

Information Dynamics across Linked Sub-Networks: Genes, Germs, and Memes Supplementary material

Included here are materials supplementary to the main paper:

- A. Supplementary sections on Hub and Wheel networks
 - 1. for infection dynamics
 - 2. for belief updating
- B. Comparison graphs for all networks considered.
 - 1. for infection dynamics
 - 2. for belief updating

A1. Infection across Hub and Wheel Networks

In hub networks a central node is connected to all others within it (the 'outer' nodes), with no connection between outer nodes except through the center (Figure 1). This pattern is also sometimes referred to as a 'royal family' in the economics literature.

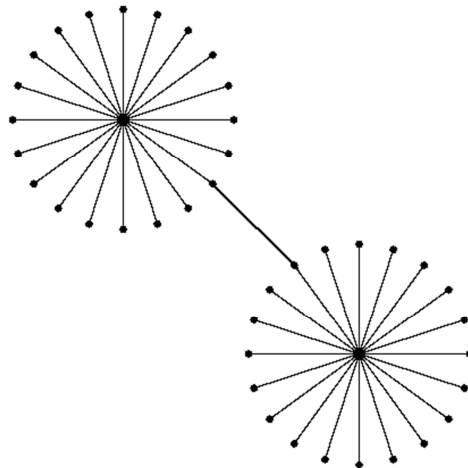


Fig. 1 Homophilous network of hub sub-networks

Consider a network with two sub-networks of equal size, incorporating a total of n nodes and m discrete links between sub-networks (links sharing no nodes). Where our links are exclusively between outer nodes, the average time to infection will be

$$\frac{5n - 4m - 2}{n}$$

provided that $n > 2m + 2$. Where $n = 2m + 2$ —every outer node is linked to another—the average time reduces to simply 3.

The possibility of links between central nodes or between an outer node in one sub-network and a central node in another complicates the situation somewhat. Where central linkages are to outer nodes exclusively, and whether we have one or two links involving central nodes, average time to infection will be

$$\frac{4n - 2m - 2}{n}$$

for any $n > 2m + 2$. If $n = 2m + 2$ and there is a single link between an outer and a central node, average time to infection will be

$$\frac{3n - 2}{n}.$$

On the other hand, if there are two links between outer and central nodes, then average time to infection will be 3 when $n = 2m + 2$ and

$$\frac{3n - 4}{n}$$

when $n = 2m$.

The remaining possibility is that we have a single link between centers. In that case the average time to infection will be

$$\frac{3n - 2}{n}$$

for any $n \geq 2m$, interestingly independent of m . The single link between centers offers a fast route between sub-networks which effectively cancels the effect of links between edge nodes, however many.

For random links between sub-networks on the assumptions above, the probability that a link will join two centers is

$$\left(\frac{1}{n/2}\right)^2 = \left(\frac{2}{n}\right)^2 = \frac{4}{n^2}.$$

The probability that a single link will join two outer nodes is

$$\left(\frac{\left(\frac{n}{2} - 1\right)}{\frac{n}{2}}\right)^2 = \frac{(n - 2)^2}{n^2}.$$

The probability that it will join a center node on one side and an outer node on the other is

$$\frac{2 \binom{n}{2} - 1}{\binom{n}{2}^2} = \frac{4n - 8}{n^2}.$$

Combining probabilities for each case with formulae for average time to infection for that case, we obtain an average time to infection with a single link, under the assumptions noted, of

$$\frac{4}{n^2} * \frac{3n - 2}{n} + \frac{(n - 2)^2}{n^2} * \frac{5n - 6}{n} + \frac{4n - 8}{n^2} * \frac{4n - 4}{n} = \frac{5n^2 - 10n + 8}{n^2}$$

As $n \rightarrow \infty$, $(5n^2 - 10n + 8) / n^2$ goes to 5.

In simulation, these results play out as follows. Figure 2 shows average time to infection over 1000 runs, adding 1 to 50 links between hub sub-networks. Though there is an effect from added linkages, that effect is minimal; average times decrease from 4.88 to 3.36. The results are understandable in terms of our cases above. Were we to add only additional linkages between outer nodes, we would have no difference in time to infection at all; all the work is already being done by the network structure within each hub and the other linkages between them. What we get with increased numbers of linkages is merely the probability of a center-to-edge connection, or a center-to-center connection, either of which do cut down average times.

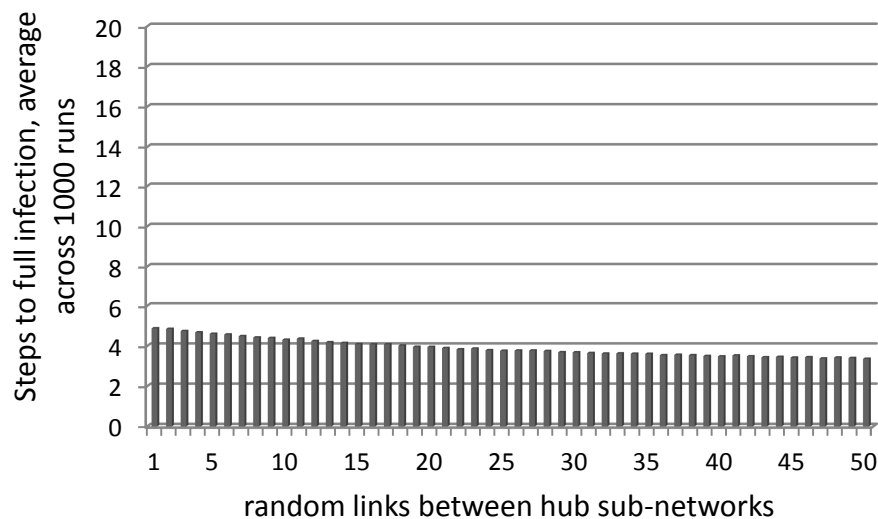


Fig. 2 Decreasing homophily: Average time to infection with random linkages between hub sub-networks

Comparison with a non-homophilous network of the same structure—a single hub—is instructive. For a single hub, the time to total infection from an initially infected edge node is simply 2. Time to infection from a central node is 1. Our average times to infection will therefore be simply

$$\frac{2(n - 1) + 1}{n} = \frac{2n - 1}{n}.$$

Here additional linkages will have no effect on results. Average times in simulation for such a case vary without pattern between 1.991 and 1.998 (Figure 3)

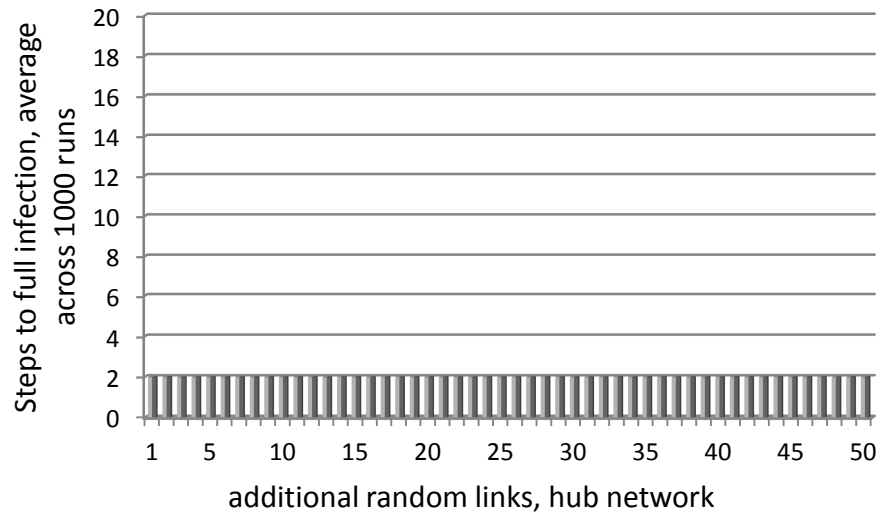


Fig. 3 Without homophily: Average time to infection with additional random links within a single non-homophilous hub network.

Wheel networks combine a ring network with the effects of a single hub; a homophilous network composed of two wheel sub-networks is shown in Figure 4.

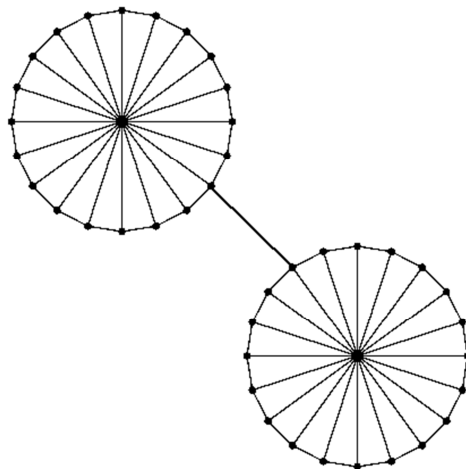


Fig. 4 Homophilous network of wheel sub-networks

Here as before we must consider a number of cases. For simplicity, we restrict to networks in which no links share nodes.

