Electronic supplementary material:

Social network dynamics: the importance of distinguishing between heterogeneous and homogeneous changes

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Additional analyses of the performance of the bootstrap and the randomization test

Additional analyses were performed to confirm that the differences in the performance of the bootstrap and the randomization test reported in the main text do not strongly depend on specific properties of the input network that we used. To this end we repeated the analyses described in the main text using artificially created networks. We used Latin hypercube sampling to investigate how varying network sizes and structures in combination with homogeneous and heterogeneous changes affect the performance of the bootstrap and the randomization tests. Latin hypercube sampling is a type of stratified Monte Carlo sampling that explores parameter space more efficiently than random sampling procedures (Seaholm et al. 1988; Rushton et al. 2000)

We conducted two separate analyses. The first analysis focused on investigating the effects of varying network structures in combination with homogeneous changes. The values of the following parameters were varied during Latin hypercube sampling: (1) number of individuals n, (2) network heterogeneity h, (3) mean interaction rate m and (4) homogeneous change q. The second analysis extends the first one by including heterogeneous changes. Thus, in contrast to the analysis described in the main text, the second analysis included combinations of homogeneous and heterogeneous changes. Accordingly the values of the following parameters were varied: (1) number of individuals n, (2) network heterogeneity h, (3) mean interaction rate m, (4) homogeneous change q and (5) heterogeneous change p. Table 1 gives the ranges in which these parameters were varied in the two analyses.

Table 1: Ranges in which varied parameters were sampled.

Parameter	Range in analysis 1	Range in analysis 2
Number of individuals n	10 - 100	10 - 100
Network heterogeneity h	0 - 10	0 - 10
Mean interaction rate m	1 - 10	1 - 10
Heterogeneous change p	0	0 – 0.5
Homogeneous change q	0 – 0.5	0 – 0.5

Each set of baseline interaction rates a_x was normalized so that the mean of all interaction rates equalled the predefined mean rate m. Modified interaction rates a_y were generated by simulating homogeneous and heterogeneous changes as described in the main text. In addition, we simulated observed interactions o_x and o_y and constructed networks following the same procedure as described in the main text. Finally, the bootstrap and the randomization test were applied to each pair of generated networks to identify changes in mean degree, global clustering coefficient and network entropy.

To investigate how network properties in combination with homogeneous and heterogeneous changes influence the performance of the statistical tests, we applied classification tree analysis (De'ath and Fabricius 2000). This analysis hierarchically splits the data set into subcategories in a way that minimizes the variance of the response variable in the generated subsets. In the analyses we conducted, the response variables were indicators of whether a test revealed a significant result (where a significant result was coded as 1 and a non-significant result was coded as 0). Predictor variables were the parameters that were varied in Latin hypercube sampling (h, m and q in analysis 1 and h, m, p and q in analysis 2). The Graphical output of this analysis helped us to visualize how basic effects and interactions among predictor variables affect the probability to obtain significant test results.

Results of the first analysis (which only included homogenous but not heterogeneous changes) confirmed that the bootstrap test is sensitive to homogeneous changes when testing for changes in mean degree, global clustering coefficient and network entropy. The respective classification trees, shown in figure S1, illustrate that the probability of obtaining significant results increases with increasing homogeneous changes q (i.e. per cent decrease in interaction rates across all dyads). In addition, the classification trees indicate that an increase in number of individuals (n) tends to increase the probability

of obtaining significant results. Classification tree analysis of the randomization tests revealed single node trees, which indicate that none of the used predictors had an important influence on the probability to obtain significant results. Across the whole data set the probability of obtaining significant results for changes in mean degree was 0.044, 0.049 for changes in global clustering coefficient and 0.051 for changes in network entropy. These probabilities are in agreement with the expected Type I error rate of 0.05, which confirms that the randomization test is insensitive to homogeneous changes.

Results of the second analysis (which included homogenous and heterogeneous changes) confirmed that both the bootstrap and the randomization test were able to detect heterogeneous changes. The respective classification trees for the bootstrap and the randomization test are shown in figure S2 and S3, respectively. In all these trees the probability of obtaining significant results increases with increasing heterogeneous changes p (i.e. the per cent relationships terminated) and both tests achieved comparable performance to detect these changes. In addition, the classification tree analysis revealed interaction effects with other predictor variables. Importantly, homogeneous changes (q) appeared only in classification trees of the bootstrap test but not in the trees of the randomization test.

