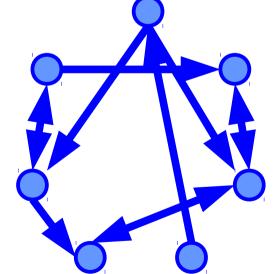




Evolving model parameters for generating a biologically plausible neural network.

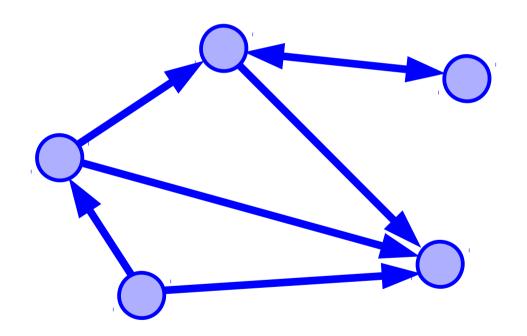
Gordon Govan

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Introduction

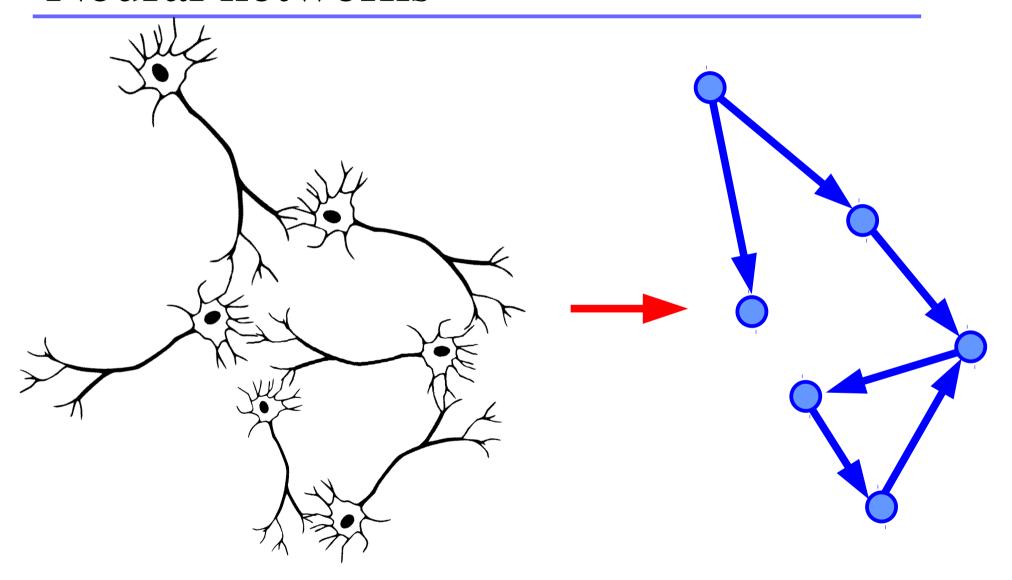
many biological concepts can be though of as **networks**



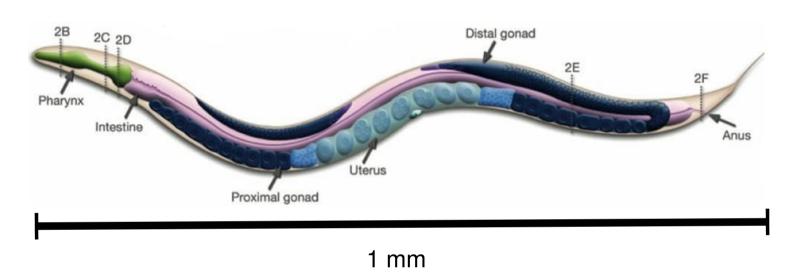
network models have been developed to aid understanding of how these networks develop and

onarata

Neural networks



Caenorhabditis elegans



Nematode worm

Human brain

Model organism with 306 neurons 2345 synaptic connections

10¹¹ neurons10¹⁴ synaptic connections

Network Models

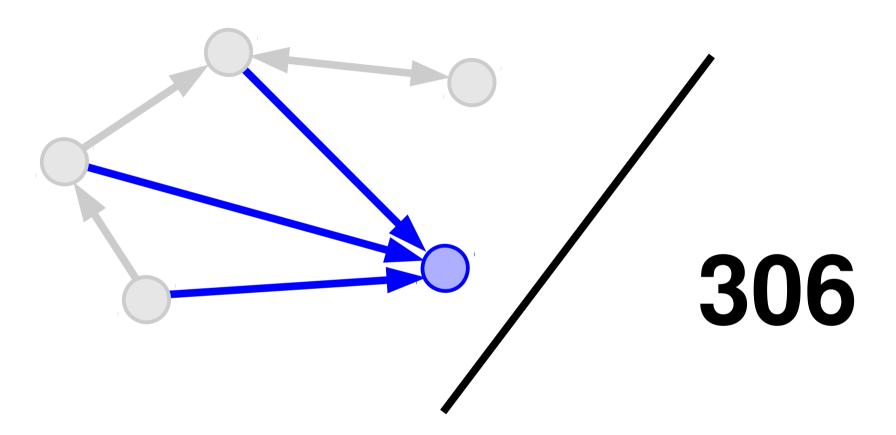
We attempt to create networks with properties similar to that of the *C. elegans* neural network.

