

# Inferring How Networks Evolved

858L

*Inferring network mechanisms: The  
Drosophila melanogaster **protein**  
interaction network*

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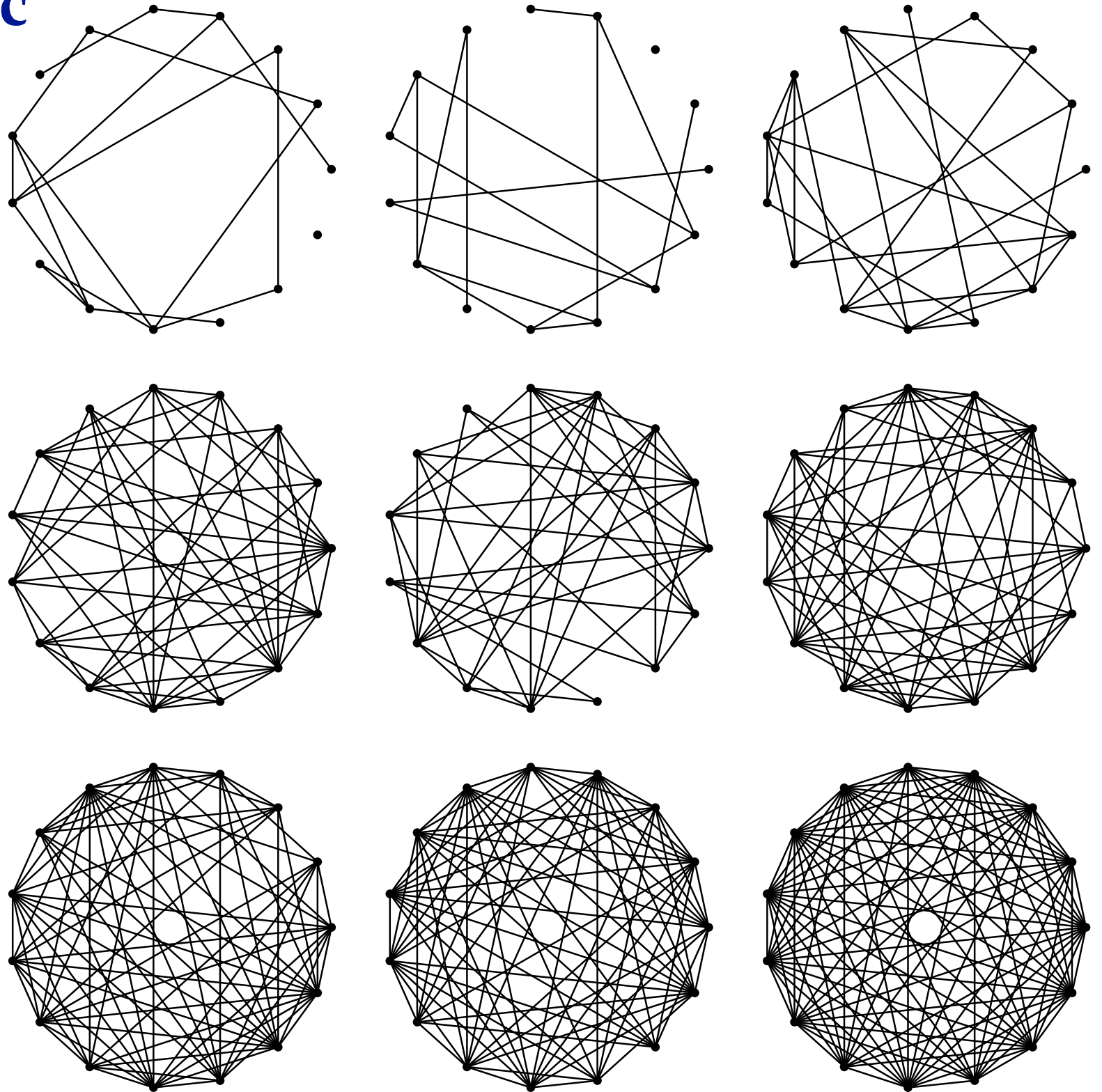
# RDS - Random Static

Erdos-Renyi (1960):

Create  $n$  vertices

Between every pair of vertices  $\{u,v\}$ , add an edge with probability  $p$ .

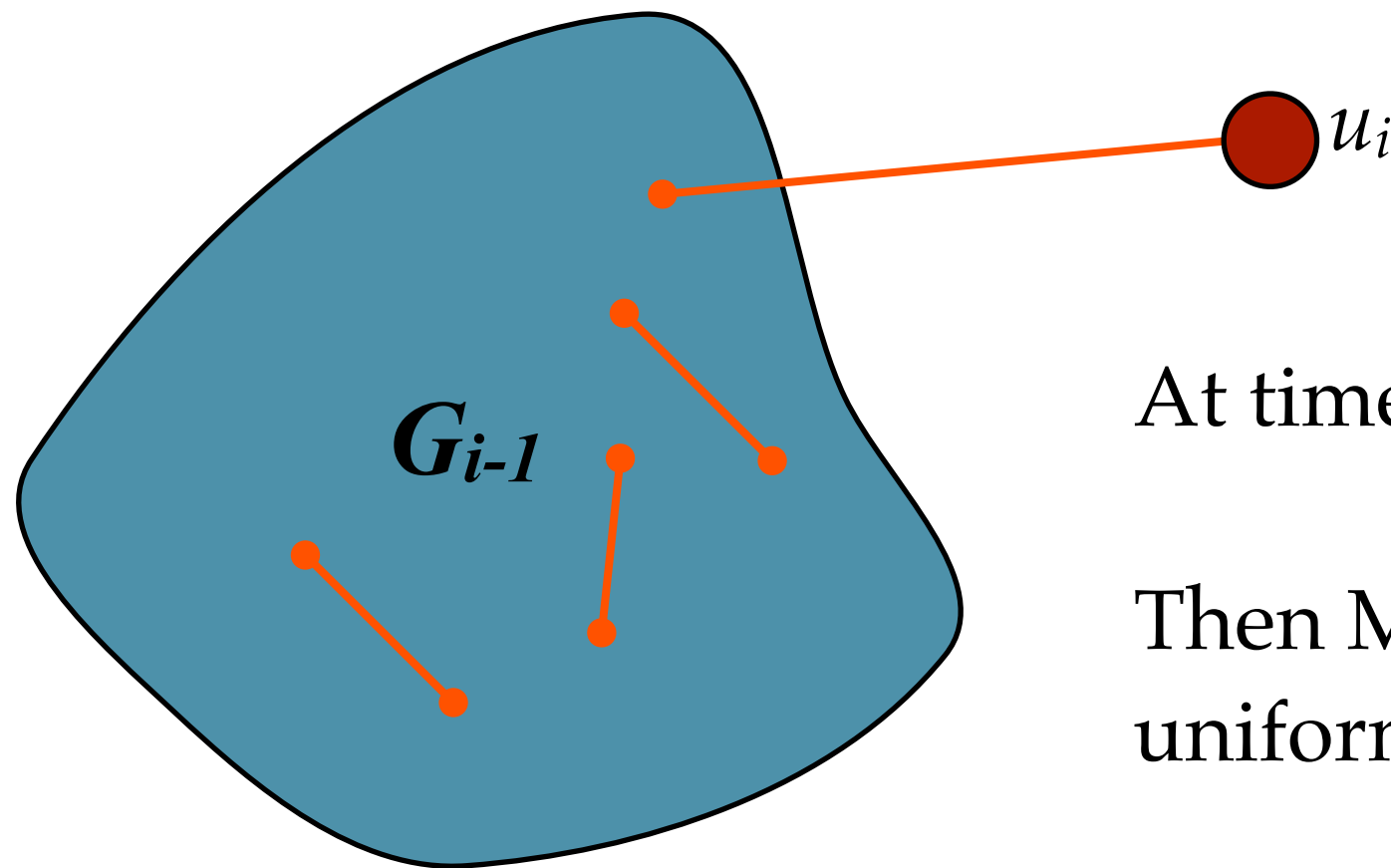
Expected degree is  $(n-1)p$



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ShowGraphArray[Partition[Table[RandomGraph[15, p], {p, 0.1, 0.9, 0.1}], 3]]
```

# RDG - Random Growing

