Appendix

Contents

A1 Agent-Based Model Algorithm

Algorithm 1: Pseudocode of a complete simulation run

Initialization

Input number of agents = *n*, group size = *FS*, iteration = 0, assign τ_i, end simulation run = *E*, matching at iteration = *X*, learning = *l*, behavioral noise = *m*, proportion prosocial agents = *PA*, chance for network dyad selection = *r*, leave (stay) rule = $\tau_i > (\leq) G_{10}$

```
while any? ungrouped agent
    if matching = rule 1
        group: unilateral first cooperation decision = 1 - $\tau_i$
        sort agents from high to low
    else
        sort ungrouped agents at random
    select FS agents for group

if matching = rule 3
    then
        if homophily = true
            initialize random spatial graph network with spatial constraints
        else
            initialize random spatial graph network
    network: unilateral first cooperation decision = 1 - $\tau_i$
```

```
while iteration < E
    if iteration ≤ X
        group: decision-making model
        if matching = rule 3
            if homophily = true
                if dyad selected = true and prior cooperation decision = equal
                    then
                        network: decision-making model
            else
                if dyad selected = true
                    then
                        network: decision-making model
        repeat

    else
        if $\tau_i > G_{10}$
            then
                ungroup agent
                threshold = $\tau_i$

        while any? ungrouped agent
            sort groups with open spots from high-low based on $G_{10}$

            if rule 1 or 2
                then
                    if rule 1 or rule 1 adjusted
                        then
                            input-for-matching = $c_{\text{all}}$
                    if rule 2 adjusted
                        then
```

```
                        input-for-matching = $c_{10}$
                if rule 2
                    then
                        input-for-matching = $G_{10}$

        if rule 3
            then
                if empty slots in a group?
                    ask agents in the group
                        if network information is available of potential candidates
                            input-for-matching = $GC_{10}$
                        else
                            input-for-matching = $G_{10}$
                else
                    ask ungrouped agent with highest $GC_{10}$
                        if network information is available of potential candidates
                            input-for-matching = $GC_{10}$
                        else
                            input-for-matching = $G_{10}$

        sort agents from high-low based on input-for-matching
        match highest agents to highest group

        end

    $X = X + X$

end
```

A2 Random Spatial Graph Algorithm

The network is as simple as possible implemented, meaning statically. The network is generated via a spatial random graph algorithm (Wong, Pattison, & Robins, 2006). The network is generated in two steps. First, agents are randomly dispersed in the cellular world. That is, we draw independently a random x and y coordinate from a uniform random distribution of coordinates, followed by assigning agents to the randomly drawn x-y coordinate if the spot is empty. The network algorithm assumes that agents tend to form ties with those geographically nearby. Second, agents are probabilistically linked to nearby agents. Each agent asks k other non-tied agents to form a tie with. Following previous implementations (Grow, Flache, & Wittek, 2017; Keijzer, Mäs, & Flache, 2018), we set $k = 5$. Agents form network ties with at least 5 others. The probability of tie creation is driven by the Euclidean distance in the cellular world (Equation A1). Two agents who are geographically closer to each other are more likely to form a tie than two agents who are farther away. Dyadic closeness is denoted as u_{ij}. The average geographical distance does not affect tie formation processes when $w = 0$. Contrarily, higher w values increase the importance of distance on tie formation, facilitating clustering levels observed in real-life networks. To ensure a representative level of network clustering, we set $w = 8$ (Grow et al., 2017; Keijzer et al., 2018). Agents form thus more easily ties with geographically nearby agents.

$$f(w, u_{ij}) = e^{(-w[u_{ij}])} \tag{A1}$$

A3 Segregation Index

We measure homophily via the Moody gross-segregation (*MS*) index (Bianchi, Flache, & Squazzoni, 2020; Moody, 2001). The coefficient allows us to compare the likelihood of ties between same and other-type agents. In Equation A2, formally, the count of same-type ties (prosocial-prosocial and proself-proself, *A*) is multiplied by all possible other-type ties (all proselfs * [all prosocials - 1] and vice versa, *D*). Next, *AD* is divided by the count of all other-type ties (prosocial-proself and proself-prosocial, *B*) and all possible same-type ties (all proselfs * [all proselfs - 1] and vice versa, *C*). *MS* reports an odds-ratio (OR). An OR of 1 denotes that the chances for a link between same and other-type agents are equal. An OR < 1 shows that the odds of linking to same-type agents are lower than linking to other-type agents. Contrarily, an OR > 1 indicates that the probability to link to same-type agents is higher than linking to other-type agents. A feature of the coefficient is that the relative group size does not affect the interpretation of the coefficient.

$$MS = (AD) / (BC) \tag{A2}$$

In the randomly-linked networks, the chances to link to the same and other-type agents are about 50/50 ($MS \approx 1.00$)[1]. But if we allow for structural homophily, the chances to link to same-type agents need to increase. We introduce a stylized implementation of increasing the chances to link to same-type agents. With homophily, we assign prosocials to a fixed area in the cellular world and draw random x-y coordinates from that restricted area, promoting clustering of prosocials due to forming ties with geographically nearby agents. Subsequently, proselfs randomly draw x-y coordinates from the whole grid, followed by moving to the drawn coordinate. Prosocials agents are firstly dispersed in the lower-left half of the network when the population consists of 20% prosocials. Whereas prosocials are sorted on the lower half of the cellular world when there are more than 40% prosocial agents.

The stylized set-up of structural homophily ensures a *MS* between 1.5 and 1.8, on average, irrespective of the percentage prosocials in the population. Estimates are based on 100 replications in a population with 20, 40, 60, and 80 percent prosocials. The stochastic nature of the spatial random graph algorithm inserts minor variance in *MS*. There remains thus some minor trembling in forming ties with other-type agents when structural homophily is implemented, meaning that the homophily procedure incorporates some faultiness. This implementation also reflects incomplete information in forming ties with similar others.

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[1] Estimate is based on 100 replications in BehaviorSpace in a population constituting either 20, 40, 60, and 80 percent prosocials.

Note that the *MS* does measure perfect segregated situations. Then, *AD* is divided by 0. We solved this issue in the code by setting $B = 1$ when no cross-type ties were available. This occurred in 33 cases when calculating *MS* in the group context, mostly when learning was slow and complete information was available. We omitted these MS odds-ratios because these incur skewness. *MS* was in such situations > 260.

A4 Two Additional Matching Rules

We took a step-wise approach to capture every small change in the matching rule and inspect how such small alterations in matching rules affect model dynamics (Flache & de Matos Fernandes, 2021). We aim to preserve, on the one hand, the importance of rigorous model building while, on the other hand, favoring less information-heavy scenarios. See the in-paper descriptions of rules 1-3.

Rule 1 adjusted. To progressively move away from the complete information assumption under rule 1, we omit the pre-game in this rule. Agents are initially randomly grouped, allowing for initial mismatching. Still, agents have, during the game, unlimited cognitive abilities to store all individual prior actions of all agents in the population.

Rule 2 adjusted. To explore the role of individual incomplete information instead of solely relying on information on the group level, we include the last 10 individual cooperation decisions (C_{10}) as input for the matching algorithm of all agents, instead of G_{10}.

A5 Parametrization of the Model

Table A1. Summary of parameters and ranges related to the agent-based model.