Suppose we have m links between sub-networks between outer nodes only, and let i be the number of non-linked nodes that are adjacent to a linked node—those immediately on one side or the other. With the linkages illustrated in Figure 4, for example, there will be two adjacent non-linked nodes in each sub-network, giving us a total $i = 4$. With two links between

sub-networks, adjacent nodes i may include 2, 3, or 4 nodes within each sub-network. If $n \geq 10$ and $m < \left\lceil \frac{n-2}{6} \right\rceil$ (where $\lceil x \rceil$ is the largest integer greater than or equal to x), our average time to infection will be a variant on the hub:

$$\frac{5n - 4m - 2 - i}{n}.$$

For the case in which there is a single link, for example, the average time to total infection will be

$$\frac{5n - 4(1) - 2 - (4)}{n} = \frac{5n - 10}{n}.$$

For a wheel network of this type with n nodes, $m - 1$ links between outer nodes and one link between an outer node and a center, with i non-linked nodes adjacent to the centrally linked node (in this case, $i = 0, 1, \text{ or } 2$), the average time to infection will be

$$\frac{4n - 2m - 2 - i}{n},$$

when $n > 20$ and $m < \frac{n}{2} - 3$. If $10 \leq n \leq 20$, this will still hold provided that $m < \left\lceil \frac{n-2}{6} \right\rceil$.

For a network with n nodes, $m - 2$ links between outer nodes and two links between an outer node and a center, with i non-linked nodes adjacent to the centrally linked nodes ($i = 0, 1, \text{ or } 2$), the average time to infection will again be

$$\frac{4n - 2m - 2 - i}{n},$$

but when $n > 20$ and $m < \frac{n}{2} - 2$. If $10 \leq n \leq 20$, the formula holds provided that $m < \left\lceil \frac{n-2}{6} \right\rceil + 1$.

For example, if $n = 22$, $m = 3$, and $i = 2$, and there is only one link between an outer node and a central node, then our average time to infection will be

$$\frac{4(22) - 2(3) - 2 - 2}{22} = \frac{78}{22}.$$

By adding one more link between an outer node and a central node and keeping $i = 2$, the average time to infection reduces to

$$\frac{4(22) - 2(4) - 2 - 2}{22} = \frac{76}{22}.$$

If the number of non-linked nodes i adjacent to the centrally linked node is increased to 3, the average time to infection decreases to

$$\frac{4(22) - 2(4) - 2 - 3}{22} = \frac{75}{22}.$$

If i is increased to 4, the time to infection becomes

$$\frac{4(22) - 2(4) - 2 - 4}{22} = \frac{74}{22}.$$

By algebraic manipulation, it can be shown that if an additional link between an outer node and a central node is inserted in a network containing one link between an outer node and a central node, the average time to infection decreases by either $\frac{2}{n}$, $\frac{3}{n}$, or $\frac{4}{n}$, depending on whether i changed by 0, 1, or 2, respectively (provided that the restrictions on m and n are satisfied).

In the final case we have a link between center nodes; given our assumption that no links share nodes we will then have no links between outer nodes and centers. In that case, for n nodes and $m - 1$ links between outer nodes, the average infection time is

$$\frac{3n - 2}{n}$$

where $n \geq 14$. Here again, subject to restrictions, our result is similar to the hub formula.

Probabilities can be calculated as follows. The number of wheel networks of the form at issue having n nodes and k links is

$$\frac{1}{k!} \prod_{j=1}^k \left(\frac{n}{2} - j + 1 \right)^2.$$

The number of such networks with k links solely between outer nodes, corresponding to the first case above, is

$$\frac{1}{k!} \prod_{j=1}^k \left(\frac{n}{2} - j \right)^2.$$

The number with $k - 1$ links between outer nodes and one link between an outer and center node is

$$\frac{n - 2k}{(k - 1)!} \prod_{j=1}^{k-1} \left(\frac{n}{2} - j \right)^2,$$

whereas the number with $k - 2$ links between outer nodes and two links between outer and center nodes is

$$\frac{1}{(k - 2)!} \prod_{j=1}^{k-1} \left(\frac{n}{2} - j \right)^2.$$

The number of networks with one center-center link and $k - 1$ links between outer nodes is

$$\frac{1}{(k-1)!} \prod_{j=1}^{k-1} \left(\frac{n}{2} - j\right)^2.$$

We obtain probabilities for each case by dividing by our total number of networks above:
For k links solely between outer nodes, we have probability

$$\left(\frac{n-2k}{n}\right)^2;$$

The probability for $k-1$ links between outer nodes and one link between an outer and center node is

$$\frac{4k(n-2k)}{n^2};$$

For $k-2$ links between outer nodes and two links between outer and center nodes, the probability is

$$\frac{4k(k-1)}{n^2};$$

For one center-center link and $k-1$ links between outer nodes, the probability is

$$\frac{4k}{n^2}.$$

Combining probabilities for each case with formulae for average time to infection for that case, we obtain an average time to infection with a single link, under the assumptions noted, of

$$\left(\frac{n-2}{n}\right)^2 * \frac{5n-10}{n} + \frac{4(n-2)}{n^2} * \frac{4n-6}{n} + \frac{4}{n^2} * \frac{3n-2}{n} = \frac{5n^2 - 14n + 16}{n^2}$$

Observe that $(5n^2 - 14n + 16) / n^2$ approaches 5 as $n \rightarrow \infty$.

In simulation, these results play out as in Figure 5, showing a decrease from 4.86 steps with a single link to 3.29 with 50 links. Here as in the case of hubs, that slight decrease is understandable as simply an increased probability of links involving central nodes.

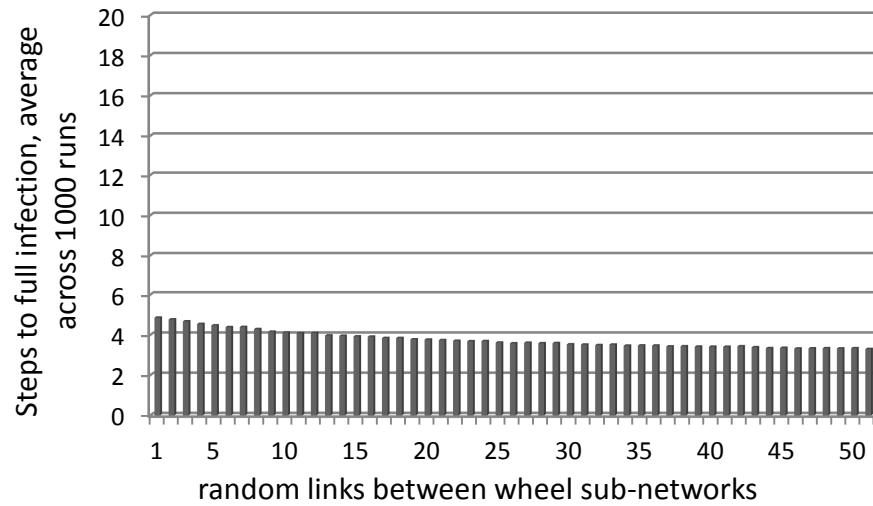


Fig. 5 Decreasing homophily: average time to infection with random links between wheel sub-networks

Comparison with a non-homophilous network of the same structure—a single wheel—is instructive. For a single wheel, the time to total infection from an initially infected edge node is simply 2 when $n \geq 5$. Time to infection from a central node is 1. Our average times to infection will therefore be simply

$$\frac{2(n-1) + 1}{n} = \frac{2n-1}{n}.$$

Simulation results for the non-homophilous wheel network are shown in Figure 6.