**Parameters:**  $n$  = number of nodes;  $M$  = expected # of edges.



At time  $i$ , a node is added.

Then  $M/n$  edges are added uniformly at random.

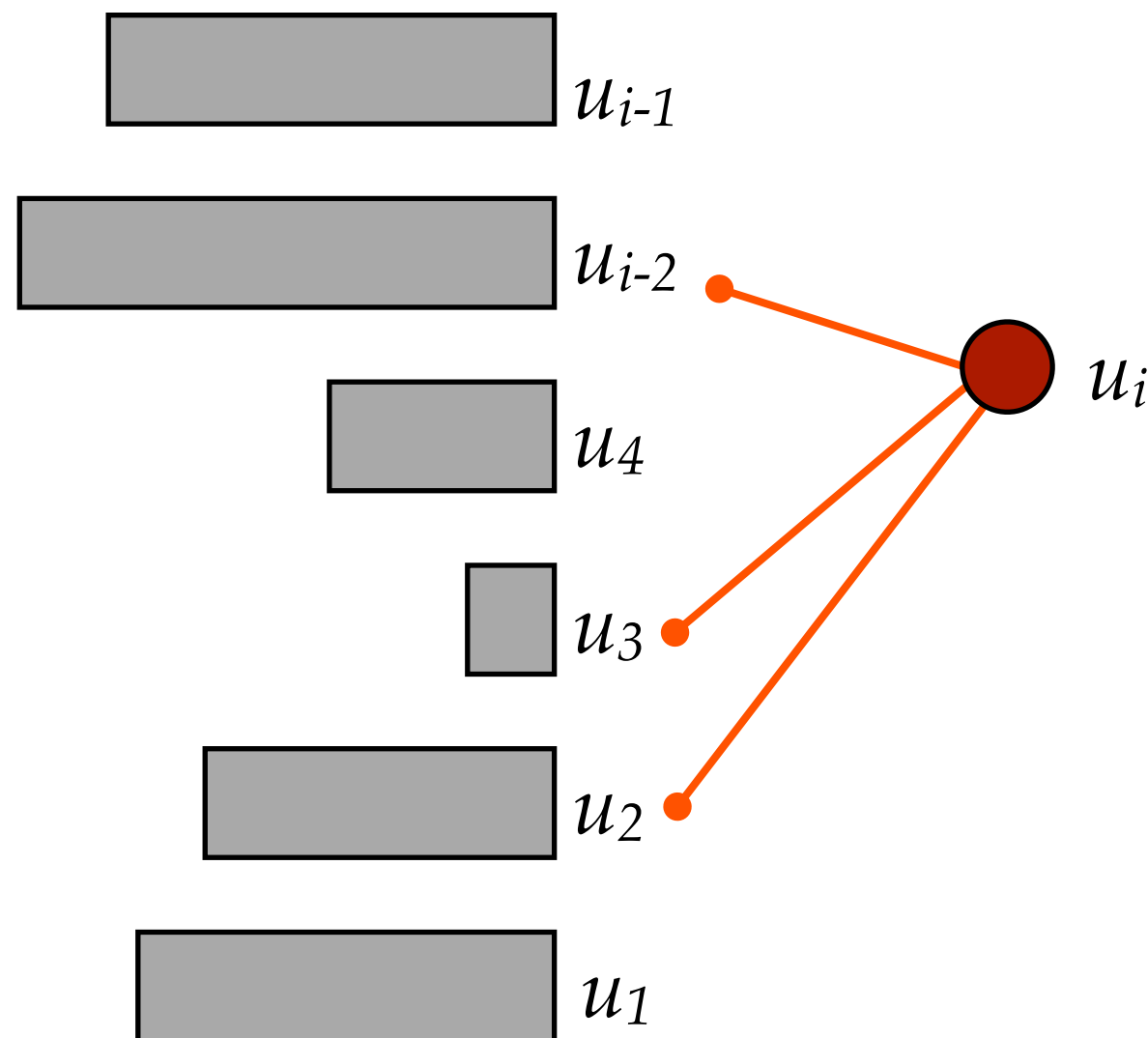
Added edges might not involve  $u_i$ .

Nodes added earlier have more chances to be adjacent to edges.

# LPA – Linear Preferential Attachment

**Parameters:**  $n$  = number of nodes;  $M$  = number of edges;  
 $a$  = smoothing parameter.

