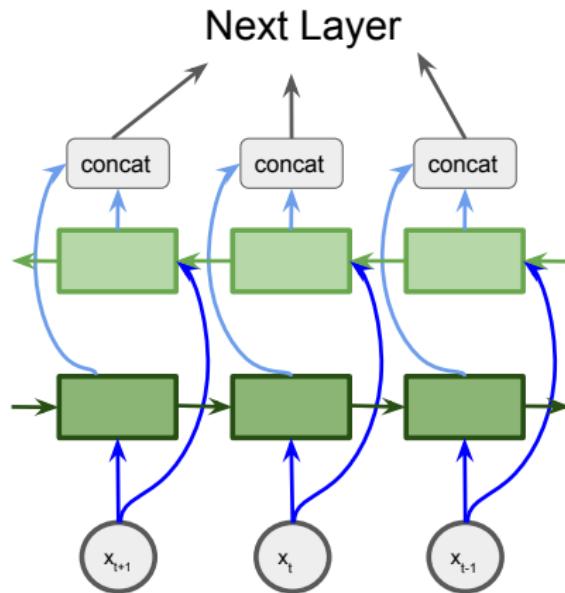


# Recurrent Neural Network (RNN)



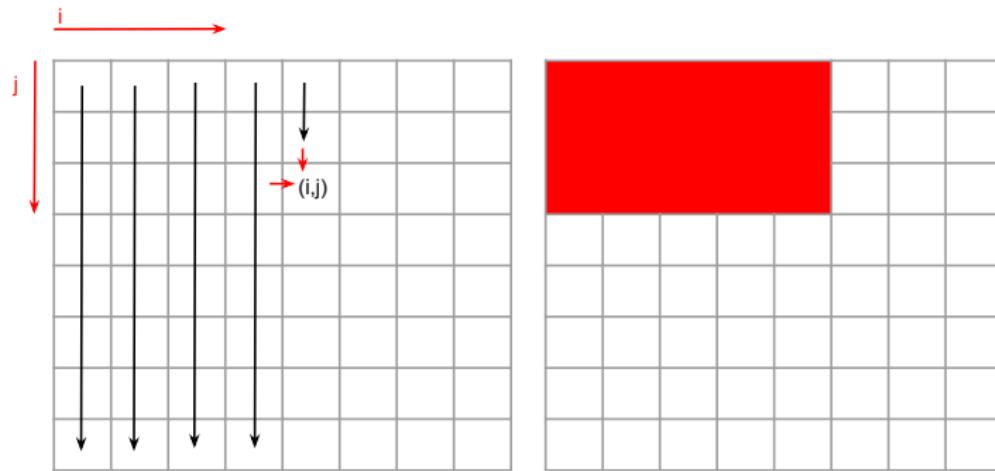
Graphic based on [colah's blog](#)

# Bidirectional RNN



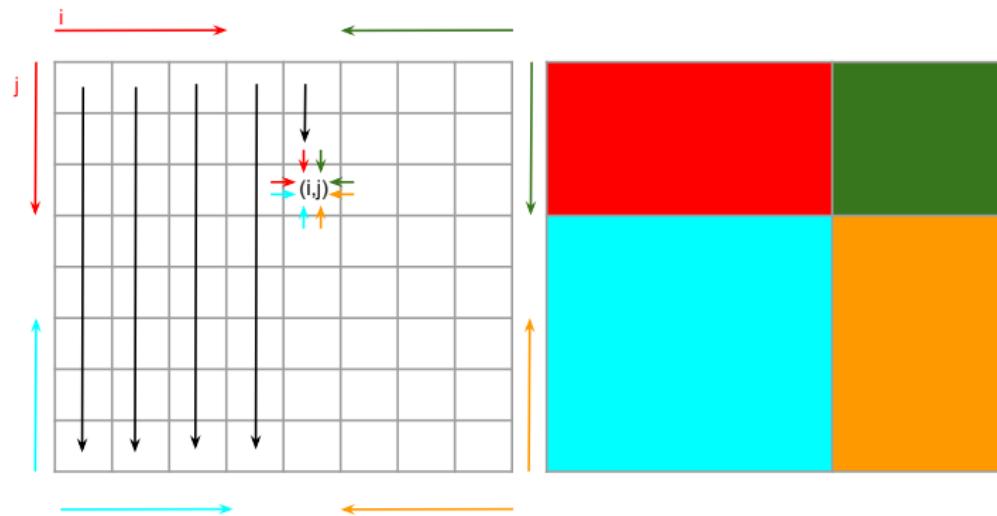
# Multidimensional RNN (2D)