To do that we use network models.

A network model is an algorithm that produces a network from a given input.

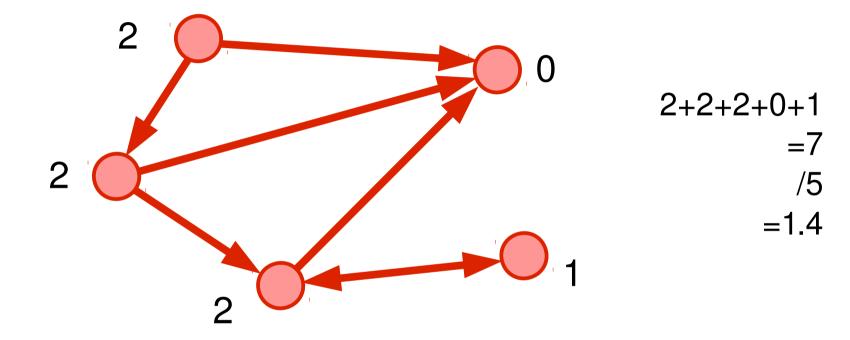
randomNetwork :: Int -> Double -> ([Node] , [Edge])
randomNetwork 5 1.75

Global topological measurements



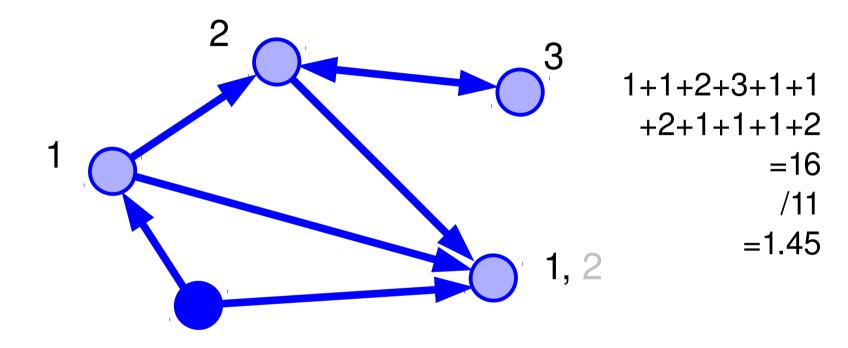
Measurements that we take from each node. We then take the average from across the network.

Average Degree



the average number of edges that a node in the network has or the total number of edges, divided by the number of nodes

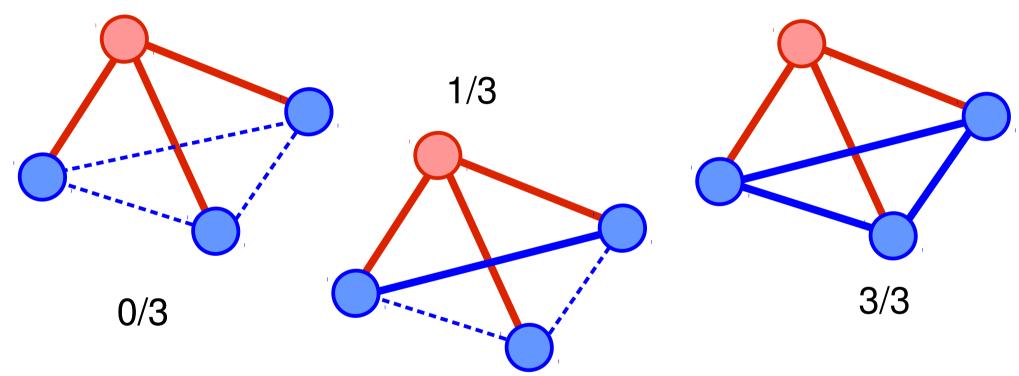
Average Path Length



the average shortest path length between two nodes

calculate the total length of all the shortest paths in the network, and then divide it by the number of paths

Average Cluster Coefficient

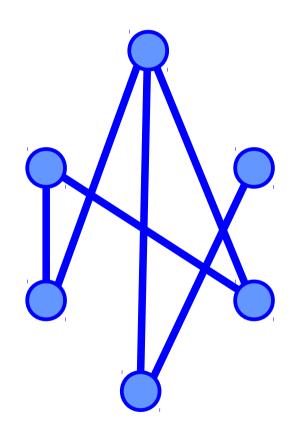


a measure of how many of a node's neighbours are connected together

number of connections between neighbours number of possible connections between neighbours

