



Modelling the transition from animal to human culture

A statistical study of community splitting

Master's thesis in Engineering Mathematics

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CHALMERS UNIVERSITY OF TECHNOLOGY

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Abstract

How human culture came to complexify in an explosive manner and become incomparable to any other animal culture is as interesting a question as it is challenging. It has recently been proposed (the social protocell hypothesis) that the earliest steps toward human culture were taken (some 2-3 million years ago) on the level of social communities and their collective behavioural patterns, rather than, as commonly believed, on the individual level of social learning with the emergence of high fidelity copying capacity of cultural know-how. The hypothesis proposes that the crucial inheritance of information occurred on the community level, through high fidelity copying of systems of culturally learned traits through events of *community splitting*.

The aim of this master thesis is to develop, test and propose some novel analytical tools for studying spontaneous community splitting that can serve in further investigations of the social protocell hypothesis. Specifically this study develops theory to predict the fidelity of primitive cultural knowledge in community splitting. Using a parameterised theoretical setting of a primitive human community, the concept of institutions as systems of traditions is introduced and serves as a hypothetical prototype of the social protocell proposed in the social protocell hypothesis. Then a theoretical expression for the institutional fidelity as a function of the parameters is derived.

The fidelity expression is tested and analysed. It is tested through simulations, both of the theoretical setting and of more general settings where some assumptions have been relaxed. Results show estimated fidelity values in the theoretical setting indeed converging with theory, and that in the more general setting, when deviations emerge, they still largely maintain the same trends and long term behaviours predicted by theory. These results indicate the expression is useful for qualitative analysis in a more general setting than in which it was derived, and that further analysis could provide relatively simple transformations for making the same expression useful also for more accurate quantitative results, in a general setting. The expression is further used to analyse fidelity behaviour in different parameter spaces, and results show high fidelity community splitting could indeed relatively easily have been achieved for institutions of primitive communities, indicating strong support for the social protocell hypothesis.

Keywords: social protocell hypothesis, cumulative cultural evolution, origin of human culture, transmission fidelity

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1 Introduction

The family of great apes of which we are proud members is called the hominid branch of the evolutionary tree, and includes today's orangutans, chimpanzees, bonobos and gorillas (Wilson and Wrangham, 2003; White et al., 2009). It emerged from the superfamily of apes (hominoids) some 20 Mya (MacLatchy et al., 2015), that in turn had emerged from the branch of old world monkeys some 5-10 million years earlier (Stevens et al., 2013; White et al., 2009). Our last branching from other still existing ape species was the divergence between the *panin* and *hominin* taxa, with the panins including today's chimpanzee and bonobos and ancestors thereof, and hominin being the ancestral bipedal branch out of which our *Homo* species emerged (Pontzer, 2012; White et al., 2009). The description of the ape-to-hominin-to-homo development as simple linear branching events is today considered a great over-simplification of what was rather a web of complex and to large extent unknown speciation and hybridisation processes stretching tens of million years (John, 2008; Milford and Caspari, 2008) but consensus is that by 4-5 million years ago the to-be *Homo* branch was distinct from the *Pan* branch (MacLatchy et al., 2015; Pontzer, 2012; Prüfer et al., 2012). While the *Pan* branch has shown relatively little changes from that point to today's modern chimpanzees and bonobos (Andersson and Törnberg, 2019; van Schaik, 2016), the *Homo* lineage has seen dramatic changes during the course of these 4 million years. It is safe if not understating to say the state of a modern human was utterly inconceivable in the mind of our primitive ancestors. Unlike all others, our lineage went on to see the mastering of fire, the complexification of tool use, an agricultural and a technological revolution, expansive civilisations, expression and language, exploration and trade, debate and morality, energy use and transportation, money and politics, philosophy and ideology. Individualism, human rights, social security, weapons, science, globalisation, world wars, finance, internet, and today's very real possibility of self destruction. To make things further more puzzling, all this happened while we still to this day genetically resemble our chimpanzee relatives by 99% (Prüfer et al., 2012; Tomasello, 1999) which is same level of relatedness as that of lions and tigers, horses and donkeys, rats and mice (Tomasello, 1999; King and Wilson, 1975).

Understanding the mechanisms behind our species' unique and explosive cultural evolution is particularly challenging considering that we are our culture's very building stones and considering that culture fundamentally defines our being. The subject lacks established theory and many proposed theories fail to fit the scarce and uncertain but continuously improving historical data (Andersson and Read, 2016; Andersson and Czárán, 2022). Recent years however have seen promising theoretical development on the subject, and it has been proposed that mechanisms from biological evolutionary theory could be relevant also in the study of human cultural evolution. A theory called the Social Protocell Hypothesis (SPH), see (Andersson and Czárán, 2022; Davidson et al., 2021; Andersson and Törnberg, 2019), suggests the complexification of our lineage took place on a social level before it took place on a individual (intellectual) one, creating and evolving new collective bodies rather than evolving our own biological bodies (brains). The theory refers to the *setting* of adaptive collective bodies as a 'social protocell', emphasising a parallel to biological evolution, where the biological protocell was the *setting* of spontaneously cooperating genomes which began to faithfully copy, leading to the emergence of life (*bionta*) (Eigen, 1971; Smith and Szathmary, 1995). In the case of the *social* protocell, it is proposed that the cooperating components of the collective body instead are abstract, specifically simple skills of primitive hominins, but that analogously the skills spontaneously joined together in a community in benefit to both individual and community. It is argued that the presence of a beneficial collective body in a community would much like in the case of the biological protocell cause incentive for increased population growth, and further that the probability of the community splitting due to instability will firmly grow with community size,

as will the probability that the community will split due to instability (Davidson et al., 2021; Feldblum et al., 2018; Dunbar, 1993). What this deduces to is that community splitting can be assumed to eventually occur in communities with beneficial collective bodies, which provides a copying mechanism for the social protocell as cell division did for the biological protocell. While referring to the beneficial *setting* as a social protocell, including the crucial dynamical components of splitting and faithful copying, the beneficial collective *body* per se is referred to as a *sociont*, another parallel to biology where *biont* refers to all living things (Survey, 1930; Andersson and Törnberg, 2019).

A vital question for the SPH is how well could socionts survive community splittings. Before the human innovation of permanent writing systems, collective knowledge and traditions would permanently disappear if crucial individuals were to forget, decease or destructively rearrange. Thus a sociont would be existentially dependent on both social spreading, and non-destructive community rearrangements. In the cases that a community split *could* be a non-destructive rearrangement for the sociont, meaning the sociont could proceed to exist in the post-split sub-communities, it would not only support stable existence of collective knowledge and skill, it would also infer a heavy evolutionary potential, or in other words the presence of a social protocell. We call the capacity of sociont persistence in a split *transmission fidelity*, a borrowed term that can be found in literature both on biological and cultural evolution (including the SPH).

1.1 Aim and scope

The aim of this thesis is to explore transmission fidelity of community splits in the hypothetical social protocell. The specific aim is to develop, test and propose analytical tools that can be used in qualitative and quantitative study of cumulative cultural evolution, with a special focus on the social protocell hypothesis (SPH). Procedures used in the SPH are followed here to develop a theoretical model community of primitive hominin agents, including a simple mechanism of community splitting and the concept of institutions as the cooperation of simple traditional skills. The setting is parameterised and analytical expression for the fidelity of institutions is derived as a function of the defined parameters. This expression is then compared to results by simulations of community splits, to determine convergence. The expression is also used to theoretically analyse fidelity in different parameter settings and identify interesting behaviour. The potential for generalisation of the expression is also explored, through simulations of more general community setting where a crucial assumption for the theoretical model is relaxed. Finally an evaluation is made of the usefulness of the defined fidelity quantity and its implications in the context of the SPH.

2 Background

2.1 Animal culture

We often claim it for ourselves, but culture is not unique for *Homo Sapiens*. Animal culture is an elaborated scientific topic on the transmittance of social behaviour of non-human species, both amongst peers and between generations (Whiten, 2019; Brakes et al., 2021). In a large variety of species one can identify evolved behavioural strategies, traditions and knowledge. Examples include socially learnt migration routes (Carroll et al., 2015; Mueller et al., 2013), avoidance of unsafe geographical areas (O’Corry-Crowe et al., 2020), vocalisations and acoustic codes for communication (Anne et al., 2011), foraging strategies (Kühl et al., 2019), and

predator avoidance strategies (Kierulff et al., 2012).

2.2 Open questions concerning cumulative cultural evolution

The idea that human culture diverged from animal culture through cumulative evolution is by now a fairly rooted proposal, not unique for SPH (Boyd and Richardsson, 1985; Foley and Gamble, 2009; Montrey and Shultz, 2020). What is meant is that cultural elements such as ideas, materials and technologies, began to evolve through social spreading and became prone to natural selection, thus growing all the more complex. A compelling definition of cumulative culture is one from the Cumulative Cultural Evolution research group at the Santa Fe Institute as follows: 'something that no individual could have produced on their own' (Ferdinand, 2018). It is established that a requirement for cumulative cultural evolution is the ability for preservation and transmission of cultural elements both between peers and generations. Also established is that this in turn requires social learning which requires faithful copying at some level. But specifics on what exactly were the cultural elements, or the driving mechanisms and level of copying, remain open topics. As a consequence so remains the historical dating of the emergence of cumulative cultural evolution (Andersson and Törnberg, 2019; Ferdinand, 2018; Tomasello, 1999).

A large variety of definitions of 'modern human behaviour' can be found in the literature. In this study I choose the emergence of clothing, art and abstract symbolism, dating up to half a million years ago (Galway-Witham et al., 2019), to define the emergence of 'early modern' (EM) *Homo Sapien*. From this point and on, it is agreed that the human brain had the capacity to imitate sophisticated cultural elements off one another (Andersson and Czárán, 2022; Tomasello, 1999). Before this point, we will refer to this period as 'pre-EM hominin' or 'early hominin', it is argued that social learning by imitation occurred only on a much more elementary level (Tennie et al., 2020b; Galef, 1992; Tomasello, 1999). To specify, (Tennie et al., 2020b) describes the pre-EM level of social leaning roughly as follows: by observing the existence of the skill in a peer, one was in principle as likely or more to produce an independent version of it alone (emulation), as of copying the exact actions of the observed skill of the other (imitation). Tennie denotes the categorical space of skills of the lowest level, as the Zone of Latent Solutions (see (Tennie et al., 2020b,a)), this notation will be used in this study as well. Given the Zone of Latent Solutions (ZLS) for pre-EM hominins, one could in hastiness conclude that cumulative cultural evolution did not begin until the emergence of the EM human. This conclusion is attractive because from the point in time of EM humans one has a clear channel of cultural knowledge: simply the faithful copying of the innovative solutions (cultural elements) of ones peers, which paves the way both for evolution of the cultural elements themselves, and for evolution of the human brain in the direction of improved social learning mechanisms.

But as the SPH argues, concluding the above leaves important issues unresolved (Andersson and Czárán, 2022). The conclusion implies that the millions of years of *Homo* evolution leading up to the point of EM humans, was simply genetically driven. Although this is a long time comparing to the 200 000 years of EM human development, in terms of genetic evolution it is very brief and arguably not enough to explain high levels of complexification leading up EM *Homo Sapien* (Andersson and Czárán, 2022; Tomasello, 1999). Further, findings show that complex cultural behaviour had emerged long before the EM human. Already around 2 million years ago, records show the homo lineage had accumulated sufficient cultural knowledge for tool aided, cooperative big game carnivory, from which followed active hunting and handling of large variation of habitats emerged (Andersson and Czárán, 2022). This marks a clear divergence

from the *Pan* lineage culture and any other animal culture to this day, and the SPH states that this is the actual point where cumulative evolution of human culture emerged. What follows is the SPH proposal of how.

2.3 The Social Protocell Hypothesis

The SPH proposes an alternative scenario where the for-cumulativity-crucial copying took place on a collective level instead of on a individual one. The scenario is one of primitive hominin communities with coexisting low level skills in individuals, that spontaneously coincide and create more complex cultural elements. The SPH calls this collective cultural element *institution*, and its components, the individual cultural elements- *traditions*. The individual traditions are in this scenario imagined simple enough to have existed and spread already in social pre-EM hominin communities, meaning they fall under the ZLS, and copied between peers by imitation or emulation. We will jointly refer to copying by imitation or emulation as pre-EM social learning (Davidson et al., 2021; Andersson and Czárán, 2022). The idea is that such institutions became prone to cumulative evolution before than any individual tradition did. (Andersson and Törnberg, 2019) calls this a 'culture first' scenario. But institutions exist on the community level, and so for cumulative evolution to emerge, there needs to have been inter-community copying. The pre-EM social learning of traditions on the individual level, although crucial for an institution to grow and adapt *within* a community, is not believed to have occurred significantly *between* communities (Davidson et al., 2021; Chivers, 1987; Wilson and Wrangham, 2003). But SPH suggests that inter-community copying did indeed occur on the level of institutional cultural organisation, via the growing and splitting of early hominin social communities.

Experimental evidence shows that social communities do not grow limitlessly, but tend to reach socio-economic population limits at which communities will split into smaller communities due to increased tension and conflict (Dunbar, 1993; Hill and Dunbar, 2003). Here lies the evolutionary potential of institutions according to the SPH. If the community split is such that existing institutions stay present in emerged sub-communities, there are now *more* communities that carry the same institution and an institutional copying has occurred. Whats more, suddenly the setting is ready to repeat this cycle. Emergence of such a steady grow-and-divide cycle, paves the way for variation and natural selection thereof (Norris and Raine, 1998). The SPH setting provides a plausible way of cumulative cultural evolution emerging earlier than the EM human and so the setting allows for the possibility that human culture complexification preceded and even caused human brain complexification. But the SPH does not settle here. Variation and natural selection happen to be the key elements for evolution of living organisms (Norris and Raine, 1998; Eigen, 1971; Ganti, 1996). The SPH proposes this is no latent coincidence. The suggestion is that adaptive institutions of traditions, went so far as to develop into an entirely novel evolutionary individual, what we refer to as the *sociont* (Andersson and Törnberg, 2019).

The adaptive institutions (socionts) are upheld and driven by *Homo* individuals and specifically their traditions, but exist and function on a level above and beyond any single individual or tradition. In evolutionary biology, events of lower level components joining together and creating a novel higher level component, is not new. Phenomena of such micro-to-macro transitions go under the name Evolutionary Traditions of Individuality (ETI) and have well established theory (Smith and Szathmary, 1995). Such transitions have occurred several times during the course of biological evolution, and are believed to account for the greatest complexification events in natural history including the origin of life, eukaryotes and multicellularity (Smith

and Szathmary, 1995; Hanschen et al., 2018; West et al., 2015). While not being the first to propose the occurrence of a cultural ETI event somewhere along the the homo lineage (Waring and Wood, 2021), SPH is first to date the event to 2-4 million years ago, possibly relating it to our divergence from the pan-lineage. It is also first to offer specifics of an actual such evolutionary entity, as well as mechanisms of its development.