Parameter	Rule	Symbol	Range
Learning rate	1-3	l	{0.1, 0.3, 0.5, 0.7, 0.9}
Slope (noise)	1-3	m	{1, 5, 10}
Adaptive threshold	1-3	$\tau_{i,t}$	(0, 1)
Cost of cooperation	1-3	h	3
Benefit of cooperation	1-3	b	4.5
Payoff when all defect	1-3	d	-0.5
Chance of network dyad selection	1-3	r	{0.01, 0.05, 0.25, 0.5}
Group context features			
Moment of matching	1-3	X	{100, 200, 300}
End iteration of a single run	1-3	E	400
Population size	1-3	$N\{0, \dots, n\}$	$n = 160$
Fixed group size	1-3	FS	8
Count of groups	1-3	G	20
Proportion prosocial agents	1-3	PA	{0.2, 0.4, 0.6, 0.8}
Fixed (initial) threshold	1-3	τ_i	{0.3, 0.7}*
Leave-stay procedure	1-3	$\tau_i > G_{10}$	{leave, stay}
Noise in leave-stay procedure	1-3		{0, 0.01, 0.05, 0.25}
Matching: Complete information			
Pre-game prob. to cooperate	1	$p_{i,t=0} = 1 - \tau_i$	{0.7, 0.3}*
Individual cooperation	1 & 1 adj.	C_{all}	(0, 1)
Matching: Incomplete information			
Individual cooperation	2 adj.	C_{10}	(0, 1)
Group cooperation	2	G_{10}	(0, 1)
Network cooperation	3	$C_{10,sn}$	(0, 1)
Network and group cooperation	3	GC_{10}	(0, 1)

* The first value refers to prosocials ($\tau_i = 0.3$) and the second to proselfs ($\tau_i = 0.7$).

A6 Exploring the Role of Two Additional Matching Rules

Figure A1 shows the average level of cooperation as a result of 100 simulation runs. Rule 1 adjusted shows that prosocials can harvest more of their innate cooperativeness compared to incomplete information rules. However, the possibility of initial mismatching, assumed under rule 1 adjusted, leads to lower cooperation among prosocials than under rule 1 (Figure A1a, yellow line). Figure A1b reports not a radical impact of additional matching rules on cooperation levels among proself agents. The collective level of cooperation, akin to cooperation levels among prosocials, benefits from rule 1 adjusted.

What is more, findings regarding rule 2 adjusted, i.e., only the last 10 individual actions are known, are also detrimental for cooperation levels among prosocials (Figure A1a, purple line). Observation of individual behavior from the last 10 iterations in the context of that group is equally bad for good apples as when merit is solely group-based.

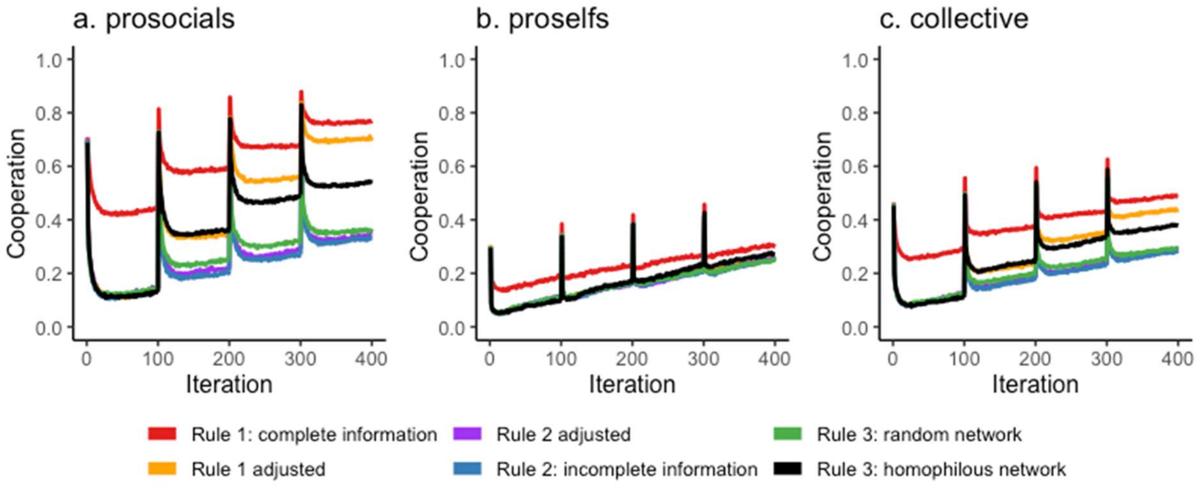

Figure A1. Average level of cooperation for prosocials (a), proselfs (b), and the collective (c), separated by the 'original' and additional matching rules. Parameter settings: $m = 5$; $l = 0.5$; $PA = 0.4$; $r = 0.05$.

A7 Consequences of Removing Meritocratic Matching: Keeping Groups Fixed

In-between matching moments, we infer that cooperation increases linearly. This leads us to conduct exploratory simulation runs and inspect the role of keeping groups fixed. Do agents quickly learn to cooperate when we remove the dynamic part out of the model? We first inspect how cooperation evolves over a timeframe of 50 rounds, specified per prosocial, proself, and overall (Figure A2a-c), followed by studying cooperation over longer periods (Figure A2d-f). Lines with lighter shades of grey point to fewer prosocials in the group. It is important to note that there is always a small chance for agents to cooperate even when defection prevails (and vice versa). Thus, due to the probabilistic nature of our model, we do not find smoothened curves in Figure A2 but mainly punctuated equilibria. We report the average level of cooperation of 100 simulation runs.

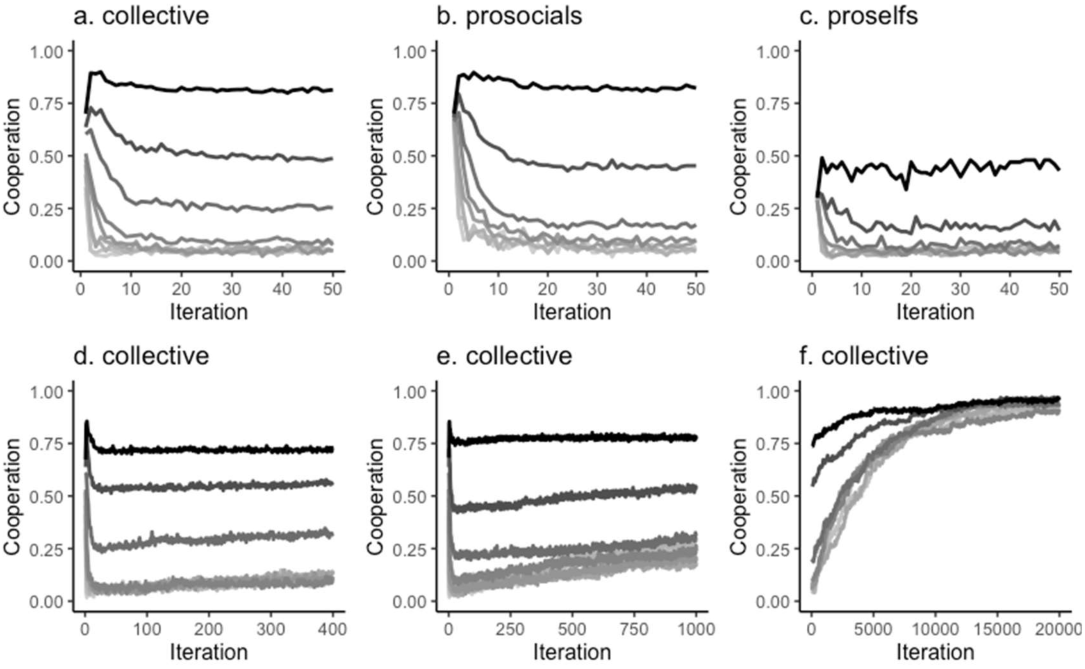

Figure A2. Average level of cooperation in fixed groups per 50, 400, 1000, and 20000 rounds (panels a, d, e, and f, respectively). Cooperation levels of prosocials (b) and proselfs (c) are reported until iteration 50. Darker shades mean more prosocials in the group (range = 0, 1, 2, …, 8 prosocials). Parameter settings: $m = 5$; $l = 0.5$; $PA = 0.4$; $r = 0.05$.