Erdős-Rényi model

nodes connected together randomly



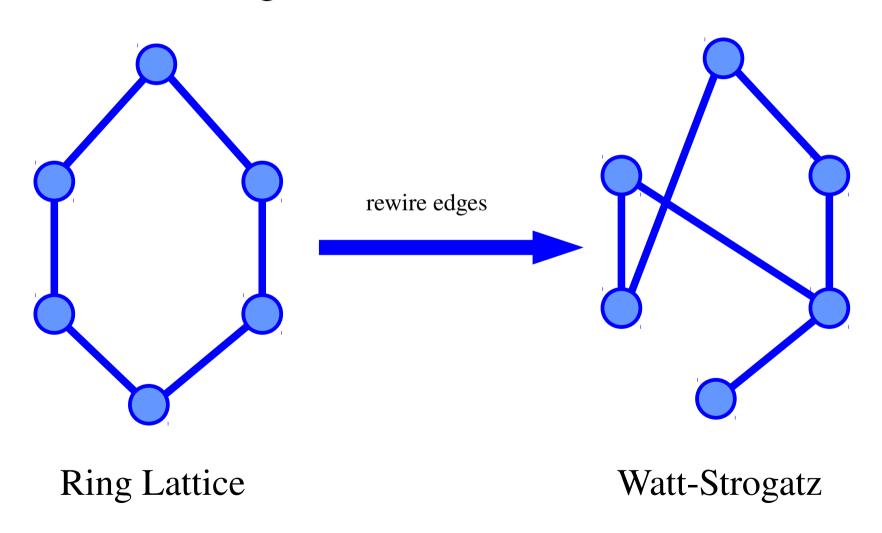
one parameter: probability to have an edge between two nodes

average degree and path length close to *C. elegans*

clustering coefficient much too low

Watts-Strogatz model

start with a regular network, then add randomness

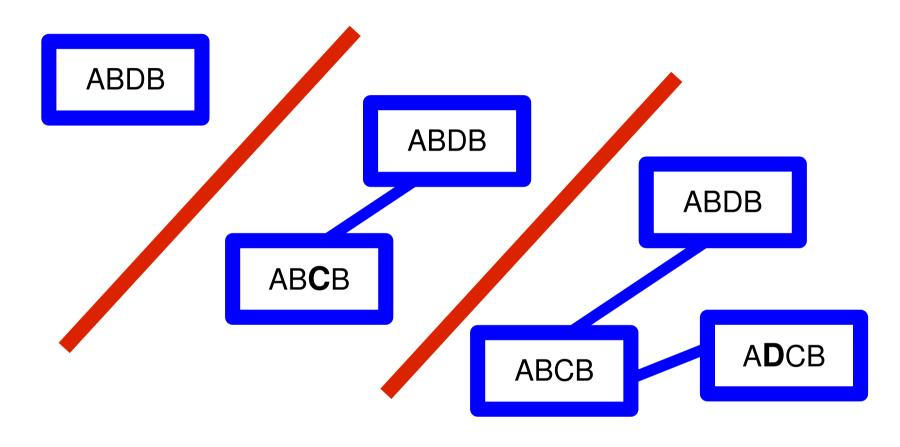


Watts-Strogatz model

two parameters: number of edges, probability to rewire an edge

average degree and path length close to C. elegans

and clustering coefficient close to target



nodes have a structure

creation of new nodes and edges based on structure

pick an existing node

ABCB

mutate its structure to form a new node



add node to network, adding edges to other nodes based on a distance measure

ABDB ADCB

repeat until you have the desired number of nodes

complex model

many parameters

found networks with values close to those of the targets

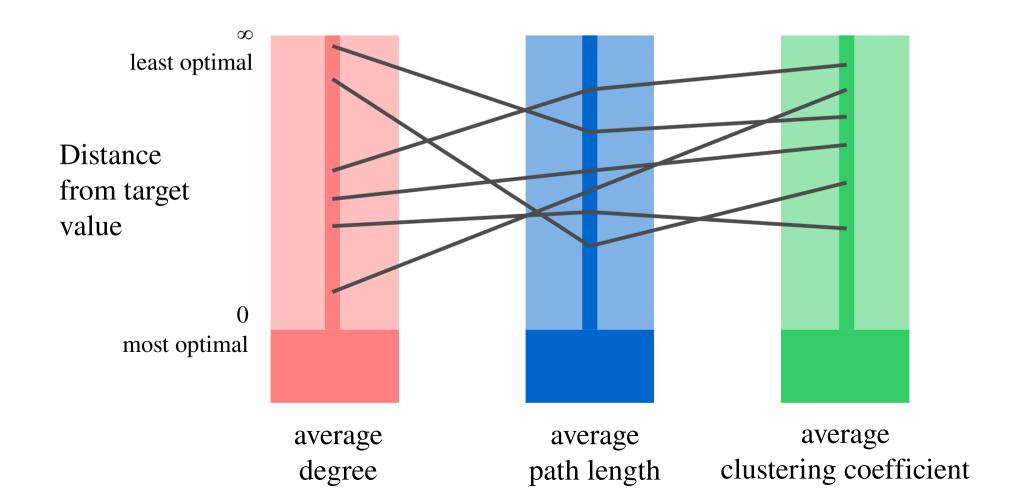
```
Counter = 38
4 Random seed = 1,3
 5 Network size = INCREMENTAL
6 Initial node = ABCDABCDABCD
 7 Num initial nodes =
8 Prob edge duplication = 0.7
9 Final remove min nodes = 0
10 Running remove min nodes = 0
  Running remove max nodes = 0
   Num new edges for each new node = 1
13 Num runs each network = 1999
14 Frequency save = 500
15 Type mutation = RANDOM
16 Mutation fix number = 1
17 Prob to mutate = 0.2
18 Prob to add = 0.8
19 Prob to delete = 0
20 Prob to duplicate = 0
21 Alphabet = A,B,C,D
22 Chosen node = RANDOM
23 Max num attempts = 1000
24 Type distance = HAMMING
25 Direction = HAMMING
                           12,1
```