The SPH was formally published in 2019 (Andersson and Törnberg, 2019), in this paper the authors extensively describe the constituting concepts and argue for their plausibility and likelihood using historical context. In (Davidson et al., 2021) the hypothesis was further strengthened, as formal criteria was used, developed for assessing evolutionary individuality of biological units, to test the theoretical social protocell setting The criteria included existence of spatial and temporal boundaries, indivisibility, and evolutionary division of labour, amongst others. The results found that the social protocell could indeed have led to evolutionary individuality according to these criteria. Further, using the *Pan* lineage (including modern day chimpanzees) as a proxy of early hominin culture, it was confirmed that evolutionary transition into individuality of the social protocell indeed could have begun already in the hominin lineage by 2-2.5 Mya. Currently in press, the paper (Andersson and Czárán, 2022) further develops the hypothesis through agent based modelling, testing by simulation the idea of institutions of simple ideas emerging and complexifying over generations through community splitting. Results show that in the presence of both social spreading of *ideas* on agent level, and community-level spreading of *systems of ideas* through growing-and-splitting mechanisms, accumulation and complexification of such systems are indeed plausible.

3 Description of setting

This section describes a theoretical setting of a hominin community. The concepts and notations of this section are borrowed from the works of SPH and some of the borrowed elements have already been mentioned and somewhat described above. Thus, although the following setting and its derivation aim be to logically plausible and self-sufficient, in the case that this was not successful, I refer to (Andersson and Törnberg, 2019; Davidson et al., 2021; Andersson and Czárán, 2022), for more extensive and historically contextualised descriptions of the components, all notations used here are shared with ones in the SPH works. A note is needed to specify that not an entire setting has been borrowed, just consisting components, one can find several more components present in the SPH works that have not been used here. In the future explicit reference to the SPH works is there only when necessary due to some specific parallel, but a constant underlying reference to the SPH exists in this section.

3.1 The community

Let us imagine a group of primitive hominin individuals coexisting on a land which offers them a sufficient amount of retrievable nutritional resources to stay and survive. We call the coexisting group of individuals a **community**, and the individuals we call **agents**. On the land there exists different types of resources with varying accessibility. Further imagine the agents have spent enough time there or on similar land to have developed certain knowledge and skills to retrieve enough from the nature to survive. These will be referred to as **traditions**, inclusive to both skill and knowledge and consistent practice: imagine simply the ability and motivation to perform a function with a certain rewarding outcome. We assume them elementary enough to have emerged from spontaneous innovation by single hominin individuals and can easily be

maintained without copying any detailed underlying know-how (ZLS, see section 2.2). The traditions remain unspecified for generality, to avoid unintentionally specifying an environment. The level of recognition in an agent of a tradition as such is not either specified, which allows for traditions to be quite unconscious/implicit (primitive). The traditions are just beneficial enough for the agent to have developed the conscious or unconscious habit of receiving its reward. Further we regard all successful learning of an agents’ tradition by other agents, as new realisations of that same tradition, and call each realisation an **instance** of that tradition.

So, in different agents there exists instances of the same tradition. Further all realisations of the tradition by the *same* individual count as the *same* single instance. Imagine that the source of new tradition types are innovating agents that have tried something new and found some new value. The aim was to keep the imagined level of traditions and social learning on a plausible level of primitive hominin culture proposed by (Tennie et al., 2020b), see section 2.2. Imagine that the source of new instances of existing tradition types is either through independent innovation, or through social learning by imitation or emulation of some able peer agent. One can further assume however that social when possible is significantly easier than innovation and therefore more frequent.

A schematic overview of the relation between the components community, agents, tradition and tradition instances is shown in the figure below.

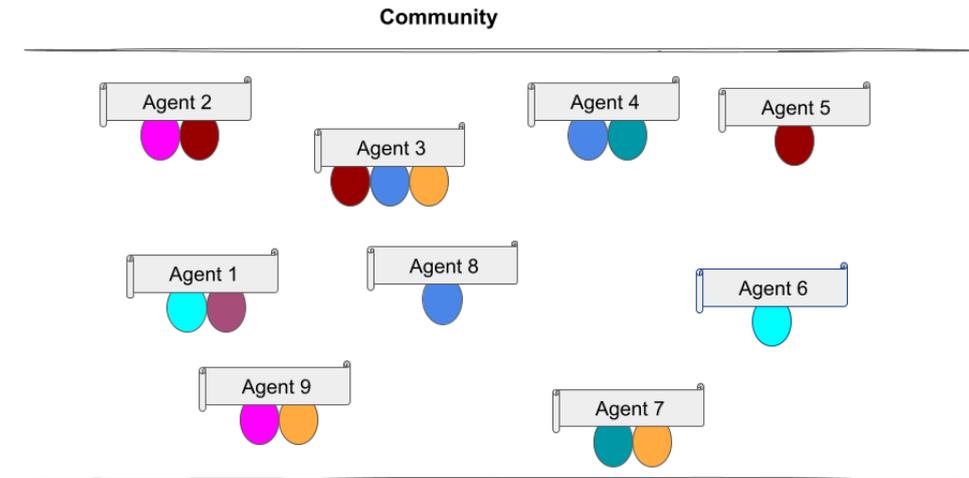


Figure 1: A schematic overview of the model components **agent**, **community**, **tradition** and **tradition instances**. The coloured circled dots are instances of traditions in able agents. Instances of the same tradition type in different agents share the same color.

3.2 The institutions

With tradition instances as building blocks, let’s proceed to assume that in some communities emerged traditions would be such that when performed together they result in a greater access to resources and so result in a fitness boost for the agents involved. We refer to such systems of synergetic traditions as *institutions*. We avoid specification of particular ways of cooperation and coordination in an institution, and just assume that it occurs as soon as the constituting tradition types sufficiently exist in the community (‘sufficiently’ will be defined through threshold parameter θ in parameter section 4.2). The institution may be organised or spontaneous, explicit or implicit, this also remains unspecified. The institutions are assumed beneficial for

both agent and community, so that once an institution is present in a community, it stays present and persists as long as 'sufficiently' many able agents exist to perform the necessary traditions. **The concept of institutions aims to serve as the prototype of a sociot.**

Figure below shows a schematic overview of an example of the model setting of a community that has an institution.

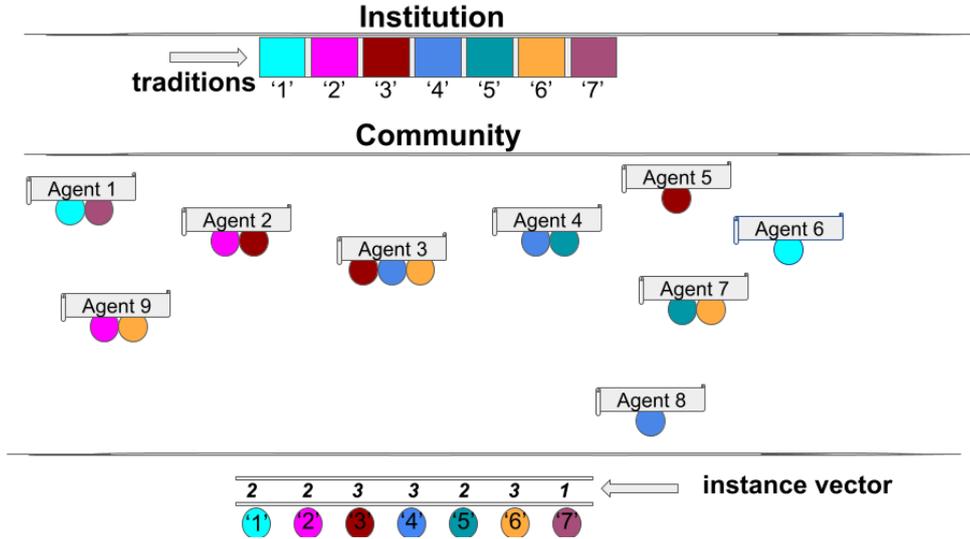
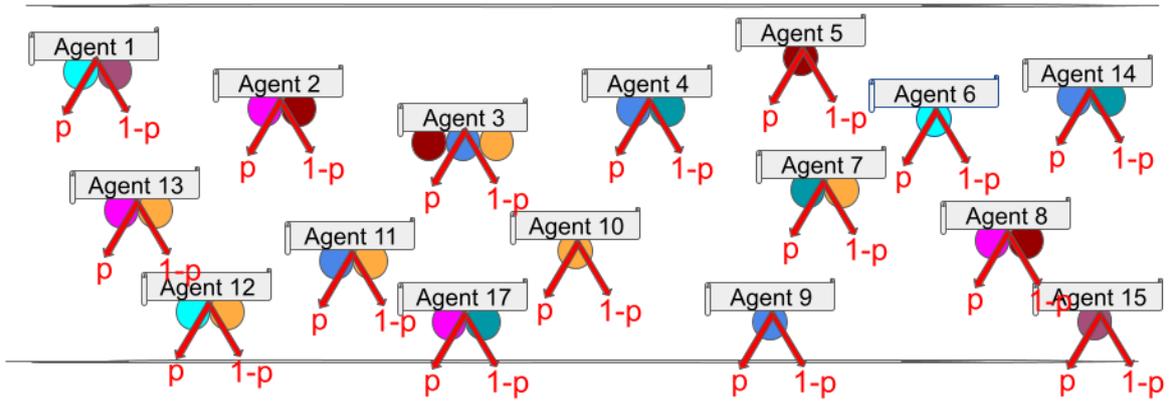


Figure 2: A schematic overview of the model components. The coloured circled dots are instances of a tradition type in able agents. The tradition types and their colours are listed above as components of the institution. Below is the instance vector, the count of instances for each tradition type.

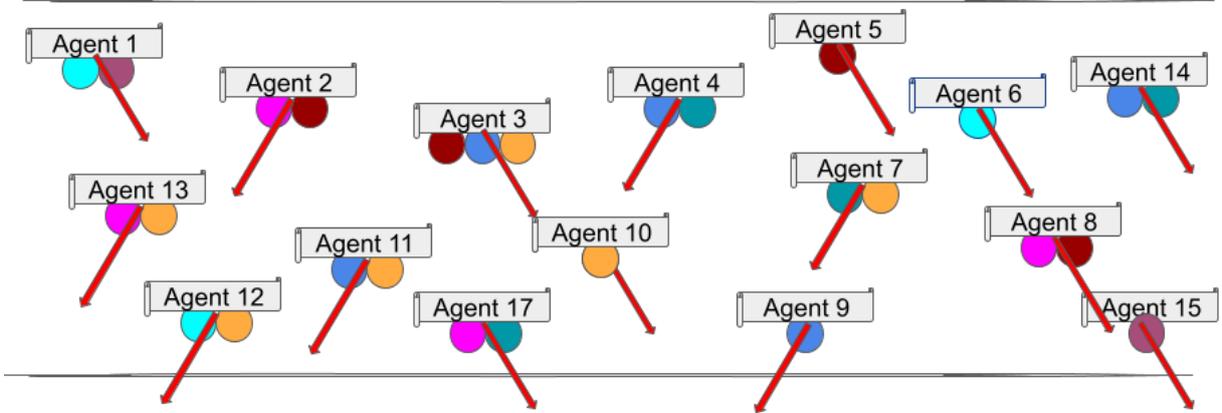
3.3 The split

The emergence of beneficial institutions is likely to cause general fitness increase for agents in the community and thus likely to cause an increase in the rate of population growth. Imagine the population grows until it reaches some socio/economic boundary of the community. It could for example be a point where the shared resources are no longer sufficient to provide for all members, or where the high population reduces peer affinity so that tension and conflicts occur. For whatever reason, instability is assumed to arise in the community structure and result in a splitting of the community into smaller stabler groups. Imagine the split splitting the population into simply two sub-populations, and being a spontaneous and unorganised event. The original community will hereon be referred to as the **mother community** and the two sub-communities emerged after split the **daughter communities**. Below figure 3 shows the schematic overview of how the split is modelled to occur. The figure includes a characterising parameter p , and shows how the split is realised by each single agent's independent choice of daughter community. The parameter p will be formally introduced and described in the following section, along with the other parameters.



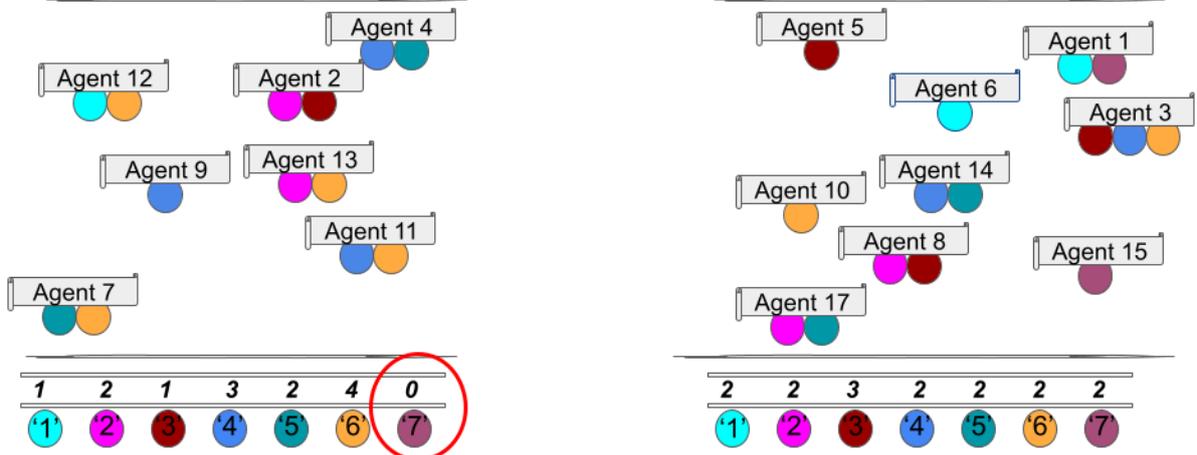
(a) Community about to split.

$p=0.4$



(b) Community under split, an example of setting $p=0.4$.

$p=0.4$



(c) Community after split, an example of setting $p=0.4$.

Figure 3: The pre, present and post stages of the splitting event shown in (a), (b) and (c) respectively. (a) shows an example model community, institution, and instance distribution. The community is under tension which has led to each member faced with a choice of between two sides. The choices are modelled as random with choice probability p of going left. (b) shows an example of the realisation of such a random choice for every agent, for the example value $p=0.4$. (c) shows the result of this realisation, the mother community has become two daughter communities in the split. Included below are the resulting instance counts for each daughter cell. One can see in this example that institution was not successfully transmitted to the left daughter community, as tradition type number '7', is missing (see red encirclement). But in the right daughter community, the institution has indeed successfully transmitted.

Recall now the main question of this study can be formulated as: what happens to the existence of institutions in a split? Or, which kinds of institutions survive and what kinds of splits? The next step will be to establish parameters inside the described setting with which one can distinguish different 'kinds' of institutions and community splits.

4 Mathematical derivation

4.1 Components

The components of the model setting derived above are gathered in the list below, after which characterising parameters of these components are introduced:

agent - a hominin individual

community - a group of agents that coexist on the same land and share resources

tradition - a simple function performed by agents to obtain some beneficial result. All functions with the same beneficial result are counted as the same tradition. The tradition is brought to the community through (possibly spontaneous) innovation by some agent and stays in the community through social learning. Realisations of tradition functions by able agents we call instances of that tradition.

instance - the realisation of a tradition by an able agent. The able agents carry one instance each and the rest carry none. Different instances of the same tradition need not share the exact actions, but have the same overall function and beneficial outcome.

institution - the spontaneous cooperation of a group of different traditions in a community. The cooperation is assumed to be a co-execution of a set of traditional types by agents, that the benefits themselves and the community as whole.

community split - the spontaneous splitting event of an unstable community into two stable daughter communities.

