

# Networks in change: how neutral can one be?

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**1§ Neutral change.** The probability with which a speaker acquires a certain linguistic variant out of a number of competing variants equals the relative frequency of that variant in the speaker's neighbourhood, *modulo* a small probability of innovating, uniformly at random, another variant from among all the biologically possible variants.

**2§ Model.** Assume:

- a symmetric, binary, uniplex network of  $N$  speakers
- $C$  competing linguistic variants
- that at each time step one speaker is removed from the network and a new one added
- that the new speaker receives their connections according to a socialization algorithm  $S$  which gives the speaker  $K$  friends in the network
- that the new speaker acquires their linguistic variant according to an adoption algorithm  $A$
- that the adoption algorithm is a neutral one, i.e. corresponds to the characterization of neutral change given above
- i.e., that there is a mutation parameter  $\mu$
- also, that there is a preferentiality parameter  $\sigma$  to control clusterization of network (Figure 1)

**3§ Good behaviour.** A language community is **well-behaved** iff it satisfies dominance, shifting and smoothness:

**Dominance** For most of the time, the language community relaxes into a state in which one variant dominates, so that most or even all speakers use that variant. There is no, or at most little, stable variation.

**Shifting** Upon introduction of an innovation or ‘mutant’, or several of them, a novel linguistic variant can nonetheless begin to spread and eventually penetrate the community; thus, the community may shift from a state of dominance by variant  $r$  to a state of dominance by variant  $r' \neq r$ .

**Smoothness** Such invasions proceed in a (quasi)monotone manner with the frequency of the invading variant increasing, and the frequency of the receding variant decreasing, along a smooth propagation curve, *modulo* stochastic noise.

**4§ Mathematical equivalent of the above.** I’ll explain these if there is time, else insert hand-waving.

For dominance (cf. Lee, Collier, Kobele, Stabler, & Taylor, 2005, 627, eqn. 3),

$$D = \left\langle \frac{C-1}{C} \left( \sum_{r=1}^C x_r(t)^2 - \frac{1}{C} \right) \right\rangle. \quad (1)$$

For shifting ability,

$$S = \left\langle \begin{cases} 1 & \text{if } |\{r = 1, \dots, C : x_r(t) = 1 \text{ for some } t\}| \geq 2 \\ 0 & \text{otherwise} \end{cases} \right\rangle. \quad (2)$$

For smoothness (monotonicity),

$$M_\tau = 1 - \left\langle \sum_{r=1}^C \sqrt{m^+(r, t_0, \tau) m^-(r, t_0, \tau)} \right\rangle / \tau. \quad (3)$$

For overall well-behavedness,

$$W_\tau = DSM_\tau. \quad (4)$$

(Cf. Table 1.)

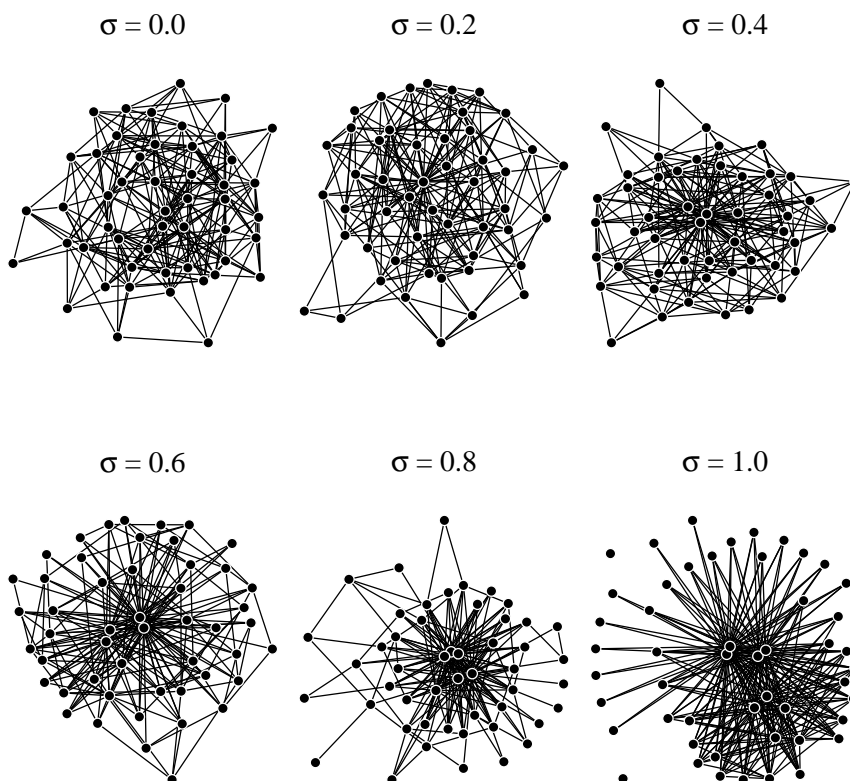
**5§ Centre-mutants.** Let  $q$  denote the probability of a speaker in the central cluster of the network distributing their variant to at least one other speaker during their (the former, not the latter) lifetime. Then it can be shown that

