

EPJ B

Condensed Matter
and Complex Systems

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Eur. Phys. J. B **75**, 373–379 (2010)

DOI: 10.1140/epjb/e2010-00128-0

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Received 21 January 2010 / Received in final form 29 March 2010

Published online 16 April 2010 – © EDP Sciences, Società Italiana di Fisica, Springer-Verlag 2010

Abstract. We introduce a model for the social structure of a two-sex population whose members form heterosexual couples with at most one partner at a time. Individuals can as well remain temporarily single. Partnership is decided on the basis of personal preferences, where members of the opposite sex are ranked according to the predilection of each individual. We distinguish between the network of potential partnership – which is defined by an acceptance threshold in the individual preferences – and the network of realized partnership – which results from dynamical rules for couple breaking and formation. The structural properties of the potential-partnership network are studied, and realized partnership is characterized in terms of the distribution of couple durations.

1 Introduction

It is by now widely accepted that in the modeling of biological, ecological, and social phenomena in populations of living beings – including humans – the representation of the pattern of contacts between individuals by means of a network brings about a substantial improvement with respect to mean field-like approaches where, at all times, any two individuals can interact with each other [1,2]. Networks, where individuals and their mutual contacts are respectively represented by nodes and links, can be built up in such a way that their structure reproduces the properties of the interaction patterns observed in real populations, such as their degree distribution, degree correlations, clustering, community segregation, etc. These properties can be static or evolve with time, and their time evolution can be coupled to other processes occurring in the population, giving rise to rich coevolutionary phenomena involving both social dynamics and structure [3,4].

It has furthermore been pointed out that, in some significant situations, it could become necessary to discern between two social networks for the same population [1,5]. On the one hand, the network of *potential* contacts represents the links that *may* be present at any given time in the population. On the other hand, at each time, one has the network of *realized* contacts. The latter is a sub-network of the former, whose links represent the possible interactions at that time. A specific context where this distinction becomes crucial is the modeling of sexually transmitted diseases in a *monogamous* human population where, however, sexual partnership can change with time.

The potential sexual contacts of an individual comprise a portion of the population, with which the individual is connected through certain social links. Meanwhile, at a given time, the realized contacts of the same individual are limited to his or her only partner. While potential contacts remain fixed or change slowly, realized sexual contacts can exhibit more agile dynamics.

In a recent work on sexually transmitted diseases in monogamous populations [6], we have introduced a model where couples are formed following a set of preferences that each individual has with respect to his or her possible partners. Inspired by the marriage problem [7,8], we have considered a two-sex population where each individual ranks all the members of the opposite sex according to his or her preferences. Heterosexual couples are thus formed and broken following a series of dynamical rules that attempt to improve matching between the preferences of all individuals.

In this paper, we present a refinement of the model, incorporating two new interrelated ingredients. First, individuals have an acceptance threshold for their potential partners, so that two individuals form a couple if each of them is sufficiently high in the other's preferences. This threshold readily implies the existence of a network of potential couples, the *potential-partnership* network. At the same time, we must allow for individuals to remain single in the case that no partnership is acceptable to, or with, him or her. Section 2 is devoted to the presentation of the model and the characterization of the structural properties of the potential-partnership network. In Section 3, we introduce dynamical rules for the evolution of partnership on the network. These dynamical rules are driven by individual preferences, and govern the breaking and formation

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of couples, as well as the abandonment of former partners, who become singles. Dynamical partnership is characterized in terms of the asymptotic fraction of singles and the distribution of couple durations. As we have shown in our previous contribution [6], the latter is a key ingredient in the dynamics of sexually transmitted epidemics.

2 Model for potential-partnership networks

We consider a population of $2N$ individuals, N men and N women, who can form heterosexual couples obeying their individual preferences. Each individual i has a preference list, where all the members of the opposite sex are ranked according to i 's predilections regarding partnership. For instance, the first woman in the preference list of a given man is his favorite candidate as a partner; the second woman is his second favorite, and so on. It is convenient to characterize preference lists using the following matrix-like notation. Let $w(i, j)$ be the rank of woman j in the preference list of man i , and $m(i, j)$ the rank of man j in the preference list of woman i . For instance, $w(i, j) = 1$ implies that woman j is the favorite candidate of man i , while $m(i, j) = 2$ implies that man j is the second favorite of woman i .