4.2 Parameters

Next some parameters are introduced to characterise the described setting. Some are taken straight from the SPH works, others are new parameters added to further nuance/specify the setting. The institution will depend on two parameters, **complexity** c , and **threshold** θ . Complexity c , is equal to the size of the institution, specifically the number of tradition types that compose it. The threshold θ is the minimum number of instances a tradition type needs to persist in the community. For the institution to be considered present, at least θ instances of all included tradition types must be present in the community. Note that all setting examples mentioned and shown in figures above have implicitly assumed a minimal threshold $\theta = 1$. The number of instances existing of each tradition type t in the institution are put in the **instance population** \mathbf{N}_t , which becomes a vector of length c , $t = 1, \dots, c$ and where each element is a count of how many agents currently hold the corresponding tradition. The community is characterised by the number of agents involved in sharing the resources and constituting the institution, **agent population** \mathbf{N}_a . A specification is needed to allow for the possibility that the number of agents involved in the institution and the number of agents enjoying its reward do not coincide. For example, if an institution leads to the seizing of a carcass, there might be resources left for a lot more agents than the ones involved in the seizing. In this case the parameter is specified to be the number of agents involved in maintaining the institution, and could also be called the *agent carrier* population. This number indicates how spread out the

tradition instances are amongst agent carriers and is more likely to affect fidelity. But the resource sharing population is likely more relevant for specifying the limit size of a community, and note this information is lost when choosing N_a as agent carrier population. Although an assumption could be made that at a moment of tension about to split, the resource population is likely not much larger than the agent carrier population. Keeping this in mind proceed with the agent population N_a is specified as the number of instance carrying agents.

The splitting event is modelled as the individual choice of each agent between the two emerging daughter communities, and the choice is random with probability p for one and $1 - p$ for the other. Probability p will define the balance between the daughter cells. If $p = 0.5$ the two daughter cells are equally chosen, in what we call a symmetric split. The further p moves from 0.5, the more unequally the daughter communities are picked, resulting in a bigger and a smaller daughter community. We call this an asymmetric split. So the level of symmetry of the split is determined by parameter p , which will be called **symmetry** p .

A table is made including all the setting parameters.

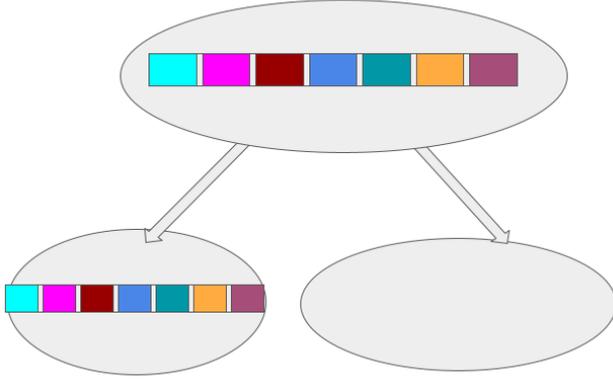
Symmetry p	The probability with which each agent chooses one daughter community over the other in a split. $p \in (0, 0.5]$ where $p = 0.5$ is a symmetric split where both daughter community choices are equally as likely
Complexity c	The number of existing traditional traits which together compose an institution
Threshold θ	The minimum number of instances that need to exist for every c traditional traits for the institution to be considered existent
Instance populations $[N_1, \dots, N_c]$	Vector including the number of instances of all tradition types in the mother community before split. Equivalent notation is $N_t, \forall t = 1, \dots, c$
Agent population N_a	The number of agents carrying at least one instance before split

Table 1: *Parameters*

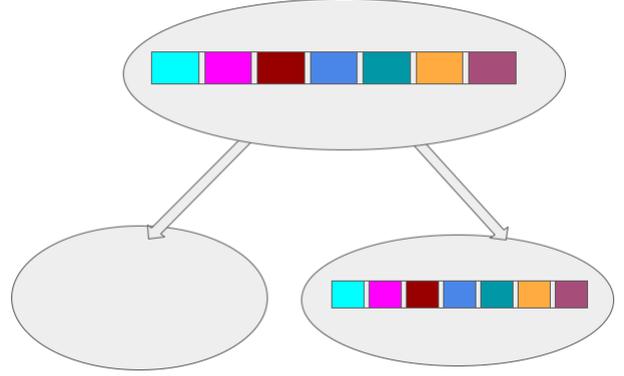
4.3 Defining fidelity

Next a quantity called fidelity is defined to determine the rate of successful institutional transmissions in a split. The aim is that the main idea of fidelity be the same here as in the works of SPH and works leading up to it, as well as lot of other literature on the subject of cultural or biological evolution: a quantification of the level of transmission of a system of information, in a rearranging event. In our case the system of information is the institution and the rearranging event is the community split.

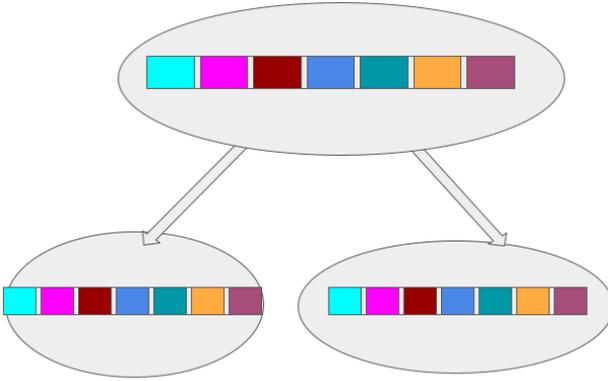
First note that the institution is considered either as complete or non-existent: as soon as one tradition from the institution is missing in the community we count the institution of complexity c as extinct. The following figure demonstrates the possible outcomes of the given community split:



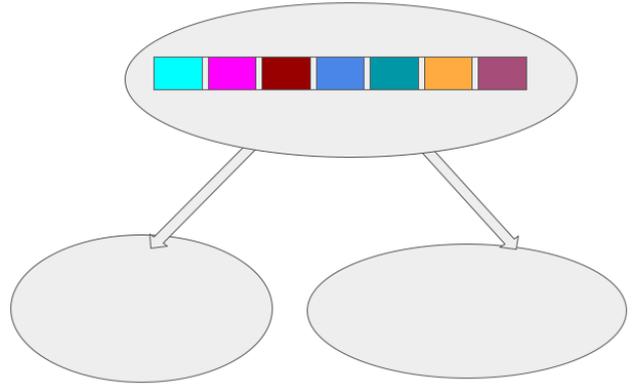
(a) The institution was successfully transmitted to one daughter community



(b) The institution was successfully transmitted to the other daughter community



(c) The institution was successfully transmitted to both daughter communities



(d) The institution was not successfully transmitted to any daughter community

Figure 4: Shows the four possible transmission outcomes of the community split

We group together outcomes 4(a) and 4(b) as the outcome of exclusively one transmission, and introduce a transmission count T indicating the number of successful transmissions after a split. Given the possible outcomes above, this number can be exactly 0, 1, or 2. Recall that successful transmission depends on θ , and is when at least θ instances of each tradition type composing the institution is present.

$$T = \begin{cases} 2, & \text{if the institution was successfully transferred to both daughter communities} \\ 1, & \text{if the institution was successfully transferred to exactly one daughter community} \\ 0, & \text{if the institution was not successfully transferred to any of the two daughter communities,} \end{cases}$$

Since the split has been defined as a random event, the transmission count T is a random variable. If the split would be repeated in the identical setting several times, an average transmission count of that particular setting can be determined. As one increases the number of repetitions towards the infinite limit, the average T starts to coincide with a theoretical expected value of the transmission count. This value is a deterministic constant uniquely defined by its particular setting. This value is what will be defined as **institutional fidelity Q** for a given setting. Recall that the setting is jointly described by the community, the institution, and the split, through parameters instance population vector $N_t, \forall 1, \dots, c$, threshold θ , complexity c , symmetry p and agent carrier population, N_a .

A note is needed because the exact definition of fidelity somewhat differs from others used in literature. The fidelity is usually defined as a likelihood between 0 and 1 of transmission. However in this setting of community splitting it is decided useful to distinguish between transmission to one or to two daughter communities, since these two outcomes implicate different rates of spreading. Expression of the likelihood of overall transmission will however also be derived and compared to the defined fidelity quantity, in section 7.4.

Another note is needed, on the question of what could be the fate of a daughter community left without institution, such as the left daughter community in 4(a) and the right daughter community in 4(b) above. In these cases at least one tradition type from the institution has gone missing. We will categorise this as a **loss** of institution, even though it was stated above in the definition of traditions that tradition types are easy enough to be innovated alone. One could argue then that the institution is likely to be resurrected. Indeed the possibility exists, but one can imagine that when the trait is present and can be socially learnt its incidence in the population will be much higher. Further, we assume that if a tradition type has disappeared it is as (un)likely to reappear as any other possible alternative is to appear. And thus we categorise an institution as lost once one of the constituting tradition types has been lost.

4.4 Interpreting fidelity

The question of what to make of a resulting fidelity value Q , needs elaboration. In rule the expected value of a discrete random variable is interpreted as the infinite average of the random variable. First note is that while the transmission count T is a discrete random variable with outcomes 0,1,2, fidelity is a theoretical mean that can take on values in between the actually possible outcomes, $Q \in [0, 2]$. When not exactly on 0,1 or 2, the fidelity value indicates that the outcome of the given setting has a significant likelihood of more than one of the possible transmission outcomes.

The three possible transmission values 0,1,2 can be ordered from closest to furthest from any given fidelity value. However, the degree with which closeness corresponds to likelihood is not unambiguous. Take the most extreme case of this for example, the mean value of 0's and 2's can land arbitrarily close to unity without including a single actual outcome of single transmission. But on the other hand unit fidelity can also be caused by exclusively single transmission outcomes. Ambiguity in the interpretation of fidelity exists for other outcomes than just unity but is indeed largest around unit fidelity due to the equidistance to 0 and 2. The region of fidelity values around unity (on both sides) will be referred to as *single transmission region*. As tools for analysing the ambiguity and obtaining more informed interpretations of fidelity, the *theoretical variance* of the transmission count will be derived along with fidelity itself, as the *fidelity variance*. The expression of overall *transmission probability* will also be derived and compared to fidelity values.

Note however that in the social protocell context, an adaptive institution (sociant) after a few generations of community splits would already exist in a good amount of communities, so that after not too long copies of the institution are frequently subject to community splitting. In this situation of a sociant in frequent community splitting the ambiguity of fidelity interpretation loses significance as the average result moves towards the fidelity value the more frequent the splits. On average the single transmission region will hold only one existing institution at the time and has thus no evolutionary spreading. It further means that the sociant is dependent on single communities which makes it existentially insecure. We will thus refer to unit fidelity and all lower values as the *maladaptive region* $Q \leq 1$ and the region above unity as the *adaptive*

region. The adaptive is the region where evolutionary spreading would be expected.

4.5 List of model assumptions

Gathered here are the crucial assumptions made for the model setting. Some assumptions have already been mentioned above (marked with 'E' below), others have up until now only been implicit (marked with 'I' below).

- **Traditions are elementary functions/skills** performed by **single agents**. Only combined with other traditions in so called institutions, can they reward a bigger group (E)
 - A tradition type has emerged by innovation of some agent at a previous point in time (E)
 - If $N_t > 1$ for tradition type t , more **instances** of the same tradition type have emerged in other agents through spreading by pre-EM social learning. (E)
 - If $N_t \geq \theta$ for tradition type t , we count tradition type as present: **adaptive and stably persisting** (E)
 - No distinction is made between tradition types, θ is the **same for all tradition types** (I)

-
- **The stable co-existence of a number of different traditions**, $t=1,\dots,c$, spontaneously permits cooperation between them in form of an **institution**. (E)
 - All existing tradition types ($N_t \leq \theta$) in the mother community will be assumed to be part of the institution (I),
 - The existence of an institution depends on **the existence of each one of its traditions**, meaning $N_t \geq \theta$ of each tradition type t are present in the community (E)
 - The existence of an institution solely depends on the above and thus is **unaffected by of the number of carrying agents**. (I)
 - **An existing institution is adaptive** by being beneficial to the agent carriers, and they continuously **express their instances in the institution** and not on their own.

-
- In this environment a **spontaneous split occurs** in the community due to instability
 - The split is **dual (E)** and **instantaneous (I)**
 - The split occurs as the **instantaneous and simultaneous choice of each agent** between **moving to one daughter community or the other**. (E)
 - The agents are conserved in the split meaning **all agents reach one out of the two emerged daughter communities** (I)
 - The traditional knowledge of each agent is also conserved in the split, **meaning each agent brings along all of its instances**.(I)
 - **The choice of an agent is independent of the other agent's choices**, and the choice probability p is **identical for all agents** (E)

4.6 The binomial assumption

One last assumption is separately added in this section. It is distinguished from the assumptions stated above in the sense that the model setting is complete without it, given the parameters and the already stated assumptions. Instead the following assumption is purely theoretically motivated, it allows for significant simplification in mathematical derivation of fidelity, as will be seen shortly. Given its independence from model setting construction, this assumption can easily be relaxed affecting only theory, not the model setting in itself. This is done as a final stage of this study.

As demonstrated in figure 3, the split is modelled as the event of every agent choosing one out of two daughter communities at random, each with the same choice probability p for one daughter community and $1 - p$ for the other. Such random dual-outcome events with constant choice probability, are called binomial trials (or Bernoulli trials) in theory of probability and statistics and are very common in priori modelling of real life situations. The split becomes a set of N_a binomial trials, one for each agent, all with parameter p . This further means that the random number of agents that reach each daughter community is a binomially distributed random variable with parameters N_a, p for the one daughter, and parameters $N_a, 1 - p$, for the other. This makes a good basis for analytical derivation since it provides well established tools and methods from probability theory and statistics for working with the probabilities of the random outcomes. Importantly we note however, that in the general case it is the number of agent carriers, in each daughter community, that is a binomially distributed number. The interesting components for defining fidelity, are not the agents but the instances of each tradition type.

We introduce a new quantity, the average number of instances per agent, aIpA,

$$\text{aIpA} = \frac{\sum_{t=1}^c N_t}{N_a}.$$

aIpA is the sum of instance populations over all traditions in the institution, divided by the total number of agent carriers, returning the average number of instances carried by the agents. We recall that an agent can only either carry *none or one* instance per tradition, so several instances in one agent are always of different tradition types.

If the aIpA is kept down to 1, this means all the agents carry only one instance from any tradition type. Even though aIpA is an average quantity in the general case, note that the number of instances must be exactly aIpA for *all* agents in the case of aIpA=1. This is so because we have defined the agent population to be equal to the agent *carrier* population, meaning that all agents included in N_a carry at least one tradition, and so an average of 1 can only occur in a homogeneous case where all agents carry one instance. In this special case of one instance per agent, the fate of each instance after split is uniquely defined by their (unique) agent carrier. Recalling that every agents fate is modelled through a binomial trial, so is then every instance in the special case of aIpA= 1. This results in N_t binomial trials with parameter p , for each tradition type t .