(a) Mean degree
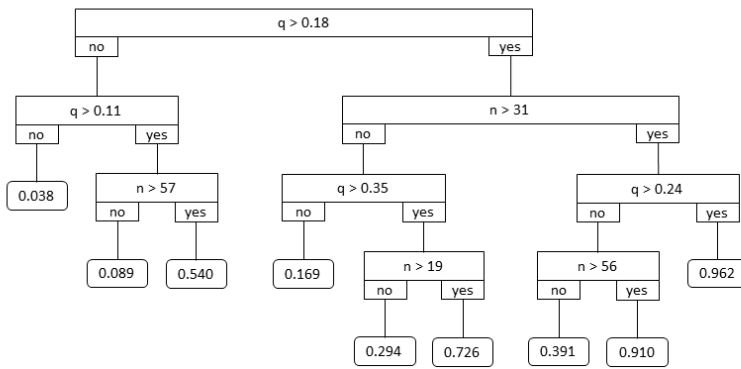
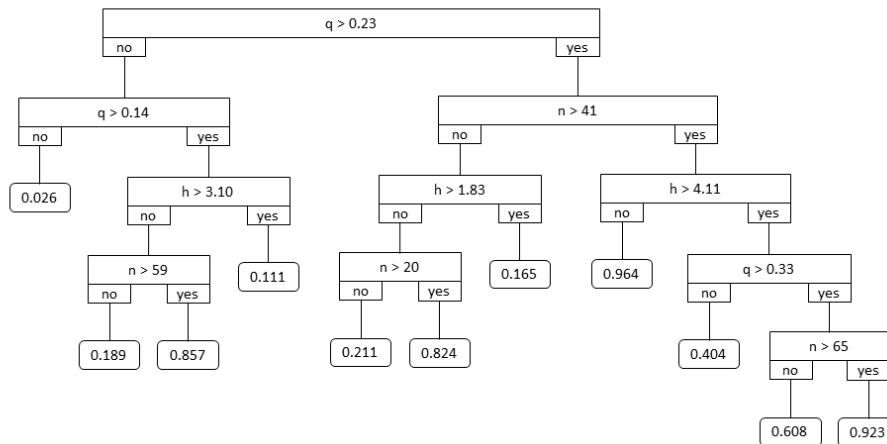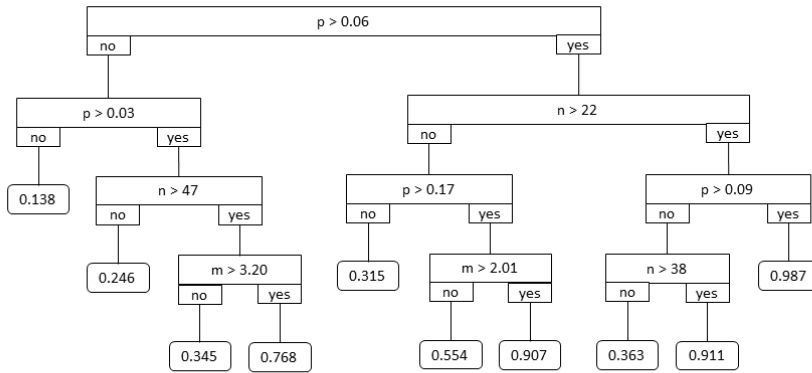(b) Global clustering coefficient
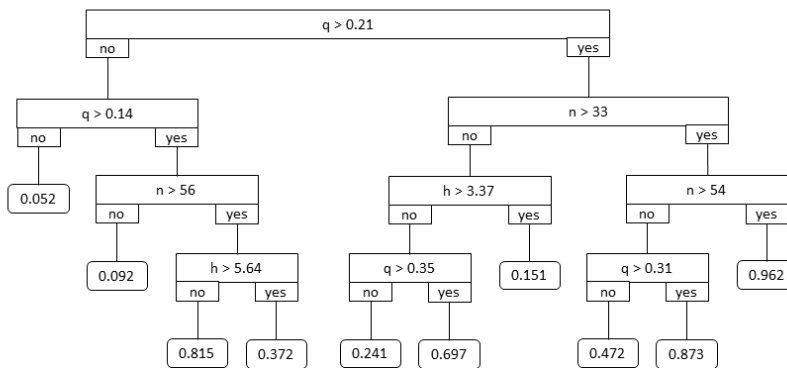
(c) Network entropy

Figure S1: Classification trees for results of the bootstrap test from analysis 1 (which only includes homogenous but not heterogeneous changes) for mean degree (a), global clustering coefficient (b) and network entropy (c). Internal nodes describe branching points where the data set is split into two subsets according to the value of the labelled predictor variable (q refers to homogenous changes, i.e. the per cent decrease in interaction rates, h refers to network heterogeneity; and n refers to number of individuals). Numerical values of the leaves indicate proportions of significant results generated by the bootstrap test in the respective subset of the data set.