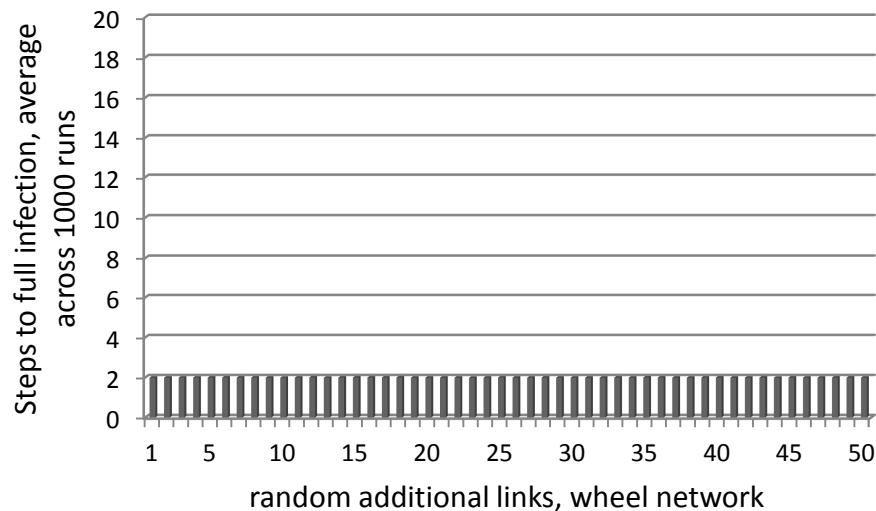


Fig. 6 Without homophily: time to infection with additional random links within a non-homophilous wheel

A2. Belief Diffusion across Hub and Wheel Networks

Figures 7 and 8 show results for times to belief convergence across hub networks, with one central node. In the case of a single non-homophilous hub, additional links are fairly redundant; the chart shows a random variance across 100 runs between 2.2 and 2.37 steps, and the graph is very similar to the case of infection. In the case of a homophilous networks with two hubs as sub-graphs, on the other hand, decreasing homophily makes a great difference; increasing links from 1 to 50 reduces time to consensus from 147 to 5.5 steps, with the same characteristic curve seen in homophilous ring and total networks above.

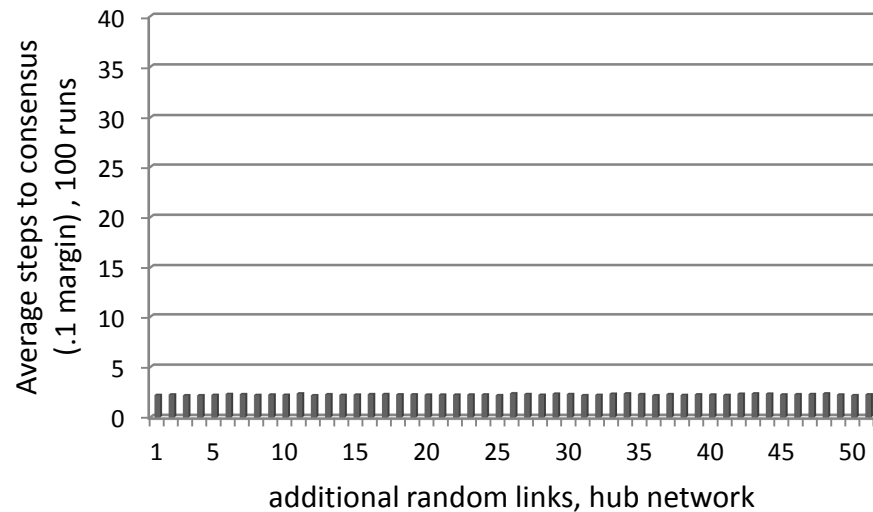


Fig. 7 Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous hub network

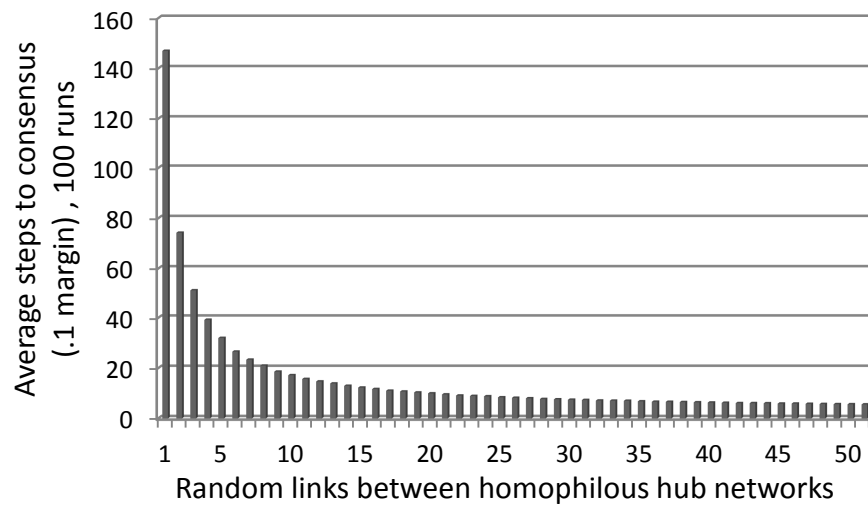


Fig. 8 Average steps to belief consensus with increasing random linkages between hub sub-networks

Results for wheel networks, shown in Figures 9 and 10, are nearly identical. Average times to consensus in the case of a non-homophilous wheel vary in the range of 2.02-2.21 steps. Average times in homophilous networks with wheel sub-networks descend sharply and characteristically from 145 to 6.06.

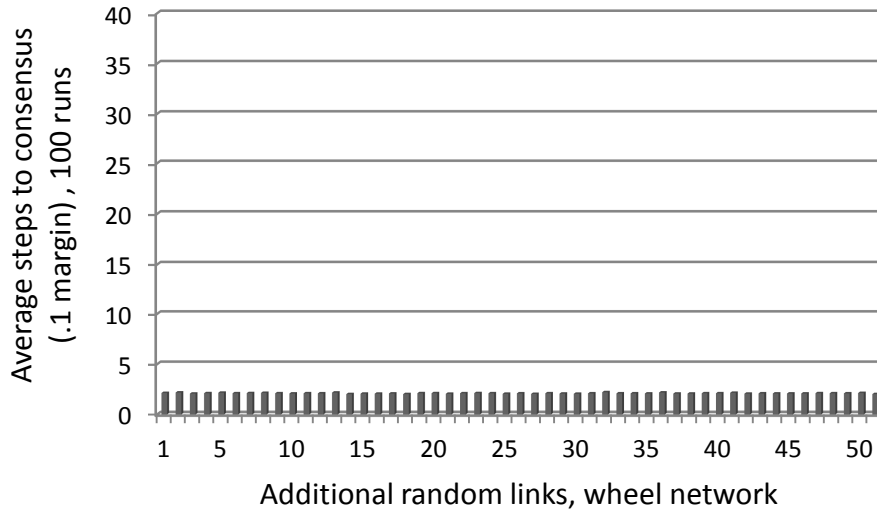


Fig. 9 Without homophily: Average steps to belief consensus with random links within a non-homophilous wheel network

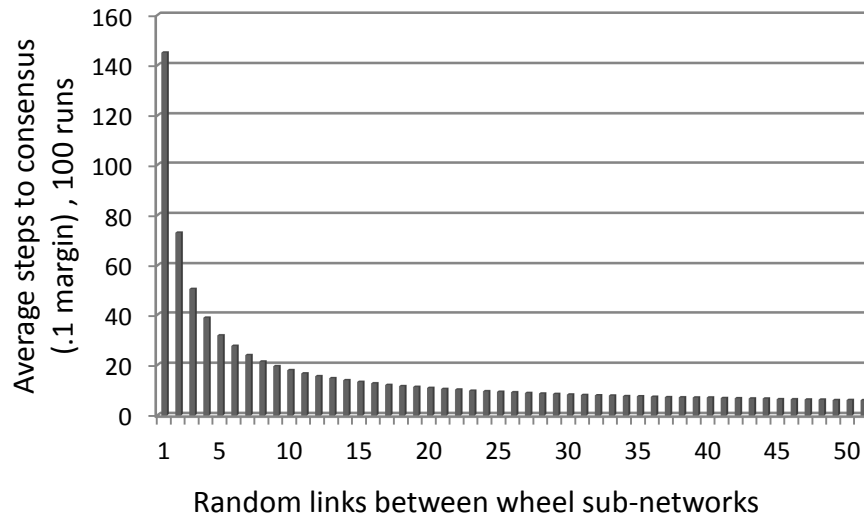
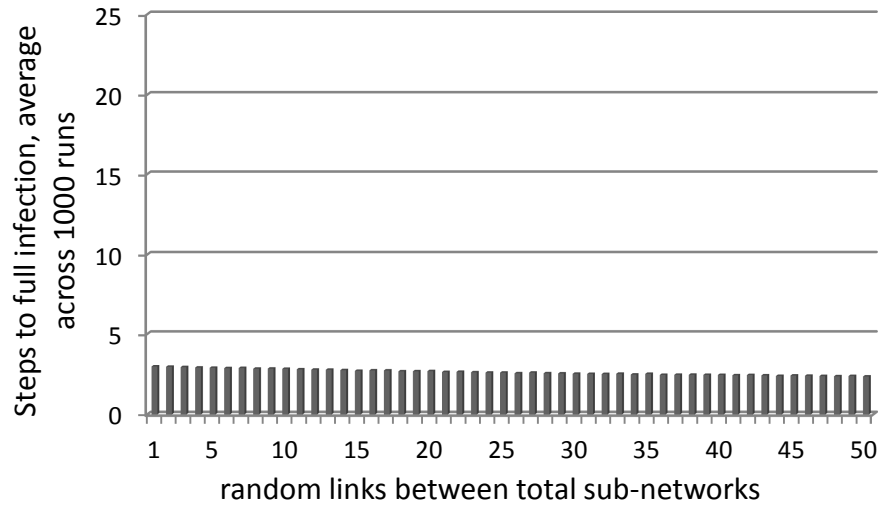