If instead aIpA > 1, several instances share the same agent carrier, and their fates are sealed by the same single binomial trial of their shared agent carrier. In this case there are less binomial trials than there are instances, ($\sum_{t=1}^c N_t > N_a$), and without introducing new information into the system, in form of new parameters, we claim we cannot know which instances share the same binomial trials. We claim (and show in appendix) that as long as one does not know the exact distributions of the instances in each agent, an inevitable uncertainty will prevail

in whatever theoretical prediction one makes of the fidelity, even in converged limits. For the general case of $aIpA > 1$, given only the parameters defined above which results in unknown exact distributions of instances in agents, mathematical derivation demands complex stochastic theory that would still result in uncertain predictions. Meanwhile the special case $aIpA = 1$, when the binomial trials of the agents are in 1:1 correlation with the instances, an exact prediction can be expected along with extensively simpler theoretical derivations. In this study we propose and test the approach of first deriving theory for the special case $aIpA = 1$, which once confirmed and elaborated, is used as a reference tool to explore the general case by relaxing the $aIpA = 1$ assumption in simulations and comparing the emerged results to the derived theory.

We call the assumption of $aIpA = 1$, **the binomial assumption** since it leads to binomially distributed instance populations in the daughter communities with exact (not stochastic) parameters. This will be our final assumption.

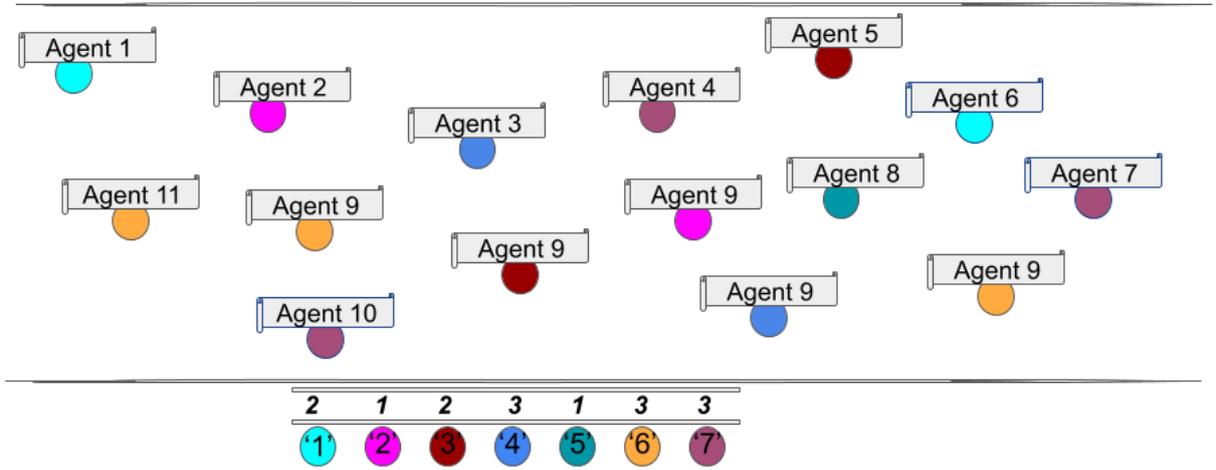


Figure 5: $aIpA=1$, A schematic overview of the related components of an example community under the binomial assumption. The instance count of an example institution is included below

In practice the binomial assumption can be seen to represent a kind of specialist community where all agents have focused on only one tradition within the institution. It could also be the model of agents not necessarily only carrying one instance each, but only dominantly practising one of them in service of the institution. However the main motivation at this point is not to be realistic, but to begin developing theory from initially strong and simplifying assumptions that will later be relaxed to move in more realistic directions. Thus we do not argue that any binomial setting was the most likely case, particularly since we have assumed that the traditions are simple enough to be included in the Zone of Latent Solutions (ZLT), which weakens the assumption that agents would not carry more than one. But we do argue that the case it is not irrelevant to study, since it is still a possible case and may well be seen as a starting point case. It is also likely to be the most challenging case for transmitting institutions, since every agent brings the minimum 'chunk' of a complete institution with them in the split. And so, when this case predicts successful emergence, this should only indicate increased such in the general case. We explore these questions in the results but first, under the binomial assumption, we are finally ready to derive mathematical predictions for the institutional fidelity Q .

4.7 Formulating fidelity under the binomial assumption

(aIpA= 1) Begin by recalling the definition of fidelity made above. The fidelity Q is defined as the expected value of the following random variable defined for every split,

$$T = \begin{cases} 2, & \text{if the institution was successfully transferred to both daughter communities} \\ 1, & \text{if the institution was successfully transferred to exactly one daughter community} \\ 0, & \text{if the institution was not successfully transferred to any of the two daughter communities} \end{cases}$$

We shall refer to one daughter community as D_x and the other one as D_y , and make the arbitrary choice of relating daughter community D_x to probability p and D_y to be the corresponding one with probability $1 - p$. This will be the order maintained throughout the study.

For compactness we will make use of the mathematical notations in further derivations, thus before proceeding we include a table of all mathematical notations used in this study.

List of mathematical notations

\in	'is in' or 'is an element of'
\forall	'for all'
\cup	'union' or 'or'
\cap	'intersection' or 'and'
\oplus /XOR	'exclusive or' or 'either one or the other'
\iff	'if and only if' or 'two way implication'
\implies	'if' or 'implies'
$P(A)$	'probability of event A'
$\sum_{t=1}^N A_t$	'sum of all terms A_t for subscripts $t=1, \dots, c$ '
$\prod_{t=1}^N A_t$	'product of all factors A_t for subscripts $t=1, \dots, c$ '
$\max(A, B)$	'returns the largest value out of values A and B'
$F_{\text{Bin}}(x; N_t, p, \theta)$	'the binomial cumulative distribution as a function of x with parameters N_t, p and θ '
$\mathbb{E}[X]$	'expected value of random variable X'

Next we introduce the pair of random variables X_t and Y_t for $t = 1, \dots, c$, a pair for each tradition t counting the number of instances that made it to daughter community D_x and D_y respectively. Note that each pair depends on each other by $N_t = X_t + Y_t$. The different outcomes of a split can then be expressed precisely in terms of the parameter θ and random variables X_t, Y_t , and denoting institutions with I . We write the three cases:

$$\text{Case 'X'} = \{I \in D_x\} = (X_t \geq \theta, \quad \forall t = 1, \dots, c)$$

$$\text{Case 'Y'} = \{I \in D_y\} = (Y_t \geq \theta, \quad \forall t = 1, \dots, c)$$

$$\text{Case 'XY'} = \{I \in (D_x \cap D_y)\} = ((X_t \geq \theta) \cap (Y_t \geq \theta), \quad \forall t = 1, \dots, c)$$

Next we will use the logical 'exclusive or' (XOR) notation: \oplus meaning for two events A and B, $A \oplus B$ is true either if only A is true, or if only B is true, but false if none or both are true. Using this we can express random variable T in terms of cases 'XY', 'X', 'Y', and 'otherwise', latter meaning none of the other cases are true. Next step will be to find the probabilities of the cases 'XY', 'Y' and 'X', to serve as building blocks for the probabilities of the outcomes of T . The binomial distribution with parameters n and p , $\text{Bin}(n, p)$ is the probabilistic progression

of the random number of 'successes' from n repeated binomial trial with success probability p . For X_t , success counts as an instance of tradition t reaching D_x in a split. There exists N_t instances of tradition type t , and under the binomial assumption $aIpA=1$, each will reach D_x with a probability p , there are N_t binomial trials of each tradition t and the random number X_t is binomially distributed with parameters N_t , and p . Further, the failures of X_t counts as successes for Y_t , and equivalently under the binomial assumption, Y_t is binomially distributed with parameters N_t and $1 - p$.

$$\begin{aligned} X_t &\sim \text{Binom}(N_t, p), \\ Y_t &\sim \text{Binom}(N_t, 1 - p). \end{aligned}$$

This allows us to utilise already established theory of binomial distributions. For example, we know the cumulative distribution functions of X_t and Y_t , meaning $F_{X_t}(x) = P(X_t \leq x)$ and $F_{Y_t}(x) = P(Y_t \leq x)$ respectively, to be:

$$\begin{aligned} F_{X_t}(x) &= F_{\text{Bin}}(x; N_t, p) = \sum_{k=0}^x \binom{N_t}{k} p^k (1-p)^{(N_t-k)} \\ F_{Y_t}(x) &= F_{\text{Bin}}(x; N_t, 1-p) = \sum_{k=0}^x \binom{N_t}{k} (1-p)^k p^{(N_t-k)} \end{aligned}$$

Note above the differences in the expressions for X_t and Y_t being a subtle switch of p and $(1-p)$ in the terms of the sum: $p^k(1-p)^{(n-k)}$ to $(1-p)^k p^{(n-k)}$.

We utilise this in the following derivation of the probability of case 'X'. We also utilise the discreteness of the outcomes, and the assumed complete independence between tradition types

$$\begin{aligned} P('X') &= P(X_t \geq \theta, \quad \forall t = 1, \dots, c) = \{independence\} = \prod_{t=1}^c P(X_t \geq \theta) = \{discreteness\} = \\ &= \prod_{t=1}^c (1 - P(X_t \leq \theta - 1)) = \prod_{t=1}^c (1 - F_{\text{Bin}}(\theta - 1; N_t, p)) \end{aligned}$$

The product is over all tradition types in the institution, where t defines the instance populations N_t in each factor, N_t are taken from the instance vector $[N_1, \dots, N_c]$. The probability of case 'Y' calls for the exact same derivation since the only difference between the cases is the parameter p .

$$P('Y') = P(Y_t \geq \theta, \quad \forall t = 1, \dots, c) = \prod_{t=1}^c (1 - F_{\text{Bin}}(\theta - 1; N_t, 1 - p))$$

For case 'XY' we define the two subcases:

'XY'(1): If $N_t < 2\theta$ for some tradition $t \implies$ case 'XY' is impossible

'XY'(2): If $N_t \geq 2\theta, \forall t = 1, \dots, c \implies$ all possible outcomes of a tradition not reaching D_y , are included in the possible outcomes of the traditions reaching D_x .

This is because if, and only if, all $N_t \geq 2\theta: (Y_t = N_t - X_t < \theta) \iff (X_t > N_t - \theta > \theta)$.

Thus in subcase 'XY'(2) for every tradition, we can remove the probability of not reaching D_y , from the probability of reaching D_x , which leaves just the probability of reaching both: $P(X_t \geq \theta) - P(Y_t < \theta)$. In subcase 'XY'(1) however this difference is not a legal probability,

because if $N_t < 2\theta$ there are cases when $Y_t < \theta$ is true without $X_t \geq \theta$ being true. In fact the difference is always negative, because no cases of $X_t \geq \theta$ can be true without $Y_t < \theta$ being true. Knowing this, if we utilise the $\max(\cdot, \cdot)$ function, which returns the maximum of two values, and write $\max(0, P(X_t \geq \theta) - P(Y_t < \theta))$ we will also get the correct probability of 0 in the subcase of 'XY'(1). Now:

$$\begin{aligned} P('XY') &= P(X_t \geq \theta \cap Y_t \geq \theta, \quad \forall t = 1, \dots, c) = \\ &= \prod_{t=1}^c (P(X_t \geq \theta \cap Y_t \geq \theta)) = \\ &= \prod_{t=1}^c \max(0, P(X_t \geq \theta) - P(Y_t < \theta)) \end{aligned}$$

We now use the following from probability theory: for any two events A and B, the exclusive or probability $P(A \oplus B)$ is found by removing the intersection ('and') of events from the union ('or'): $P(A \oplus B) = P(A \cup B) - P(A \cap B) = P(A) + P(B) - 2P(A \cap B)$, since $P(A \cup B) = P(A) + P(B) - P(A \cap B)$. In our case,

$$P('X' \oplus 'Y') = P('X') + P('Y') - 2P('XY')$$

and we are equipped to express the institutional fidelity, Q, the expected value of T, given parameters p, θ, c and instance vector $[N_1, \dots, N_c]$

$$\begin{aligned} Q = \mathbb{E}[T] &= \{the\ three\ possible\ T\} = \\ &= 2 \cdot P('XY') + 1 \cdot P('X' \text{ XOR } 'Y') + 0 \cdot P('otherwise') = \\ &= 2P('XY') + P('X') + P('Y') - 2P('XY') = \\ &= P('X') + P('Y') \end{aligned}$$

And so the final fidelity expression becomes:

$$Q = \prod_{t=1}^c (1 - F_{\text{Bin}}(\theta - 1; N_t, p)) + \prod_{t=1}^c (1 - F_{\text{Bin}}(\theta - 1; N_t, 1 - p)) \quad (1)$$

We note case 'XY' disappeared due to the values of T. Done with expected value, we proceed to the variance.

4.8 Formulating fidelity variance

The theoretical variance of a random variable X is defined as,

$$\text{Var}(X) = \mathbb{E}[(X - \mu)^2]$$

where, μ is the mean value of the random variable, that is $\mu = \mathbb{E}[X]$. In words the variance is the expected value of the squared difference between the variable and its mean. We can rewrite the variance as,

$$\text{Var}(X) = \mathbb{E}[(X - \mathbb{E}[X])^2] = \mathbb{E}[X^2] - \mathbb{E}[X]^2$$

In our case, the random variable is the transmission count T , for which the expected value is the derived fidelity Q . Thus the second term in the variance formula will be just Q^2 . The first term, using the case notations and derivations from above, becomes

$$\begin{aligned}
\text{Var}(T) &= \mathbb{E} \left[\tilde{Q}^2 \right] = 2^2 \cdot P('XY') + 1^2 \cdot P('X' \oplus 'Y') + 0^2 \cdot P('otherwise') = \\
&= 4 \cdot P('XY') + P('X' \oplus 'Y') = \\
&= 4 \cdot P('XY') + \prod_{t=1}^c \left(1 - F_x(\theta - 1; N_t, p) \right) + \prod_{t=1}^c F_x(\theta - 1; N_t, p) - 2 \cdot P('XY') = \\
&= 2 \cdot P('XY') + Q = \\
&= 2 \cdot \prod_{t=1}^c \max \left(0, 1 - F_{\text{Bin}}(\theta - 1; N_t, p) - F_{\text{Bin}}(\theta - 1; N_t, 1 - p) \right) + Q
\end{aligned}$$

And so the variance becomes, for any given parameters p, θ, c and $[N_1, \dots, N_c]$:

$$\text{Qvar} = 2 \cdot \prod_{t=1}^c \max \left(0, 1 - F_{\text{Bin}}(\theta - 1; N_t, p) - F_{\text{Bin}}(\theta - 1; N_t, 1 - p) \right) + Q - Q^2 \quad (2)$$

For simpler notation, we have denoted the variance $\text{Var}(T) = \text{Qvar}$, but this is not to be confused with $\text{Var}(Q)$. What is always referred to is the theoretical variance of the random variable T , as Q is the deterministic expected value, it is without theoretical variance.

4.9 Some special cases

The proposed fidelity formulas have the advantages of being fairly simple, and can be simplified even further for some special cases presented below.

Single tradition fidelity case

The fidelity of a single tradition t in a split, is included in the institutional fidelity Q as a special case of $c = 1$, an institution of one. This is not really an institution and we call it single tradition fidelity $q_t = Q(c = 1 = t)$. This special case reduces the instance vector to a single value of N_t , which leaves just the parameters p, θ and N_t .

$$q_t = 1 - F_{\text{Bin}}(\theta - 1; N_t, p) + 1 - F_{\text{Bin}}(\theta - 1; N_t, 1 - p)$$

For its simplicity will be used for initial study in the results.