(a) Mean degree

p > 0.06 — no / yes

p > 0.03 — no / yes | n > 22 — no / yes

0.138 | n > 47 — no / yes | p > 0.17 — no / yes | p > 0.09 — no / yes

0.246 | m > 3.20 — no / yes | 0.315 | m > 2.01 — no / yes | n > 38 — no / yes | 0.987

0.345 | 0.768 | 0.554 | 0.907 | 0.363 | 0.911

(b) Global clustering coefficient

p > 0.06 — no / yes

p > 0.03 — no / yes | n > 27 — no / yes

0.141 | 0.428 | p > 0.24 — no / yes | p > 0.12 — no / yes

m > 4.98 — no / yes | m > 2.10 — no / yes | n > 52 — no / yes | 0.980

0.262 | 0.561 | 0.381 | 0.809 | 0.658 | 0.926

(c) Network entropy

p > 0.05 — no / yes

p > 0.01 — no / yes | n > 21 — no / yes

0.090 | n > 52 — no / yes | p > 0.17 — no / yes | 0.983

0.272 | m > 4.98 — no / yes | 0.500 | m > 2.01 — no / yes

0.446 | 0.854 | 0.634 | 0.960

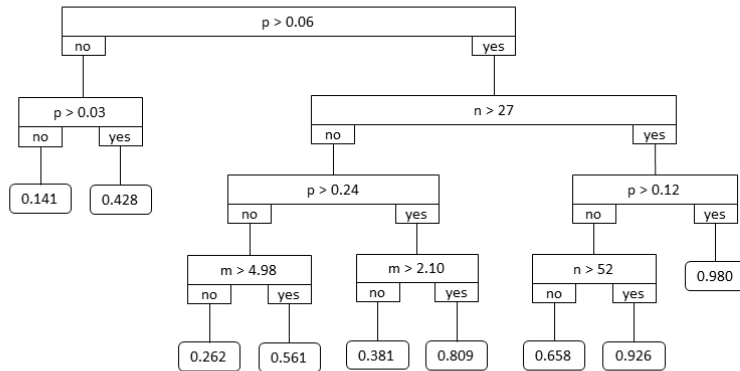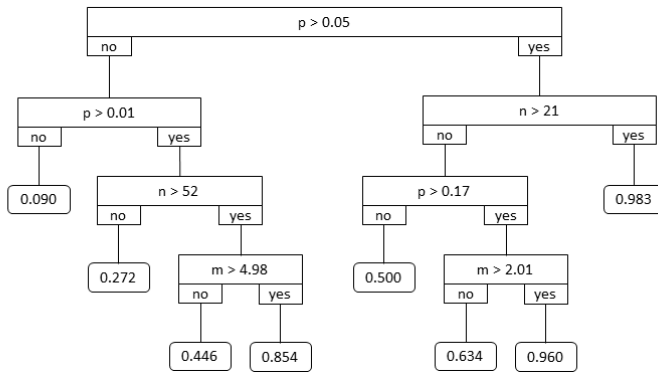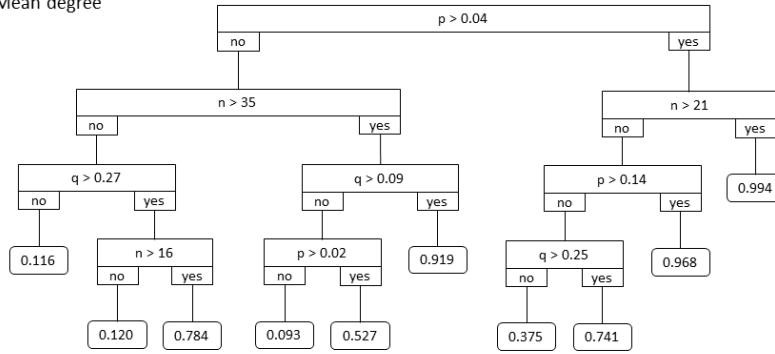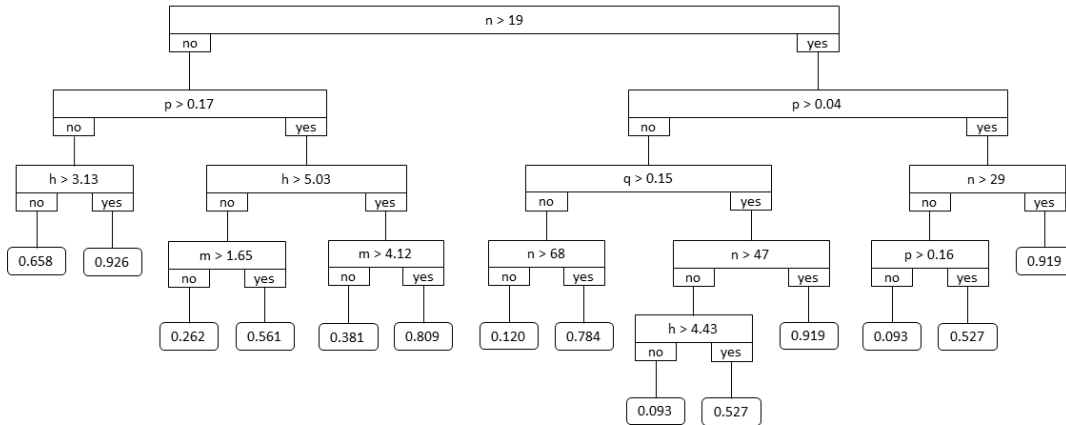**Figure S2:** Classification trees for results of the bootstrap test from analysis 2 (which includes homogeneous and heterogeneous changes) for mean degree (a), global clustering coefficient (b) and network entropy (c). Internal nodes describe branching points where the data set is split into two subsets according to the value of the labelled predictor variable (p refers to heterogeneous changes, i.e. the per cent relationships terminated; q refers to homogenous changes, i.e. the per cent decrease in interaction rates; m refers to mean interaction rate across all dyads; and n refers to number of individuals). Numerical values of the leaves indicate proportions of significant results generated by the bootstrap test in the respective subset of the data set.