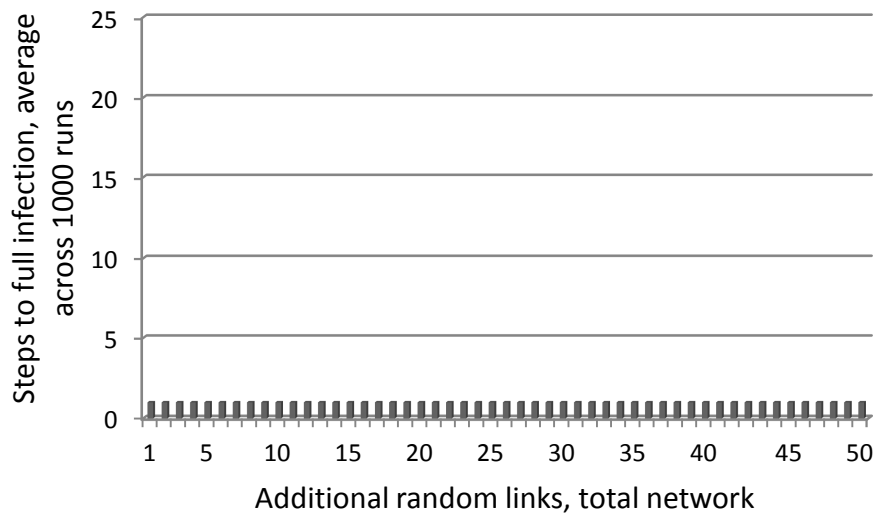
Fig. 10 Decreasing homophily: Average steps to belief consensus with increasing random linkages between wheel sub-networks

B1. Comparison Graphs for Infection Dynamics

Total networks

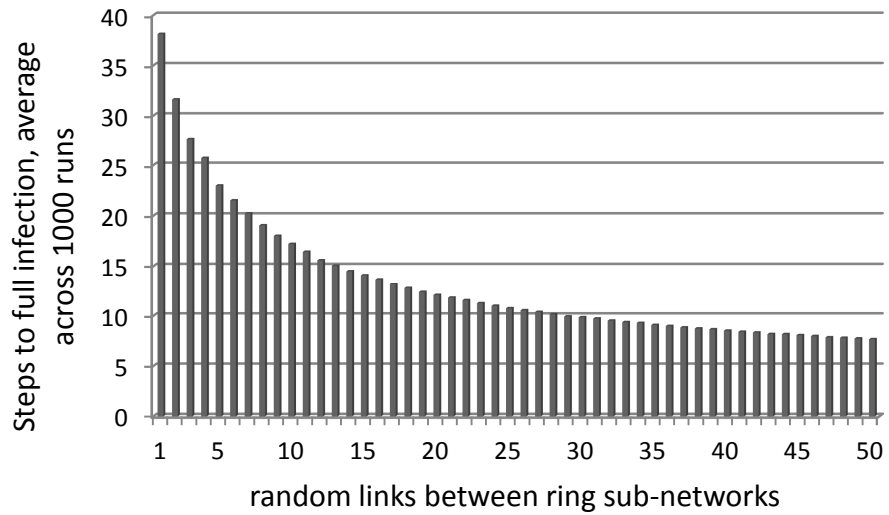


Decreasing homophily: Average time to total infection with increasing links between total sub-networks

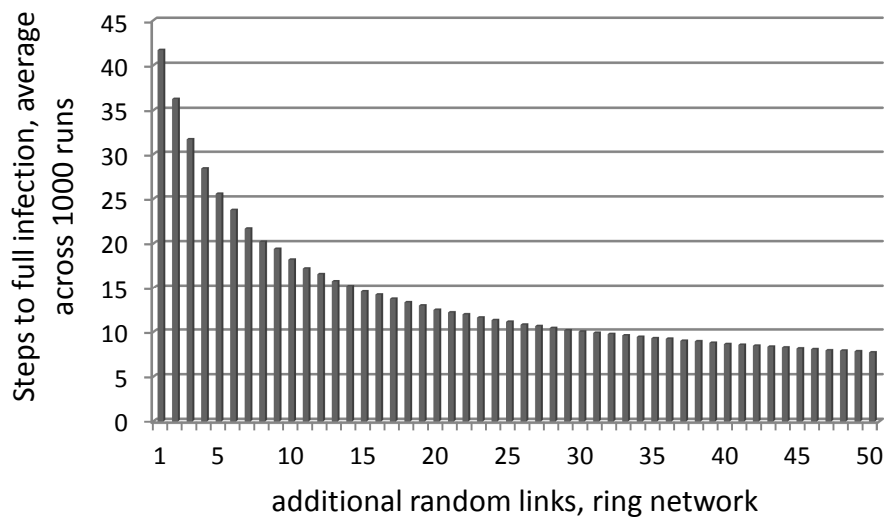


Without homophily: Average time to total infection with additional links within a non-homophilous total network

Ring Networks

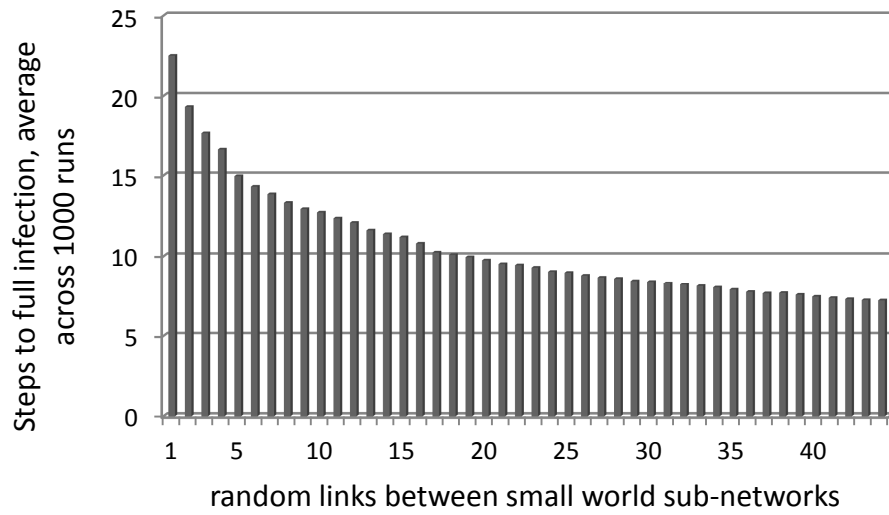


Decreasing homophily: Average time to total infection with increasing links between ring sub-networks

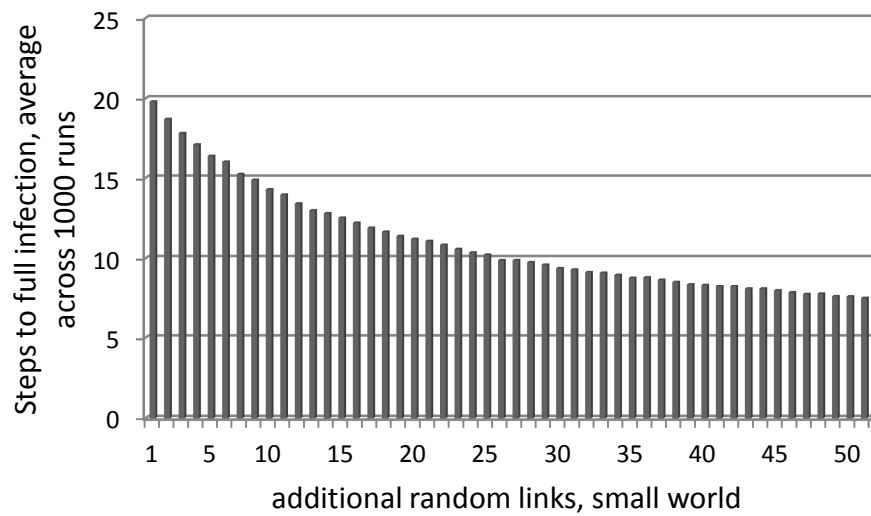


Average time to total infection with increasing links within a non-homophilous ring network