Symmetric case

In the symmetric case of daughter community D_x and D_y being equally frequently picked by the agents, the two terms in the fidelity expression 2, become equal. We get

$$Q_{\text{sym}} = 2 \prod_{t=1}^c F_{\text{Bin}}(\theta - 1; N_t, p) \quad (3)$$

Case of minimum θ

The minimum case for the threshold θ is $\theta = 1$, which is when the presence of a single instance is enough for the tradition to be counted as present in the community. In this case, the cumulative distribution functions become easily explicitly expressed, since their sums include only one the term of zero:

$$\begin{aligned} F_{\text{Bin}}(0; N_t, p) &= (1 - p)^{N_t} \\ F_{\text{Bin}}(0; N_t, 1 - p) &= p^{N_t} \end{aligned}$$

$$\begin{aligned} Q &= \prod_{t=1}^c (1 - F_x(0; N_t, p)) + \prod_{t=1}^c (1 - F_x(0; N_t, 1 - p)) = \\ &= \prod_{t=1}^c (1 - (1 - p)^{N_t}) + \prod_{t=1}^c (1 - p^{N_t}) \end{aligned} \quad (4)$$

For the case of both a symmetric split and $\theta = 1$, the fidelity expression becomes,

$$Q = 2 \prod_{t=1}^c (1 - p^{N_t}) \quad (5)$$

In the future this case will be referred to as the *base case*.

Case of a homogeneous instance vector $[N, N, \dots, N]$

The instance populations of c traditional traits in the institution compose the instance vector N_t $t = 1, \dots, c$. The fidelity formula handles every component in separate factors in the product series. In the quite narrow case of a homogeneous instance vector, or in a more inclusive set of cases of estimations of actual heterogeneous instance vectors by homogeneous ones of a single value perhaps in lack of knowledge or perhaps with the purpose of generality. For whatever reason a homogeneous vector into the formula greatly simplifies the expression, for a homogeneous instance vector $[N, N, \dots, N]$ of length c the fidelity becomes,

$$Q = \left(1 - F_{\text{Bin}}(\theta - 1; N, p)\right)^c + \left(1 - F_{\text{Bin}}(\theta - 1; N, 1 - p)\right)^c$$

5 List of population names

The study will proceed to frequently refer to some different types of populations. To make it easier to distinguish them the following list is included with the used population names and a short description. Make a note here that some of these populations are not necessarily realistic scenarios, but are used because they are central or extreme points in different population dynamics.

- **agent population** - referring to the agents existing in a community
- **instance population** - referring to the instances existing in the agent population
- **homogeneous instance population** - referring to the instances in a agent population with a homogeneous instance vector $[N, N, \dots, N]$ meaning there are the same number of instances of all tradition types existing in the institution. This population quantity will be denoted as N .

- **heterogeneous instance population** - referring to the instances in a agent population with a heterogeneous instance vector $[N_1, N_2, \dots, N_c]$, meaning there are tradition types with various number of instances in the community (various frequencies). The mean of this quantity will be referred to as the mean instance population and denoted as \bar{N} .

Another note is that it is not necessarily excluded that there could be instances of other existing tradition types in the community as well, that are not included in the institution. However these tradition types have no impact in this setting and thus will be neglected so that by tradition types we refer only to the types included in the existing institution.

6 Testing procedure

The results presented in this study are a combination of theory and simulations, this section describes how the simulation parts have been performed. First are a set of simpler simulations subject to all the same assumptions upon which the theory was derived, to confirm the derivations and the convergence of the estimated quantity. Second part of simulations are more generalised when the one instance per agent assumption is relaxed, and settings of several instances per agent (IpA) is included and the effects of increasing aIpA on the behaviours predicted by theory is studied.

The simulations were all performed in *python* and to evaluate the cumulative distribution function points necessary in the theoretical expressions, the cdf function from the *scipy.stats.binom* classes was used.

6.1 Simulations of single tradition fidelity qt

The theory is first tested for the simplest case of $c = 1$, in which the institution is only a single tradition, and we have called this the single tradition fidelity qt. In this case the binomial assumption always holds since there can always only be one instance per agent. Thus the agents can be neglected in the simulation, as the agents who do have an instance can be represented by that instance, and agents who don't have an instance are not included (as mentioned in the parameter section 4.2 we count only the *agent carrier* population). The mother community population is represented simply as the instance population N_t which in case $c=1$ is a single number, which will be equal to or larger than threshold parameter θ . The simulated split becomes the random choice of N_t instances between two groups, with choice probability p , or as called the symmetry parameter. The populations in both groups are counted after the split, the number of successful transmissions is decided. This is simply how many daughter communities have a population of at least θ , 0,1, or 2, for each split. The institutional fidelity is estimated as the long term average of this outcome over many repetitions of the split. The resulting quantity is compared by the one predicted by theory for the given parameters $c, p, \theta, [N_1, \dots, N_c]$.

6.2 Simulations under binomial assumption

In the following simulations, institutions ($c > 1$) are included by introducing the presence of c different types of traditions in a mother community, the instance population of each tradition type is determined by the instance vector parameter $[N_1, \dots, N_c]$. As we stay in setting of aIpA= 1, the split is still simulated on the instance level, independent binomial trials with parameter p one for every instance. The difference is that now there are c different types in the mother community that all need to be separately present after split. The resulting outcome is

found by counting the instance populations of tradition types in both daughter communities after split, and counting a successful institutional transmission if there are θ or more of each tradition type.

Testing is performed first for homogeneous instance vectors, vector $[N, N, \dots, N]$ of length c . Then heterogeneity is included, and the number of parameters increase with c and the parameter space to be tested grows exponentially (number of dimensions increased with c). To cover as large a region of this space as possible, we create heterogeneous instance vectors at random, and then for analysis sort them into parameters θ , c , mean and range (the difference between highest and lowest value in the instance vector), but also if needed other useful statistics such as median, and upper and lower quantiles. Random heterogeneous instance vectors were generated as follows:

- Create a vector of length **numMeans** spanning a desired interval of mean instance populations.
- For each mean instance population \bar{N} , create a number of **numVars** different variances by randomly drawing from a uniform distribution from a determined minimum value **minVar** to a determined maximum value **maxVar**.
- For each variance, of each mean instance population, create an instance vector by drawing c numbers from a normal distribution with the mean and the created variance, and rounding the c numbers to their closest integer value.
- For each created instance vector, calculate and save the actual mean (which will vary somewhat from the desired due to randomness and rounding but will on average be the desired value), the range, and if shown necessary any other statistic to be studied as a parameter.

This procedure is used both for study with simulations but also just for creating a large variety of parameter points for theoretical study. With this procedure a total of **numMeans**·**numVars** different instance vectors is created within a controlled mean interval and a controlled range interval. One can go towards a fixed range by reducing the range interval, and study a dense interval of means by increasing the **numVars**. This is done for testing of convergence of simulated values to theory. One can also increase the range interval, and keeping the **numVars** value high, for some specific means, study the effect of ranges, this was also done, theoretically, given confirmation of convergence. Note that $2 \cdot \sqrt{(\mathbf{maxVar})}$ indicates the expected maximum range of the created instance vectors.

6.3 Simulations in the more general setting

In the general setting, $aIpA \geq 1$ instances of different tradition types in an institution can be carried by the same agent. Consequently the community split can no longer be simulated on the instance level since the one to one correspondence between instance and agent is lost. Necessarily agents are introduced into the simulations, each agent carrying a so called *tradition repertoire*. The tradition repertoire is a binary vector of length c , indicating with 1s the tradition types which that agent carries at the time of the split, and 0s for the rest. The split is then simulated as a binary trial for each agent carrying along its tradition repertoire to the daughter community. What follows is the procedure of generating a variation of communities with the same instance population vector, but different instance carrier population N_a .

→ Generate random heterogeneous instance vectors generated using the procedure described above. The range interval is however kept low to reduce sources of variation, (without excluding heterogeneity per se).

For each instance vector, create **numCom** mother communities for which the generated instance vector holds as follows:

- Create a copy of the instance vector which is the *available instance vector* (**AIV**)
- Until the **AIV** is emptied:
 - (1) Add a new agent
 - (2) Draw a random sample of the available tradition types (the tradition types which have positive values in the **AIV**). Let the size of the sample be a random integer number between one and a certain predetermined maximum value **maxaIpA**, if the **AIV** allows, if not, as many as it allows.
 - (3) Assign an instance of each tradition type to the new agent, by setting these tradition types to one in the instance vector, while reducing the number of these tradition types in the **AIV**, by one.
 - (4) If the **AIV** remains unemptied, go back to (1).

This procedure creates **numCom** distinct communities all with the same parameters (and thus with the same theoretical fidelity value, if p , θ are also kept the same), but distributed distinctly in distinct communities amongst a distinct number of agents. By this procedure, the agent population of each community becomes a random number, and so becomes the aIpA of each community. What is controlled apart from the instance vector is the interval of possible aIpA values (defined by **maxaIpA**). This procedure serves for creating a large number points for varying aIpA values for the same instance vector to study the variation of effect .

But communities with *controllable* aIpA values are also desired for more specific study of the effects. The procedure described above is in this case repeated just with a change in step (2). Instead of step (2) the size of the drawn sample for each agent is in this case instead constantly the desired value of aIpA. We note here that due to the randomness of the sampling from the available traditions, the available tradition vector might not allow the *full* number of aIpA to be assigned for the last agent. The resulting aIpA for the community will then be slightly lower than the desired (but results show not more than a few tenths of a percentage point). Note that the number of agent carriers becomes determined upon the determination of aIpA.

7 Results

Results begin by a brief look at the single tradition fidelity, which is special case of $Q(c=1)=q_t$, and informs of how well a homogeneous group of instances reach the daughter communities in a dual split. The few parameters and simple nature of this case makes it more intuitive and helps to identify and explain the effects of the primary parameters, p , θ , and N_t , on the fidelity function. We choose to study q_t as functions of varying instance population N_t , leaving symmetry p and threshold θ as the parameters. Recall that θ is the minimum number of instances that needs to reach a daughter community for successful transmission of the tradition. We recall the instance population is the number of instances of the tradition t present in the community before split and that we refer to case of symmetrical split and minimal $\theta, p = 0.5, c = 1$, as the base case.

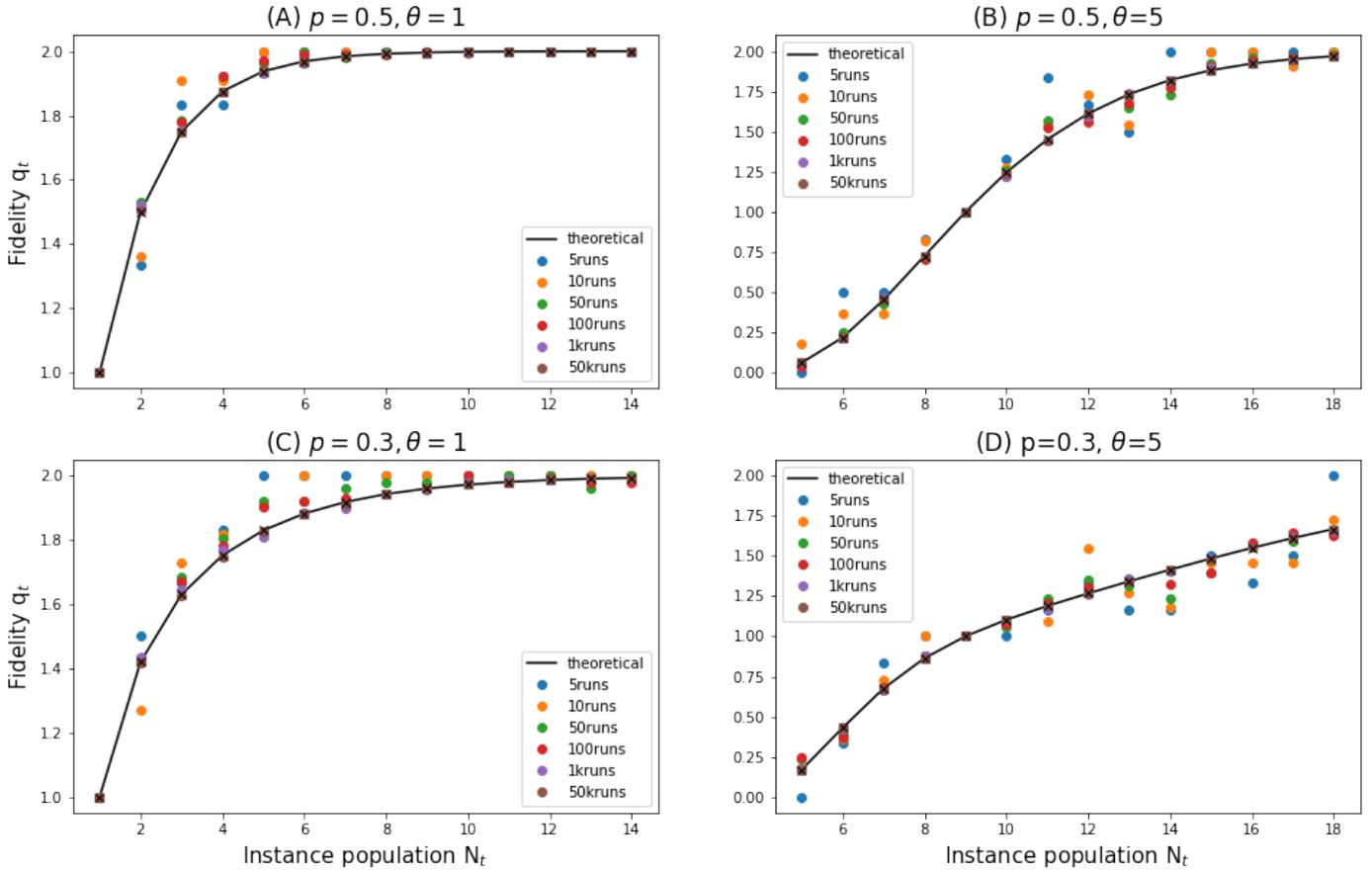


Figure 6: Shows the convergence of simulated estimations of fidelity values q_t to the derived theoretical values as a function of instance population N_t . Each sub-figure (A)-(D) shows results for a different set of parameters p and θ , the values stated above. For every N_t point, the dotted points show the average fidelity outcome value calculated over 5, 10, 50, 100, 1 000 and 50 000 simulated splits. At each N_t , the black x-point shows the theoretical value. Note that all curves start at $N_t = \theta$, since for smaller values there is no tradition present in the mother community.

The figure confirms that fidelity monotonously grows with instance population until it reaches and stabilises at the maximum value of 2 for sufficiently large instance populations N_t . It is clear by definition, figure and formula that it will stay there for any larger instance populations. The figure shows that for the base case of (A) 'sufficiently large instance populations' are in fact not large at all. Naturally for the base case fidelity starts at unity since one instance is certain to reach one and only one community, and it has reached 2 by eight instances. Figure (B) compared to (A) shows that greater thresholds θ worsened not only all the fidelity values but also the over all growth of fidelity, because the larger the threshold, the less significant becomes the addition of a single instance. Figures (C) and (D) indicate that also *asymmetry* $p < 0.5$ reduces likelihood in the adaptive region of transmission $q > 1$, but that it helps in the maladaptive region $q \leq 1$. This is also intuitive since a bias split makes it more likely to reach *one* community, but an unbiased split makes it more likely to reach *both*. Finally figure also confirms convergence of the simulated splits fidelity toward the expected theoretical function for all cases (A)-(D) by 1 000 runs, and shows a faster convergence for the base case that appears to have converged by 50 runs whilst several values for the other parameter sets had

not yet converged at 100 runs. On this note we proceed to look at the variance of the fidelity of a single tradition.