Input from two directions instead of one  
 $(i,j)$  only reached after  $(i,j-1)$  and  $(i-1,j)$

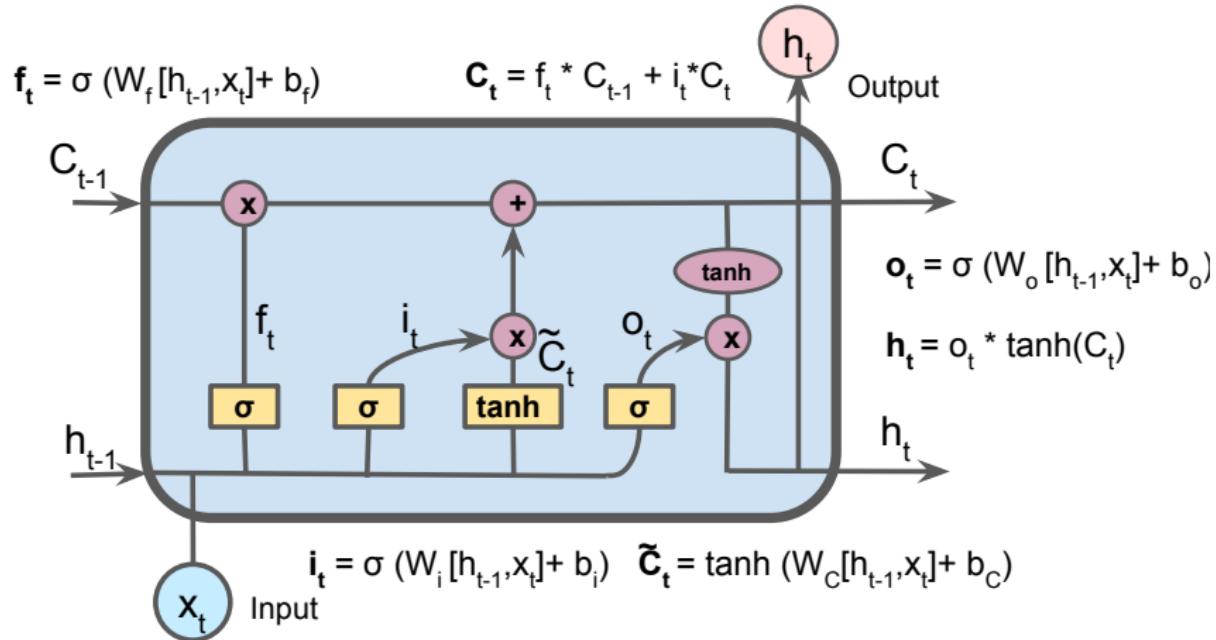


# Multidimensional RNN (2D)

At every point context from 4 directions



# Long Short Term Memory (LSTM) Network



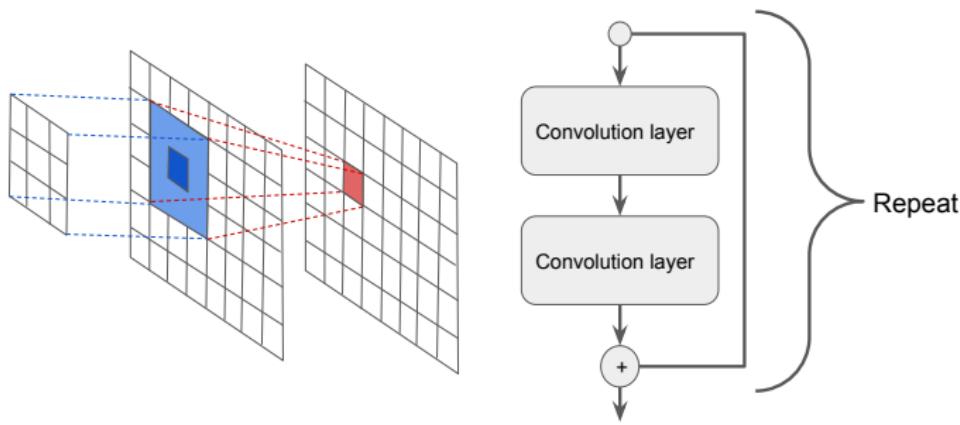
Hochreiter, S. & Schmidhuber, J. (1997)  
Graphic based on [colah's blog](#)