In our model, partnership preferences are defined by the following rules. We start by assigning identical preference lists to all the individuals of each sex, say $w(i, j) = m(i, j) = j$ for all i . In this situation, preferences for the members of the opposite sex do not vary over the population. This represents the case where the intrinsic appeal of each individual completely determines the predilection of potential partners, disregarding possible variations from person to person. This intrinsic appeal has sometimes been called *beauty* [9,10]. In this case, correlation between the preference lists of different individuals is maximal. To partially destroy this correlation, we now take the preference list of each individual and perform q transpositions, choosing at random two members of the list and exchanging their ranks. The number of transpositions is independently drawn for each individual from the geometric distribution $p(q) = c^q / (1 + c)^{q+1}$, with $q = 0, 1, 2, \dots$. The parameter c is the mean value of q , thus representing the average number of transpositions in each list. Varying c interpolates between the situation where preferences are fully dominated by the intrinsic appeal of the possible partners (identical lists; $c = 0$) and the situation where they are determined by personal affinities, not shared with other members of the same sex (random lists; $c \rightarrow \infty$) [6].

We assume that each individual would accept partnership with any of the first rN individuals in his or her preference list, while would reject as partners the remaining candidates. In other words, man i would accept woman j as a partner if $w(i, j) \leq rN$, and woman i would accept man j if $m(i, j) \leq rN$. The threshold $r \in (0, 1)$ thus defines how choosy individuals are: smaller and larger values of r represent, respectively, more selective and more indifferent tastes. When the preference lists are identical for all the members of each sex ($c = 0$), the threshold r splits the whole population into two well differentiated

groups, namely, the rN top individuals in the lists, and the remaining $(1 - r)N$ individuals. Recalling that, for $c = 0$, the rank in the preference lists can be interpreted in terms of the intrinsic appeal of each individual, we may respectively call the two groups *attractive* and *unattractive*. For $c \neq 0$, attractive and unattractive individuals are those that, before disordering the preference lists, are respectively above and below the threshold.

Partnership between man i and woman j is potentially possible if j is among the rN individuals in the top of i 's list and, concurrently, i is among the rN individuals in the top of j 's list, i.e. if both $w(i, j) \leq rN$ and $m(j, i) \leq rN$. Potential partnership thus defines links between individuals of opposite sexes or, in other words, a bipartite network which we call *potential-partnership network* (PPN). Our aim in the remaining of this section is to characterize the PPN generated by the above rules – which, we point out, are symmetrical with respect to men and women. Clearly, for a fixed population size N , the quantitative properties of the PPN will depend on the parameters c , which measures the degree of randomness in the preference lists, and the threshold r , a measure of how indifferent are the partnership predilections of any individual.

We note, first of all, that in a sufficiently large population the total number of links in the PPN is $L = r^2 N^2$, irrespectively of the value of c . On the average, in fact, from the rN members of the opposite sex in the top of an individual's preference list, a fraction r will in turn have him or her in the top of their respective lists. The mean number of potential partners per individual is therefore $r^2 N$.

The distribution of the L links over the population, on the other hand, strongly depends on the value of c . For $c = 0$, potential partnership occurs between attractive individuals only. Each one of the rN attractive individuals of each sex is connected with all the rN attractive individuals of the opposite sex, while all unattractive individuals are disconnected. In the limit $c \rightarrow \infty$, in contrast, attractive and unattractive individuals are connected at random, and – up to fluctuations due to the finite size of the population – each individual will be connected to $r^2 N$ potential partners.

To evaluate the expected number of potential partners for intermediate values of c , we must take into account the effect of the possible transpositions in the preference lists. Consider, for instance, that the preference list of man i is subjected to q transpositions. A necessary condition for an attractive woman j to be a potential partner of i is that she remains among the top rN places of i 's list after the transpositions. This may happen because she does not participate of any transposition, with probability $(1 - N^{-1})^{2q}$, or because after one or more transpositions she ends in one of the top places, with probability $[1 - (1 - N^{-1})^{2q}]r$. An unattractive woman, on the other hand, depends on participating of at least one transposition to end in the top part of the list. To establish potential partnership it is additionally necessary that man i is in the top part of j 's list, which happens with overall probability r . Of course, the same arguments hold if i is a woman