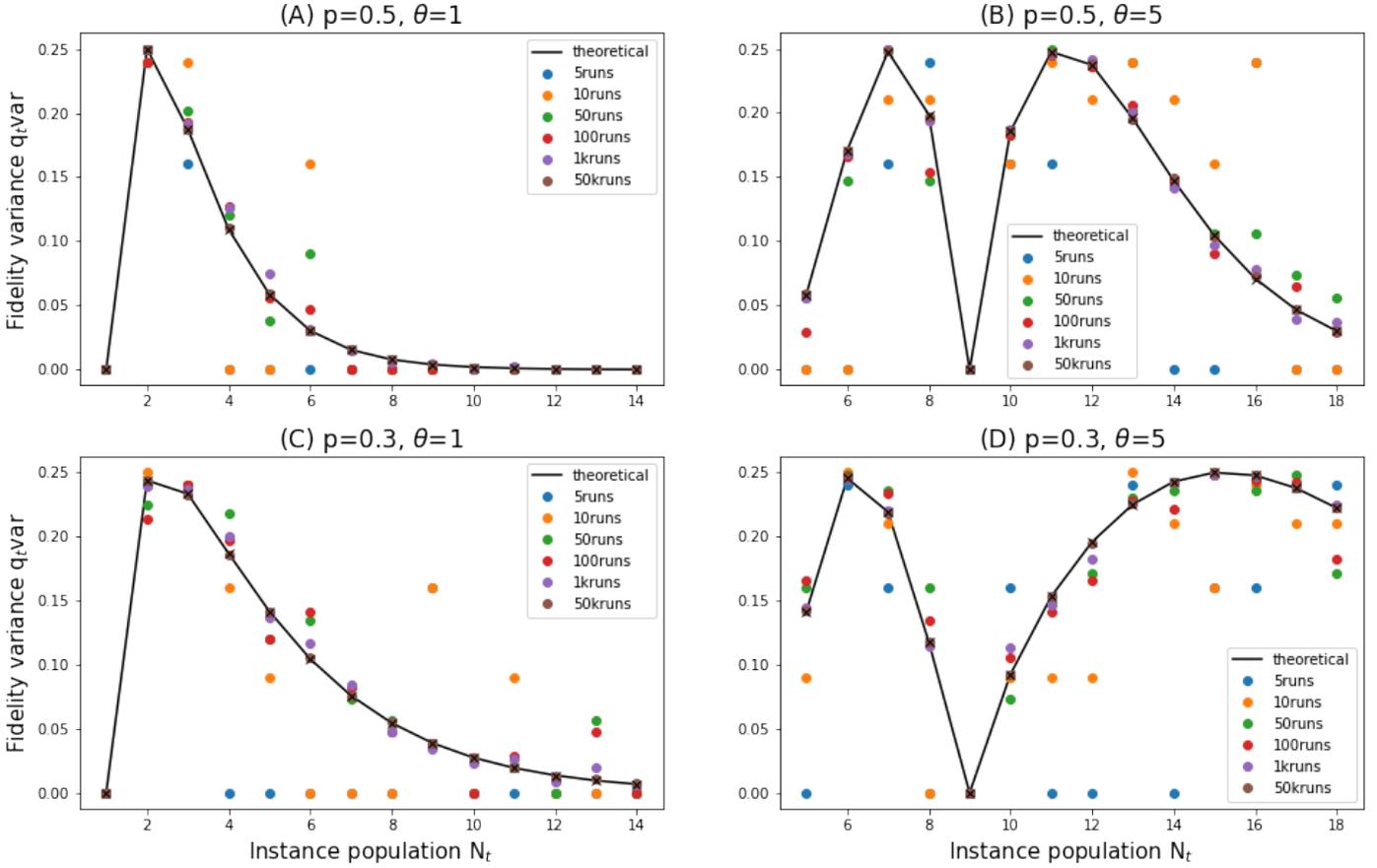


Figure 7: Convergence of the variance of simulated fidelity values q_{tvar} to the theoretical values. as a function of instance population N_t . A different set of parameters p, θ for each sub-figure (A)-(D), values stated above. At each N_t , colored dotted points show the progression of the fidelity average calculated over an increasing number of splits: 5, 10, 50, 100, 1 000 and 50 000. At each N_t , the black x-point shows the theoretical value.

The simulated values in figure 7 were calculated as the estimated variance of transmission counts T from all simulated splits up to that point. This figure confirms convergence of the simulated variance to theory, but at a somewhat slower rate than for the fidelity values. This is expected for the estimation of a variance of an unknown mean, compared to of simply the mean. A variance is often easier interpreted when put into the context of its mean and so we do best to proceed to the following figure.

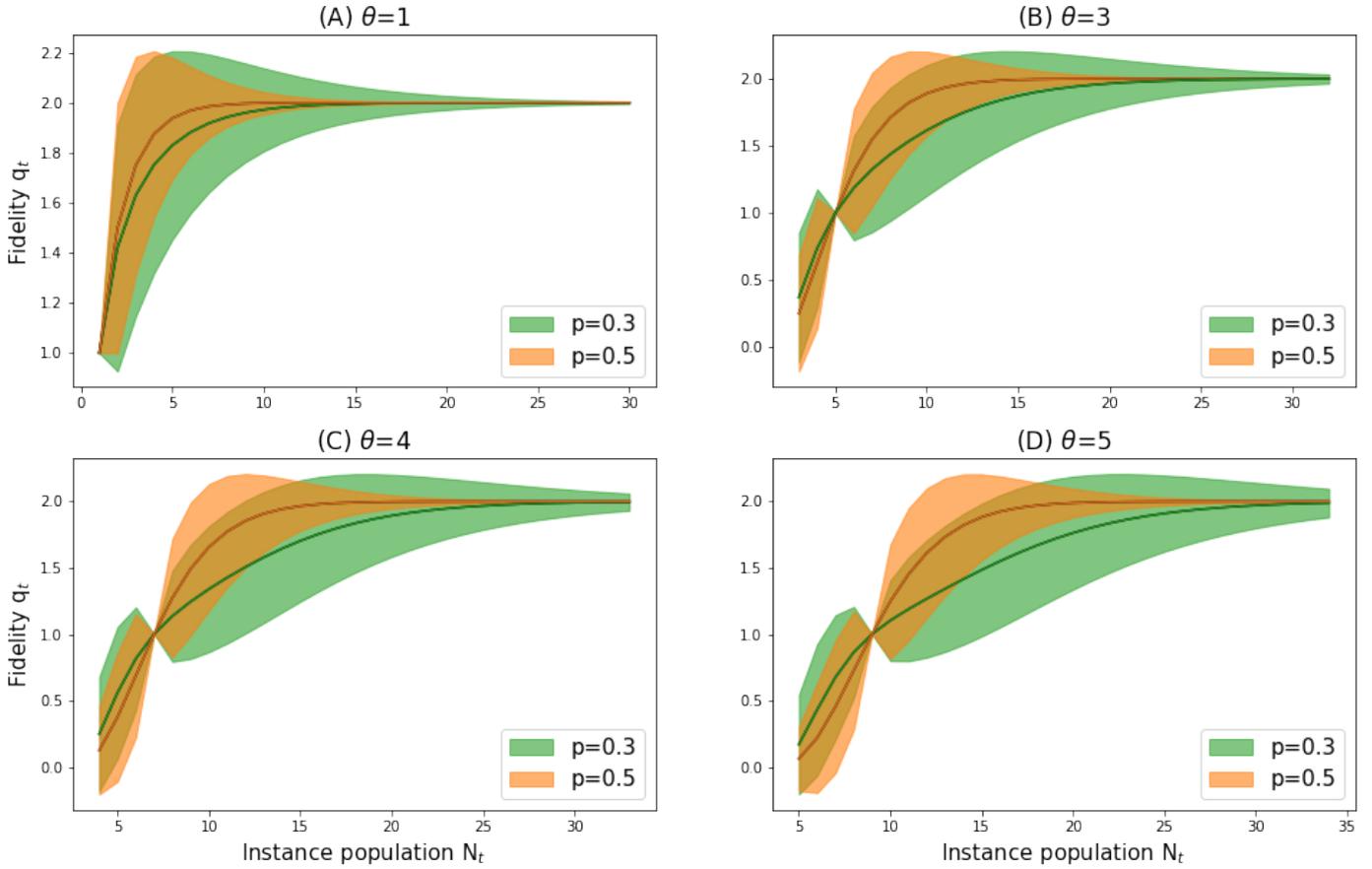


Figure 8: Theoretical values of fidelity q_t as a function of N_t plotted together with the theoretical standard deviation of q_t , the square root of the variance $q_t \text{var}$, coloured as a symmetrical deviation. Different values of p and θ in each sub-figure. As they share the same parameters, sub-figure (A) is a merger of above sub-figures 6(A), 6(C), 7(A) and 7(C) and the same goes for sub-figure (D) with 6(B), 6(D), 7(B) and 7(D).

Figure 8 shows the standard deviation as a symmetrical deviation, for an unknown deviation, this is the best uninformed guess. However in our case one knows that the fidelity does not cross under 0 or over 2, thus in the regions in figure for which the symmetrical deviation does, we can conclude that the true variation is asymmetrical and heavier towards the other way than is shown.

We note there is a point of zero variance in all tested cases when fidelity exactly crosses unity. Any way such a group is split into two, one group will be certain to have θ instances and the other one will be certain to not. Note that zero variance can only occur exactly on the true possible transmission count values 0,1, or 2. Thanks to the cumulative nature of the fidelity function, such a zero variance point for fidelity $q_t=1$ further implies that values *above* that point cannot either ever deviate below 1, because fidelity monotonously grows with instance population. On the same note, no values below this point can ever deviate above 1. The zero variance points can be noted also by the convergence of the fidelity plot in figure 6. See there that the corresponding instance population points, show no variance of the simulation values from the theoretical, not even for the smallest number of runs.

Zero variance points can be assumed much more unlikely in the case of institutions $c > 1$ as other traditions can easily remove any certainty of a single tradition fidelity. However we can look for low variance points, specifically at fidelity 1, since the implication that this introduces *probable* edges to all other points would still hold and can be used in future analysis.

7.1 The effect of adding complexity ($c > 1$)

We now put the concept of institution to the test, introducing complexity $c > 1$. Recall the complexity parameter c is the number of different traditions types which compose the institution. Recall the threshold θ holds for all c tradition types and is the minimum number of instances that must exist in the community the institution to be present.

The symmetry parameter p is still the probability of an agent (and instance, since $aIpA=1$) reaching one of the daughter cells, leaving probability $1 - p$ for the other. The instance population parameter is now a vector $[N_1, N_2, \dots, N_c]$, specifying the instance population of each tradition type in the institution. We begin this section with a theoretical plot. The theoretically expected effects of growing complexity of the institutions on fidelity Q is shown in the following figure. To keep the number of parameters low, we begin by assuming a homogeneous instance vector, $[N, N, \dots, N]$ defined by parameters N and length c . This means all c traditions have the same number of instances spread out amongst agents in the community before split. Under the binomial assumption $aIpA=1$ we get the following results:

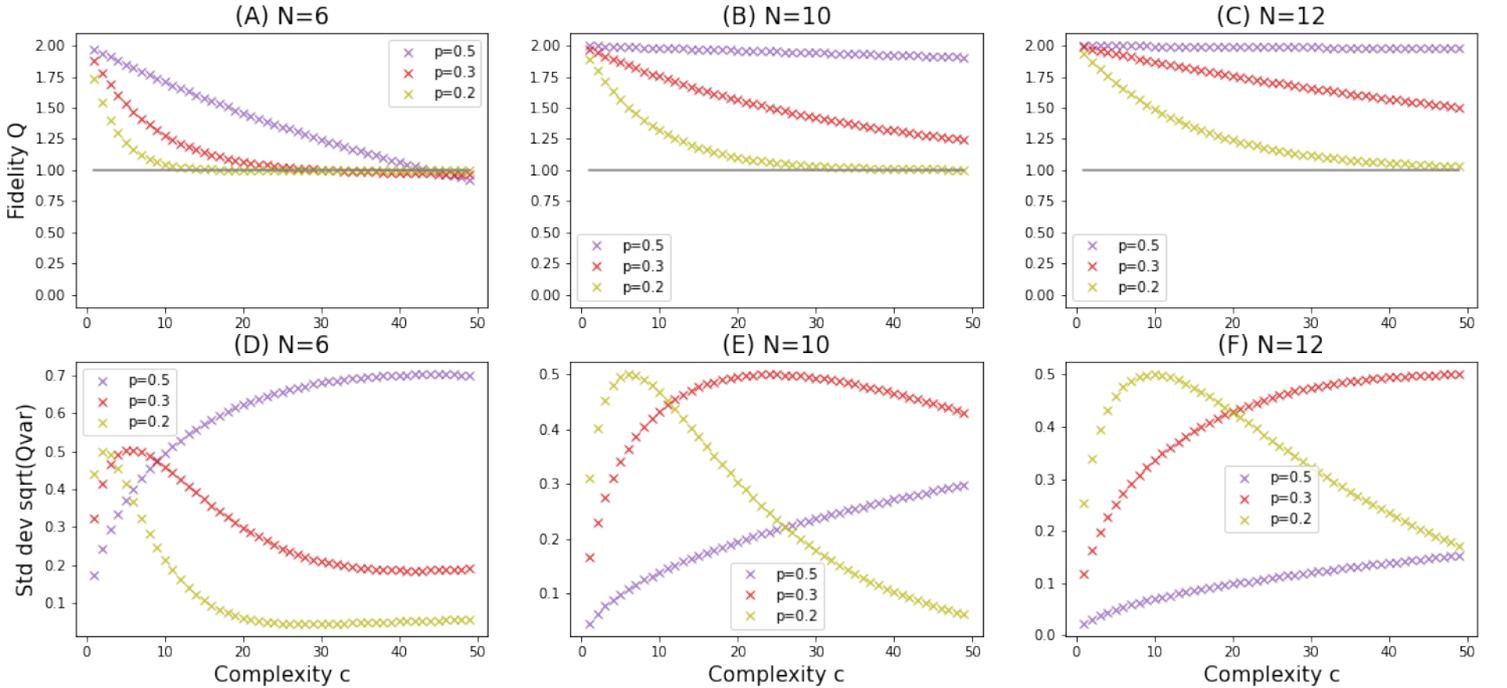


Figure 9: $\theta=1$. First row (A)-(C) shows the theoretical fidelity Q as a function of complexity c for the threshold value $\theta = 1$, for different values of the homogeneous instance populations N in different columns, and different symmetries p for different coloured curve. Second row (A)-(C) shows the corresponding theoretical variance $Qvar$ for the same complexity region and same parameter values as the fidelity Q shown above.

