

# Gene Prediction

Bioinformatics algorithms | Winter Semester 2015

J. Setnička & J. Citorík

## Finding genes with neural networks

1) Simplistic approach:

Input: subsequence of length  $w$

Output: position of gene start or end (output layer of size  $w$ )

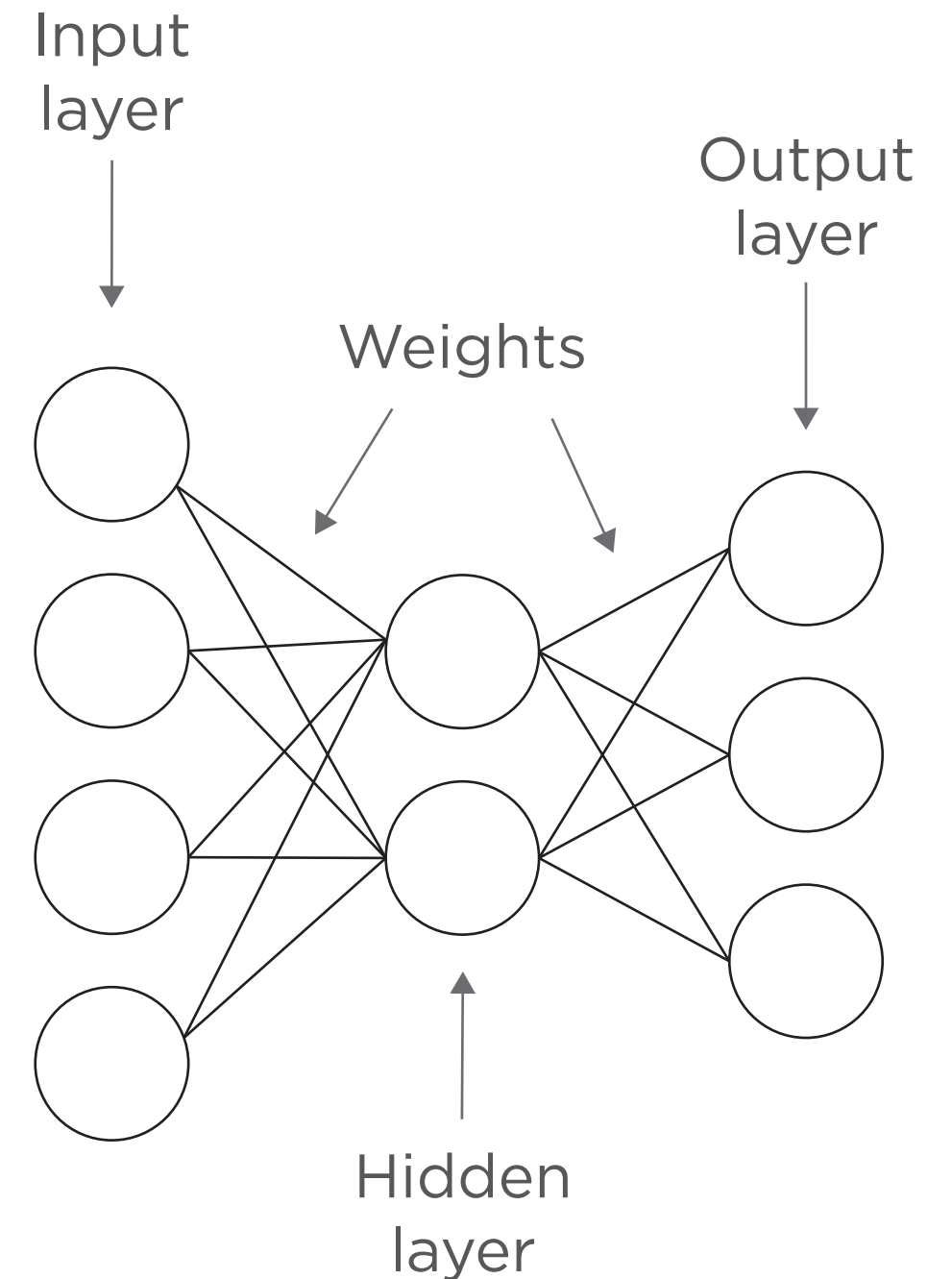
Results: terrible

2) k-mer frequencies:

Input: number of occurrences for each k-mer within a window of size  $w$

Output:  
coding region: 1  
non-coding region: 0

Results: it's complicated...



## Problems

What data should be used to teach?

(# of positive/negative samples, where to put the window)

Papers recommend using 6-mers

...but then we have 4096 input neurons and we have to compute frequencies of 4096 6-mers many many times

Window size

Evaluation

How to use the network once we've trained it?

## Results:

Coding/Non-coding distinction

Increasing k-mer length didn't help much

k = 3, 4, 5 didn't differ significantly, couldn't try k = 6 due to technical limitations

Window size that worked best: 100

Number of neurons in the hidden layer: 200

Best result for 3-mers

83.8% on training, 85% on test

Finding start/end of a gene

Move the window along the sequence, until NN says the region is a coding region

Find Start codon within that window, continue moving window while NN labels the region as coding region. In the first window which NN labels as non-coding, find stop codon.

Genes found were too long, real average was 1181 bases, found average was 1820

Approach: ORF Length ( $> 150$  bases)

Average % genes found: 48.97%

Average % nonexistent genes found: 3294.42%

Sequences:

Bacteroides\_fragilis\_YCH46,

Bacteroides\_ovatus\_strain\_ATCC8483,

Bacteroides\_thetaiotaomicron\_VPI5482,

Bacteroides\_vulgatus\_ATCC8482 ,

Bacteroides\_xylanisolvens\_XB1A

Approach: ORF start surroundings

Average % genes found: 38.38%

Average % nonexistent genes found: 59.83%

Trained on: *Bacteroides\_fragilis*\_YCH46, *Bacteroides\_ovatus*\_strain\_ATCC8483,  
*Bacteroides\_thetaiotaomicron*\_VPI5482

Tested on: *Bacteroides\_vulgatus*\_ATCC8482 , *Bacteroides\_xylanisolvens*\_XB1A

Approach: CG islands

Average % genes found: 25.24%

Average % nonexistent genes found: 1147.87%

Trained on: *Bacteroides\_fragilis*\_YCH46, *Bacteroides\_ovatus*\_strain\_ATCC8483,  
*Bacteroides\_thetaiotaomicron*\_VPI5482

Tested on: *Bacteroides\_vulgatus*\_ATCC8482 , *Bacteroides\_xylanisolvens*\_XB1A