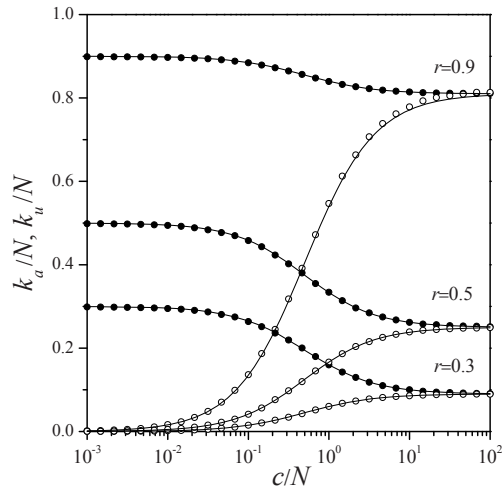


Fig. 1. Normalized mean number of links, k_a (●) and k_u (○), for attractive and unattractive individuals as a function of c/N , for three values of r . Dots correspond to numerical results for $N = 10^3$, averaging over six realizations of the preference lists for each dot. Lines correspond to the analytical results of equations (1) and (2).

and j is a man. Averaging over the distribution $p(q)$ for the number of transpositions, we get the expected number of links for attractive and unattractive individuals, which respectively read

$$k_a = rN \frac{(N^2 - cr + 2crN)}{N^2 + c(2N - 1)} \rightarrow rN \frac{1 + 2cr/N}{1 + 2c/N}, \quad (1)$$

and

$$k_u = rN \frac{cr(2N - 1)}{N^2 + c(2N - 1)} \rightarrow rN \frac{2cr/N}{1 + 2c/N}. \quad (2)$$

To the right of the arrows, the above equations give the limits of k_a and k_u for $N \rightarrow \infty$, keeping terms of order c/N . The limits for $c \rightarrow 0$ and $c \rightarrow \infty$ discussed previously are readily reobtained from these equations.

Figure 1 compares the analytical results of equations (1) and (2) with numerical realizations of the PPN for populations of size $N = 10^3$. It shows the average number of links of attractive and unattractive individuals normalized by N as a function of c/N , for three values of the threshold r . In each numerical realization of the preference lists, k_a and k_u are evaluated as averages over each kind of individual. Each dot is in turn an average over six realizations of the lists. For this population size, the agreement between analytical and numerical results is excellent. Note that the transition between the regimes for small and large c occurs in a well-defined interval around $c/N \approx 1$, spanning from about $0.1c/N$ to $10c/N$.

In our numerical realizations of the preference lists we have also recorded the fraction of links in the PPN corresponding to each kind of potential couple, namely, attractive-attractive (aa), attractive-unattractive (au), and unattractive-unattractive (uu). Figure 2 shows these fractions as a function of c/N for four values of the threshold r . For small thresholds, the number of unattractive individuals in the population is large and, as a consequence,

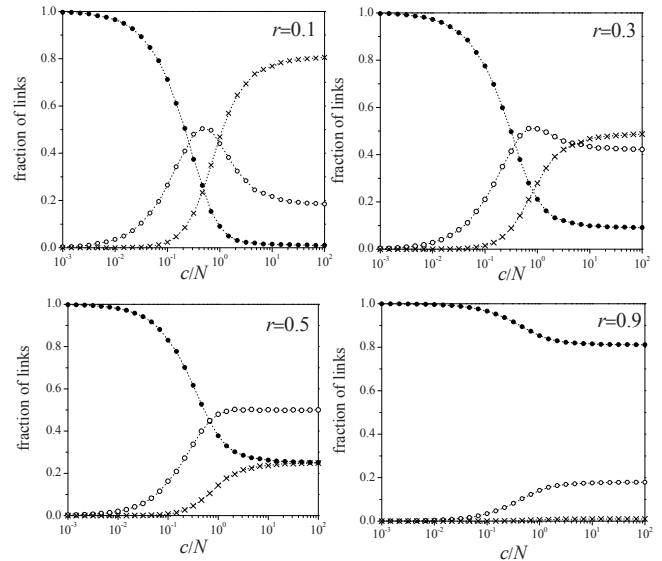


Fig. 2. Fractions of attractive-attractive (●), attractive-unattractive (○), and unattractive-unattractive (×) links in the PPN as functions of c/N , for four values of the threshold. Average values obtained from numerical realizations of the preference lists in the same conditions as described for Figure 1.

the fraction of aa -links decreases drastically as the preference lists are disordered. Concurrently, the fraction of uu -links increases monotonically, while au -links reach a maximum and then decreases. For large thresholds, on the other hand, most individuals are attractive, and the fraction of aa -links is therefore the largest for all values of c/N .