As seen in figure 6, it is also seen in figure 9 that the fidelity values for the chosen instance populations are almost all at the maximum of $qt = 2$ at the starting case $c = 1$ (slightly under for (A) $N = 6$). Figure 9 shows as expected a decay of fidelity for increasing complexity, as for a growing institution an increasing number of tradition types need to make it to the same daughter community for successful transmission. As fidelity equation 2 states, the decay is exponential. For the symmetrical case (purple) it is slow enough to appear linear, and as the instance populations grow, it appears more so also for the asymmetrical splits. Slower decay of the symmetrical split is shown to come with a rapidly growing standard deviation, which is as high as 0.7 in (A) as the symmetrical split fidelity crosses one. This implies that decay will firmly continue as fidelity falls into the maladaptive region, because the increasing deviations must be caused by increasing cases of zero transmission outcomes $T = 0$. For the higher instance populations $N \leq 10$, (B) and (C) fidelity of symmetric splits appears almost stable on 2, however the growing variance seen in (E) and (F) reveals its decay.

Unlike the symmetrical split where the variance seems to peak at 1, the variance for the asymmetrical splits seem to stabilise for a minimum at 1. On the other note, the asymmetrical splits show a decaying variance as fidelity approaches 1. Case (A) $p = 0.2$ reveals that variance will slowly start growing after that and the fidelity as a consequence will start moving toward zero. For $p = 0.3$ the variance appears to stabilise above zero and therefore does not really stay on unity. Of the tested cases only the case $p = 0.2$ appears to have approximately zero-variance. As mentioned for figure 7, we propose this reveals not only that the transmission outcome is almost exclusively unity (and not a balance of 0s and 2s). We propose it also reveals 'edges' at fidelity 1, meaning that the values *above* point 1 do not (significantly) deviate to 0 and the values *below* 1 do not (significantly) deviate to 2.

The effect of increasing the threshold θ on the functions $Q(c)$ and $Qvar(c)$ is shown in the next figure.

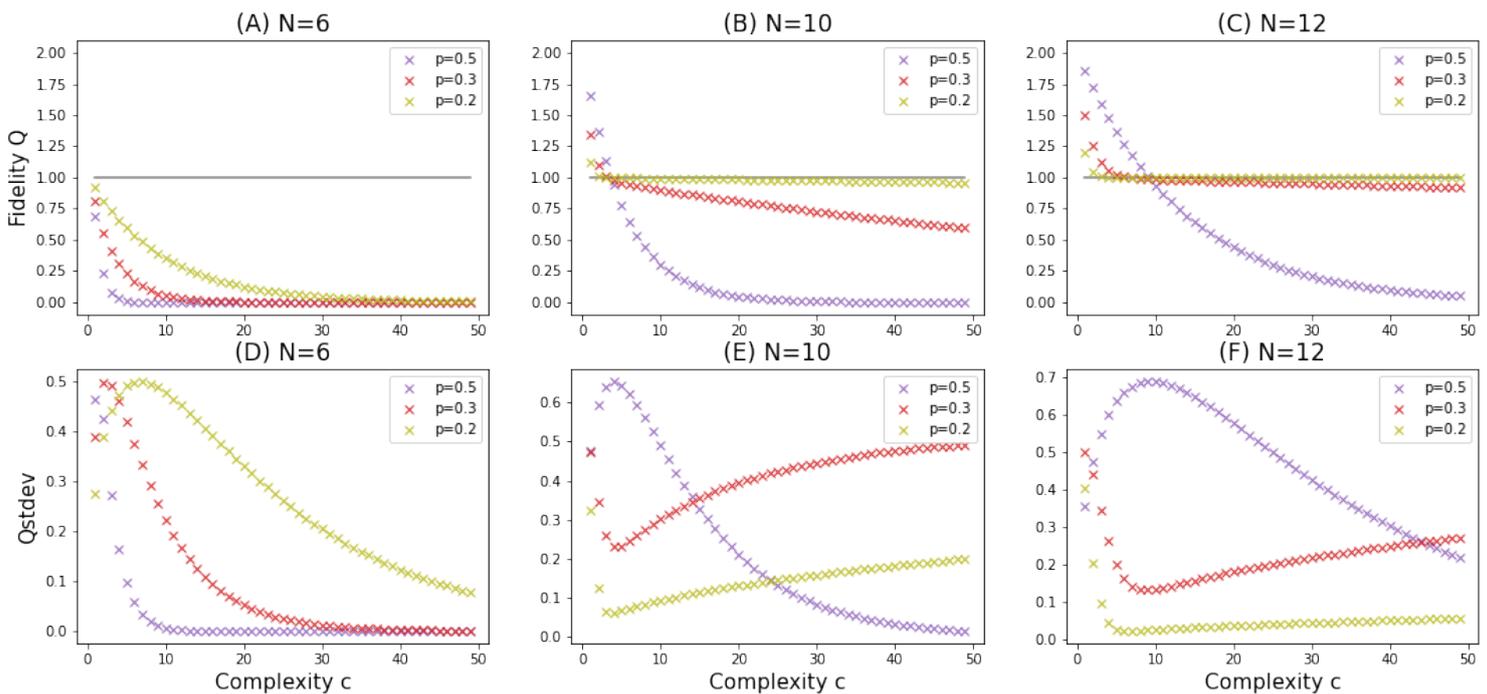


Figure 10: $\theta=4$. (A)-(C) shows the theoretical fidelity Q as a function of complexity c , now for the threshold value $\theta = 4$, for different values of instance populations N in each column and different symmetries p for each colour. The instance population holds for all c tradition types, as do the parameters p and θ . (D)-(F) shows the theoretical variance $Qvar$ for the same complexity region and corresponding parameter values as the fidelity Q shown above it.

Figure 10 shows that increasing the threshold from $\theta = 1$ to $\theta = 4$, allows none of the tested cases to stay in the adaptive region for particularly long. The symmetrical splits show again the slowest decay when in the adaptive region. Below the crossing of unit fidelity however, the asymmetrical splits seem better for staying over zero, as was understood also in figure 6 for the single tradition fidelity q_t .

Overall both figures show that for low thresholds symmetrical splits would allow institutions (incipient socients) to complexify substantially in the adaptive region, for fairly low instance populations like (A) $N = 6$. By complexification we imagine the phenomena of an institution growing by adding newly emerged tradition types over time. Asymmetrical split is shown to instead allow institutions to complexify substantially in and around the single transmission region $Q \sim 1$ without/before reaching the loss region. Recall however that a $Q \sim 1$ most likely indicates an eventual loss of institution. This is because it does not allow spread, only survival. For higher threshold values or comparably lower instance populations, the fidelity shows all the quicker exponential decay down to 0. Figures 9 and 10 show for all tested cases that the fidelity behaviour even at such high complexity values have not yet stabilised. Another complexification figure is included showing long term values.

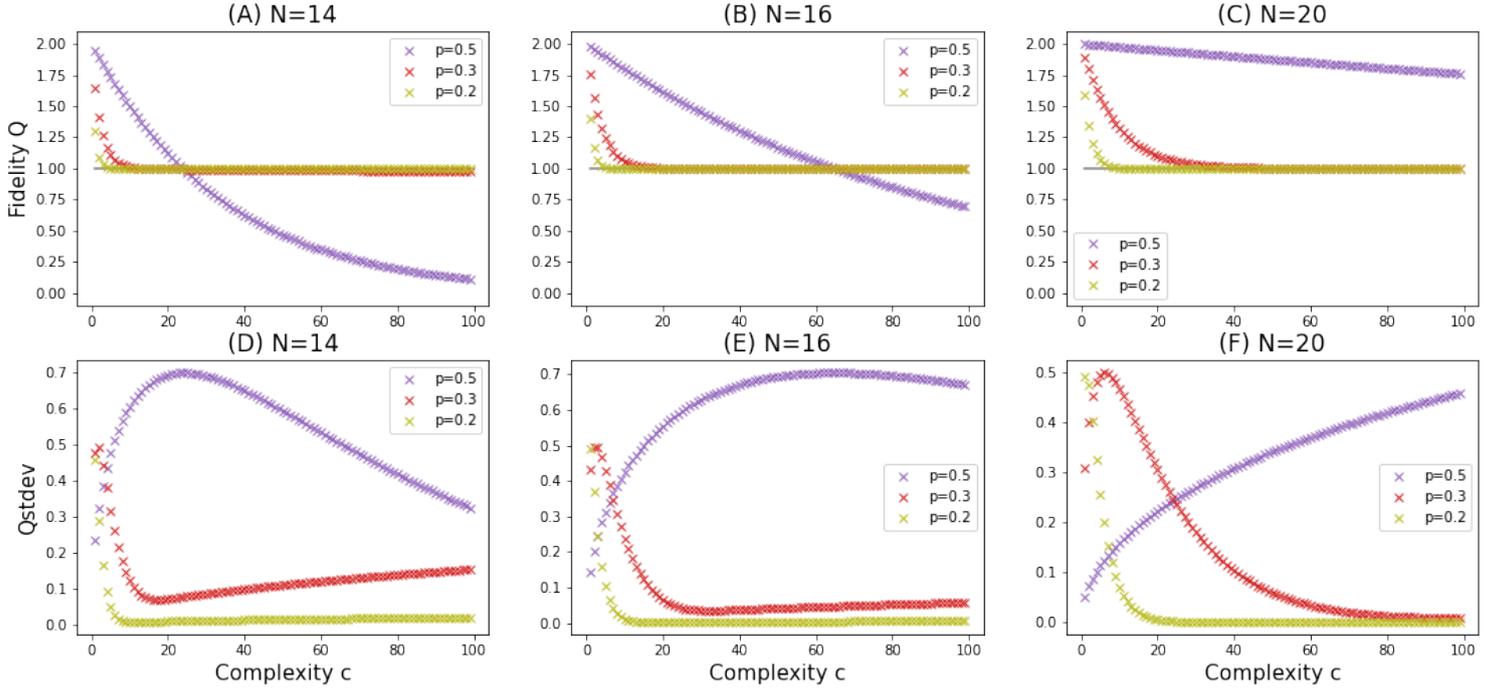


Figure 11: $\theta=4$. Same figure as 10 with double the range of complexity values.

The long term figure 11 shows slow but firm declination to zero for the symmetrical cases, as instance population grows the declination slows down quite rapidly. The asymmetrical cases instead show a quick stabilisation on unit fidelity that for the most cases has yet started decline by $c = 100$. The red $p = 0.3$ in (A) is the only asymmetrical case where slow declination towards zero has begun as revealed also in (D) by the growing variance.

The next figure shows the convergence of simulations for the institutional fidelity $c > 1$. All simulations are still under the binomial assumption $aIpA = 1$ (and will proceed to be until stated otherwise) which allows us to disregard the agents and handle the community as a population of instances, of c different types. The population of each type is given by the instance vector $[N_1, \dots, N_c]$. The fidelity is estimated as the average tradition count over all repetitions. The instance population vectors are still kept homogeneous, to focus solely on the effect of complexity. Instance vector is $[N, \dots, N]$ given parameter N and length c . To easier compare how complexity has changed to Q from q_t , the figures show the same parameter sets as previous figures 6 and 7, only with $c = 10$ instead of $c = 1$. The corresponding $c = 1$ curve is shown in grey in each sub-figure.

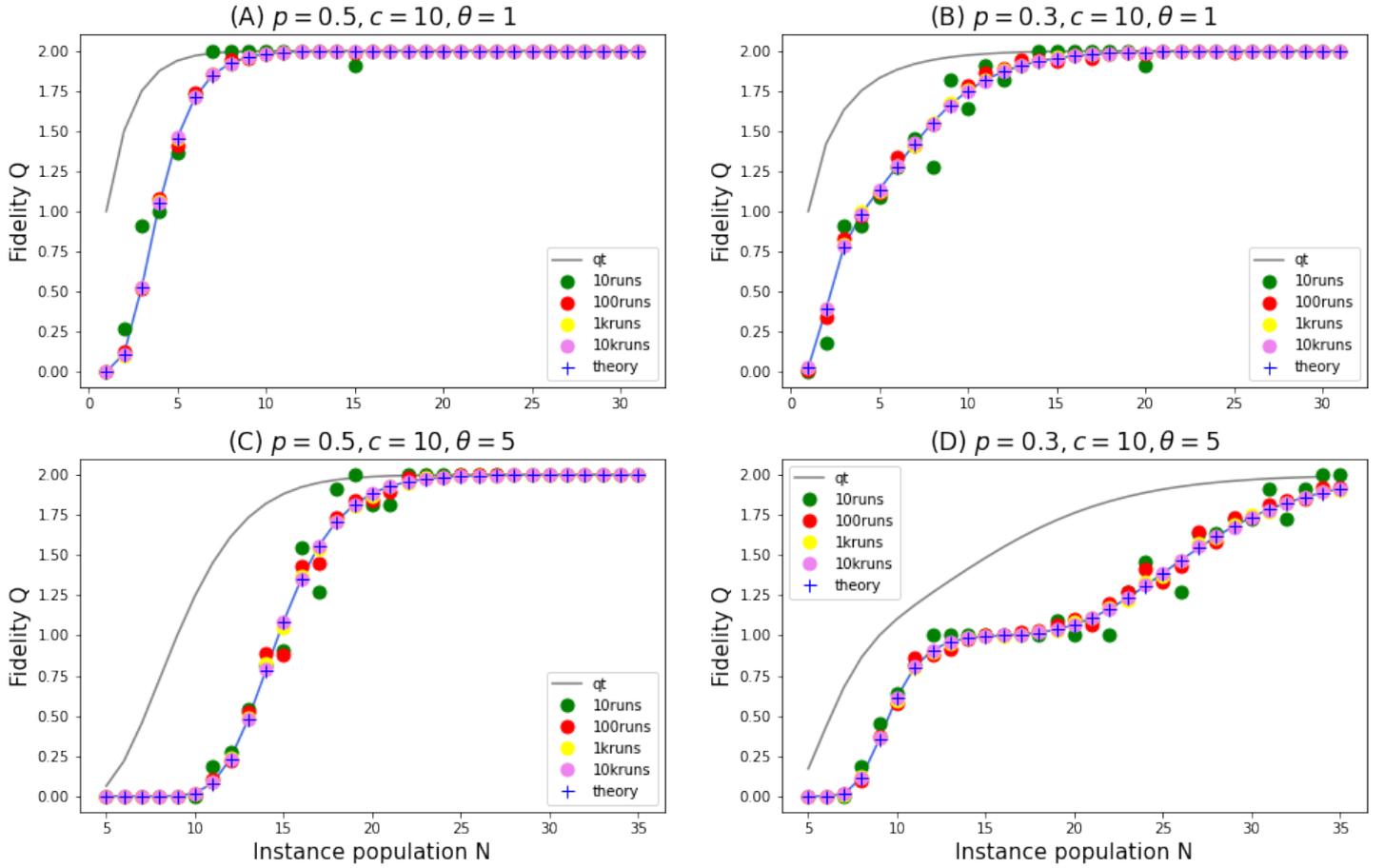


Figure 12: $c=10$ Shows the function of fidelity Q for an institution of $c = 10$ traditions in a community split of symmetry p , with threshold θ , both of which hold for all tradition types. On the x-axis is the instance population N which is same for all tradition types, meaning a homogeneous instance vector $[N, N, \dots, N]$ of length c . The dots show the simulated fidelity Q for increasing number of runs, 5, 10, 100, 1 000, and 50 000 in different colours. Included as a grey line for comparison are the corresponding single fidelity ($c = 1$) functions from figure 6.