creating networks from the SN model is more difficult many parameters means multi-objective optimisation

used a genetic algorithm to find a suitable set of parameters

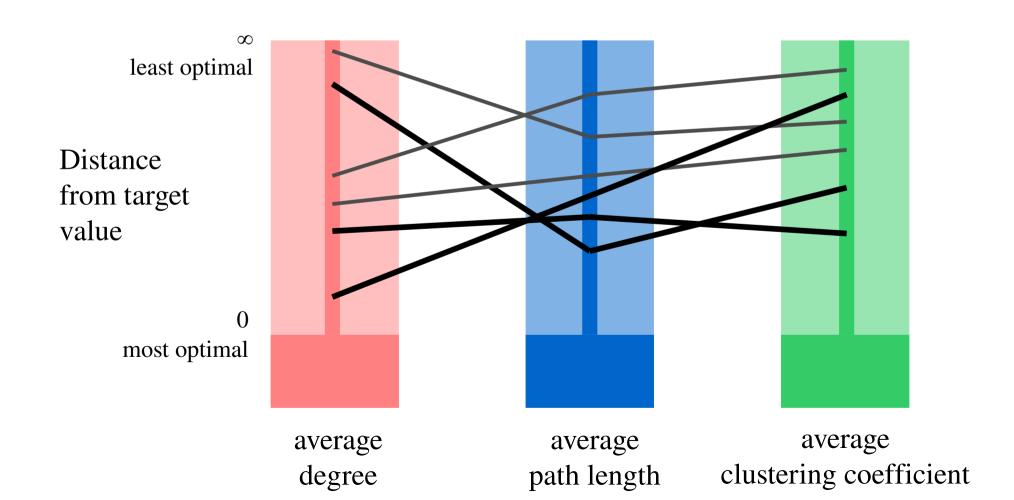
Multi-Objective Optimisation

Want to get the generated network to match as closely as possible the empirical network on 3 measurements



Paerto Front

The set of solutions which are not irrefutably worse than any others



Fitness Function

For each solution the fitness needs to be calculated

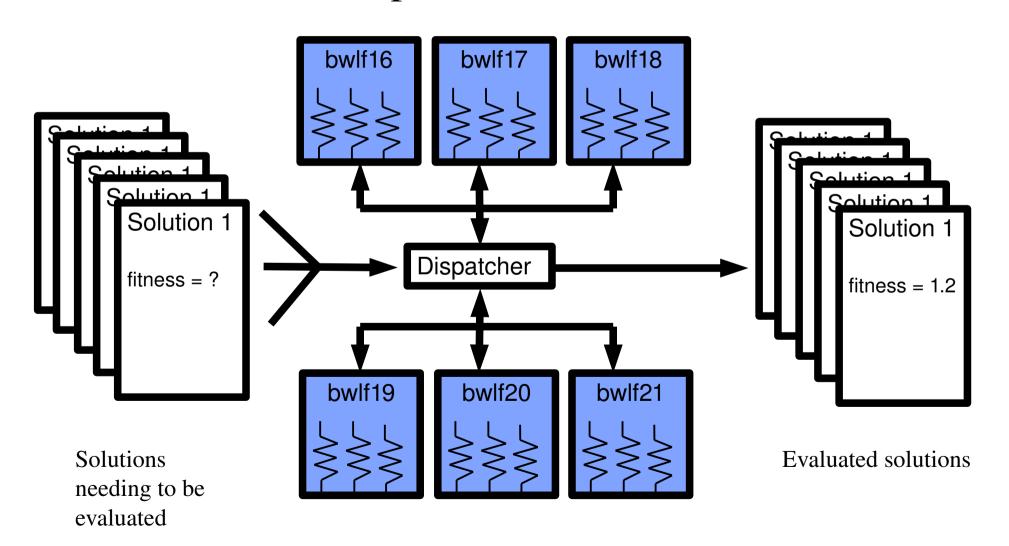
The SN model needs to be run with the parameters from the solution

For large networks this could take up to an hour or more

For large populations and many generations this would take a long time to run.

Fitness Function

Run the SN model in parallel



Global topological measurements

For each network model we created 10 networks.

We took measurements for each of the networks, and then averaged them.