Figure A2f shows that cooperation needs time to arise. All group configurations tend to converge at all-out cooperation if we set the time horizon to 20000 rounds. However, especially groups with fewer prosocials tend to cooperate at lower levels when they interact over ≤ 5000 rounds. Prosocials are more able to cooperate when there are more prosocials in the group (darker lines), but defective outcomes are more likely when there are too many bad apples (lighter lines) in the group (Figure A2d-e). Keeping groups fixed is thus a solution to promote collective success in the long run, but it may be an unrealistic scenario if we translate this finding to real-life where groups are usually dynamic while facing external influences.

Our explanation for the low levels of cooperation in groups with fewer prosocials in Figure A2a-c is as follows. Prosocials generally cooperate initially but quickly fall in line with their group mates' defective behavior if the outcome of cooperation tends to be negative (Figure A2b-c). Figure A2b shows that the average level of cooperation at the start relates to the initial probability to cooperate for prosocial and proself agents, 0.7 and 0.3 respectively. But if cooperation does not generate positive outcomes – which is more likely in groups with more proself agents – we see that cooperation of prosocials stabilizes at substantially lower levels than the initial probability to cooperate, visualized by lighter shades of grey (Figure A2a-c). Prosocials are the drivers of cooperation in our model and if they do not show up, defection prevails.

A8 Network Cooperation

Please find the BehaviorSpace (100 simulation runs per condition) findings of network cooperation levels specified per network condition in Figure A3. The single run is reported in the paper.

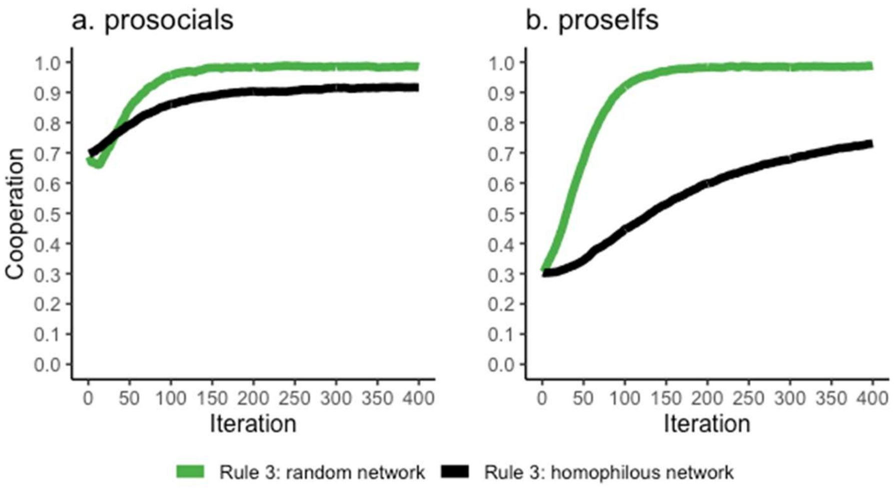

Figure A3. Average level of cooperation in the network, separated by random (green) and homophilous (black) network. Parameter settings: $m = 5$; $l = 0.5$; $PA = 0.4$; $r = 0.05$.

A9 Sensitivity Analysis

A9.1 Testing the Impact of *m*, *l*, and *PA*

To check the impact of little or much noise in the decision algorithm, we incorporate values of $m = \{1, 5, 10\}$. Also, we inspect the implications for slow and rapid learning by assuming $l = \{0.1, 0.3, 0.5, 0.7, 0.9\}$. Next, we control for how the initial distribution of prosocial agent affect model outcomes, $PA = \{0.2, 0.4, 0.6, 0.8\}$. We run 100 independent simulations per condition. There are overall 6 x 3 x 5 x 4 conditions – matching, slope, learning rate, and proportion prosocials, respectively – realizing a total of 36000 simulation runs, all things being equal.

We present the average level of cooperation of prosocials (Figure A4), proselfs (Figure A6), and the collective (Figure A7) as well as for the prosociality segregation MS index (Figure A5). We only included the last interaction of runs. Although the variance across matching rules decreases when comparing rules per *PA*, the order of rule 1 (complete information) > rule 3 (homophily) > role 2 (incomplete information) remains fairly the same when inspecting cooperation levels of prosocials, leading us to infer that our findings are relatively robust when $m = 5$ and $l < 0.9$. In what follows, we only discuss findings regarding prosocials given that the picture does not radically change when inspecting how robust the findings are for proselfs and the collective.

Changes in cooperation outcomes regarding learning and noise may be expected. Macy (1991, p. 739) states that "rapid learning suggests pragmatic error-correction, while slow learning may indicate habitual or norm-guided behavior […] that take somewhat longer to change." We find the same in Figure A4, middle row. High learning rates allow agents to quickly coordinate on the best course of action. Whereas slow learning rates, $l = 0.1$ or 0.3, show the necessity of more time to learn to steer away from negative outcomes.

More noise ($m = 1$) leads to a self-correcting equilibrium (Macy & Flache, 2002) where cooperation levels hover around 0.34 (Figure A4, top row). In such an equilibrium, the expected change of cooperation levels is minimal as the benefits of cooperation and defection counter each other out. Contrarily, prosocials end up in an equilibrium of all-out cooperation (Figure A4, bottom row) if noise decreases to $m = 10$. Macy and Flache dubbed this as a self-reinforcing equilibrium in which positive payoffs lead to a reinforcement of behavior even if alternative actions, i.e., defection, may lead to a higher payoff.