# Convolution NNs & ResNets

Capture local surroundings

Problems with very deep networks → performance decrease

Skip Connections



He, K. & Zhang, X. (2015)

CNN graphic based on River Trail Documentation

# ML for RNA structure

## What?

AACGCAUUGGAUACCUGUGUAUGAUUAUUACACGGUAGAGUACGCGCUCGCGGA  
↓  
0011100000011110111110000000111111111111000011111100  
..(((((.....((((.((((((.....))))))))))) (((((....))))))..

## Why?

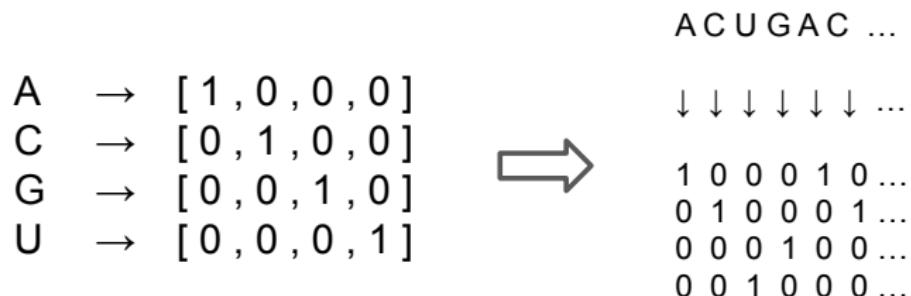
- ▷ Used for similar tasks
- ▷ Possibly capture complicated dependencies
- ▷ Already used in publications
- ▷ No performance comparisons

# Current situation + project

- ▷ First Networks published
  - Very good performances reported
  - No comparisons between new models
  - Possible bias introduced by datasets
  - Predictions specific for different types of RNAs
- ▷ Tests with artificial random RNA sequences predicted by RNAfold
  - Similar performance reachable ?
  - Dataset size dependency
  - Capacity dependency

# Input

One hot encoding



# Input

Concatenation of one hot encodings  
Matrix of size LxLx8

	A	C	U	...
A	[1, 0, 0, 0 , 1, 0, 0, 0]	[0, 1, 0, 0 , 1, 0, 0, 0]	[0, 0, 0, 1 , 1, 0, 0, 0]	
C		[0, 1, 0, 0 , 0, 1, 0, 0]	[0, 0, 0, 1 , 0, 1, 0, 0]	
U			[0, 0, 0, 1 , 0, 0, 0, 1]	
...				