**Theorem 1.** *Suppose that  $\sigma = 1$ ,  $K \leq N - 1$  and  $\mu \leq 1/K$ . Then  $q > 1 - e^{-1} \approx 0.63$ . Moreover, as the ratio  $K/N$  tends to 0 (as the centre of the network becomes smaller and smaller in relation to the whole network)  $q$  tends to 1.*

Thus, *it is always more probable for variants flowing from the centre of the network to be replicated than not to be replicated* if  $\sigma$  is very large (Figure 7). This explains both conservatism and progressivism, and hence the ‘punctuated equilibrium’ sort of (good) behaviour of strongly clusterized communities: if no innovatory variants manage to invade the centre, the centre suppresses any mutations; but if a ‘mutant’ is able to invade, it has a very good chance of propagating.

## References

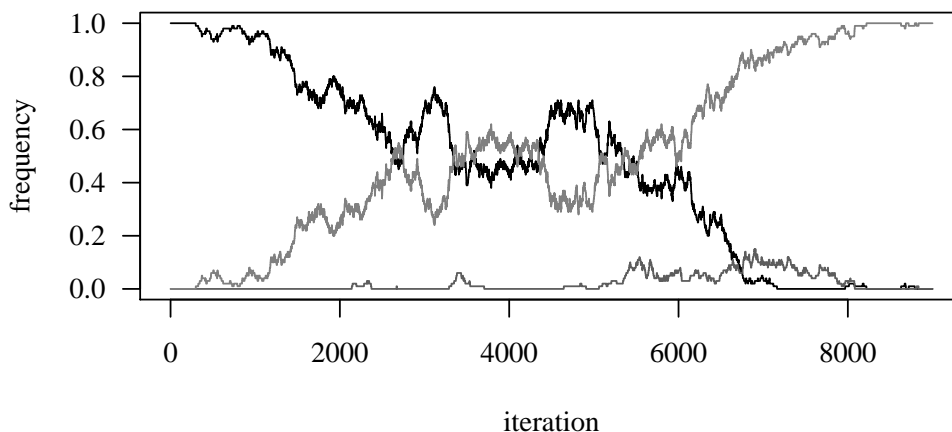
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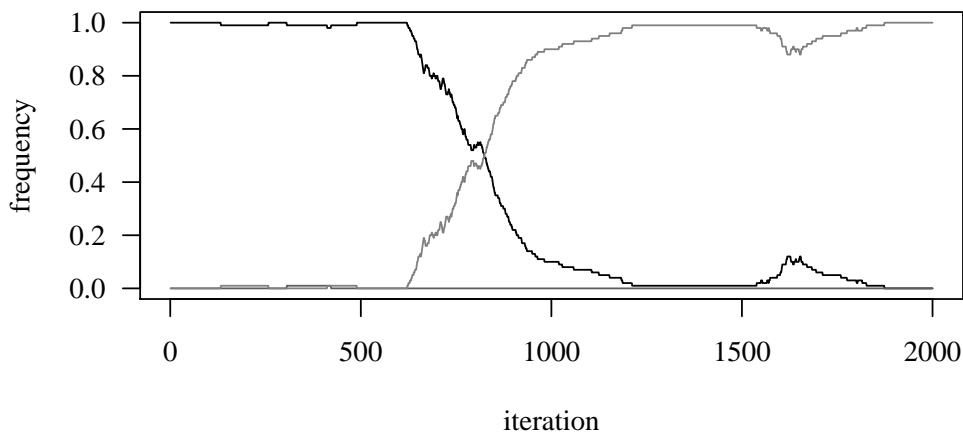
**Figure 1.** Different values of the preferentiality parameter  $\sigma$  lead to networks with different amounts of clusterization. Note that the networks are not static but are constantly rewired over time by the removal and addition of speakers. For these networks,  $N = 50$  and  $K = 5$ .