Small world

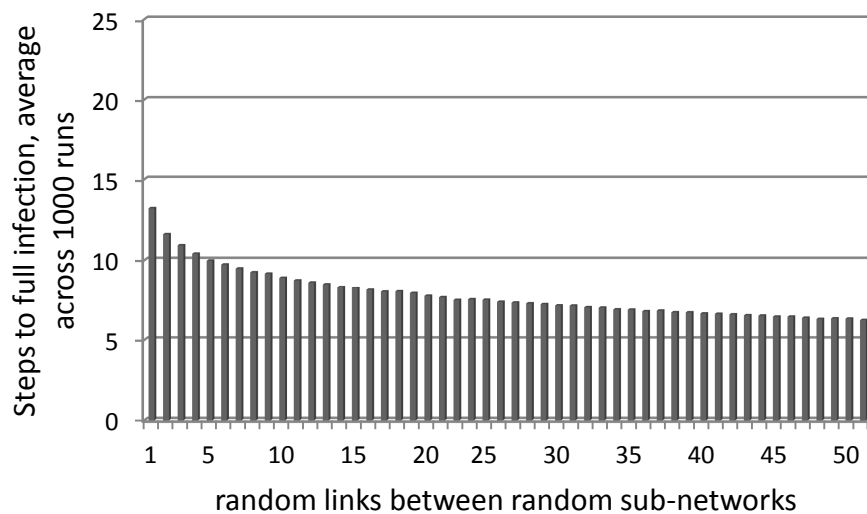


Decreasing homophily: Average time to infection with increasing random links between small world sub-networks.

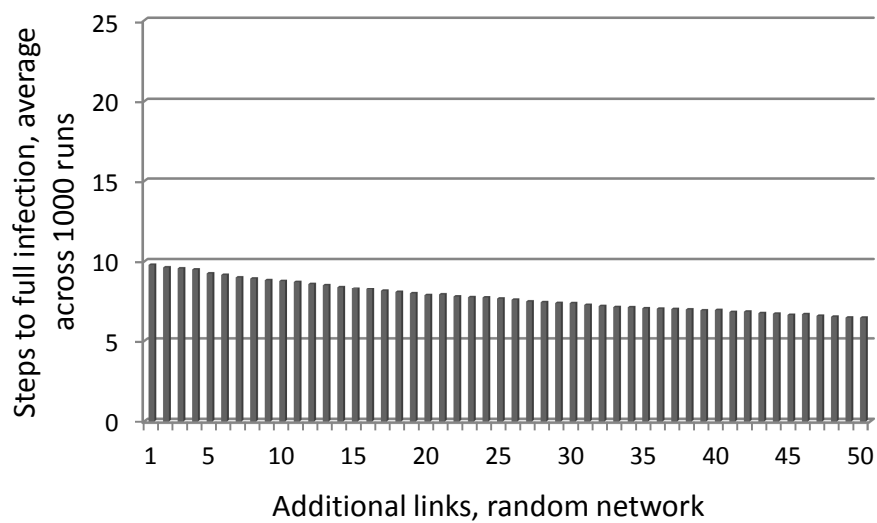


Without homophily: Average time to infection with additional links within non-homophilous small world

Random

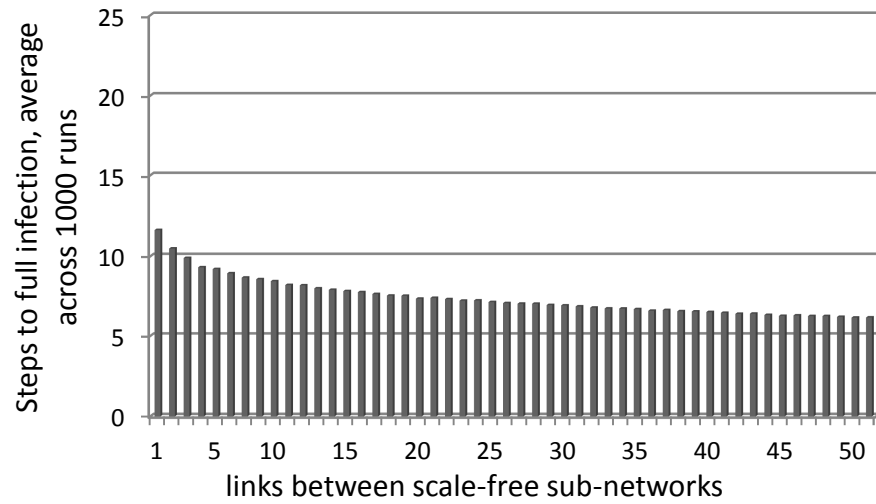


Decreasing homophily: Average time to infection with random links between random sub-networks

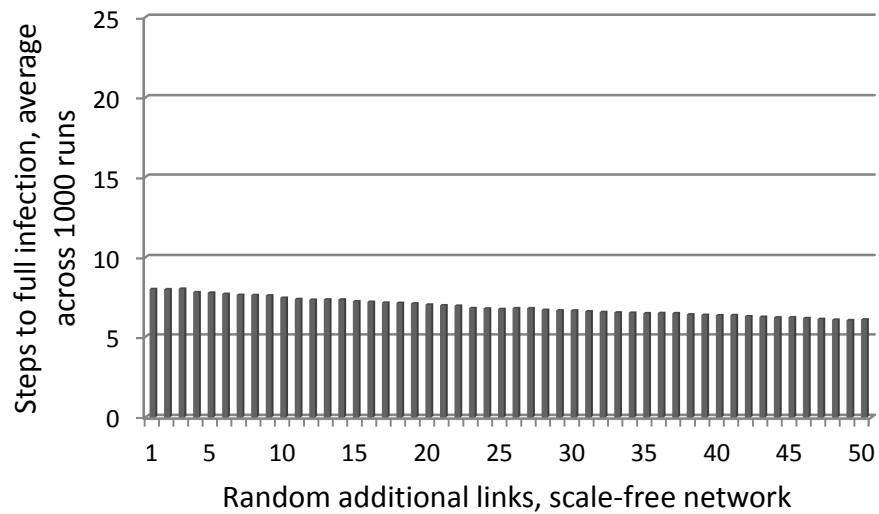


Without homophily: Average time to infection with additional links within a non-homophilous random network

Scale-free

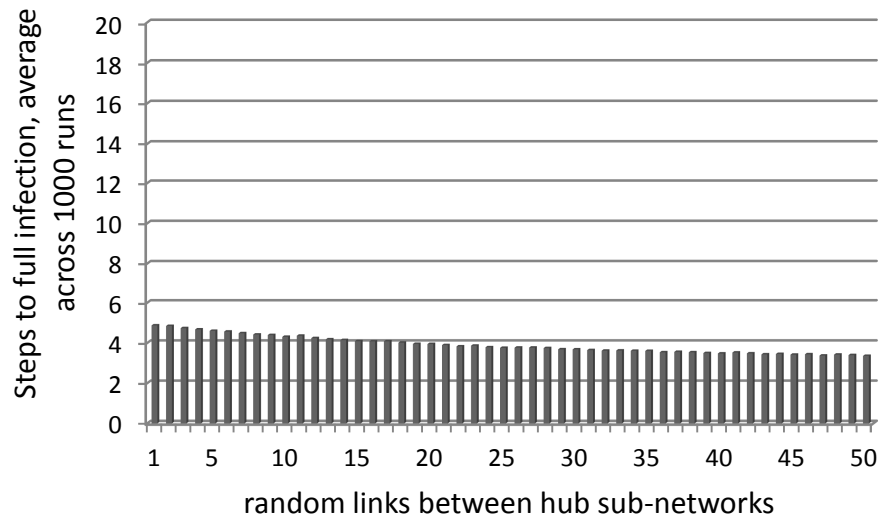


Decreasing homophily: Average time to infection with random links between scale-free networks.

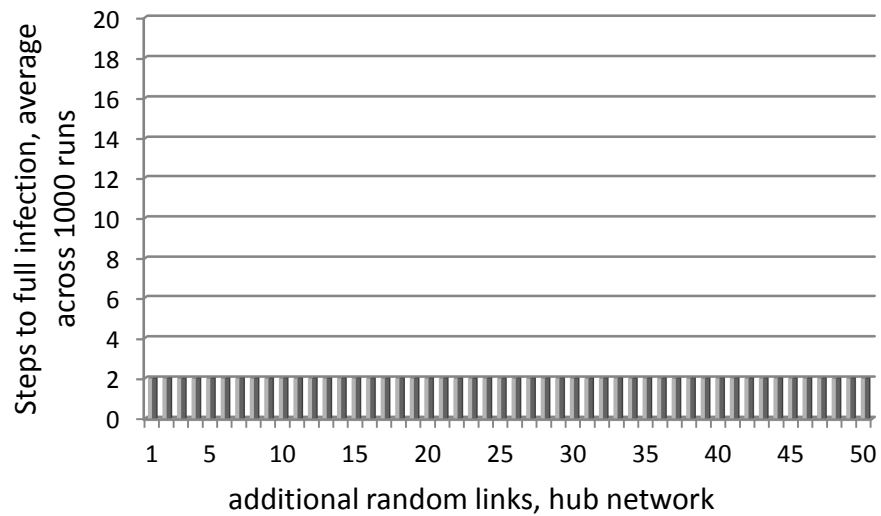


Without homophily: Average time to infection with additional links within a non-homophilous scale-free network.