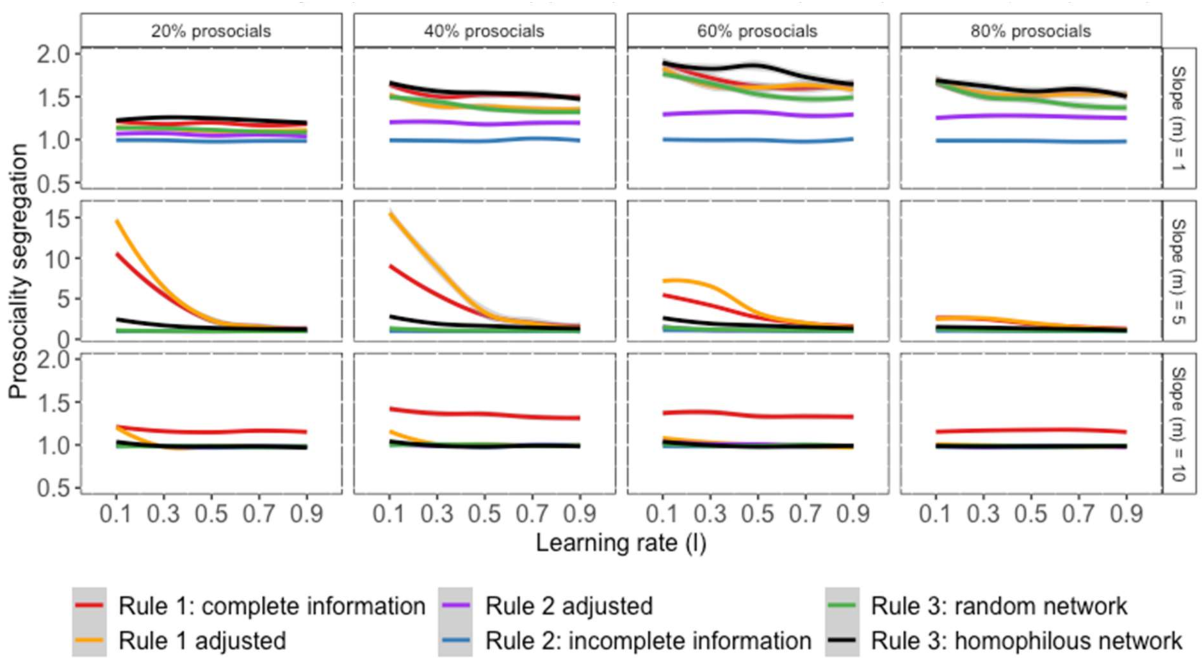

Figure A4. Sensitivity analysis of prosociality segregation per *l*, *m*, and *PA*. Mean and 95% confidence interval are depicted. Note that we report different values for the y-axis when *m* = 5.

Figure A5 allows us to further assess the robustness of our prosociality segregation finding. The middle row in Figure A5 shows that prosociality does not arise when prosocials quickly can learn to cooperate when *l* = 0.7 or 0.9, omitting the need to team up to spur cooperation. Next, more noise (*m* = 1) in the behavioral algorithm has a peculiar effect, on homophily as it becomes the go-to matching rule to spur prosociality segregation. Still, cooperation levels hover around 0.34. Furthermore, lower levels of noise (*m* = 10) point to the importance of initial grouping for prosociality segregation to arise. The possibility of pre-game grouping – in which prosocials are more likely to team up – leads to substantially higher levels of prosociality segregation compared to initial random grouping, irrespective of *PA* and *l*.

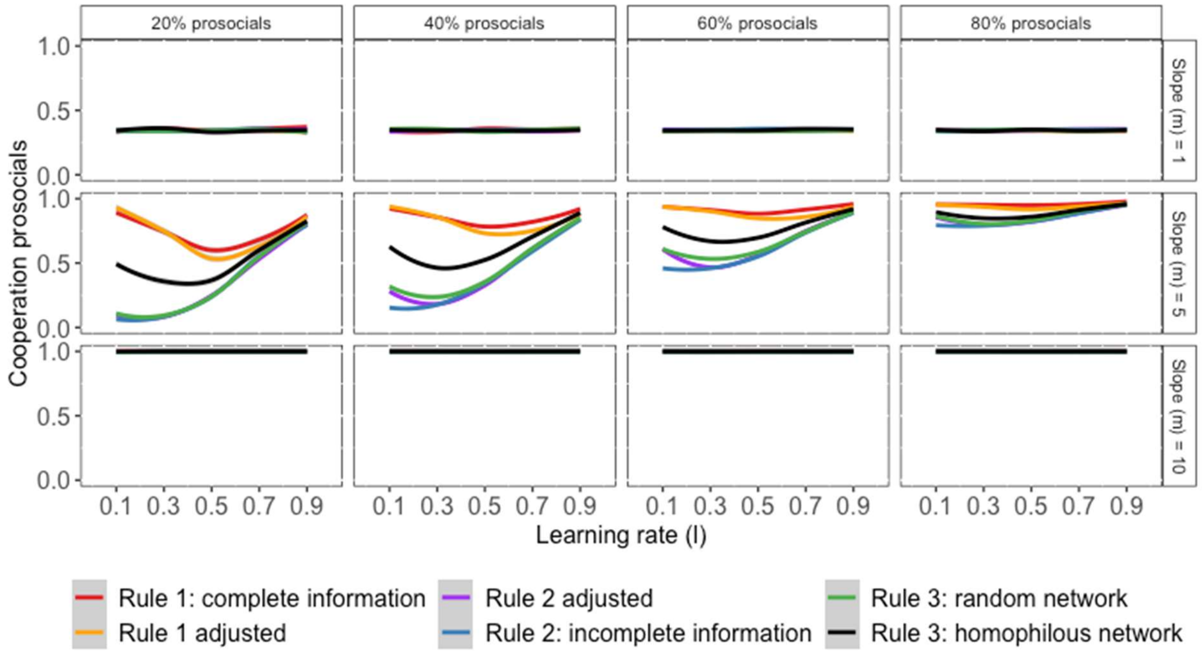

Figure A5. The effect of *m*, *l*, and *PA* on the mean level of cooperation of prosocials at iteration 400. Mean and 95% confidence interval are presented per rule.

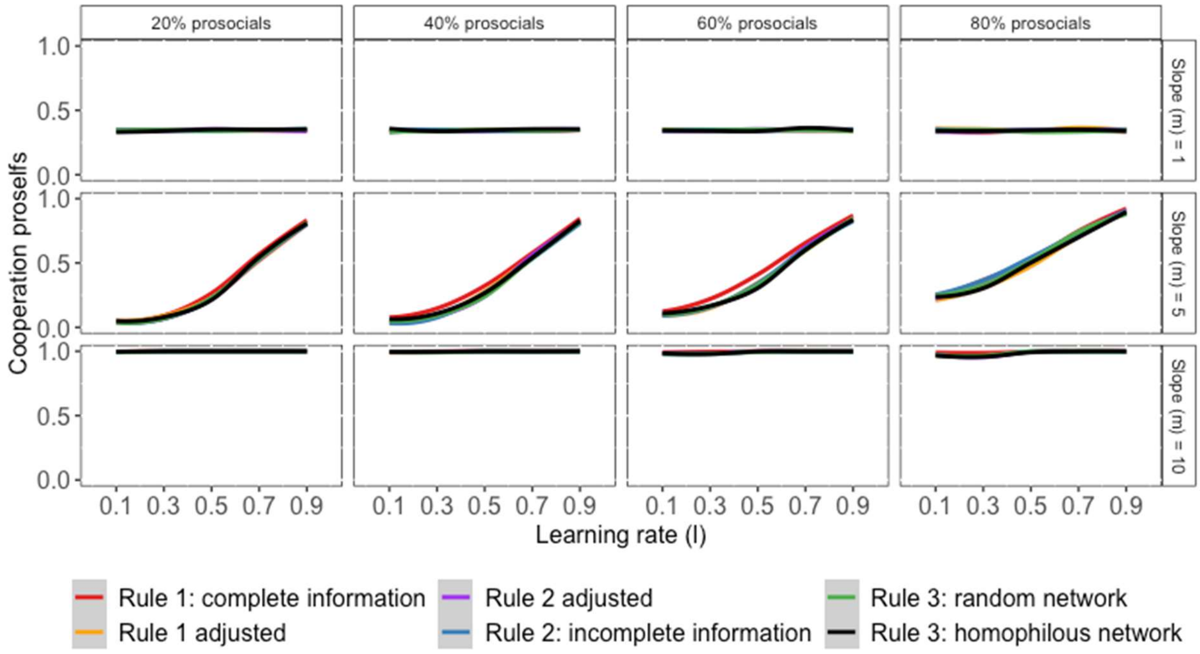

Figure A7. The effect of *m*, *l*, and *PA* on the mean level of cooperation of proselfs at iteration 400. Mean and 95% confidence interval are presented per rule.