	$D$	$S$	$M_{10}$	$W_{10}$
Figure 2	0.53	1	0.72	0.38
Figure 3	0.85	1	0.96	0.82

**Table 1.** Dominance ( $D$ ), shifting ( $S$ ), monotonicity ( $M_{10}$ ) and well-behavedness ( $W_{10} = DSM_{10}$ ) for the histories depicted in Figures 2 and 3.

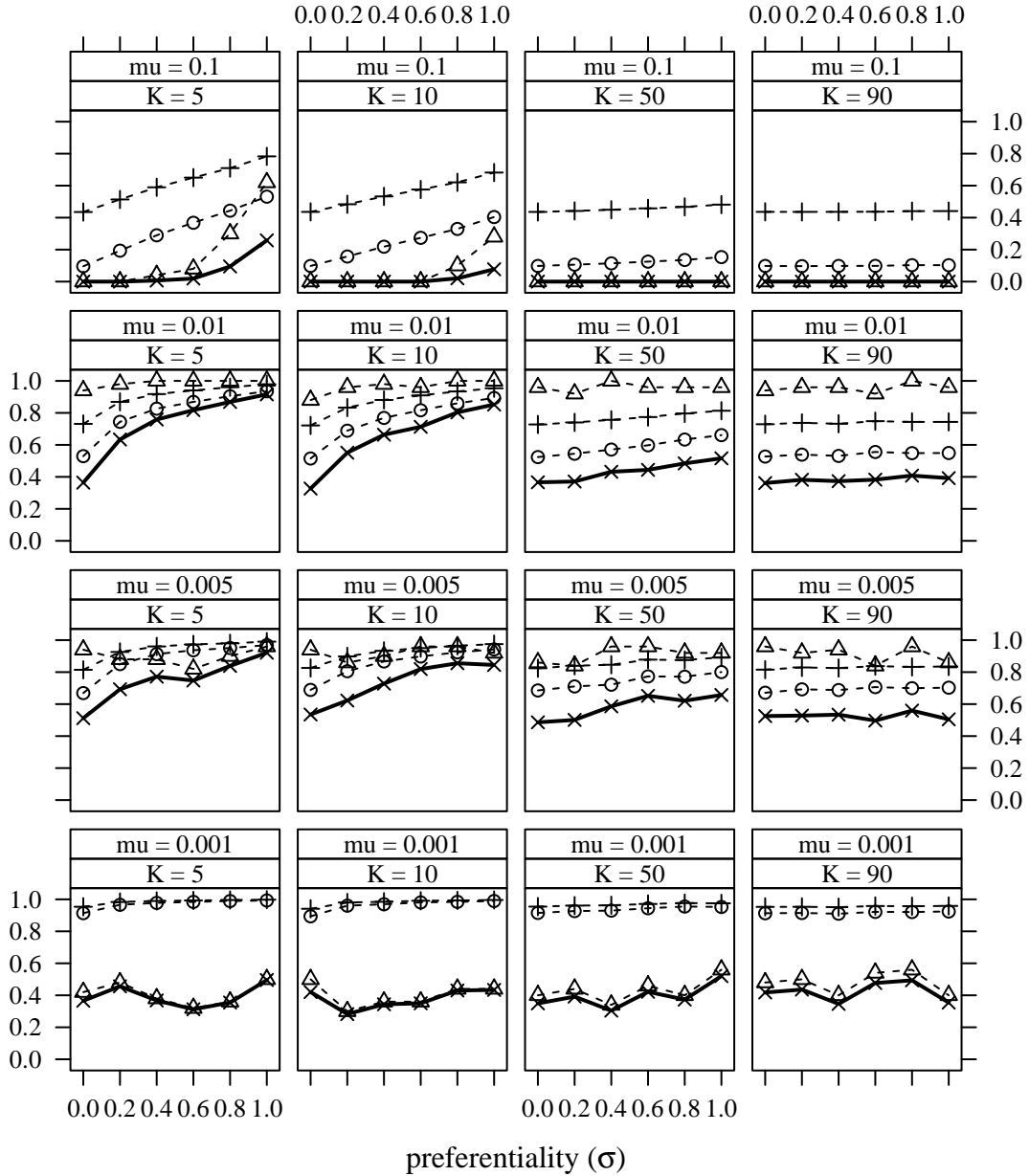


**Figure 2.** Portion of an ill-behaved history that violates dominance and smoothness in a system of three variants. This trajectory was generated with parameter settings  $N = 100$ ,  $K = 10$ ,  $C = 3$ ,  $\mu = 0.005$  and  $\sigma = 0$ .