Hubs

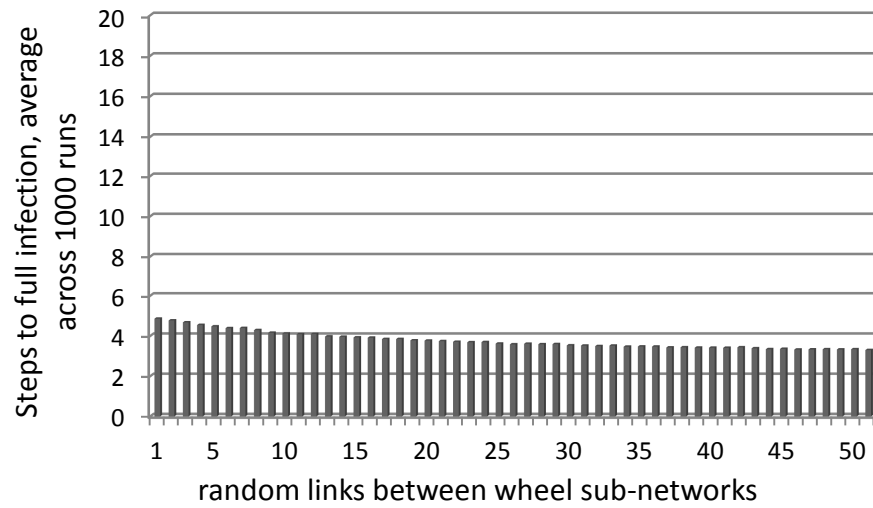


Decreasing homophily: Average time to infection with random linkages between hub sub-networks

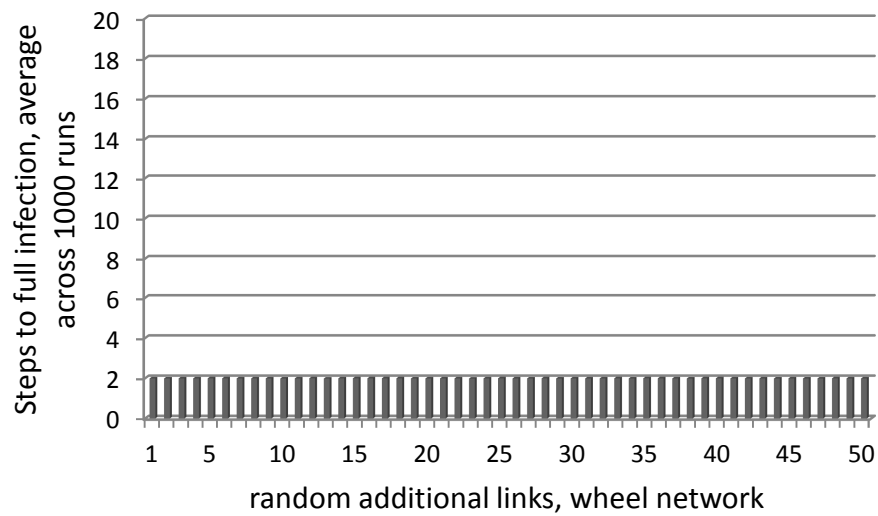


Without homophily: Average time to infection with additional random links within a single non-homophilous hub network

Wheels



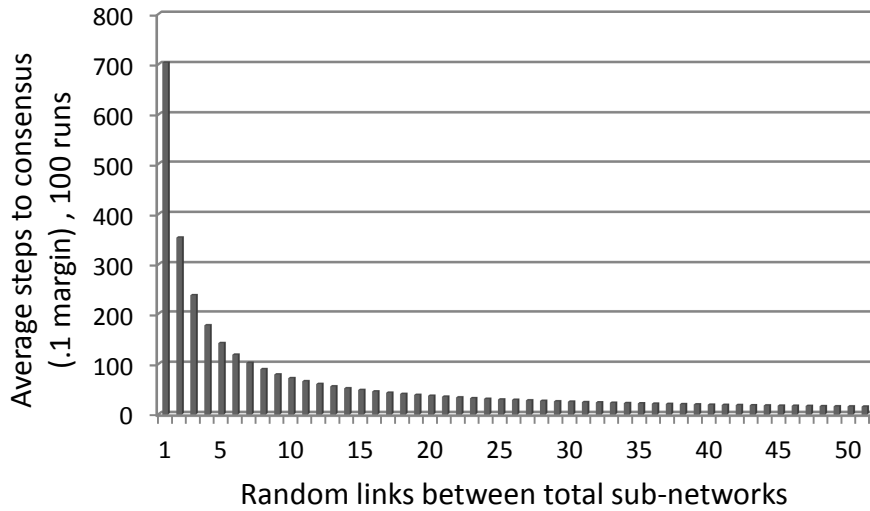
Decreasing homophily: average time to infection with random links between wheel sub-networks



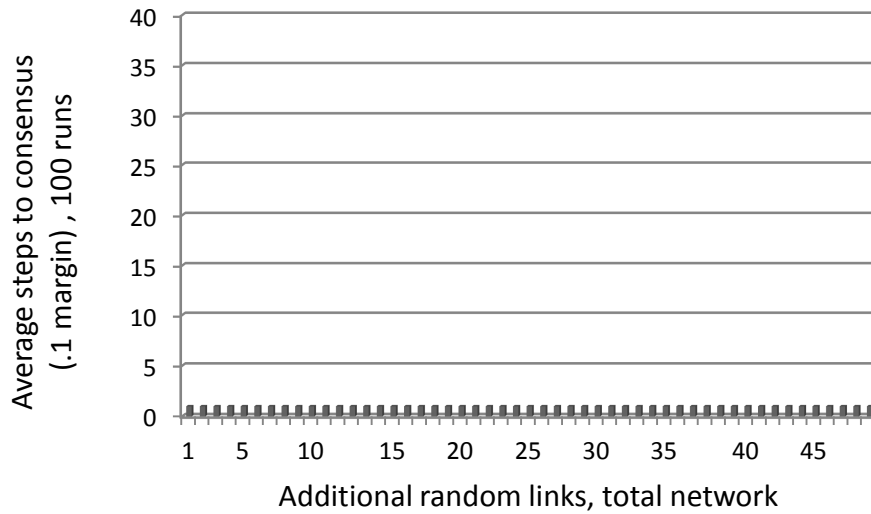
Without homophily: time to infection with additional random links within a non-homophilous wheel

B2. Comparison Graphs for Belief Dynamics

Total networks

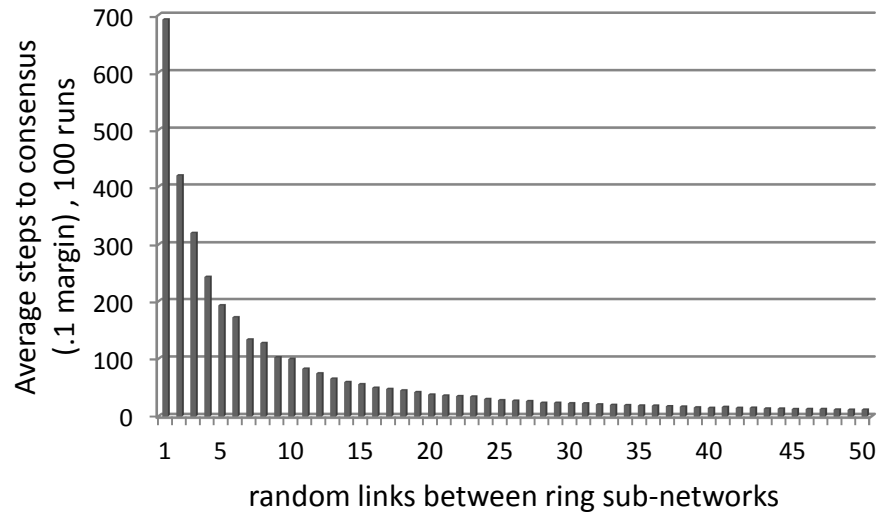


Decreasing homophily: Average steps to belief consensus with increasing random linkages between total sub-networks