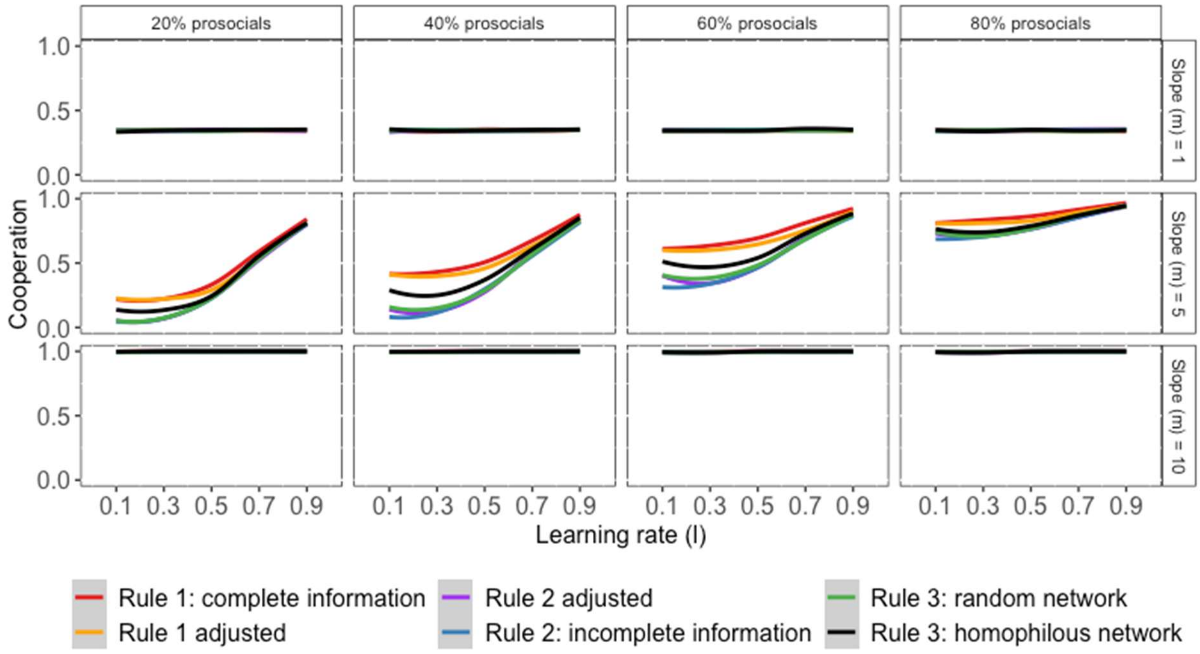

Figure A6. The effect of *m*, *l*, and *PA* on the mean level of collective cooperation at iteration 400. Mean and 95% confidence interval are presented per rule.

A9.2 Noise in Leave-Stay Procedure

Noise plays an important role in threshold models (Macy & Evtushenko, 2020), but it may also impact the leave-stay procedure. Some may wrongly want to leave the group, even if they are happy with group performance. We aim to answer if a higher level of noise in the leave-stay procedure impedes or promotes the effectiveness of meritocratic matching in the long haul (noise leave-stay incorporates values: 0, 0.01, 0.05, 0.25), all other parameter settings being equal. The parameter set refers to the chance of activation, meaning that with 0.25 there is a 25 percent chance of noise implementation. Also, the parameter refers to the proportion of stayers who are put in the leavers pool. For example, when we set noise to 0.25, then a random selection of 25 percent of stayers is put in the leavers pool. We run 100 independent simulations per condition. There are in total 6 x 4 conditions – matching and noise in leave-stay, respectively – realizing a total of 2400 simulation runs. We report the average level of cooperation of prosocial agents in Figure A8.

Figure A8 elucidates that noise in the leave-stay procedure does not promote or impede cooperation among prosocials, proselfs, or the collective, as well as for prosociality segregation in comparison to our main findings reported in the paper. Inserting more empty slots in groups and promoting more movement does not make our solution to the bad barrels problem stronger or weaker.