(a) Mean degree

p > 0.04
 — no — n > 35
   — no — q > 0.27
     — no — 0.116
     — yes — n > 16
       — no — 0.120
       — yes — 0.784
   — yes — q > 0.09
     — no — p > 0.02
       — no — 0.093
       — yes — 0.527
     — yes — 0.919
 — yes — n > 21
   — no — p > 0.14
     — no — q > 0.25
       — no — 0.375
       — yes — 0.741
     — yes — 0.968
   — yes — 0.994

(b) Global clustering coefficient

n > 19
 — no — p > 0.17
   — no — h > 3.13
     — no — 0.658
     — yes — 0.926
   — yes — h > 5.03
     — no — m > 1.65
       — no — 0.262
       — yes — 0.561
     — yes — m > 4.12
       — no — 0.381
       — yes — 0.809
 — yes — p > 0.04
   — no — q > 0.15
     — no — n > 68
       — no — 0.120
       — yes — 0.784
     — yes — n > 47
       — no — h > 4.43
         — no — 0.093
         — yes — 0.527
       — yes — 0.919
   — yes — n > 29
     — no — p > 0.16
       — no — 0.093
       — yes — 0.527
     — yes — 0.919

(c) Network entropy

p > 0.04
 — no — n > 42
   — no — q > 0.28
     — no — 0.101
     — yes — h > 3.33
       — no — 0.755
       — yes — 0.240
   — yes — q > 0.18
     — no — p > 0.02
       — no — 0.157
       — yes — 0.612
     — yes — 0.922
 — yes — n > 21
   — no — p > 0.17
     — no — p > 0.11
       — no — 0.259
       — yes — 0.559
     — yes — p > 0.26
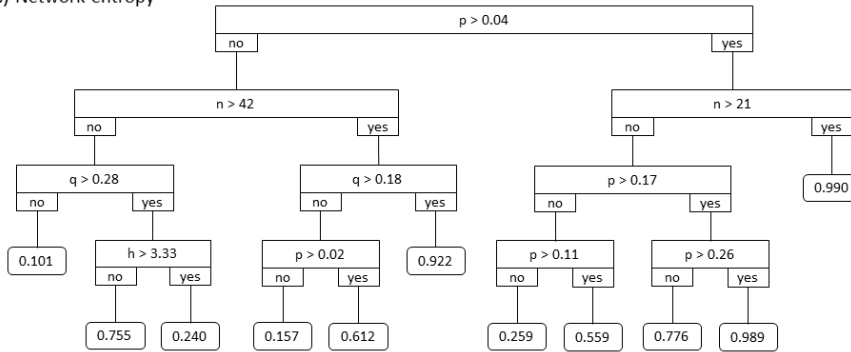   — no — 0.776
       — yes — 0.989
   — yes — 0.990

Figure S3: Classification trees for results of the randomization test from analysis 2 (which includes homogeneous and heterogeneous changes) for mean degree (a), global clustering coefficient (b) and network entropy (c). Internal nodes describe branching points where the data set is split into two subsets according to the value of the labelled predictor variable (p refers to heterogeneous changes, i.e. the per cent relationships terminated; q refers to homogenous changes, i.e. the per cent decrease in interaction rates; h refers to network heterogeneity; m refers to mean interaction rate across all dyads; and n refers to number of individuals). Numerical values of the leaves indicate proportions of significant results generated by the randomization test in the respective subset of the data set.