# Input

Matrix with value "rating" basepair

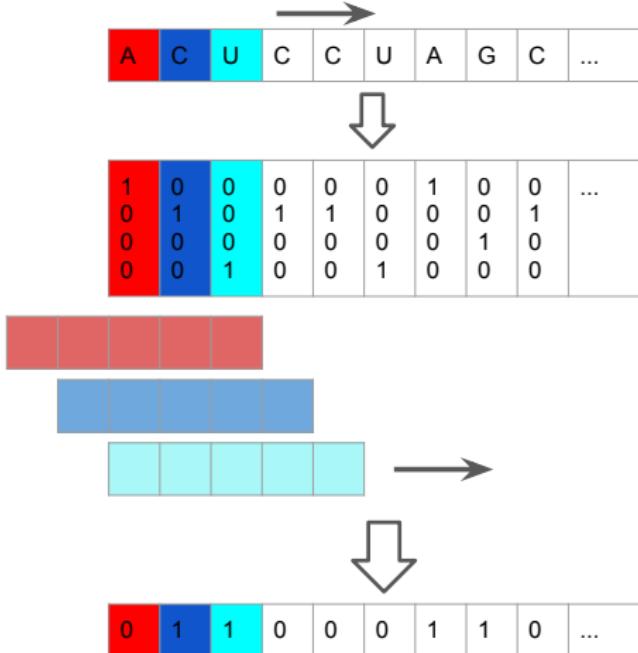
Matrix of size LxLx1

	A	C	G	U
A	0	0	0	2
C		0	3 $+2 * b$	0
G			0	0.8
U				0

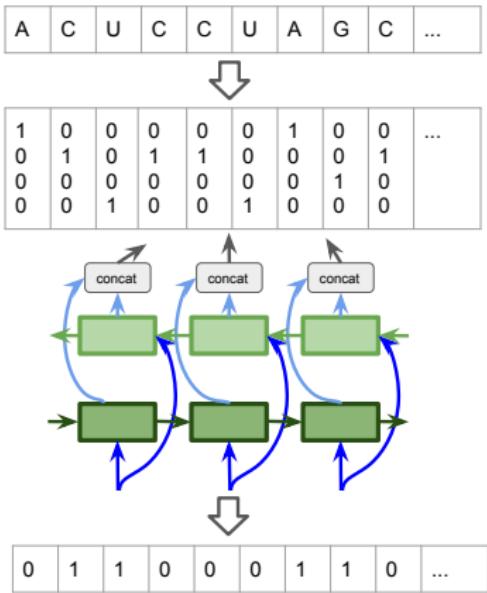
# Output

- ▷ Problem of incorrect secondary structure
  - Incorrect pairing partners
  - Opening and closing brackets → different number
  - Separate label for every base → conflicting basepairs  
eg.  $i+j$ ,  $j+k$
- ▷ Classify additional interactions (Pseudoknots, Triple and Non-canonical basepairs)
- ▷ Additional Corrections
- ▷ Simplification (1/0 for Paired/Unpaired)