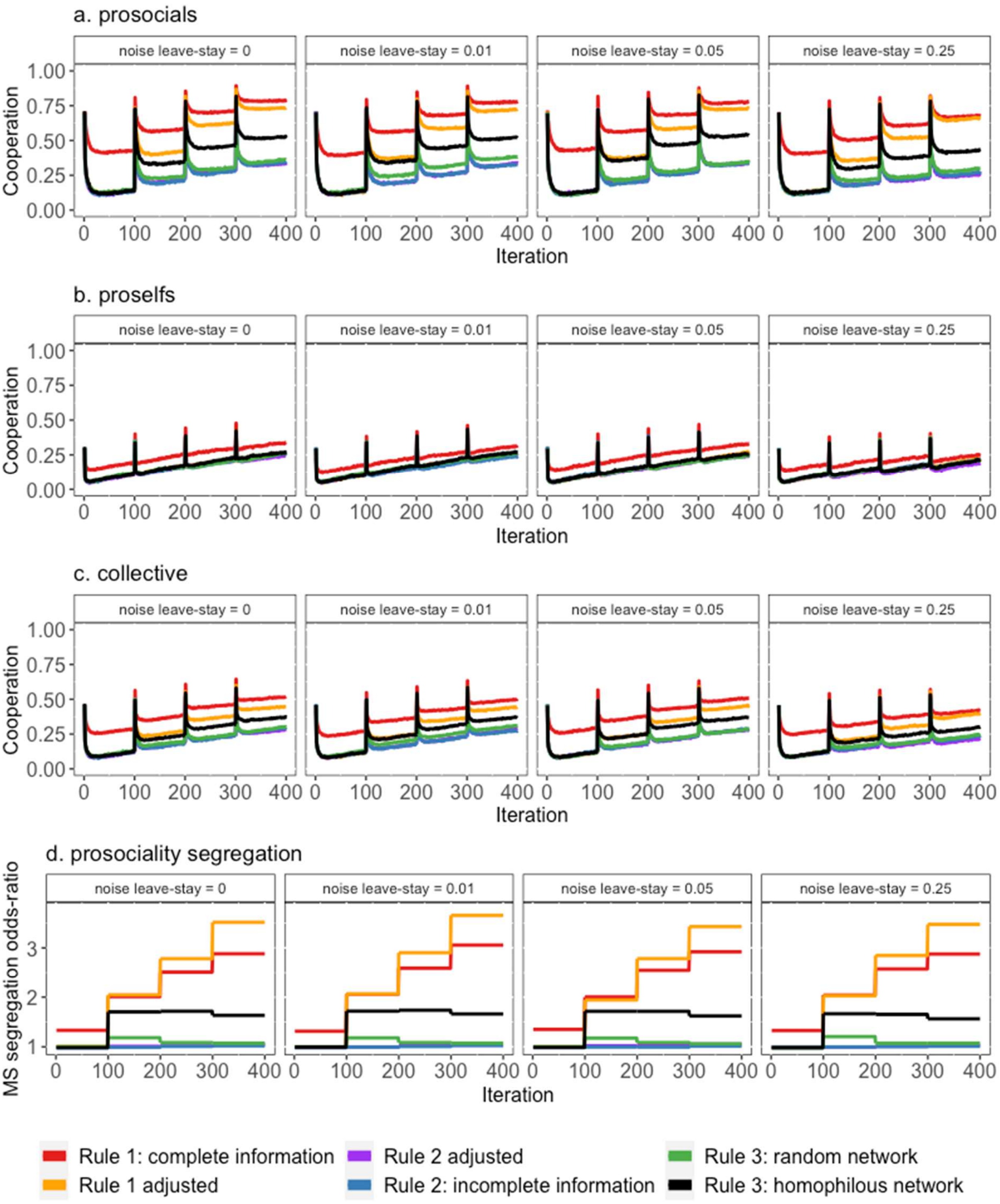

Figure A8. Robustness check of noise in the leave-stay procedure, separated per matching rule. We report the average level of cooperation among prosocial (a) and proself (b) agents as well as for the collective (c). The degree of prosociality segregation in the group context is reported in panel d. Parameter settings: $m = 5$; $l = 0.5$; $PA = 0.4$; $r = 0.05$.

A9.3 Altering Input Leave-Stay Procedure

Figure A9 shows that our findings are robust when altering agent-level input in the leave-stay procedure. 100 independent simulation runs per condition, a total of 1800 runs (6 x 2 x 100).

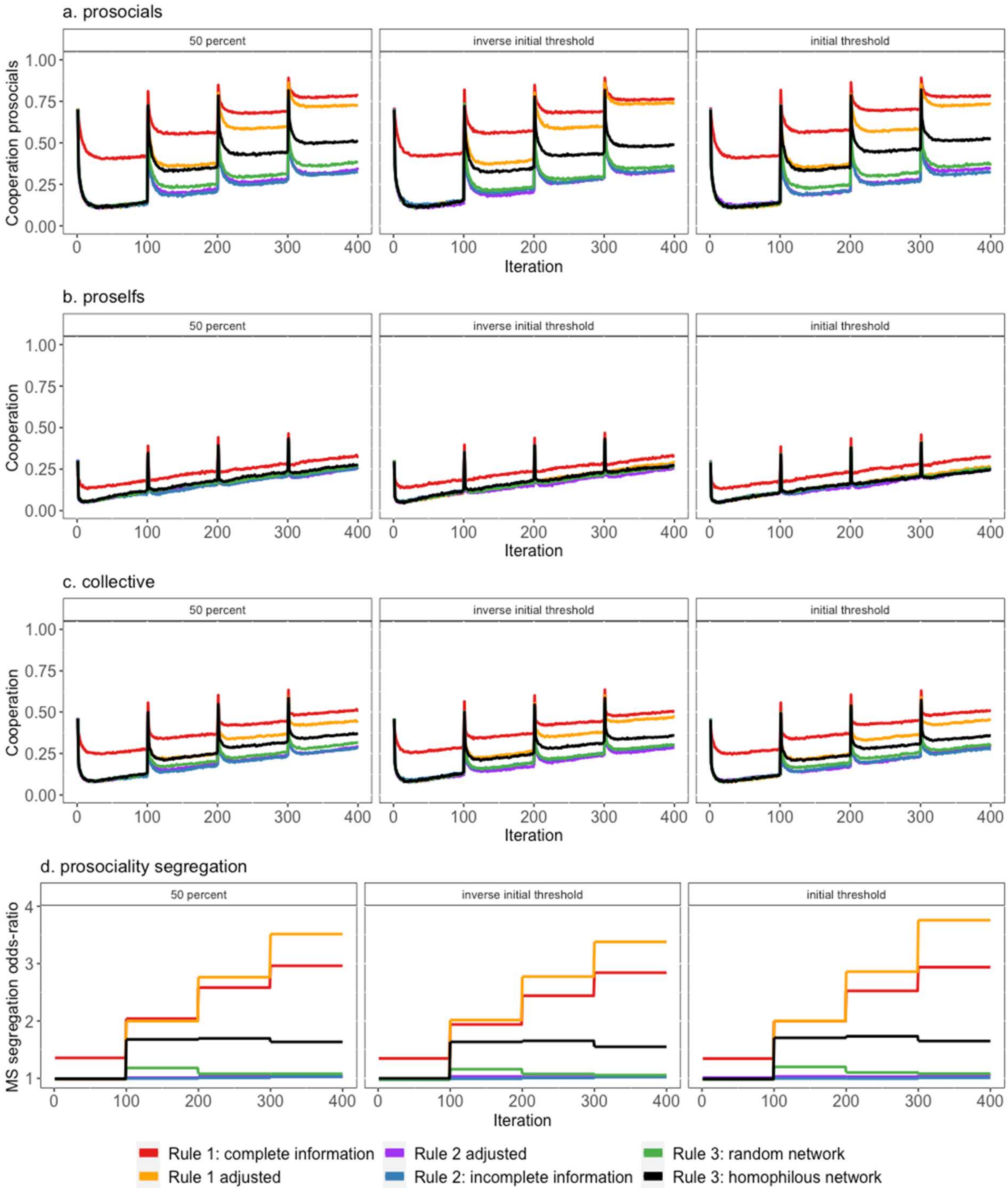

Figure A9. Robustness check of input in the leave-stay procedure, separated per matching rule. Agents leave either when $0.5 > G_{10}$, $1 - \tau_i > G_{10}$, or $\tau_i > G_{10}$. The baseline in the paper is $\tau_i > G_{10}$. We report the average level of cooperation among prosocial (a) and proself (b) agents as well as for the collective (c). The degree of prosociality segregation in the in the group context is reported in d. Parameter settings: $m = 5$; $\iota = 0.5$; $PA = 0.4$; $r = 0.05$.

A9.4 Chances Network Dyad Selection

In this section, we inspect if the homophily solution still works when we vary the chances of dyad selection. Parameter *r* was set to 0.05, reflecting a 5% chance of being selected as a dyad to play the 2-person PD in the social network. We question if agents are still able to differentiate in the social network between prosocials and proselfs when the chances of interaction are slimmer or higher ($r = \{0.01, 0.05, 0.25, 0.5\}$), all things being equal. The upper bound is $r = 0.5$ because a dyad consists of two agents. We run 100 independent simulations per condition. There are in total 6 x 4 conditions – matching and *r*, respectively – realizing a total of 2400 simulation runs. We replicate all figures reported in the paper but separate per value of *r*.