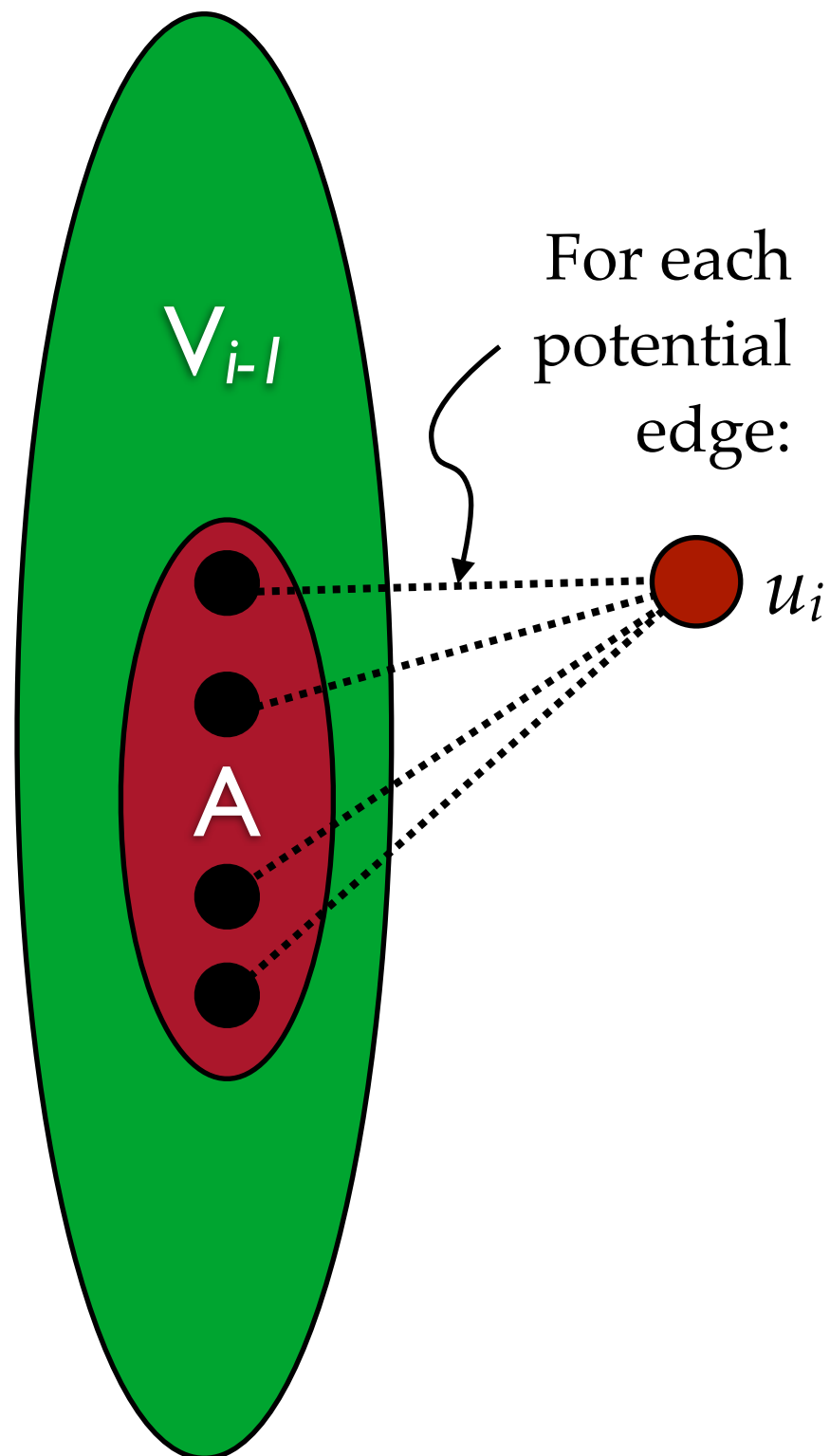
Histogram:  $\text{degree}(u_j) + a$ , normalized  
to be a probability distribution:



At time  $i$ , a node  $u_i$  is added.

$M/n$  edges are added  
between  $u_i$  and the existing  
nodes drawn randomly  
according to the histogram.

# AGV – Aging Vertices



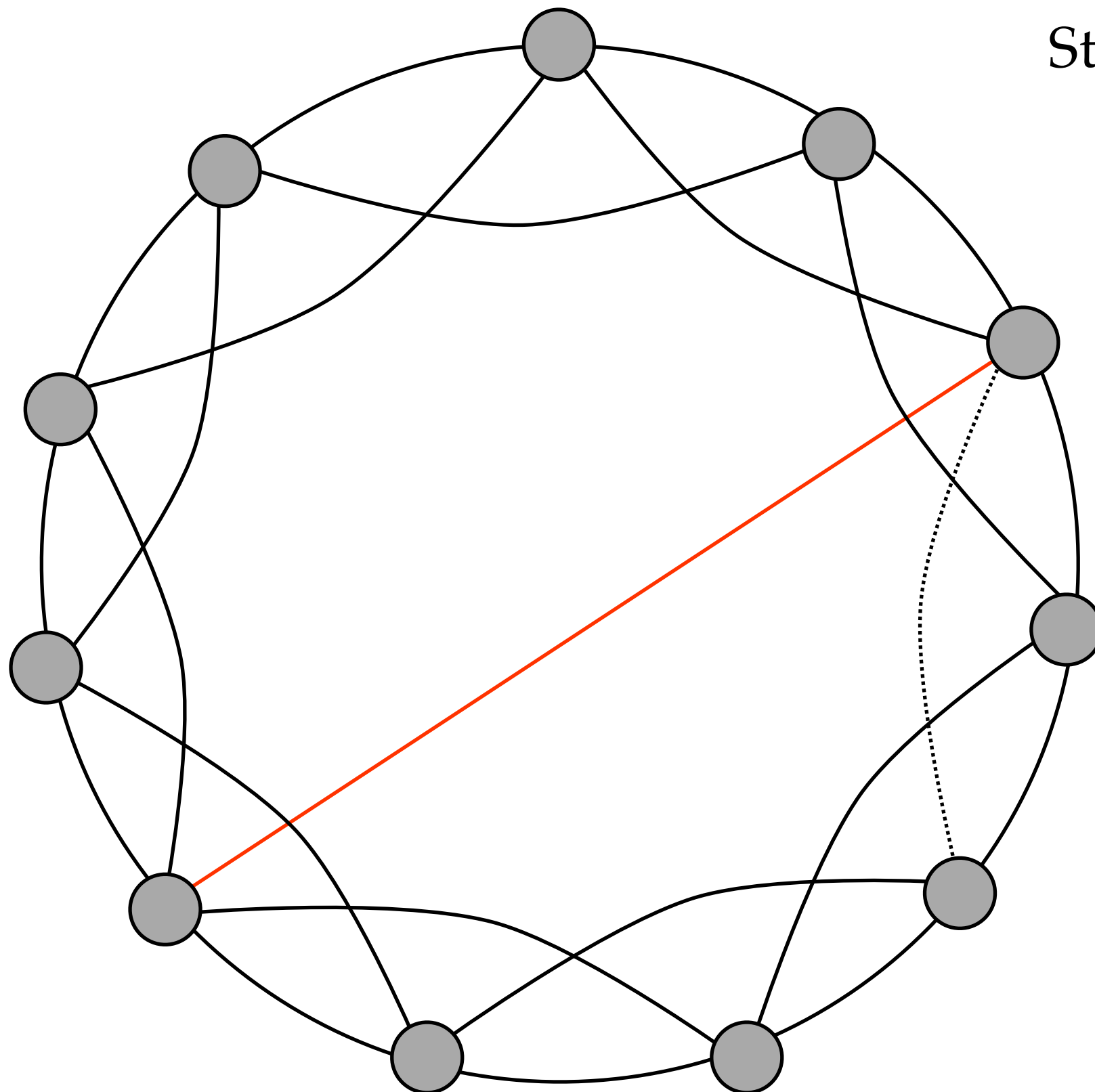
With probability  $\mu$ , add the edge.

With probability  $(1-\mu)$ , add a random edge between  $u_i$  and any node in  $V_{i-1}$ , chosen according to the existing degrees.