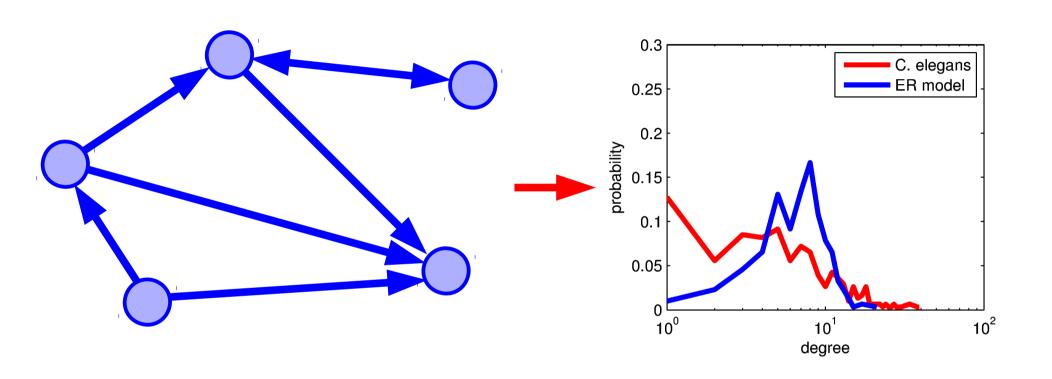
Global topological measurements

| Network | Average Degree | Average Path Length | Average Clustering Coefficent |
|------------------|----------------|---------------------|-------------------------------|
| C. Elegans | 7.66 | 2.46 | 0.284 |
| Erdos-Renyi | 7.56±0.15 | 2.41±0.02 | 0.05±0.00 |
| Watts-Strogatz | 8 | 2.78±0.01 | 0.29±0.01 |
| Structured Nodes | 6.43±0.41 | 3.73±0.12 | 0.36±0.03 |

Watts-Strogatz is a very good match to *C. elegans*

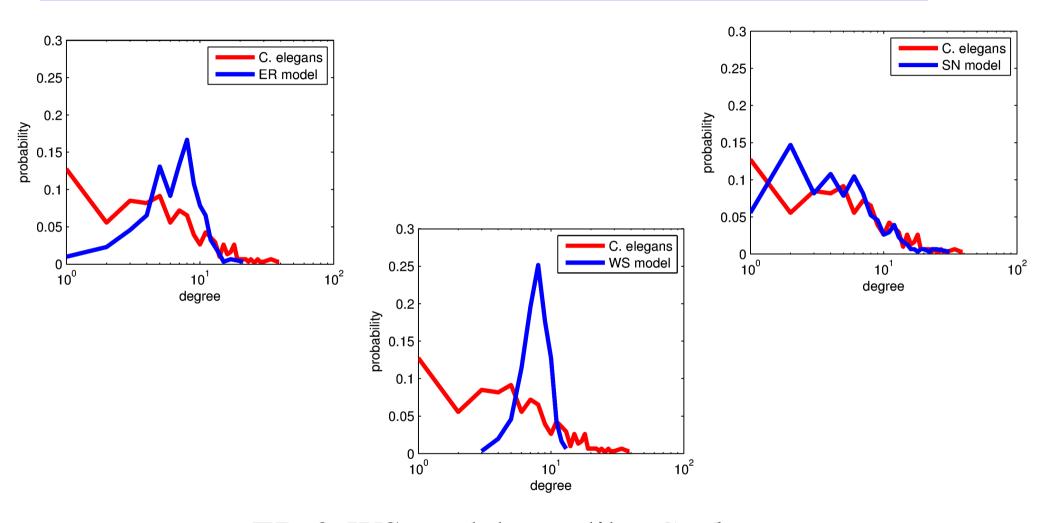
SN model is in second place

Distribution of topological measurements



Tells us more than just the global averages, but are harder to analyse as they provide multidimensional data