3 Partnership dynamics on the PPN

Once we have determined the potential-partnership network (PPN) of our population from the individuals' preference lists, we proceed to the realization of partnership by defining dynamical rules for the formation and dissolution of couples. Our model is based on the so-called *bar dynamics* for the marriage problem [6,8], with the addition that we admit both married and single individuals. Partnership is assumed to be always monogamous, so that, at any time, each individual can be either single or have at most one partner of the opposite sex.

At each evolution step, a man i and a woman j , not partners to each other, are drawn at random from the population. If they are linked by the PPN, the following rules are applied. (1) If both i and j are single, they become partners and a new couple is thus formed. (2) If i is single but j is the partner of another man i' , i and j become partners if i ranks higher than i' in j 's preference list, i.e. if $m(j, i) < m(j, i')$. Thus, partnership between j and i' is dissolved and i' becomes single. If, on the other hand, $m(j, i) > m(j, i')$, nothing happens. (3) Correspondingly, if j is single but i is the partner of another woman j' , i and j become partners and j' becomes single if i prefers j to j' , i.e. if $w(i, j) < w(i, j')$. (4) Finally, if

both i and j already have respective partners j' and i' , they establish partnership if both $m(j, i) < m(j, i')$ and $w(i, j) < w(i, j')$, in which case i' and j' become single. The unit of time lasts N evolution steps. On the average, thus, each individual is chosen once per time unit.

Numerical simulations with these rules for partnership evolution, which we start from an initial condition where all individuals are single, show two well-differentiated regimes. For any value of c and sufficiently small r , the population rapidly reaches a frozen state with a certain number of couples and singles. In this state, no man-woman pair in the whole system would simultaneously prefer to change their present status, i.e. to quit their present partners or to abandon their singleness, in order to form a couple with each other. Frozen states of this kind are analogous to the Nash equilibria of the original marriage problem (without singles, [8,11]), so that we refer to them as *Nash states*. For large r , on the other hand, couples keep breaking and re-forming at a sustained rate, for extremely long times. In our simulations for $N = 10^3$, this was tested to persist during periods of the order of 10^6 time units without reaching a Nash state. Of course, this regime is the most interesting in relation to the dynamics of processes such as epidemics [6] in evolving social structures.

The inset of Figure 3 depicts the regions corresponding to the two regimes, either Nash states or persistent dynamics, in the parameter plane $(r, c/N)$. In the main plot, we show the long-time total fraction of singles in the population, s , as a function of c/N for several values of the threshold r . Note that for $r = 0.1, 0.2$ and 0.3 , our results span both regimes. While, when a Nash state is reached, the fraction s attains a fixed value, in the persistent dynamics regime s fluctuates around an average asymptotic value as couples form and break down. For this latter case, the plot shows the average value of s .

As expected, the fraction of singles decreases with c , as preference lists are disordered and more couples become feasible. For larger r , when preferences are less selective, s is also smaller. For $r \gtrsim 0.2$ and large c the fraction of singles approaches a uniform value, $s \approx 0.16$.

Figure 4 shows the long-time fractions of each kind of couple as functions of c/N , for four values of r . Comparing with Figure 2, we find that these fractions follow roughly the same trend as the corresponding kinds of link in the PPN. A closer inspection, however, reveals substantial differences. Specifically, consider the fraction of attractive-unattractive couples and links (empty dots in both figures). For small c , i.e. when the preference lists are only slightly disordered, the number of au -links in the PPN is insignificant as compared with that of aa -links, irrespectively of the value of r (Fig. 2). During the realization of the dynamics, on the other hand, au -couples occur in small, but not negligible quantities, with fractions around 10% of the total number of couples. This implies that even small differences in the preference lists induce significant partnership of unattractive individuals, in spite of the fact that they are reached by relatively very few links in the PPN. Note also that the maximum of the