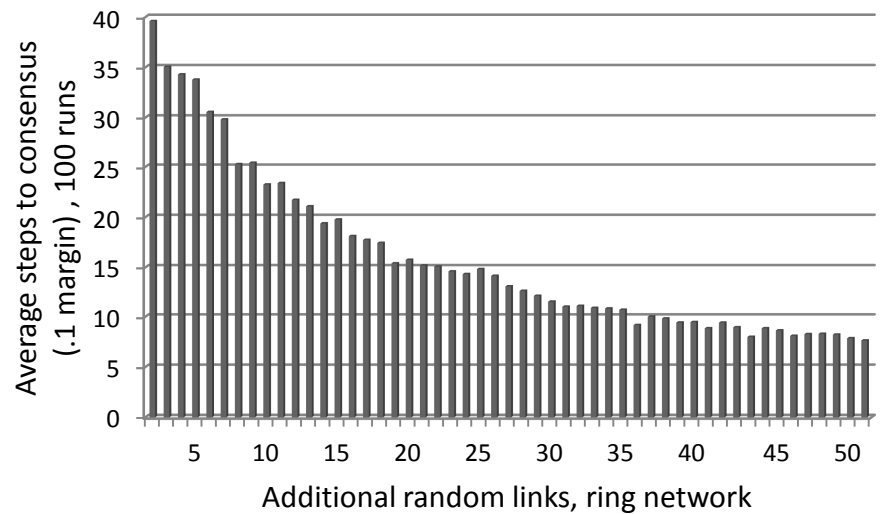


Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous total network

Ring networks

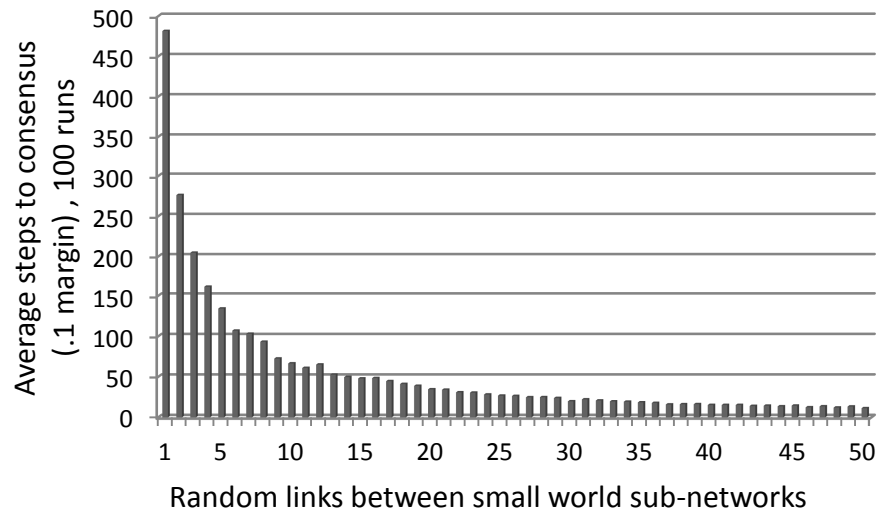


Decreasing homophily: Average steps to belief consensus with increasing random linkages between ring sub-networks

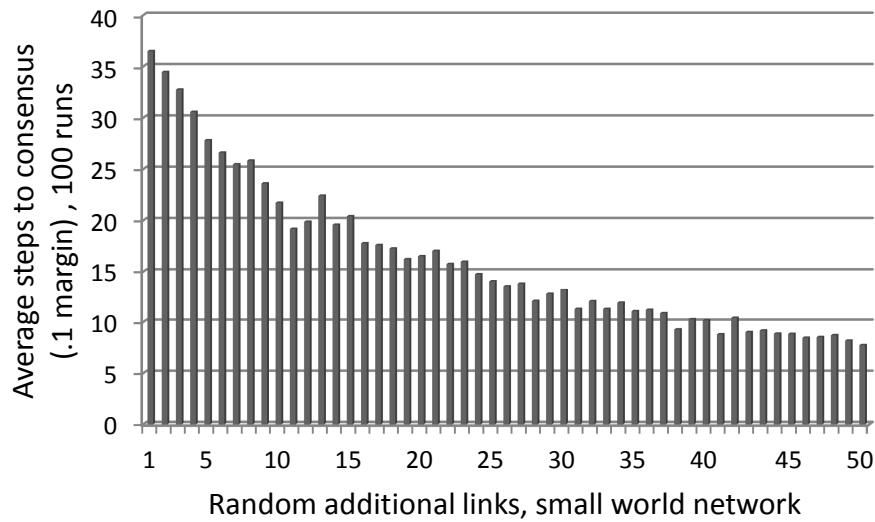


Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous ring network

Small world

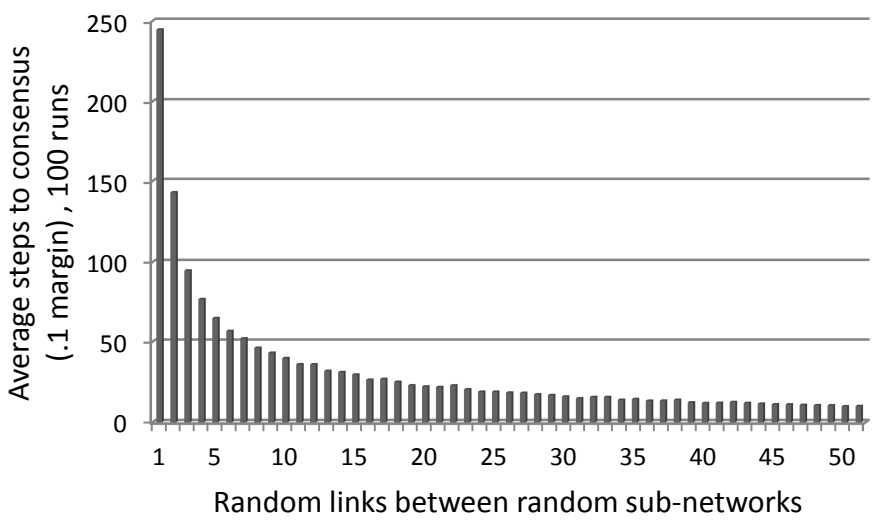


Decreasing homophily: Average steps to belief consensus with increasing random linkages between small world sub-networks

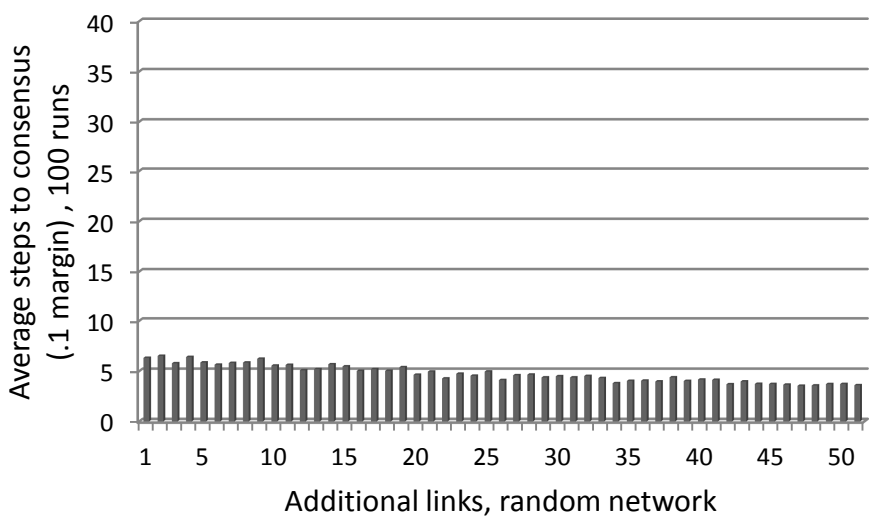


Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous small world network

Random

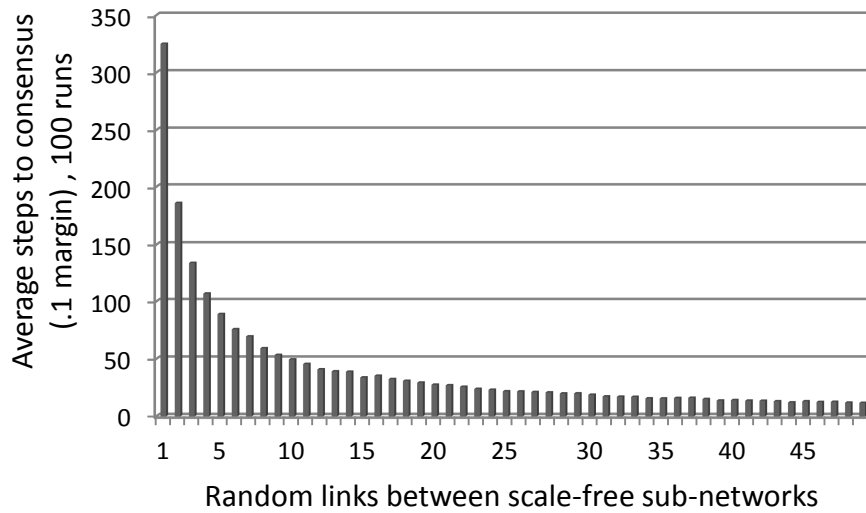


Decreasing homophily: Average steps to belief consensus with increasing random linkages between random sub-networks