The effects of homogeneous and heterogeneous changes on weighted clustering coefficients

We extended the analysis described in the main text on the effects of homogeneous and heterogeneous changes on network measures. Specifically we investigated the effects on four measures of weighted clustering coefficients. Similar to the binary measure, the weighted measures aim to capture information about the 'cliquishness' of interactions or associations. Several different versions have been proposed for incorporating edge weights into such measures. Here we used four versions that are implemented in the R package *tnet* (Opsahl 2009), which differ in the way edge weights are used to calculate the value that make up the triplet: arithmetic mean, geometric mean, maximum, and minimum (Opsahl & Panzarasa 2009). Results for all four measures (figure S4) show the same basic pattern that we reported for the binary clustering coefficient (figure 2 b, e); i.e., both simulated homogeneous changes and simulated heterogeneous changes tended to decrease the weighted clustering coefficients. This result highlights the importance performing tests that can distinguish heterogeneous from homogeneous changes, if one seeks to determine whether network patterns change over time or as a result of perturbations.
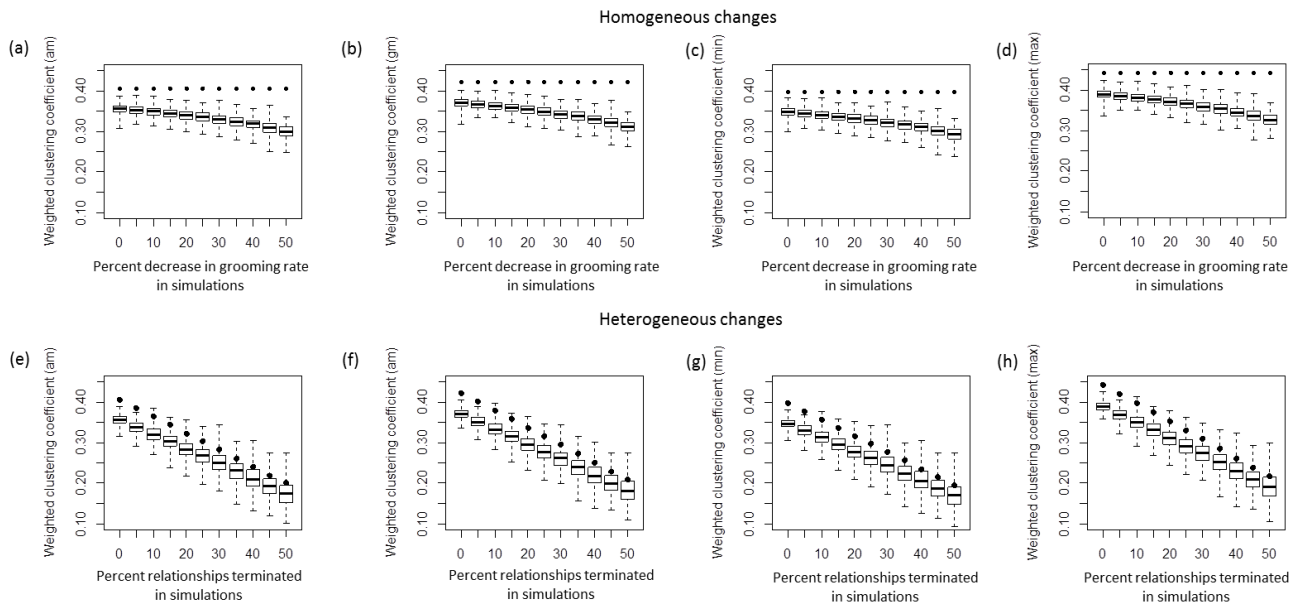

Figure S4: Homogeneous changes (a, b, c, d) and heterogeneous changes (e, f, g, h) can result in similar apparent changes on different versions of global weighted clustering coefficients: arithmetic mean (am), geometric mean (gm), maximum (max), and minimum (min). Dots indicate the mean network measures of networks based on true interaction rates (a_x). Boxplots indicate network measures (max, 75%ile, median, 25%ile, minimum) of networks based on simulated observations of interaction rates (o_x).

References

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