We deduce from Figure A10 that it becomes harder to differentiate between prosocials and proselfs in the social network when the chances for dyad selection increase. Prosocial agents cooperate across the board at a higher degree (Figure A10a), albeit somewhat lower in homophilous social networks. This makes sense because cooperation cannot cascade freely through the network but is restricted via behavioral homophily. A prosocial defector, surrounded by cooperators, may not be selected as an interaction partner when behavioral homophily is allowed. Proselfs learn more quickly to cooperate when chances for dyad selection increase, facilitating possibilities to learn how to cooperate (Figure A10b).

Our network and homophily solution for the bad barrels problem only works when agents can readily differentiate between types. Rule 3 with homophily is still more beneficial than other incomplete information rules when $r = 0.25$ (Figure A10c-e). However, the benefits of homophilous networks and information derived thereof disappear completely when $r = 0.5$. When *r* increases, the complete information matching rules are the best solution to increase cooperation. Prosociality segregation decreases from approximately 1.60 to 1.05, $r = 0.05$ and $r =0.5$, respectively (Figure A10f).

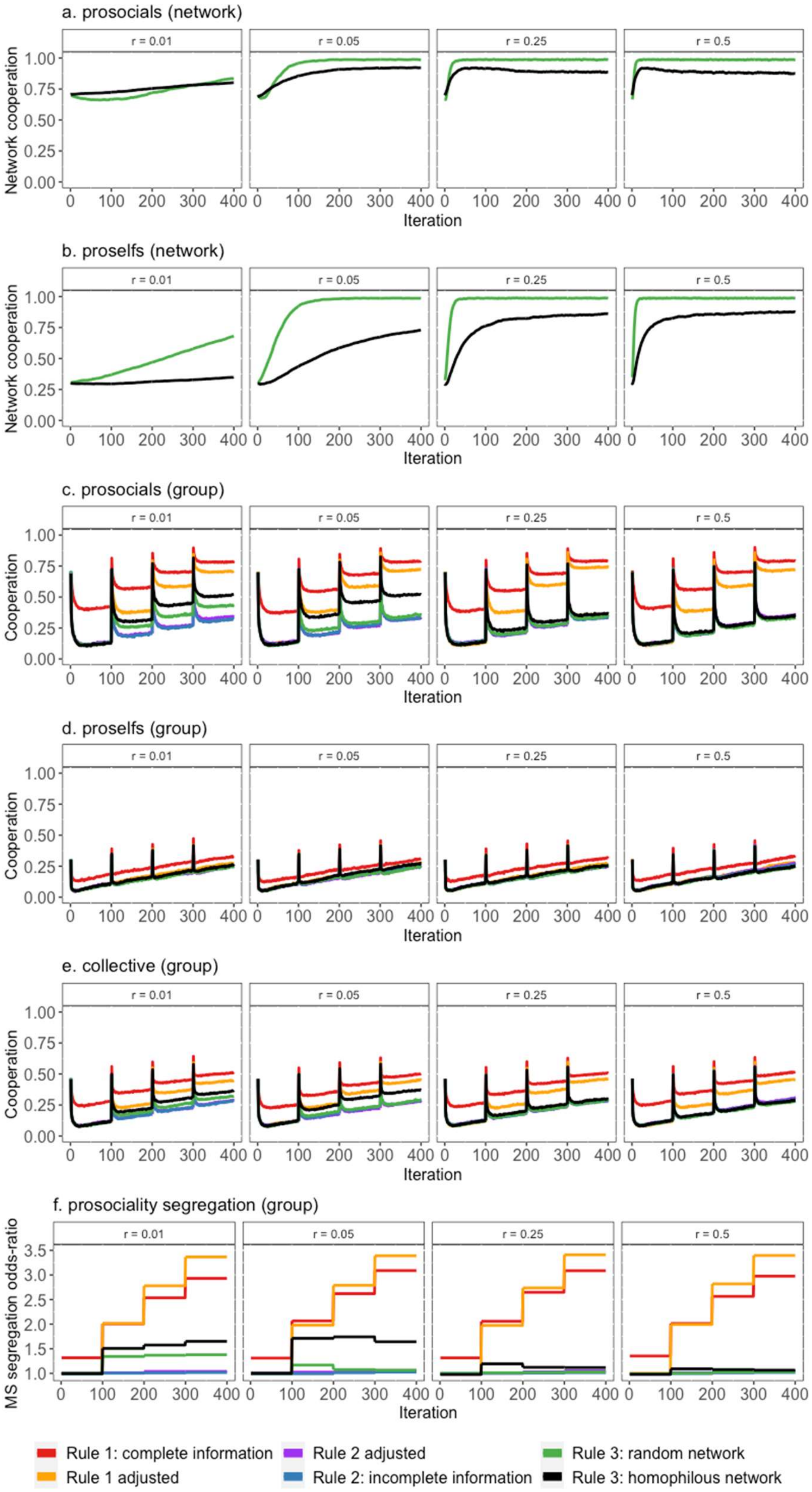

Figure A10. Impact of the chances of network dyad selection (r) on network cooperation (a-b), cooperation in the group (c-e), and prosociality segregation in the group context (f), separated by matching rules. The chances for dyad selection in the network differ, ranging from the lower bound ($r = 0.01$) to the upper bound ($r = 0.50$). Parameter settings: $m = 5$; $l = 0.5$; $PA = 0.4$.

A9.5 Impact of Behavioral Homophily on Model Outcomes

Here, we test how robust our findings are when behavioral homophily is implemented or not. We noted in the paper how structural homophily is implemented in the network. Prosocials are more likely to form ties to prosocials than to proselfs. The network solution is rather probabilistic, still allowing for ties between proselfs and prosocials. We also implemented homophilous tendencies in 2-person PDs. Namely, behavioral homophily governs the interaction of agents. Cooperators only interact with other cooperators, leaving defectors to interact with other defectors. The only option for defectors to interact with cooperators is to change behavior from defection to cooperation. We inspect the consequences of removing behavioral homophily as rule affecting who interacts with whom in the network. As such, we inspect the upper boundary of a favoring behavioral homophily rule protecting cooperators from exploitation by defectors and a lower boundary in which all linked agents can interact with one another. We ran 100 independent simulation runs per condition, matching rule 3 (homophily) x 2 (behavioral homophily), realizing a total of 200 runs. The findings of this robustness check are visualized in Figure A11.

We find that our model outcomes reported in the paper are fairly robust, qualitatively speaking. Yet, we find quantitively that our homophily solution fares slightly worse when behavioral homophily is not implemented. Prosocials still benefit when information from homophilous network is paired with information from the group context, but not as good compared to the condition when behavioral homophily is allowed (Figure A11c). An important reason why prosocials cannot harness their cooperative potential is the inability to differentiate between proselfs and prosocials regarding network cooperation. Figures A11a and b indicate that both types quickly learn to cooperate when behavioral homophily is not implemented. The inability to identify similar others then affects the chances to group up with similar others (Figure A11f). The homophily solution is thus less effective when behavioral homophily does not govern network interactions.