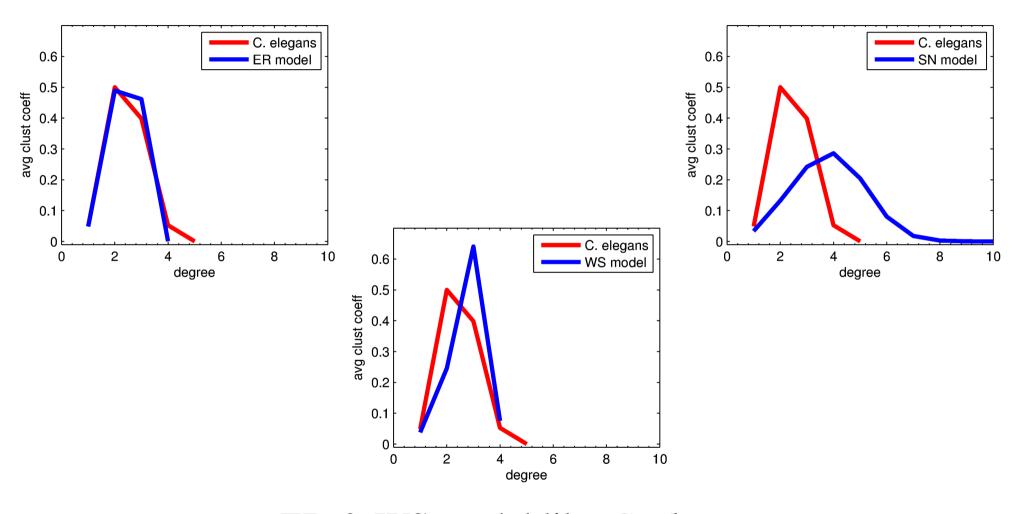
Degree distribution



ER & WS models not like C. elegans

SN model similar to *C. elegans*

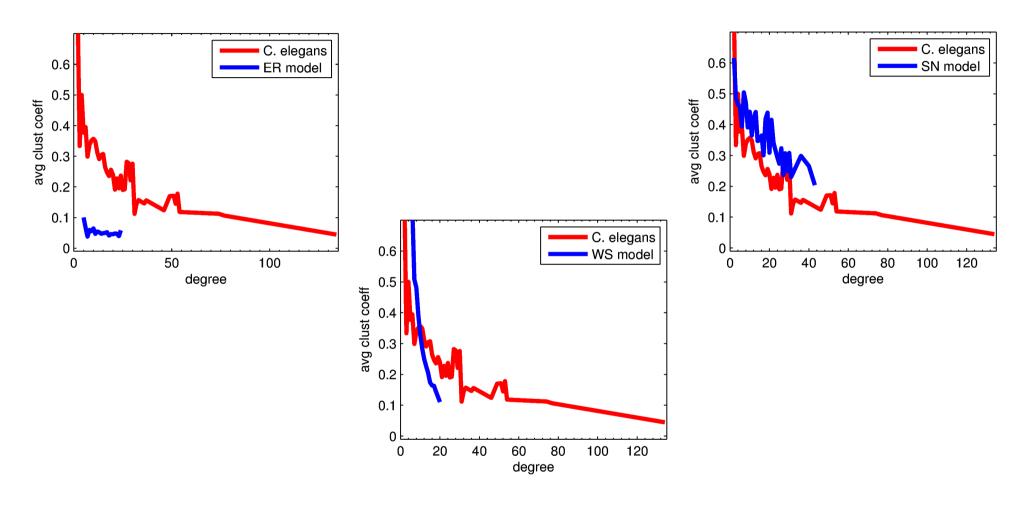
Path Length distribution



ER & WS model like C. elegans

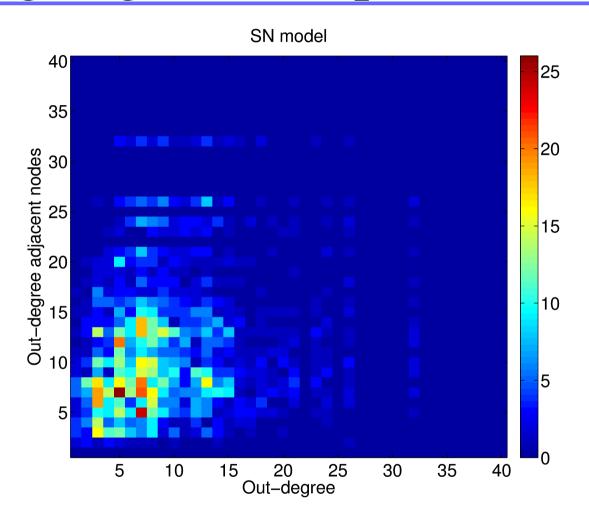
SN model not like *C. elegans*

Cluster Coefficient distribution



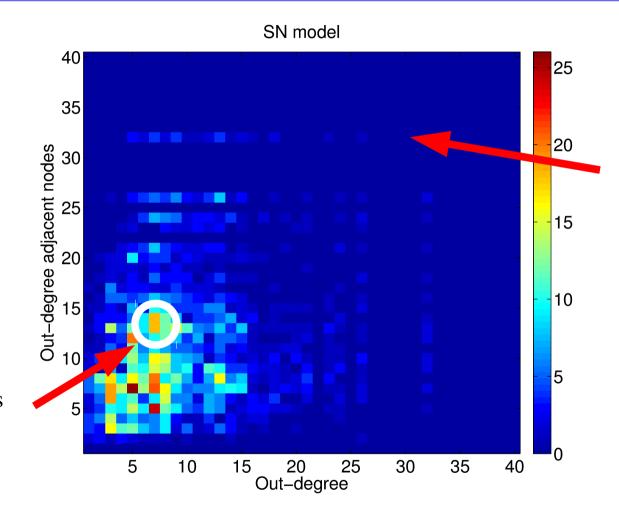
ER model not like *C. elegans*WS model like *C. elegans*SN model more like to *C. elegans*

