

Table S2. SAOM model parameter values, meta-analysis and post-hoc goodness-of-fit test results

Final models were run with number of subphases in phase 2, nsub=6, and number of runs in phase 3, n3=6000
 For good model fit, need tconv.max < 0.25, and 4x post-hoc GOF tests p > 0.01

(a) Parameter values and meta-analysis

Source colony	Treatment	Groups	Overall fit			Degree act + pop			Jaccard similarity			from.w.ind		Boldness ego & alt		Bold linear		Bold quadratic		Average alter effect	
			tconv.max	Density Mean	s.e.	Mean	s.e.	Mean	s.e.	Mean	s.e.	Mean	s.e.	Mean	s.e.	Mean	s.e.	Mean	s.e.	Mean	s.e.
	1 all bold	3	0.0816	0.3313		0.2781	-0.2203	0.0409	2.5424	0.5388	0.1196	0.0478	-0.0816	0.0401	-1.2921	0.1922	0.4914	0.3144	1.0681	0.504	
	2 all bold	2	0.0778	-0.9900		0.2079	-0.0772	0.03	4.4013	0.4171	0.029	0.0145	0.0079	0.0469	-1.4076	0.261	0.3874	0.3535	0.4872	0.8307	
	1 keystone	4	0.1262	-0.2240		0.1981	-0.1449	0.0289	3.0195	0.3283	0.0756	0.0159	0.0809	0.0459	-2.1259	0.2189	1.0814	0.1866	0.0252	0.5894	
	2 keystone	4	0.107	0.1910		0.3371	-0.2291	0.0454	3.484	0.4199	0.1135	0.0297	0.0853	0.0466	-1.8654	0.3848	0.5062	0.1088	-1.2969	2.1981	
	3 keystone	3	0.1157	0.0725		0.2889	-0.1855	0.0364	3.2216	0.4938	0.0918	0.029	-0.0171	0.0481	-2.4788	0.3134	1.2565	0.2426	0.9325	0.7006	
	1 all shy	3	0.0939	-0.2699		0.2241	-0.1423	0.0307	3.4944	0.4482	0.0661	0.0246	0.0304	0.0429	-2.3475	0.3039	1.2662	0.2513	0.8995	0.4702	
	2 all shy	3	0.0874	-0.2345		0.2094	-0.1734	0.0304	3.7606	0.3244	0.0824	0.0205	-0.0041	0.0703	-3.6575	0.4952	1.5912	0.3226	0.6886	1.0723	
	3 all shy	2	0.0796	-0.2190		0.2975	-0.1591	0.0445	3.1215	0.5017	0.0866	0.0364	0.0011	0.0698	-3.506	0.4798	1.7168	0.3232	0.7411	0.8996	
Mean & s.e., normality assumption					-0.2063	0.1379	-0.16	0.016	3.4278	0.1762	0.0735	0.0108	0.0126	0.0212	-2.2516	0.2699	1.0191	0.1619	0.7118	0.2416	
IWLS modification of Snijders & Baerveldt (2003)					-0.2031	0.1444	-0.1607	0.017	3.4229	0.1909	0.073	0.0104	0.0126	0.0209	-2.2664	0.3001	1.0233	0.1775	0.7118	0.164	
two-sided p (normality)					0.178		< 0.001		< 0.001		< 0.001		0.57		< 0.001		< 0.001		0.022		
two-sided p (IWLS)					0.203		< 0.001		< 0.001		< 0.001		0.566		< 0.001		< 0.001		0.003		

(b) Goodness of fit test results

Monte Carlo Mahalanobis distance test p-values
 One tailed test used (i.e. estimated probability of greater distance than observation).
 Calculated joint MHD

Boldness does not have an effect on the likelihood of forming (or avoiding) ties with other spiders

Social interactions increase boldness, on average

Source colony	Treatment	Groups	Outdegree Distribution		Geodesic Distribution		Triad Census		Behavior Distribution	
			Joint MHD	p	Joint MHD	p	Joint MHD	p	Joint MHD	p
	1 all bold	3	91.52	0.893	73.41	0.884	54.07	0.996	153.54	1
	2 all bold	2	498.07	0.281	132.07	0.694	121.59	0.991	142.3	1
	1 keystone	4	912.77	0.055	195.09	0.555	238.41	0.962	90.3	1
	2 keystone	4	3418.98	0.242	119.28	0.025	195.69	0.972	163.1	0.054
	3 keystone	3	253.42	0.203	110.26	0.134	78.97	0.99	99.4	1
	1 all shy	3	205.08	0.334	91.56	0.851	59.26	0.997	75.28	1
	2 all shy	3	1136.37	0.108	134.61	0.012	113.46	0.959	107.36	1
	3 all shy	2	308.55	0.089	86.46	0.978	70.53	0.998	67.55	1