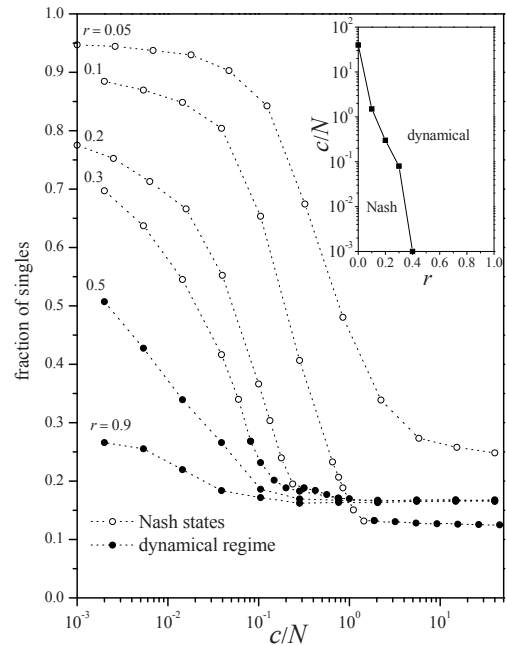


Fig. 3. Asymptotic fraction of singles as a function of c/N for different values of r , in a population with $N = 10^3$. Full and empty dots respectively stand for the persistent dynamical regime and the Nash-state regime. The inset shows the critical curve separating the two regimes in the $(r, c/N)$ -plane.

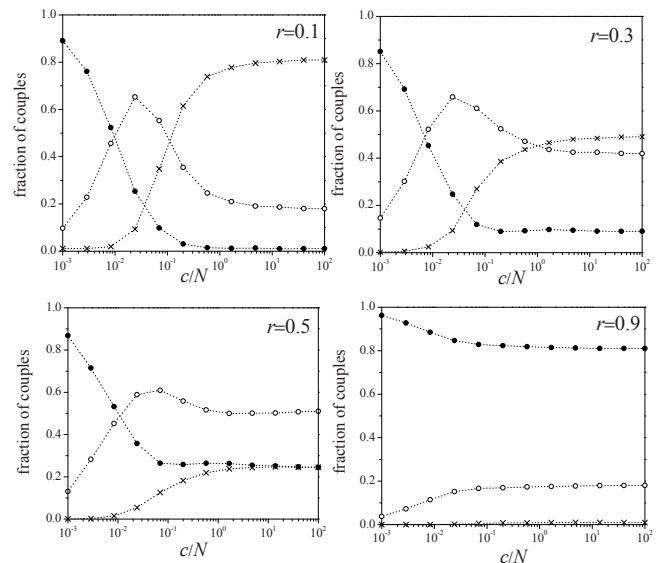


Fig. 4. Asymptotic fractions of attractive-attractive (\bullet), attractive-unattractive (\circ), and unattractive-unattractive (\times) couples as functions of c/N , for four values of the threshold r and $N = 10^3$.

fraction of au -couples occurs for values of c/N systematically smaller than for the fraction of au -links.

The main characterization of the dynamical regime of partnership in the PPN is given by the distribution of partnership durations, i.e. of the times between formation and dissolution of each couple. In the application to sexually transmitted diseases, for instance, this distribution

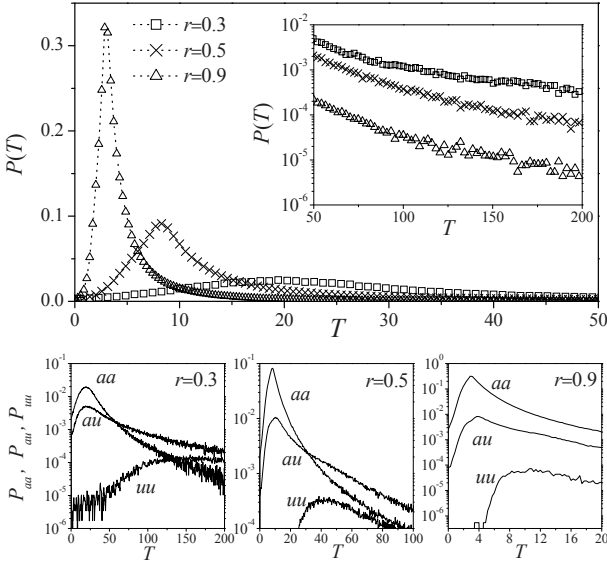


Fig. 5. Upper panel: Numerical results for the distribution of couple durations, $P(T)$, in a population with $N = 10^3$ for $c/N = 0.2$ and three values of the threshold r . The inset shows a detail of the same data for large T . Lower panels: Contributions to $P(T)$ from each kind of couple: attractive-attractive (aa), attractive-unattractive (au), and unattractive-unattractive (uu).

controls whether and infected couple is cured or not before it breaks down or, in other words, whether the infection will be confined or will spread over the population [6].