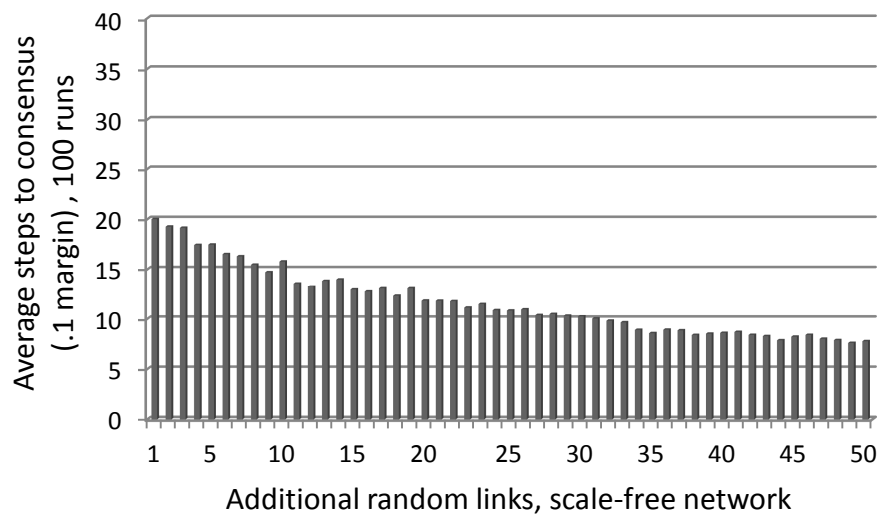


Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous random network

Scale-free

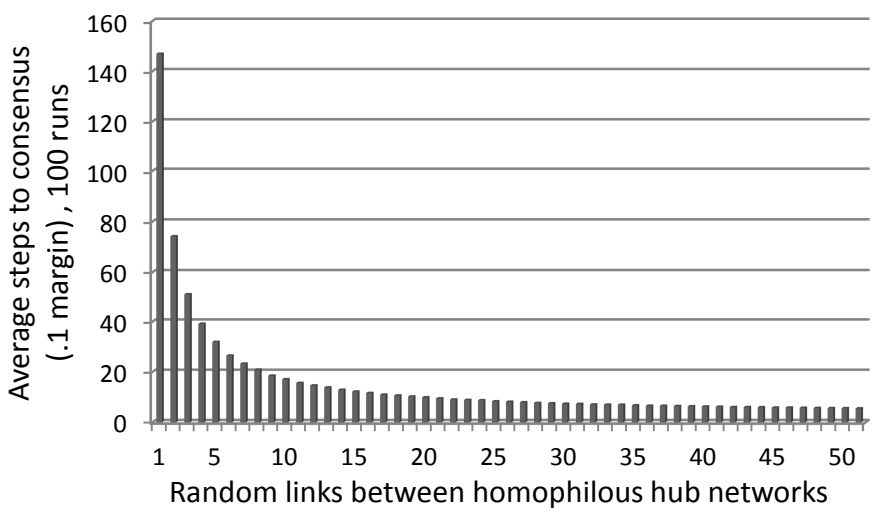


Decreasing homophily: Average steps to belief consensus with increasing random linkages between scale-free sub-networks

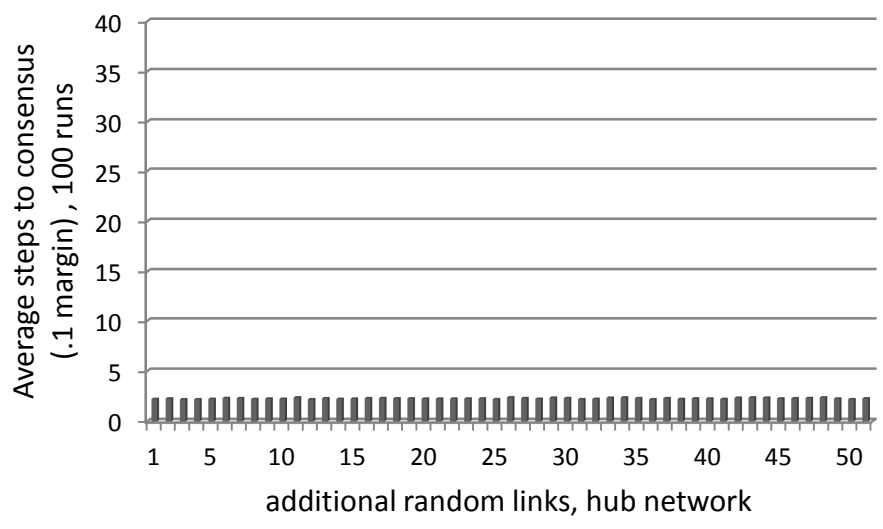


Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous scale-free network

Hubs

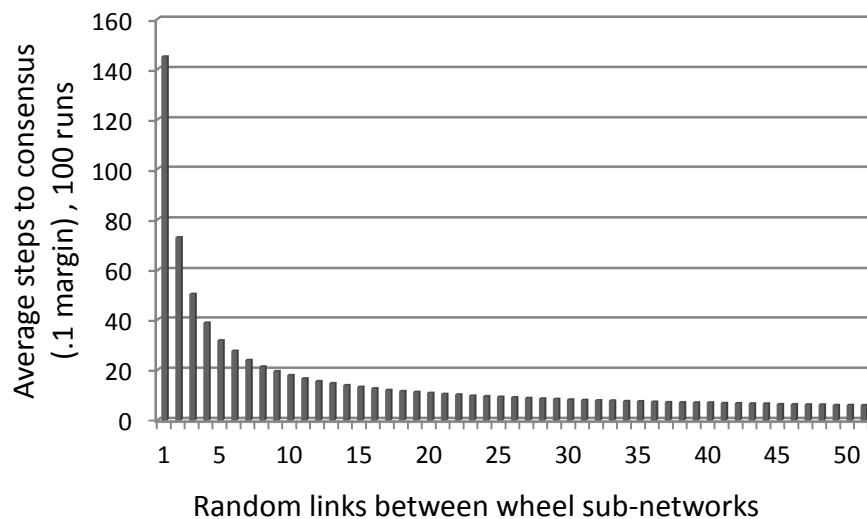


Decreasing homophily: Average steps to belief consensus with increasing random linkages between hub sub-networks

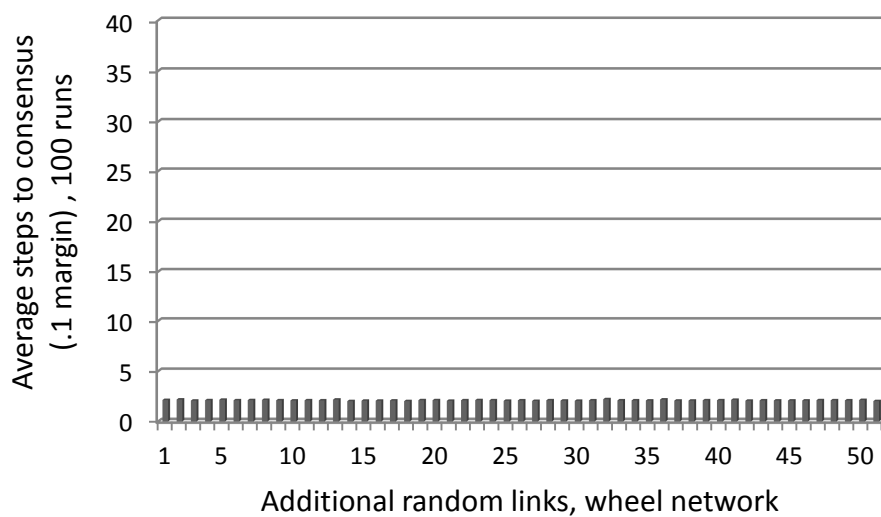


Without homophily: Average steps to belief consensus with increasing random linkages within a non-homophilous hub network

Wheels



Decreasing homophily: Average steps to belief consensus with increasing random linkages between wheel sub-networks



Without homophily: Average steps to belief consensus with random links within a non-homophilous wheel network