Outgoing edge heatmaps



shows how nodes are connected to other nodes based on their degree

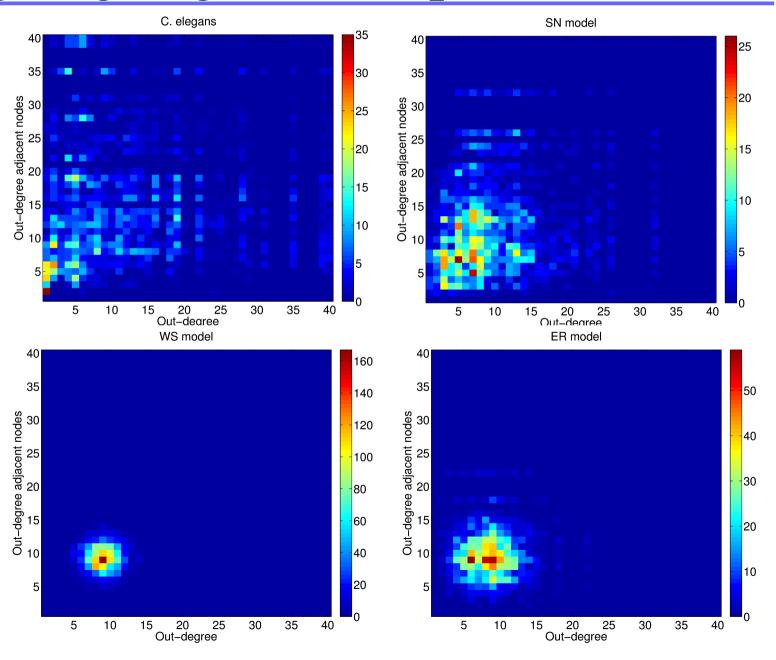
Outgoing edge heatmaps



Nodes of degree 32 have very few incoming nodes, but those are all from nodes with smaller degrees.

There are many nodes of degree 7 connected to nodes of degree 13 & 14.

Outgoing edge heatmaps



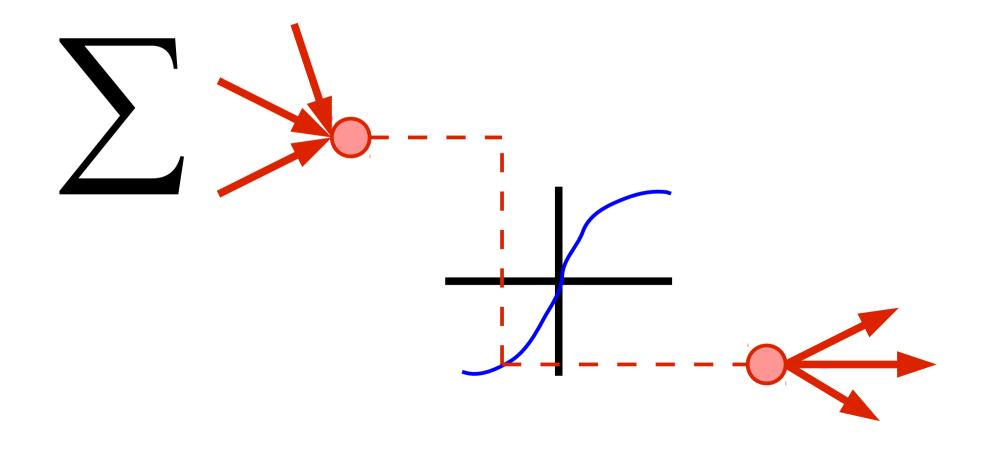
Distributions of measurements

| network | avg. degree | avg. path length | avg. clustering coefficent | similar to degree distribution |
|------------------|-------------|------------------|----------------------------|--------------------------------|
| C. Elegans | 7.66 | 2.46 | 0.284 | |
| Erdos-Renyi | 7.56±0.15 | 2.41±0.02 | 0.05±0.00 | No |
| Watts-Strogatz | 8 | 2.78±0.01 | 0.29±0.01 | No |
| Structured Nodes | 6.43±0.41 | 3.73±0.12 | 0.36±0.03 | Yes |

the SN model is the best fit of the distribution, depending on the measurements considered