**Then:** Pick a random node  $x$  in  $A$ , inversely proportional to the node degrees (i.e. prefer low-degree nodes)

Remove  $x$  from  $A$  and add  $u_i$  to  $A$ .

# SMW – Small World Networks



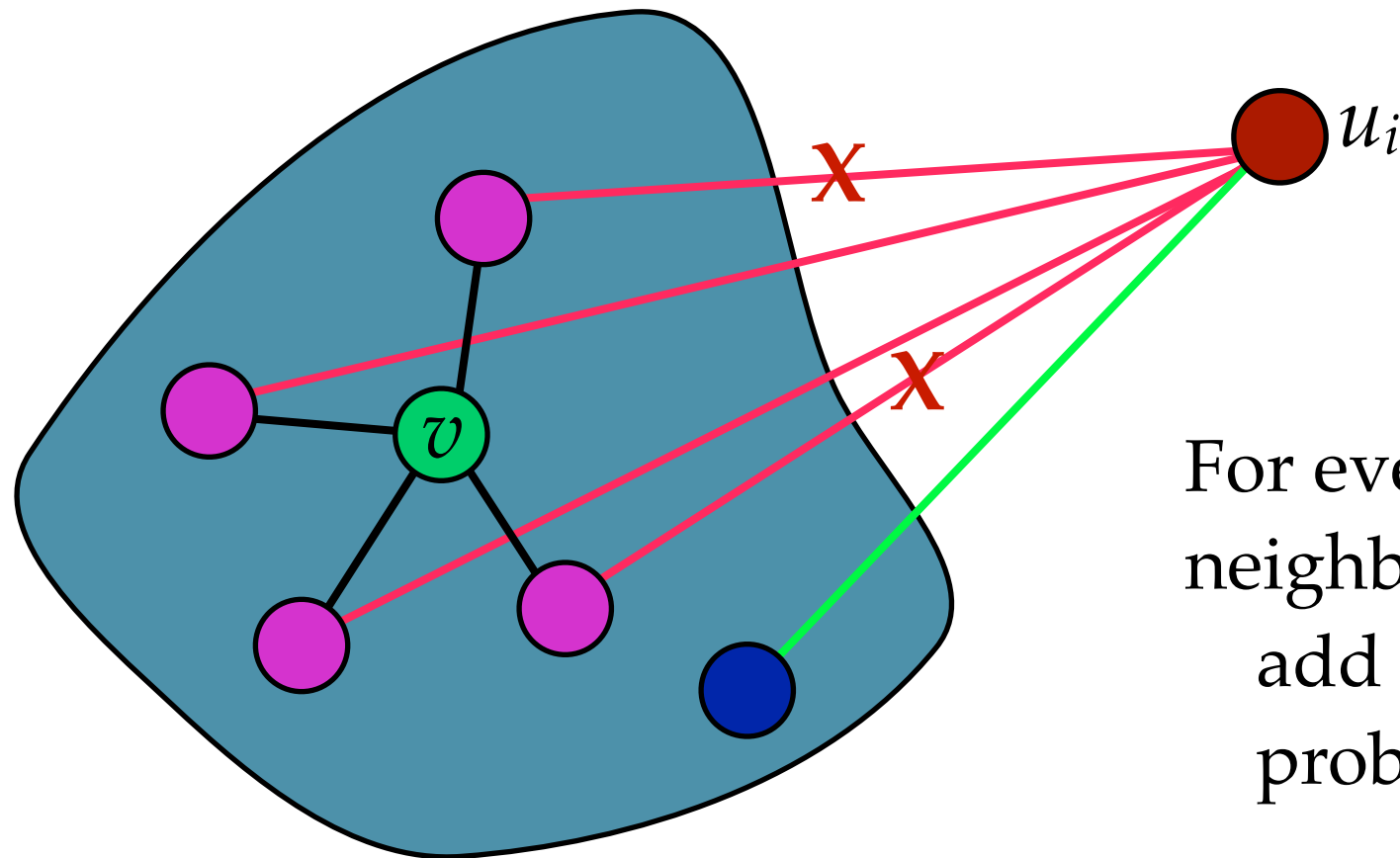
Start with ring lattice

For each edge  $(i,j)$ , in  
random order:  
with probability  $q$ ,  
rewire it to be an  
edge  $(i, v)$  for a  
random vertex  $v$ .

# DMR – Duplication With Mutations

Choose a node  $v$  at random, and connect  $u_i$  to all the neighbors of  $v$ .  
 $u_i$  is now a “clone” of  $v$ .

For each added edge, remove it with probability  $q_{\text{del}}$



For every node  $w$  that is not now a neighbor of  $u_i$ ,  
add an edge  $(u_i, w)$  with  
probability  $q_{\text{new}} / (i-1)$

↑  
probability  
decays over time.

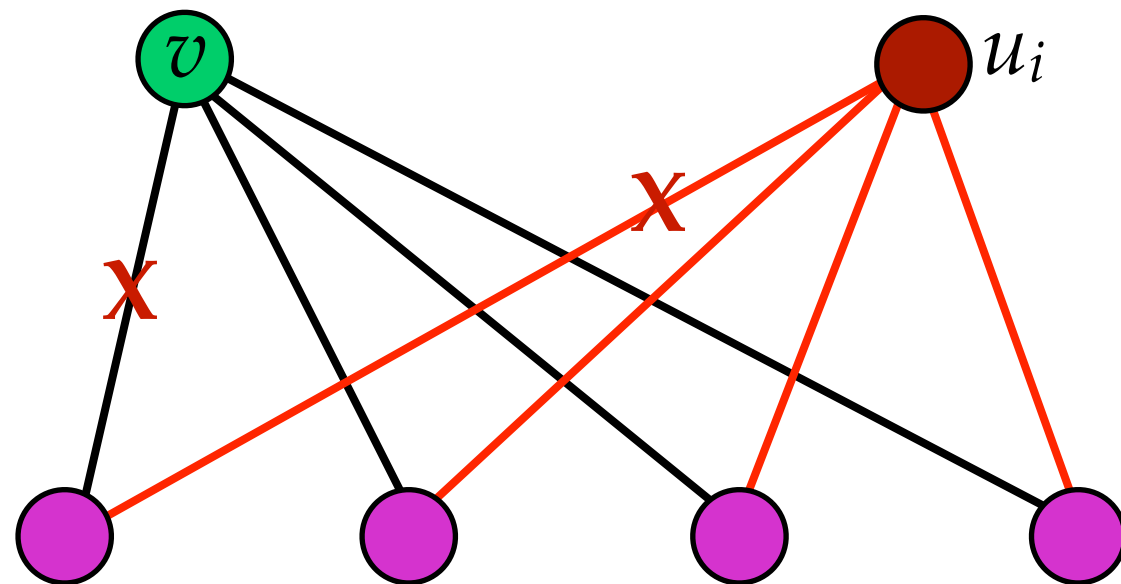


# DMC – Duplication, Mutation with Complementarity

Choose a node  $v$  at random, and connect  $u_i$  to all the neighbors of  $v$ .  