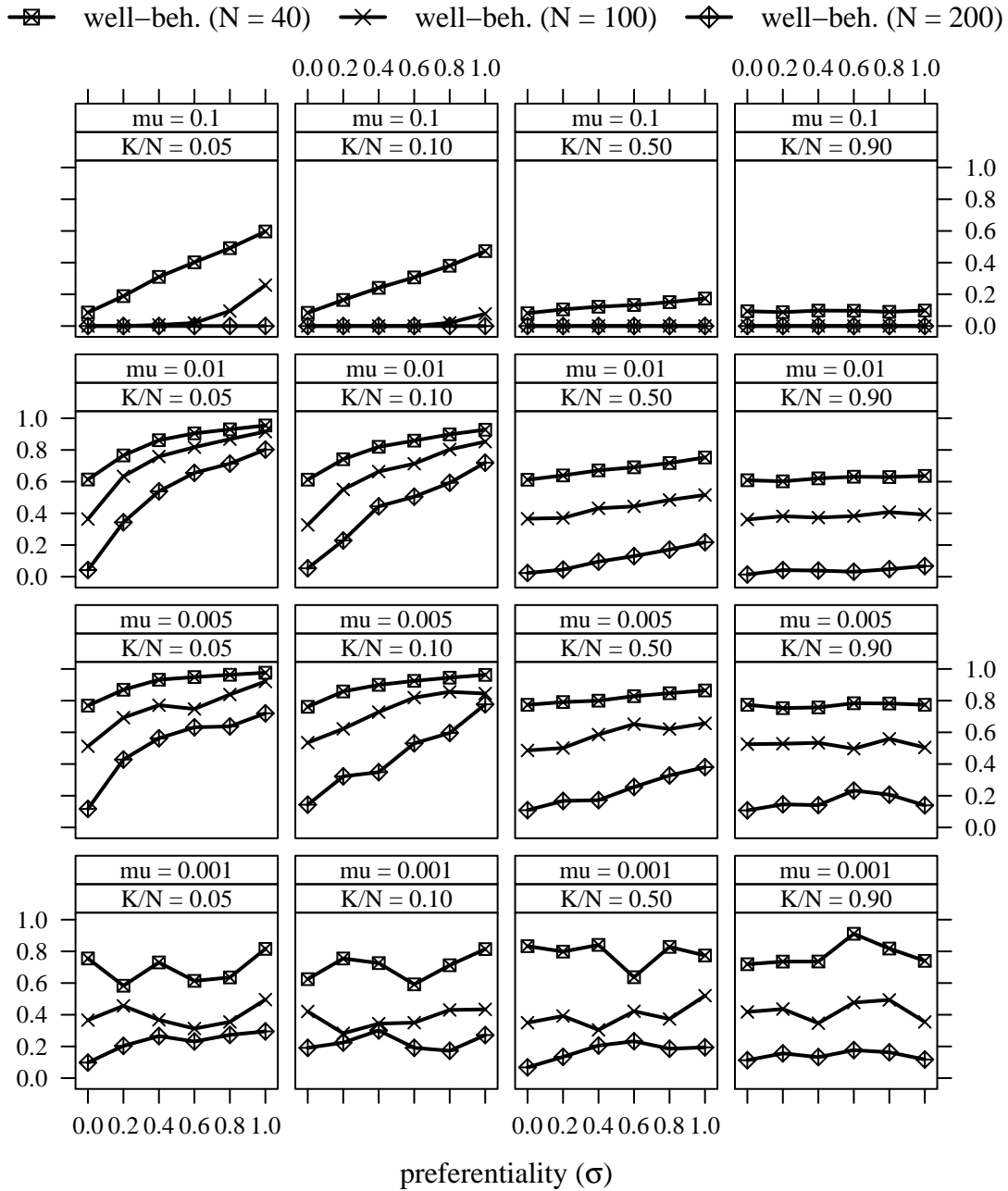


**Figure 3.** Portion of a well-behaved history satisfying dominance, shifting and smoothness. For this simulation,  $N = 100$ ,  $K = 10$ ,  $C = 3$ ,  $\mu = 0.005$  and  $\sigma = 1$ .