Let i and j respectively be a man and a woman linked by the PPN. The mean duration time of the couple formed by i and j , $T(i, j)$, is numerically computed as the average duration of all the periods during which the couple was effectively present in the partnership configuration. Figures 5 and 6 show numerical results for the distribution $P(T)$ of $T(i, j)$ over all the PPN links in populations with $N = 10^3$, respectively, for small and large c ($c/N = 0.2$ and 40). Three values of the threshold r were considered.

Comparison of the upper panels of both figures reveals that there is no strong qualitative dependence on c . In both cases, the distribution $P(T)$ is rather sharp for large r , and broadens and shifts to larger T as r decreases. This shift reveals that, as individuals become more selective in their partnership choices, the couples they form are more stable and last longer. We stress that the width of the distribution – namely, the dispersion around the average from couple to couple – is a direct consequence of the heterogeneity in the mutual preferences between men and women. In a population where partnership changes at random [6], all couples would have the same average duration.

Differences between small and large values of c appear when we analyze the duration between different kinds of couple, as illustrated in the lower panels of Figures 5 and 6. For large c , when preference lists are essentially random (Fig. 6), the contributions of each kind of couple to the distribution $P(T)$ are mutually proportional, and their differences can be ascribed just to the different

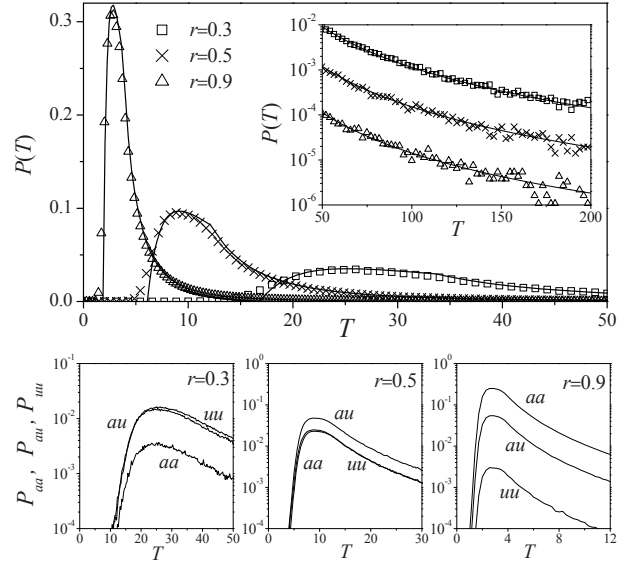


Fig. 6. As in Figure 5, for $c = 40$. Curves in the upper panel correspond to the analytical evaluation of $P(T)$, equation (6).

number of individuals of each kind in the population. For $r = 0.9$, for instance, aa -couples are more abundant just because the number of attractive individuals is larger. On the other hand, for small c (Fig. 5), the three contributions have different relative values and shapes. In particular uu -couples are now generally less frequent, irrespectively of the threshold r . In fact, for small c , most unattractive individuals remain below the threshold after disordering the preference lists. However, we also note that uu -couples tend to last longer than aa and au -couples: once coupled with each other, unattractive individuals will rarely have the chance of changing their partners.

In the limit of uncorrelated preference lists ($c \rightarrow \infty$), mean field-like arguments make it possible to semi-analytically calculate the expected value of $T(i, j)$ – and, as a byproduct, the distribution of couple durations – as follows. Let us assume that man i and woman j are partners to each other at a given time. The probability per evolution step that the couple breaks, because either i or j attempt to form a couple with other potential partners (say, j' and i'), is approximately given by

$$P_b(i, j) = \frac{1}{N} \left[\frac{w(i, j) - 1}{N - 1} + \frac{m(j, i) - 1}{N - 1} \right] [sr + (1 - s)p_b]. \quad (3)$$

The prefactor N^{-1} is the probability that either i or j is selected at that step. The ratio $[w(i, j) - 1]/(N - 1)$ is the probability that, given that man i is selected, the selected woman j' is better ranked than j in i 's list. Analogously, $[m(j, i) - 1]/(N - 1)$ is the probability that, if woman j is selected, the selected man i' is better ranked than i in j 's list. Finally, $sr + (1 - s)p_b$ approximates the probability that woman j' accepts man i or, analogously, man i' accepts woman j . The contribution sr stands for the case in which the new partner is single, while $(1 - s)p_b$ stands for the case in which he or she already has a partner. Here, p_b is the probability that an individual who already has a

partner, when chosen at any given evolution step, decides to break his or her couple in order to form a new one. For this probability, which generally depends on c and r , we do not have an analytic approximation. In our calculation of $P_b(T)$ for $c \rightarrow \infty$, p_b is evaluated numerically for each value of r . The fraction of singles s is also got from numerical simulations.