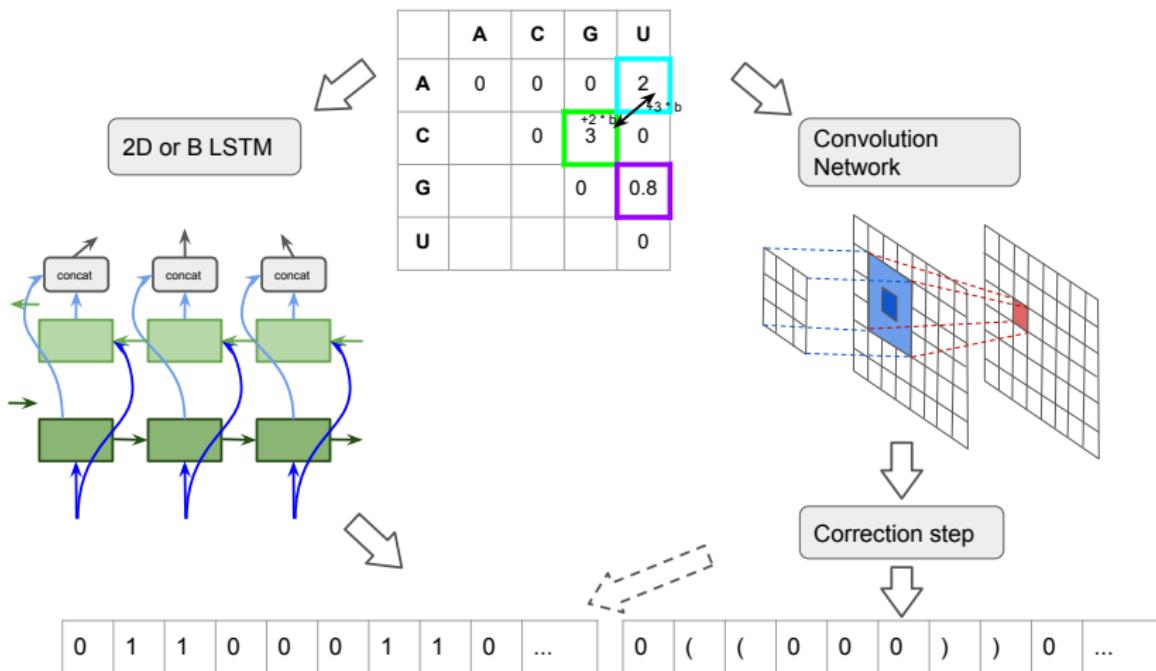
# Sliding Window



# B-LSTM

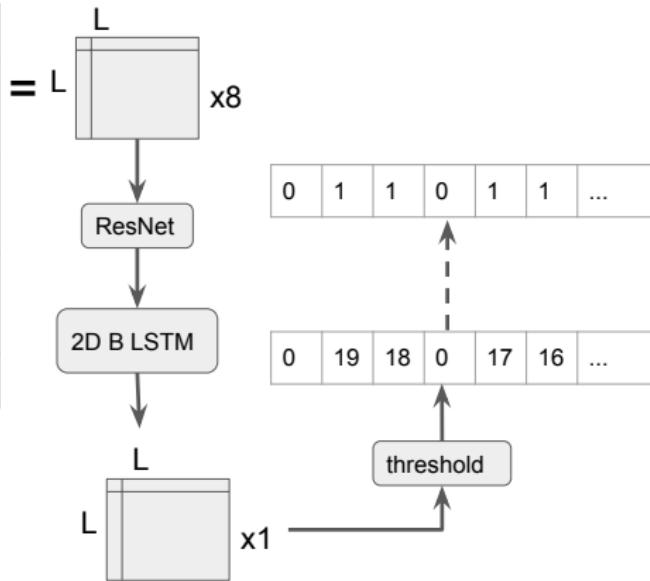


# LSTM / CNN



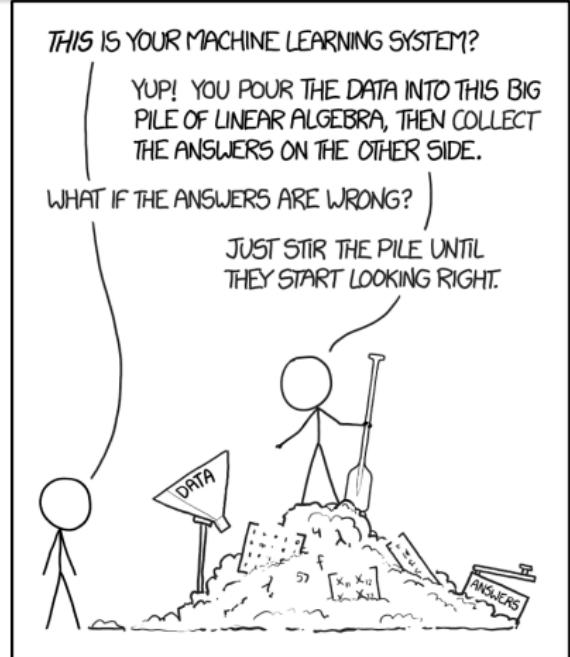
# ResNet & 2D BLSTM

	A	C	U	...
A	[1,0,0,0 ,1,0,0,0 ]	[0,1,0,0 ,1,0,0,0 ]	[0,0,0,1 ,1,0,0,0 ]	
C		[0,1,0,0 ,0,1,0,0 ]	[0,0,0,1 ,0,1,0,0 ]	
U			[0,0,0,1 ,0,0,0,1 ]	
...				



## Acknowledgements:

- ▷ Christoph Flamm
- ▷ Ivo Hofacker
- ▷ Michael Wolfinger
  
- ▷ Gregor Entzian
- ▷ Irene Katharina Beckmann
- ▷ Maria Waldl



<https://xkcd.com/1838/>

# Supplement 1 (Metrics)

	Actually Positive	Actually negative	
Predicted Positive	True positive ( $T_P$ )	False positive ( $F_P$ )	Precision/Positive Predictive Value: $T_P / T_P + F_P$
Predicted Negative	False negative ( $F_N$ )	True negative ( $T_N$ )	Negative Predictive Value: $T_N / T_N + F_N$
	Sensitivity: $T_P / T_P + F_N$	Specificity: $T_N / T_N + F_P$	

$$F_1 = 2 \times \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}}$$

$$\text{Accuracy} = \frac{T_P + T_N}{T_P + T_N + F_P + F_N}$$

$$MCC = \frac{T_P \times T_N - F_P \times F_N}{\sqrt{(T_P + F_P)(T_P + F_N)(T_N + F_P)(T_N + F_N)}}$$