-○ dominance -△ shifting -+ monotonicity ✕ well-behavedness

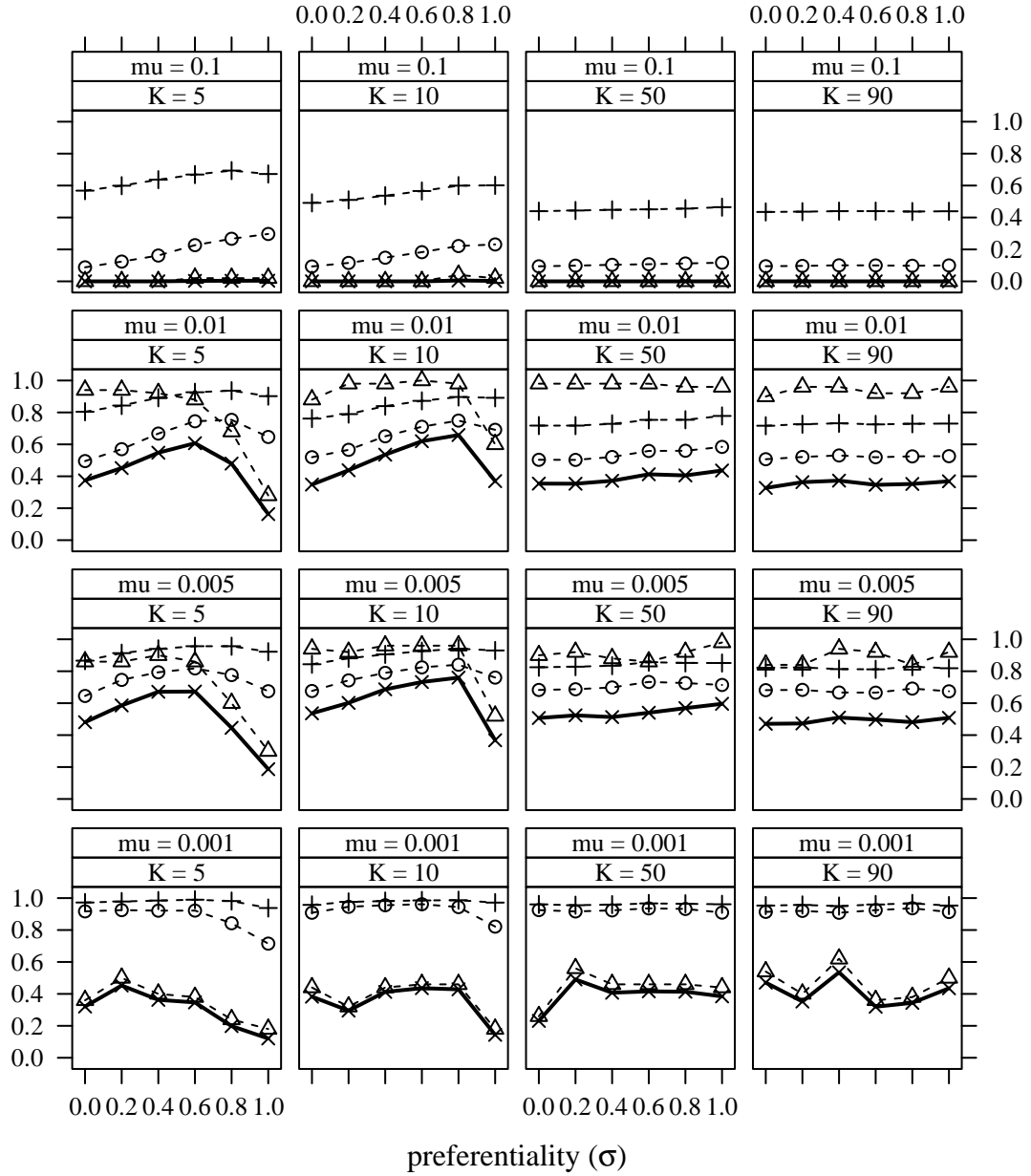


**Figure 4.** Dominance, shifting, monotonicity ( $\tau = 10$ ) and well-behavedness for an ensemble of 50 histories with network size  $N = 100$  and  $C = 3$  variants, for varying values of attachment set size  $K$ , preferentiality  $\sigma$  and mutation rate  $\mu$ . A subset of the parameter space (small  $K$ , large  $\sigma$  and suitable  $\mu$ ) exists where the language community displays well-behaved neutral change.

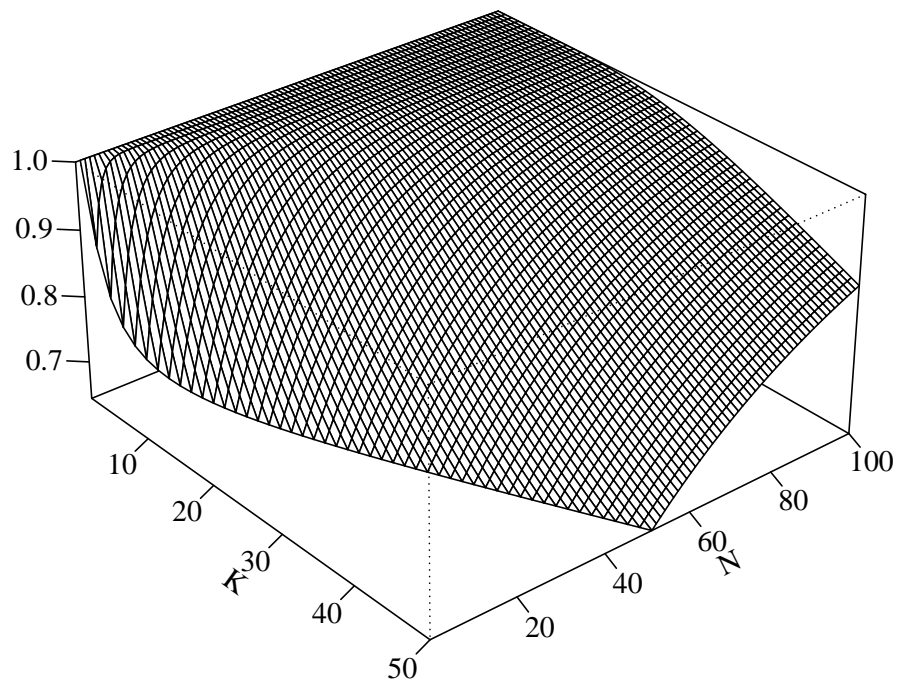


**Figure 5.** Well-behavedness ( $W_{10}$ ) scores for three ensembles of 50 histories each, with network sizes  $N = 40, 100, 200$  and  $C = 3$  variants, for varying values of attachment set size  $K$ , preferentiality  $\sigma$  and mutation rate  $\mu$ . Smaller populations sustain well-behaved neutral change for a wide range of parameter values; for a larger population, well-behaved neutral change is only attested in the strongly clustered (small  $K$ , large  $\sigma$ ) case.

-○ dominance -△ shifting -+ monotonicity ✕ well-behavedness



**Figure 6.** Dominance, shifting, monotonicity ( $\tau = 10$ ) and well-behavedness for the simulation ensemble with rewiring turned off.



**Figure 7.** Probability of successful centre-mutant propagation  $q$  as a function of attachment set size  $K$  and network size  $N$ , for mutation rate  $\mu = 0.001$  and number of competing variants  $C = 100$ .