 $u_i$  is now a “clone” of  $v$ .

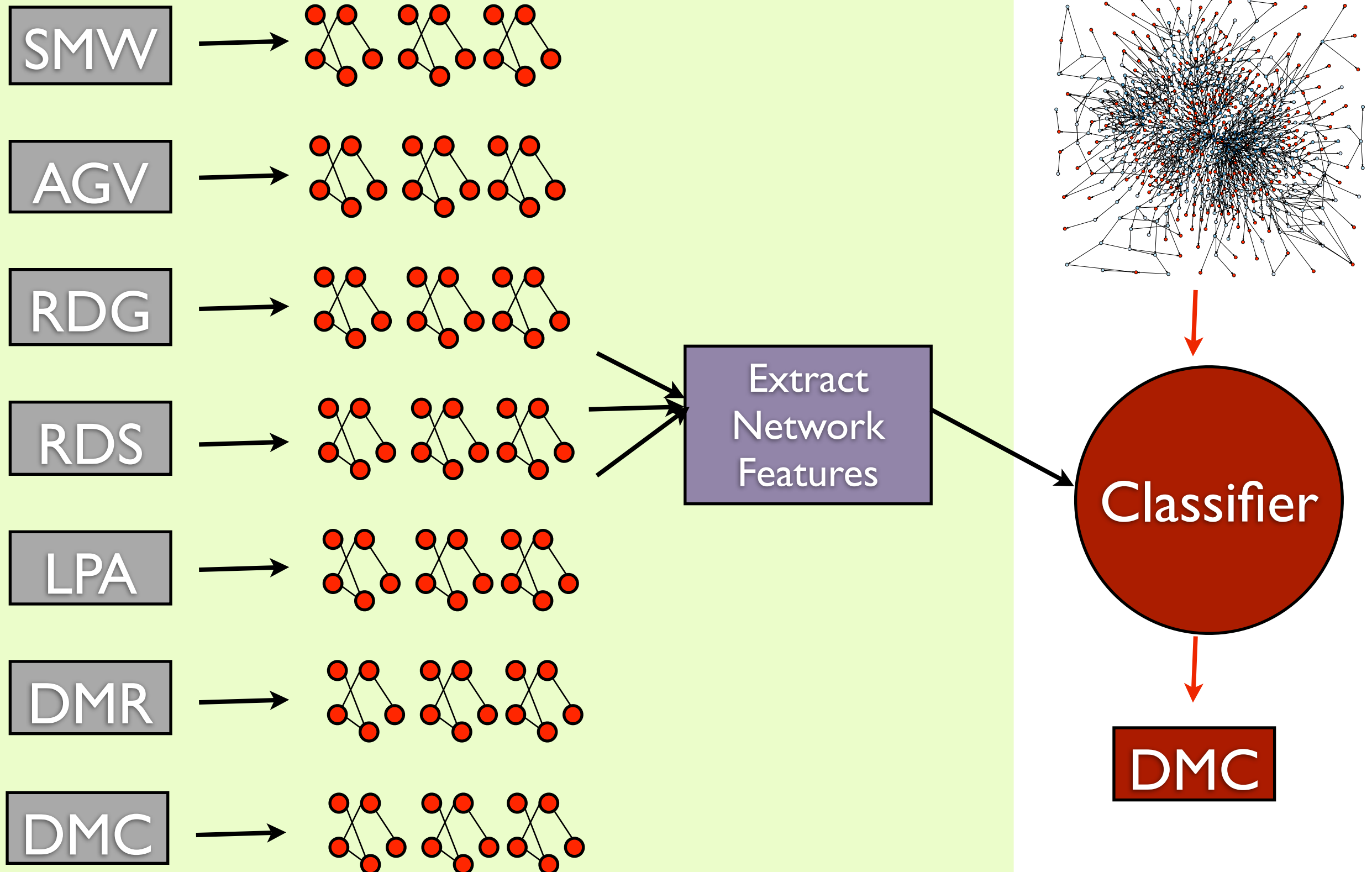
For every added edge, decide to delete with probability  $q_{\text{del}}$

If you decide to delete, delete the new or corresponding old edge (choosing which one by flipping a coin):



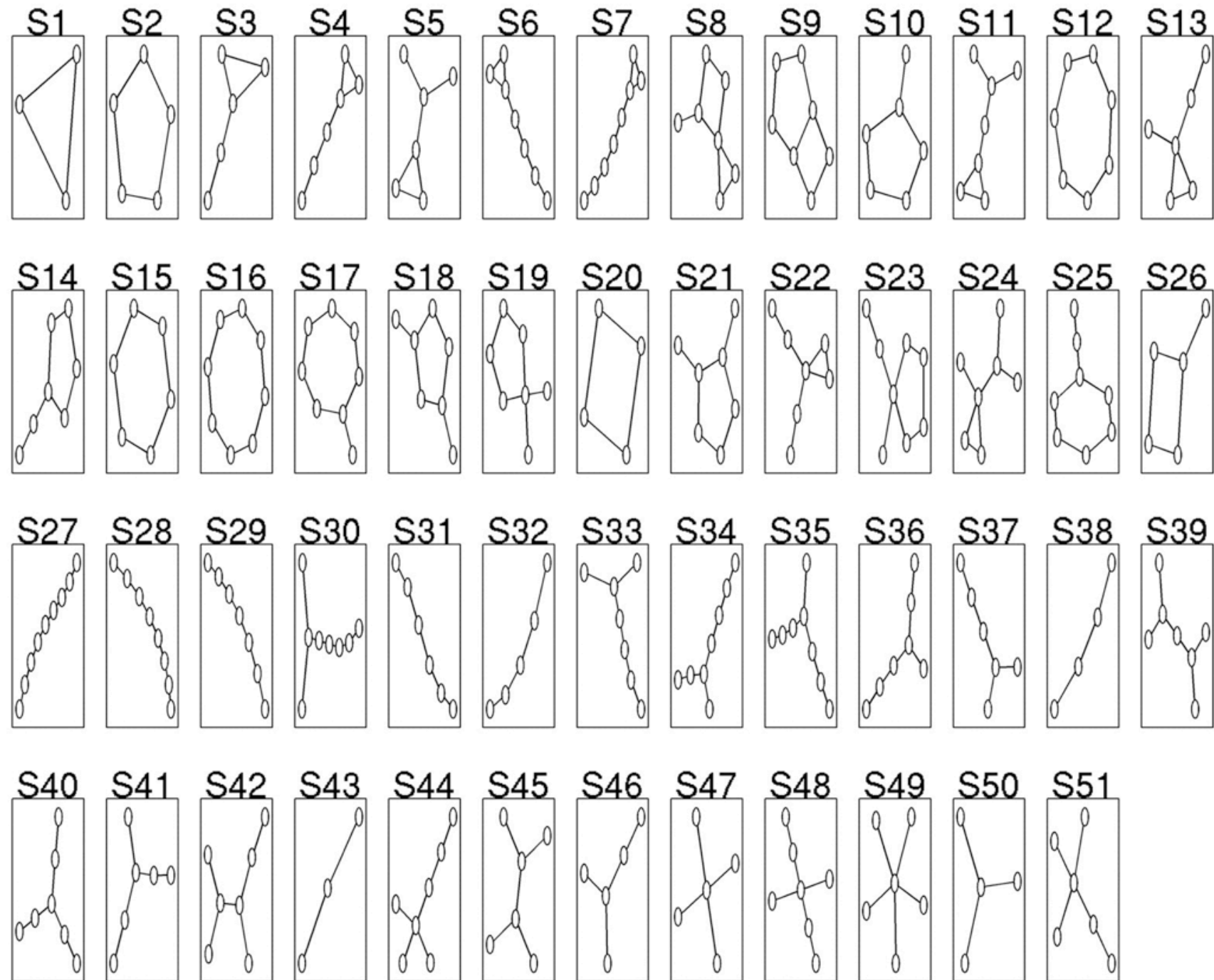
Finally, with probability  $q_{\text{con}}$ , add an edge  $(v, u_i)$

# Supervised Learning → Predict Network Models



# Network Features – Subgraph Census

Count the occurrences of  
the following subgraphs:



Walks Of Length  $\leq 8$   
(148 possible graphs)

Subgraphs with  $\leq 7$  edges  
(130 possible graphs)

(Figure from Middendorf, 2004)

# Classifier - Alternating Decision Trees

Trained via Boosting

To predict a class,  
traverse the tree in the  
following way:

Start a root node

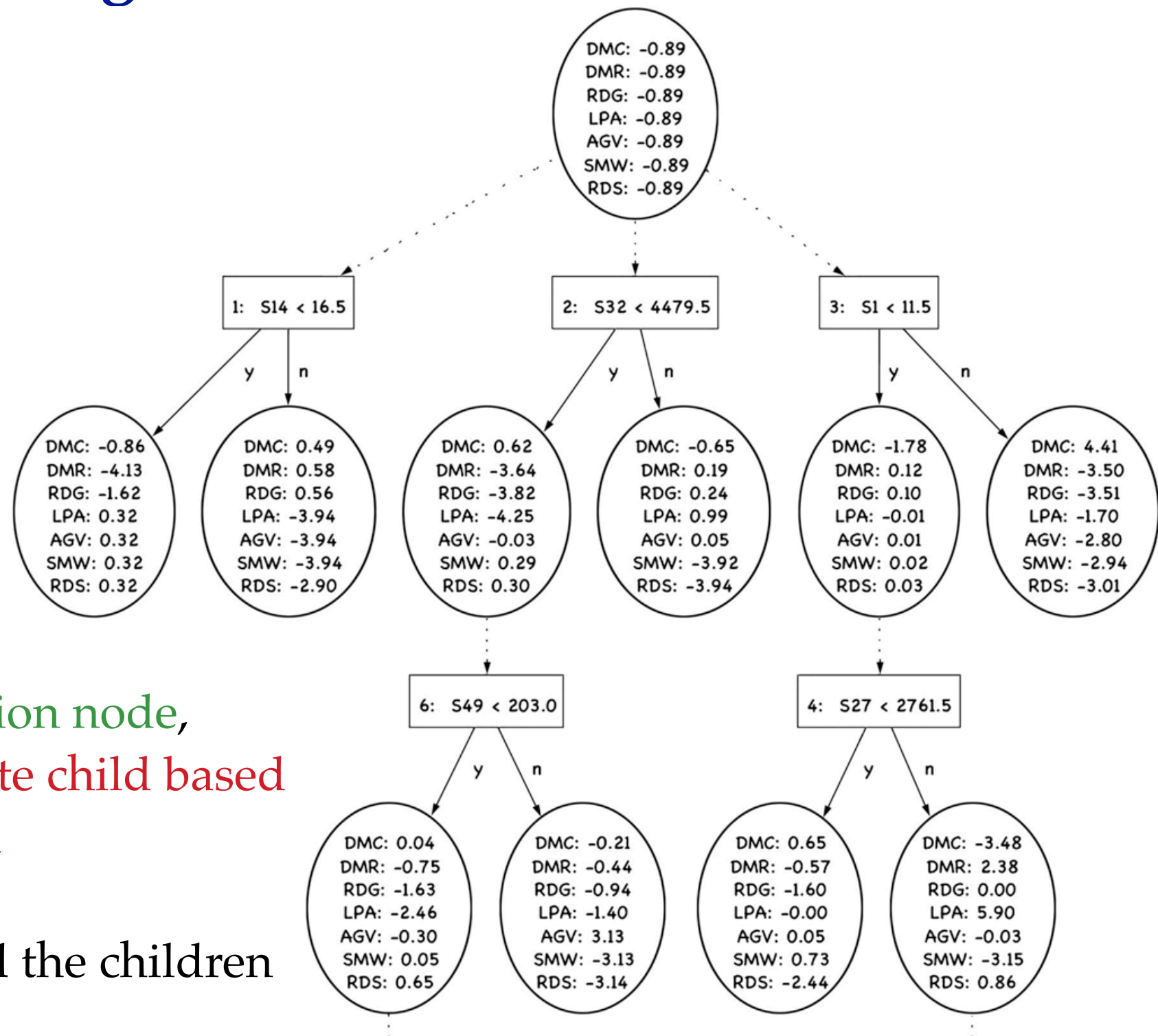
**Repeat** until leaf:

if current node is a decision node,  
move to the appropriate child based  
on the node's question

else

recursively move to all the children  
of the current node