The probability that the couple lasts exactly t steps is $P_t(i, j) = [1 - P_b(i, j)]^{t-1} P_b(i, j)$, which gives an average duration of $T(i, j) = [N P_b(i, j)]^{-1}$ time units. Calling $g(i, j) = w(i, j) + m(j, i)$, we get

$$T(i, j) = \frac{N - 1}{[sr + (1 - s)p_b][g(i, j) - 2]}. \quad (4)$$

Since $w(i, j)$ and $m(i, j)$ are integers uniformly distributed between 1 and rN , the possible values of $g(i, j)$ follow a triangular distribution between 2 and $2rN - 2$:

$$\Upsilon(g) = \frac{1}{(rN - 1)^2} \begin{cases} g - 1, & 2 \leq g \leq rN, \\ 2rN - g - 1, & rN < g \leq 2rN - 2. \end{cases} \quad (5)$$

The distribution of couple durations is then calculated as

$$P(T) = \Upsilon[g(T)] \frac{dg}{dT}(T), \quad (6)$$

where $g(T)$ is obtained by inverting equation (4). Curves in the upper panel of Figure 6 show our semianalytical evaluation of $P(T)$, with the probability p_b measured in numerical simulations. The agreement with numerical results is excellent over most of the considered range.

Finally, as we have discussed at length elsewhere [6], dynamical processes such as infection transmission and the establishment of endemic diseases involve not just the duration distribution $P(T)$ of all couples permitted by the PPN links, but the duration distribution $Q(T)$ of the couples actually present in the population at any given moment. Since $Q(T)$ depends both on the mean duration of each possible couple and on the frequency at which each couple forms, it turns out to be independent of $P(T)$. Figures 7 and 8 present numerical results for the distribution $Q(T)$ in populations with $N = 10^3$, for small and large c and three values of the threshold r . While the shape of $Q(T)$ is qualitatively similar to that of $P(T)$, comparison of the two distributions reveals that $Q(T)$ is systematically broader than $P(T)$ and, correspondingly, its tail is fatter. This implies that, for the couples present in a snapshot of our population, the distribution of durations differs from the case of random partnership even more than in an integrated, time-averaged picture of configuration of couples. This further emphasizes the role of preference lists in determining the evolving social structure of partnership in the present model.

4 Conclusion

Discerning between potential and realized contacts may be crucial in the description of many processes related to social dynamics. We have here considered the extreme

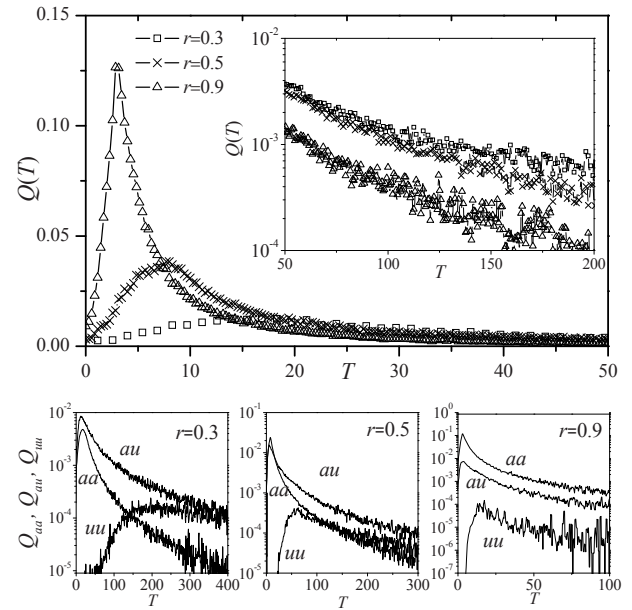


Fig. 7. Upper panel: numerical results for the distribution of couple durations for the couples present at any given time, $Q(T)$, in a population with $N = 10^3$ for $c/N = 0.2$ and three values of the threshold r . The inset shows a detail of the same data for large T . Lower panels: Contributions to $Q(T)$ from each kind of couple: attractive-attractive (aa), attractive-unattractive (au), and unattractive-unattractive (uu).