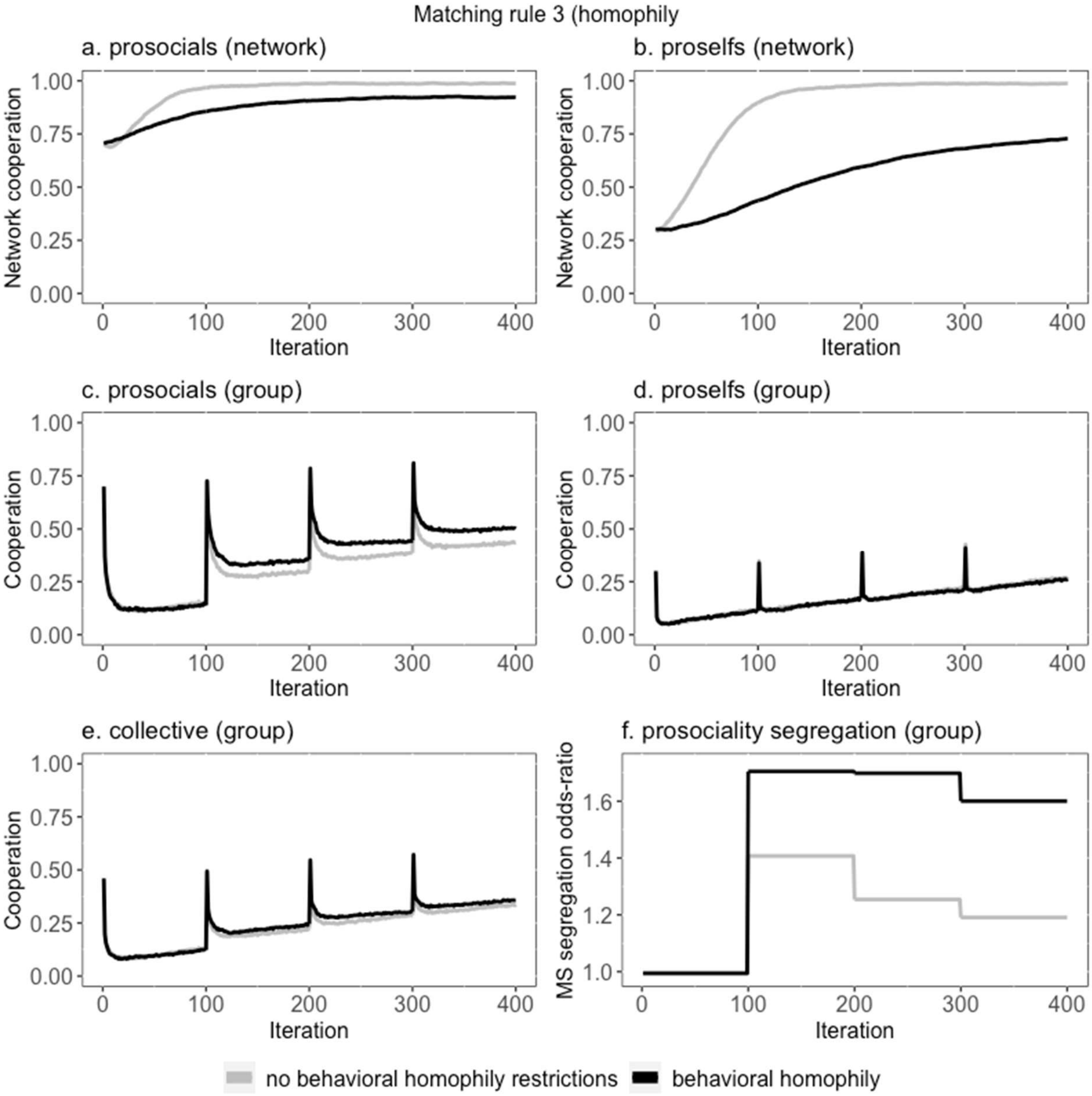

Figure A11. Impact of behavioral homophily on network cooperation (a-b), cooperation in the group (c-e), and prosociality segregation in the group context (f), separated by matching rules. Parameter settings: $m = 5$; $l = 0.5$; $PA = 0.4$; $r = 0.05$.

A10 Potential Model Extensions

Our model leaves room for several model extensions. Without specifying in-depth model adjustment, we report seven potential avenues for extensions. First, we aimed to build on the current literature on meritocratic matching by studying both prosocial and proself types as well as fixed next to adaptive thresholds to resemble individual and situational (i.e., group and network) influences. In the future, however, we may want to study more heterogeneity in the distribution of thresholds. For instance, agents could randomly draw an initial threshold from a normal, uniform, or polarized distribution (Macy & Evtushenko, 2020).

Second, initial thresholds can be affected by long-term learning effects in which one gradually adapts thresholds accordingly. Positive (negative) outcomes may gradually lower (increase) one's initial threshold. Agents may, for example, lower their initial threshold to a new initial threshold ($\tau_{i,\mathrm{new}}$) when $\tau_{i,t}$ is lower than τ_i.[2] Contrarily, ($\tau_{i,\mathrm{new}}$ increases when $\tau_{i,t}$ is larger than τ_i. For example, if a prosocial has a $\tau_{i,t} = 0.9$, then ($\tau_{i,\mathrm{new}} \approx 0.5$. This extension would lead to an all-out adoption of the learning perspective.

Third, prosocials' fixed initial thresholds play an important role after joining a new group, but adaptive thresholds may incorporate some fixedness. For example, prosocials may throughout the game be more likely to cooperate than proselfs.[3] Normally, prosocials cooperate at a probability of 0.18 when $\tau_{i,t} = 0.3$, $k_t = 0$, and $m = 5$ compared to 0.26 with an added fixed prosociality effect of, for example, $a_i = 0.1$. Then we have a reversed ceiling effect. Practically, including $a_i = 0.1$ would shift the logistic function structurally upwards for prosocials.

Fourth, a step towards adding more matching dynamics can be to rely on a-synchronous matching in which agents can try to leave and join groups on their own accord. This resembles situations in real life when individuals quarrel with others in their group, resulting in some wanting to leave. Still, a-synchronous matching requires other fixed parts of the ABM to be adjusted, e.g., deviating from fixed group sizes and centralized leave-stay moments, while requiring a group acceptance and exclusion procedure. We leave this for future model considerations.

Fifth, including network information incorporates asymmetry of information. Some have local information about others' social network efforts, while others only have group information. But asymmetry can also occur within and between matching rules. Some agents may have complete information about the individual merits of a subset of agents, while they have incomplete information about another subset. Even a tiny piece of individual information shows to ease the detrimental effect of group merit for cooperation in general (Nax, Perc, Szolnoki, & Helbing, 2015).

Sixth, homophily shows to buffer the bad barrels problem, but we can also envision findings the 'sweet spot' of homophily. We could question the upper and lower level of homophily required to aid spoiled prosocial agents. A consequence of this extension would be that we depart from the probabilistic nature of the random spatial graph algorithm, allowing us to vary the degree of homophily, e.g., from 0 (no homophily) to 1 (full homophily).

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[2] $\tau_{i,\mathrm{new}} = \tau_i \, / \, \{\tau_i + exp[-(\tau_i + \tau_{i,t})]\}$

[3] $p_{i,t}\,(c_{i,t} = 1) = 1 \, / \, \{1 + exp[m(\tau_{i,t} - k_t - a_i)]\}$

Seventh, agents may have different dyadic information per partner. Some may have a positive view of an agent, while others perceive the agents to be defective. Agents would then have different tabs about their network partners. Again, the consequence for the model may be severe as this extension may create peculiar dynamics of some not wanting an agent in the group while others do. We would then need to design an acceptance rule.

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