**Return** vector of sums of all the weights visited.



(Figure from Middendorf, 2004)



# Classifier - Alternating Decision Trees

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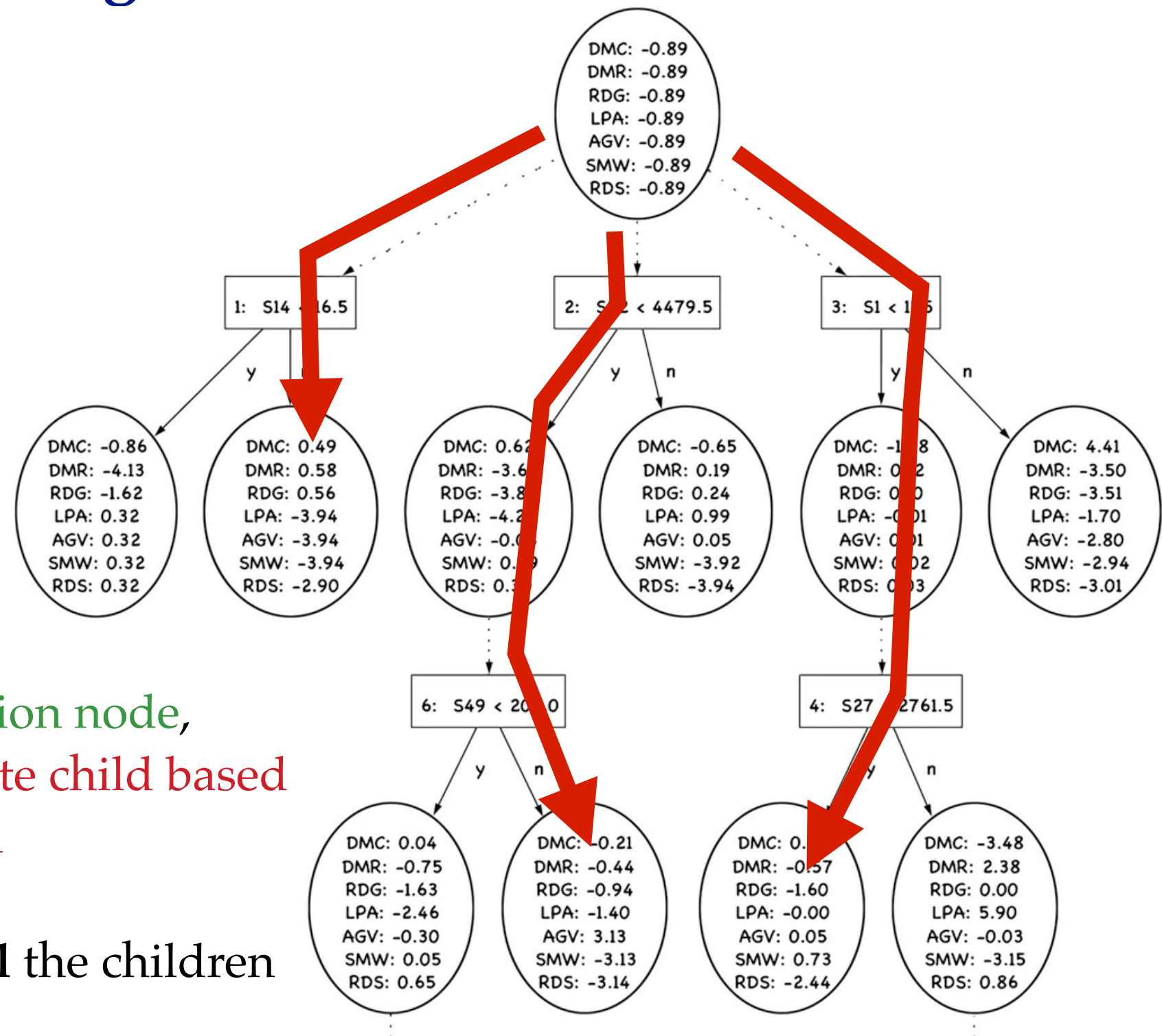
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(Figure from Middendorf, 2004)

**Return** vector of sums of all the weights visited.

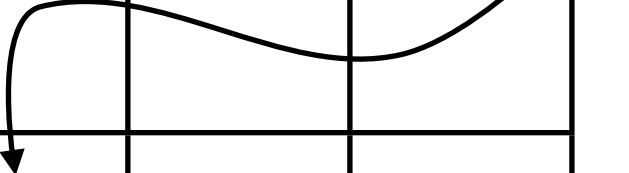
# Error on Simulated Data

Prediction

Correct Answer

	DMR	DMC	AGV	LPA	SMW	RDS	RDG
DMR	99.3						
DMC		99.7					
AGV		0.1	0.84	13.5	1.2	0.5	
LPA			10.3	89.6			0.1
SMW			0.6		99.0	0.4	
RDS			0.2		0.8	99.0	
RDG	0.9			0.1			99.0

Percentage of  
time predicted  $x$   
when correct  
answer was  $y$ .



# Drosophila Network

- Yeast 2-hybrid with probabilities assigned by Giot et al. (34).
- Two different cutoffs for probability an edge really exists:  $p^* = 0.5$  and  $p^* = 0.65$
- (0.65 chosen because this is when the two largest components are merged).
- When  $p^* = 0.65$ , 3,359 vertices and 2,795 edges.

# Predictions on Dros. Network:

Eight-step subgraphs ( $p^* = 0.65$ )			Subgraphs with up to seven edges ( $p^* = 0.65$ )		Eight-step subgraphs ( $p^* = 0.5$ )	
Rank	Class	Score	Class	Score	Class	Score
1	DMC	$8.2 \pm 1.0$	DMC	$8.6 \pm 1.1$	DMC	$0.8 \pm 2.9$