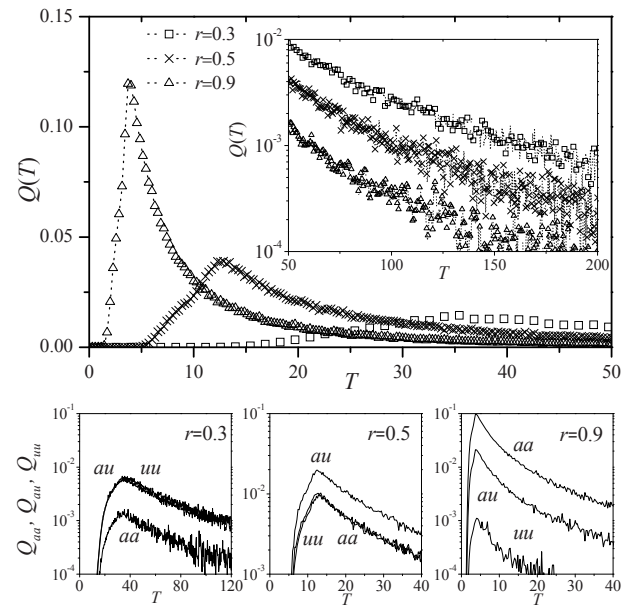


Fig. 8. As in Figure 7, for $c = 40$.

situation where, while the potential contacts of an individual can span a substantial part of the whole population, at most one of those contacts is effectively realized at any given time. Specifically, we have modeled the social structure and dynamics of a monogamous two-sex population where, at a given time, individuals either form heterosexual couples or remain single. Both the network of potential partnership and the dynamics of formation and

dissolution of couples are driven by individual preferences for the members of the opposite sex.

Our model is controlled by two parameters, c and r , which respectively measure the diversity of preferences between different individuals and how selective they are with respect to either accept a partner or remain single. When all individuals have the same preferences ($c = 0$), selectiveness naturally splits the population between “attractive” and “unattractive” individuals. In this limit, only attractive individuals can form couples but, as preferences become more diverse, also unattractive individuals can participate of partnership. The resulting potential-partnership network has a bimodal degree distribution, with distinct number of contacts for each kind of individual. This difference, however, decreases as preference diversity grows.

The dynamical rules for couple formation and dissolution add no new parameters to the model. As in the bar dynamics for the marriage problem [6,8], we find two regimes. In the first regime, realized partnership reaches a frozen (Nash) state with a certain number of fixed couples and single individuals. As expected, the number of singles decreases with selectiveness and when preference diversity grows. In the second regime, which occurs for low selectiveness (large r), couples keep breaking and re-forming and the number of singles fluctuates with time. We have characterized this dynamical regime by studying the distribution of couple durations. It turns out that, when selectiveness is large (small r), couples are on the average more stable and last longer. Among them, when preferences are not much diverse (small c), partnership between unattractive individuals is the most durable. Sadly, however, this is not due to their excess of

fidelity but rather to the fact that unattractive individuals find it more difficult to get new partners.

The present contribution is a step towards modeling social structure on the basis of a sensible factor – in this case, individual partnership preferences – and, at the same time, taking into account the difference between patterns of potential and realized contacts. Generalizations may point toward a more realistic representation of preference and selectiveness diversity. Applications beyond disease spreading, such as information transmission, decision making, ecological and game-like interactions, and other processes of biological or social inspiration, would also be worth considering.

References

1. M.J. Keeling, K.T.D. Eames, *J. Roy. Soc. Interface* **2**, 295 (2005)
2. M.E.J. Newman, A.-L. Barabási, D.J. Watts, *The Structure and Dynamics of Networks* (Princeton University Press, Princeton, 2006)
3. T. Gross, B. Blasius, *J. Roy. Soc. Interface* **5**, 259 (2008)
4. C. Castellano, S. Fortunato, V. Loreto, *Rev. Mod. Phys.* **81**, 591 (2009)
5. K.T.D. Eames, M.J. Keeling, *Math. Biosci.* **189**, 115 (2004)
6. S. Bouzat, D.H. Zanette, *Eur. Phys. J. B* **70**, 557 (2009)
7. D. Gusfield, R.W. Irving, *The Stable Marriage Problem: Structure and Algorithm* (MIT Press, Cambridge, 1989)
8. A. Lage-Castellanos, R. Mulet, *Physica A* **364**, 389 (2006)
9. G. Caldarelli, A. Capocci, *Physica A* **300**, 325 (2001)
10. G. Caldarelli, A. Capocci, P. Laureti, *Physica A* **299**, 268 (2001)
11. S. Bouzat, D.H. Zanette, *Physica A* **380**, 539 (2007)