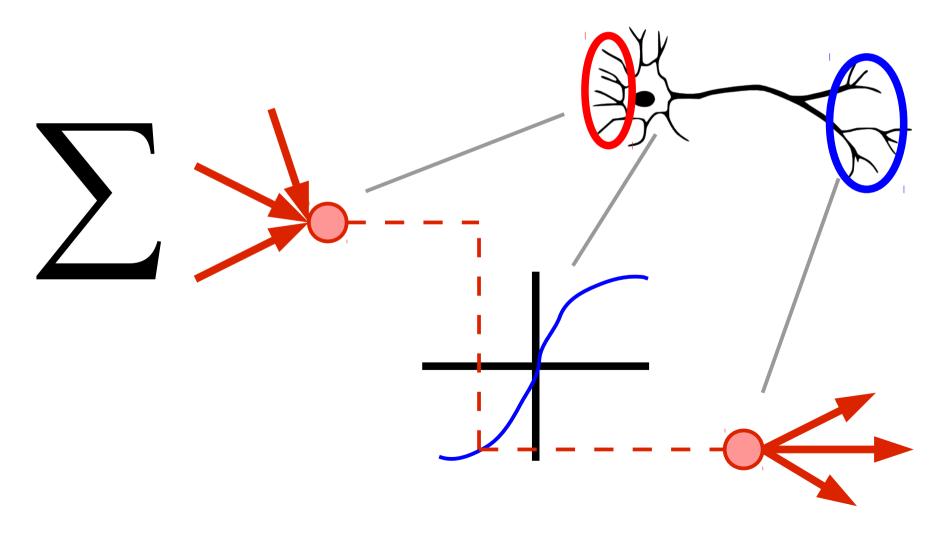
Random Recurrent Neural Networks

simple model of a neural network



Random Recurrent Neural Networks

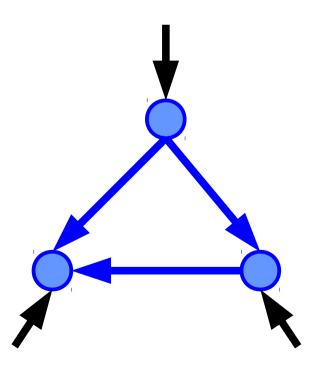
simple model of a neural network



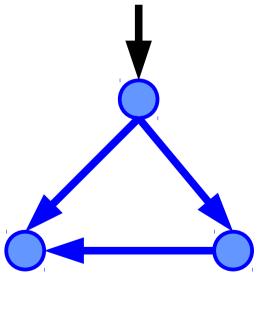
Adding an Influence

Three different methods of adding an influence were used

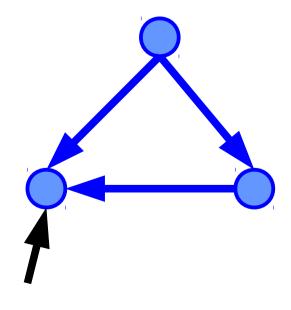
All Neurons



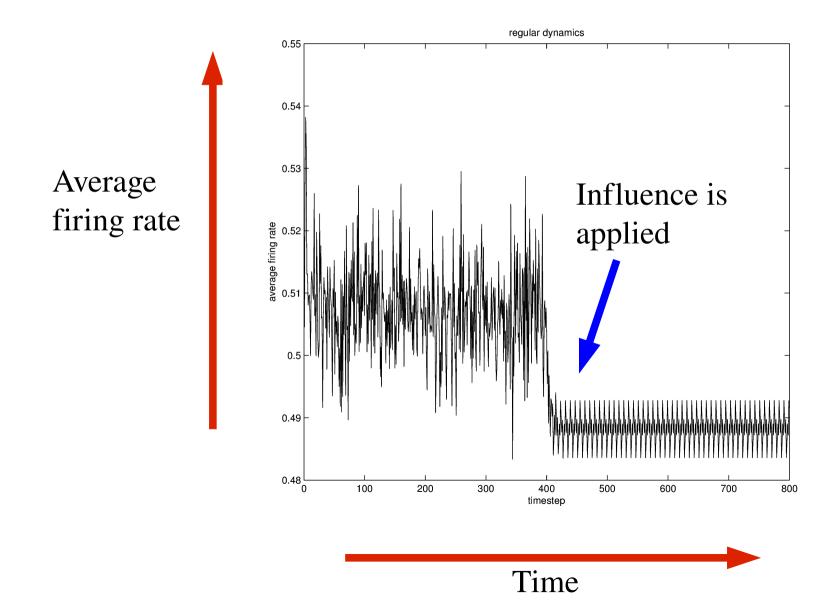
Most Outgoing Synapses



Least Outgoing Synapses

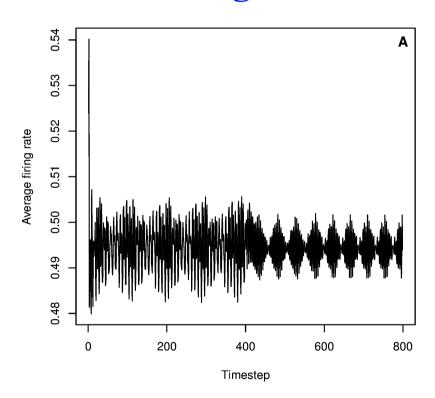


Observing the Dynamics

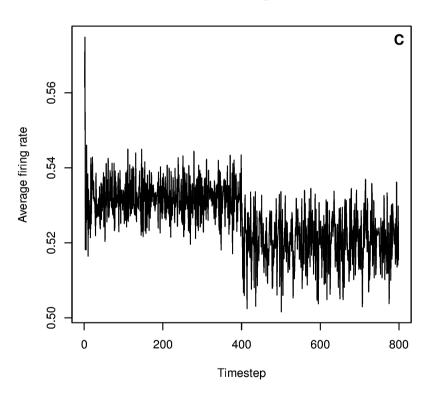


Regular Dynamics

Regular



Not Regular



Exploring the dynamics

| network | % regular all nodes | % regular most connected nodes | % regular least connected nodes |
|------------------|---------------------|--------------------------------|---------------------------------|
| C. Elegans | 100 | 100 | 90 |
| Erdos-Renyi | 94 | 67 | 54 |
| Watts-Strogatz | 75 | 27 | 29 |
| Structured Nodes | 82 | 52 | 40 |

C. elegans has by far the most regular dynamics!

Conclusions

The WS model, though widely used, fails to model any distributions of measurements.

The SN model closely matches the distributions of measurements

None of the examined models come close to matching the regularity of the dynamics shown by the *C. elegans* network.

Future models may need to draw inspiration from neural development.



Thanks for listening,

any questions?

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PhD Students' Short Talks 14/3/2013