2	DMR	$-6.8 \pm 0.9$	DMR	$-6.1 \pm 1.7$	DMR	$-2.1 \pm 2.0$
3	RDG	$-9.5 \pm 2.3$	RDG	$-9.3 \pm 1.6$	AGV	$-3.1 \pm 2.2$
4	AGV	$-10.6 \pm 4.2$	AGV	$-11.5 \pm 4.1$	LPA	$-10.1 \pm 3.1$
5	LPA	$-16.5 \pm 3.4$	LPA	$-14.3 \pm 3.2$	SMW	$-20.6 \pm 1.9$
6	SMW	$-18.9 \pm 0.7$	SMW	$-18.3 \pm 1.9$	RDS	$-22.3 \pm 1.7$
7	RDS	$-19.1 \pm 2.3$	RDS	$-19.9 \pm 1.5$	RDG	$-22.5 \pm 4.7$

(Table from Middendorf, 2004)

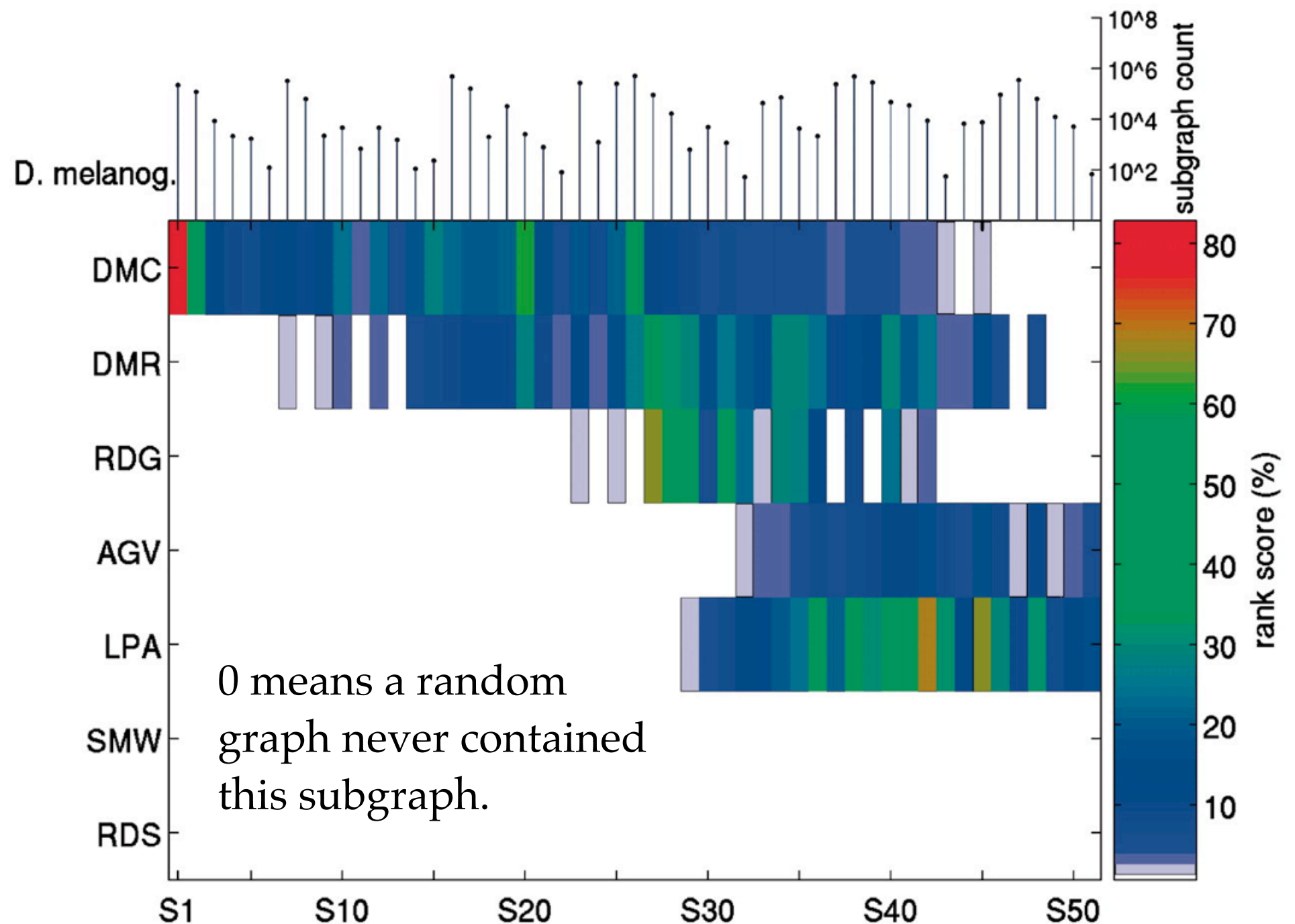
↑  
stddev over cross-  
validation folds

Note: random  
growing preferred  
over preferential  
attachment



# Which random processes can produce which subgraphs?

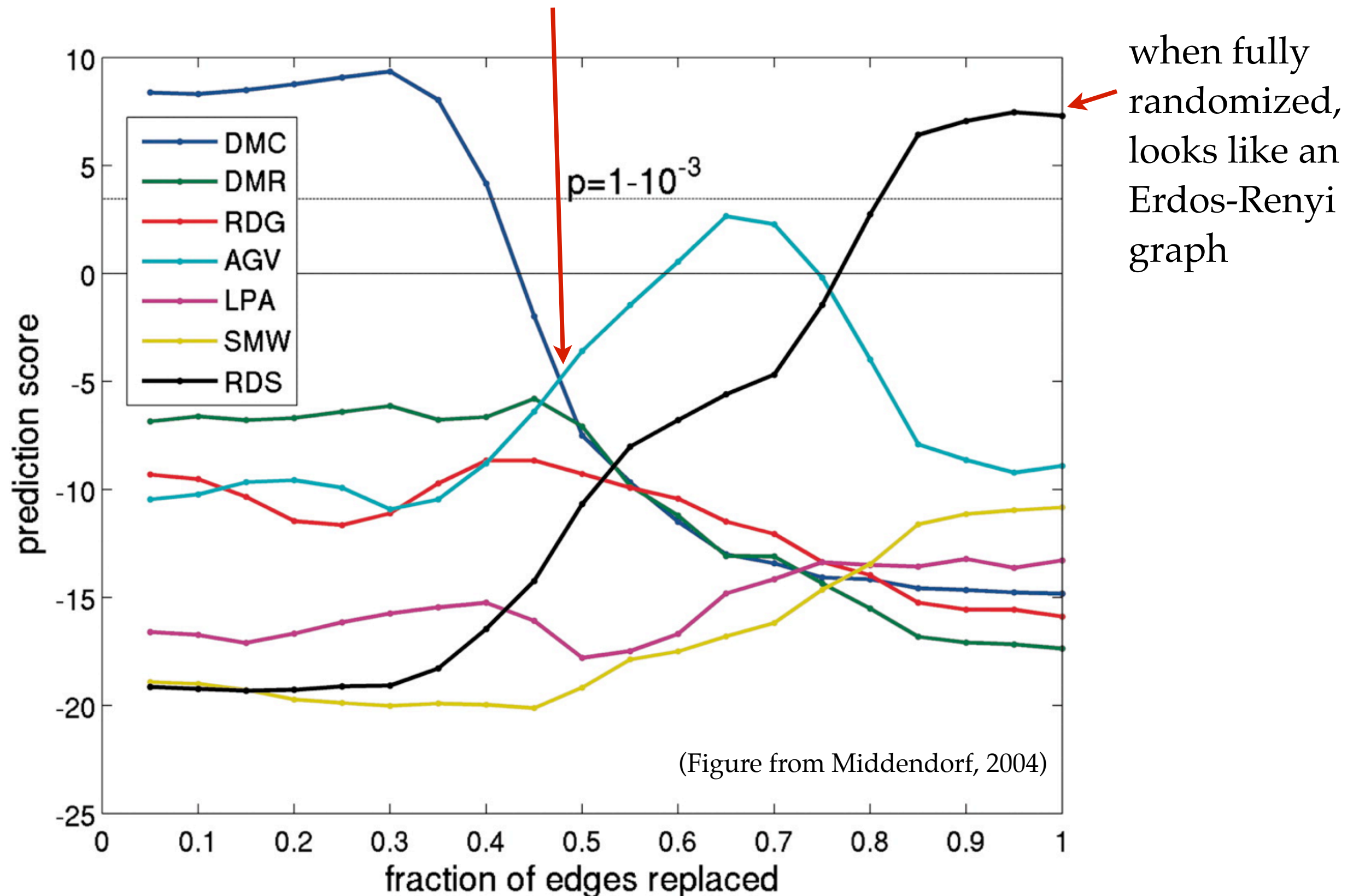
**Rank score:** % of random graphs that contained  $\geq$  instances of the subgraph than exist in Dros.



(Figure from Middendorf, 2004)

# Robustness to Noise

Place where  
prediction changes



# Summary

- Lots of random models for growing networks (there are still others we haven't covered)
- Each gives rise to networks with different properties.
- These networks can generally be distinguished by looking at the counts of various subgraphs that they contain.
- Using that idea, Middendorf et al. work backwards, and guess which model seems to fit real data.
- DMC seems like the best-fitting model for fly.