Figure 12 shows, as expected, drops for all the fidelity functions of institutions compared to single traditions. All sub-figures show that the starting point values have dropped to 0, which in (A) and (B) with lowest threshold $\theta = 1$ is directly followed by rapid growth, in symmetrical (A) all the way to the maximum 2, in the asymmetrical (B) up to 1 where growth slows down. For higher threshold such as $\theta = 5$, symmetrical (C) still shows rapid growth to maximum, although somewhat slower and starting at much higher instance populations, at $N = 10$ in case (C). Before that, transmission shows to be steadily impossible. Asymmetrical split fidelity (D) begins growth somewhat earlier around $N = 7$, stays rapid until fidelity reaches unity where a plateau has formed of certain transmission of exactly one, unaffected by growing instance populations until a sufficient number has been reached so that transmission is possible also for the second, lower populated/unpopular, daughter community. In (D) this appears to be a number slightly lower than $N = 20$. Fidelity then grows although slowest of all cases, weighted both by the high threshold and the biased choice of daughter community in the splits. Figure shows convergence to theory more or less by 1 000 runs in all cases, and certainly by 10 000 runs.

Next we look at the corresponding variance functions.

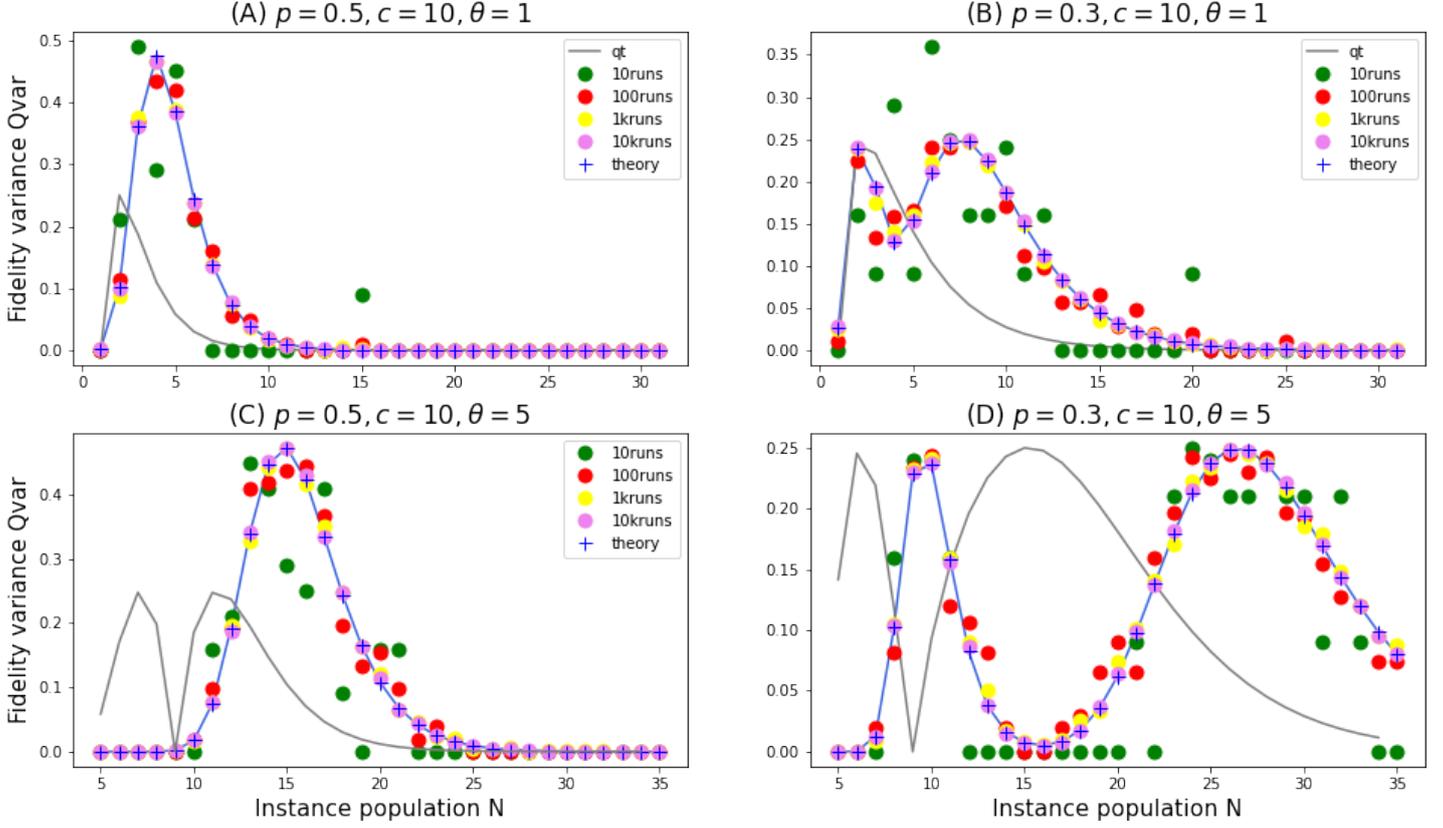


Figure 13: $c=10$ Shows the function of fidelity variance $Qvar$ for an institution of $c = 10$ traditions in a community split of symmetry p , with threshold θ , both of which hold for all tradition types. On the x-axis is the instance population N which is same for all tradition types, meaning a homogeneous instance vector $[N, N, \dots, N]$ of length c . The dots show the simulated fidelity Q for increasing number of runs, 5, 10, 100, 1 000, and 50 000 in different colours. Included as a grey line for comparison are the corresponding single fidelity ($c = 1$) functions from figure 7

Figure 13 shows that institutions will have a higher variance in fidelity than single traditions, which is very reasonable since the value is determined by *several independent* tradition outcomes. Figure (A) shows a high variance peak which seems to reflect the region of growth in figure 12(A). Same for the other figures (B)-(D), the variance peak regions reflect the growth regions in the corresponding fidelity curves above in figure 12. Whats more this seems to be regions in between possible transmission outcome values of 0,1 and 2. This is understood since in these regions the true values actually always deviates from the expected value. The fact that the peaks are *double* in height from the single tradition fidelity for the symmetric cases (A) and (C) should indicate now that the fidelity is expected to jump significantly often between all the three possible values, while in the single fidelity only jumps between two. In the asymmetrical cases (B) and (D) the peaks remain the same heights as the single tradition fidelity, indicating that the outcomes remain significantly between only the two closest possible values, for institutions as for single traditions. We note that by significantly we mean the third outcome could

still occur but not to a statistically significant level. An example of this seems to show in (B) at a point on the second peak, where the estimated variance after five simulations (green dot) is closer to the double height, indicating that higher jumps might indeed have occurred, although seems not often enough to heighten the mean variance value. The crossing of unit fidelity in the asymmetrical cases seem to correspond to a dip in variance as opposed to the peak in the symmetrical case. This should mean that in the asymmetrical cases, unit fidelity to a much larger extent is caused by the actual unity outcome value, and not by the balanced frequency of values 0 and 2.

7.2 The effect of a heterogeneous instance population

The instance vectors have up till now been homogeneous, meaning all c instance populations are the same. This is likely not often a realistic case, especially as complexity grows. True that the institutions are assumed to be made up of fairly equally challenging/impactful traditions, since no distinction of value or role has been made between them (homogeneous θ). Someone could argue that they for that reason indeed should be found with similar frequency in the community. However at closer consideration there can be found several reasons that would cause varying instance populations, that still allow for homogeneous θ . For example one can imagine some tradition types are newer than others, that is more recently added as components of the institution. These tradition types might then not have had as much time to spread to many agents, at the time of the split, and thus have lower instance populations, even though equally they are significant to the (now larger) institution. Another setting could be the that different tradition types are correlated with different demographic groups in the community. Perhaps by age groups or by varying physical versus intellectual fitness, and can still be equally valuable to an institution. We will study now how the introduction of heterogeneity in the instance vectors affects the institutional fidelity.

This is done by creating a large set of random instance vectors of varying mean and range, as described in simulations section 6.2. By range we mean the difference between the highest and the lowest values in the instance vector. Complexity is kept at $c = 15$ in the following figure. The fidelity value Q is then calculated by equation 2 and the values are visualised as dots in figure 14 below. In (A) each point is sorted on the x axis by the mean of its instance vector. In (B) the same group of points are instead sorted by the minimum value of its instance vector. In both (A) and (B) the ranges in the instance vectors are indicated by colours.

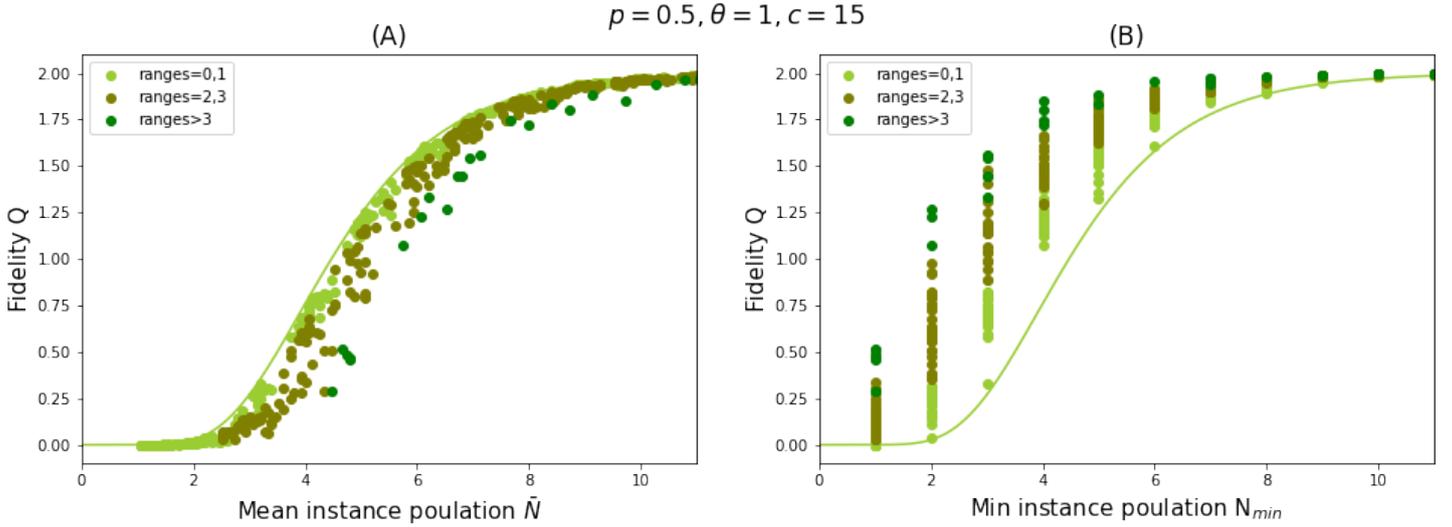


Figure 14: Institutional fidelity Q of heterogeneous instance vectors $[N_1, N_2, \dots, N_{c=15}]$ in a symmetrical split $p = 0.5$, complexity $c = 15$ and threshold $\theta = 1$. Each dot is the Q value of a single randomly created instance vector sorted on the x-axis by their mean values in (A) and their minimum values in (B). The range of each vector is specified by its colour. Range is simply the difference between the highest and the lowest value in the instance vector. The drawn curves show the functions of the homogeneous cases $[N_{\text{mean}}, N_{\text{mean}}, \dots, N_{\text{mean}}]$ in (A) and $[N_{\text{min}}, N_{\text{min}}, \dots, N_{\text{min}}]$ in (B).

In both (A) and (B) the line shows the fidelity of a homogeneous instance vector, in (A) the homogeneous vector of the mean value N_{mean} , in (B) of the min value N_{min} . As the line and the points on the same x value in (A) share the same mean, the figure shows that any vector with varying instance populations, will always have lower fidelity than if all values had been replaced by the mean value. Furthermore the higher the range of different population values in the vector, the lower the fidelity will be.

A heterogeneous vector contains both higher and lower values than its mean and by definition the higher values must together be as much higher than the mean as the lower values are lower. The phenomena seen in figure 14(A) thus implies that lower instance populations weigh *down* more on the fidelity than what the higher instance populations weigh *up*, making all the heterogeneous results lower than the homogeneous mean result. This is generally the case for concave functions as they grow all the less for increasing values and thus two points equally far from a mean in different directions on the x axis, will result in a greater distance downward than upward on the y axis. We see in figure 14(A) that the fidelity function is indeed concave for the most part, and that the part where it is convex it is so only very slightly and is right as the function starts leaving zero, for which we can see the differences are insignificantly low. The other parameter cases in figure 12 indicate the fidelity function is overall a concave function for all parameter variations expect for the very lowest values, and the slight exception of case (D) $p = 0.3$ and $\theta = 5$, where at the value of unit fidelity when leaving the plateau and reaching for the adaptive region, but again the convexity appears so slight that it is practically linear, which would indicate agreement with homogeneous mean case.

In a less surprising result, (B) shows that the homogeneous instance vector composed of a smallest value in a heterogeneous vector, will have much lower fidelity, than the heterogeneous case, and that the deviation will grow with range since high range implies existence of higher values (instance populations). Case (B) was included to show that there is both an upper and

lower limit for the fidelity value of a heterogeneous vector, using its mean value and its minimum value, and the homogeneous formula. This gives a much simpler formula and a significant parameter reduction. The fact that the intervals seem to grow on both sides with range in the heterogeneous vector, although undeniably more in (B), would indicate the interval changes relatively slowly in shape (shape here meaning relation of distance on both sides from the true value). This gives hope that some combination of these limit values could serve for reasonable estimate for the true heterogeneous value.

Before doing that, we also mention that the convergence of simulated fidelity in the heterogeneous case was confirmed by additionally simulating splits for all created instance vectors. The result was a perfect overlap for all dots by 10 000 runs, see these results in appendix.

7.3 On the estimation of a heterogeneous instance population

The results of the previous section was that a upper and lower limit can be found for the fidelity value of any heterogeneous vector using its mean and minimum value respectively, in the homogeneous fidelity equation. Here some possible estimators of the true fidelity are proposed, using the homogeneous Q function of the mean and the min. First a reminder of the homogeneous Q function, we denote our cases, Q_{mean} and Q_{min} ,

$$Q_{mean} = (1 - F_{Bin}(\theta - 1, N_{mean}, p))^c + (1 - F_{Bin}(\theta - 1, N_{mean}, 1 - p))^c$$

$$Q_{min} = (1 - F_{Bin}(\theta - 1, N_{min}, p))^c + (1 - F_{Bin}(\theta - 1, N_{min}, 1 - p))^c$$

Next follows three proposed combinations of Q_{mean} and Q_{min} values to be tested as estimators for the true value. The first one is a perfect balance between the values.

$$Q_{est1} = \frac{Q_{mean} + Q_{min}}{2}$$

However, seeing in figure 14 that the underestimation of Q_{min} (B), seems more severe than the overestimation of Q_{mean} (A), for almost all points, we propose two other combinations which way somewhat heavier on Q_{mean} , so as to compensate.

$$Q_{est2} = \frac{2Q_{mean} + Q_{min}}{3} \qquad Q_{est3} = \frac{3Q_{mean} + Q_{min}}{4}$$

Figure below shows the result of estimation, in the plots below together with the true homogeneous value, the figure shows this for the base case, for two complexity values $c = 5, 10$.

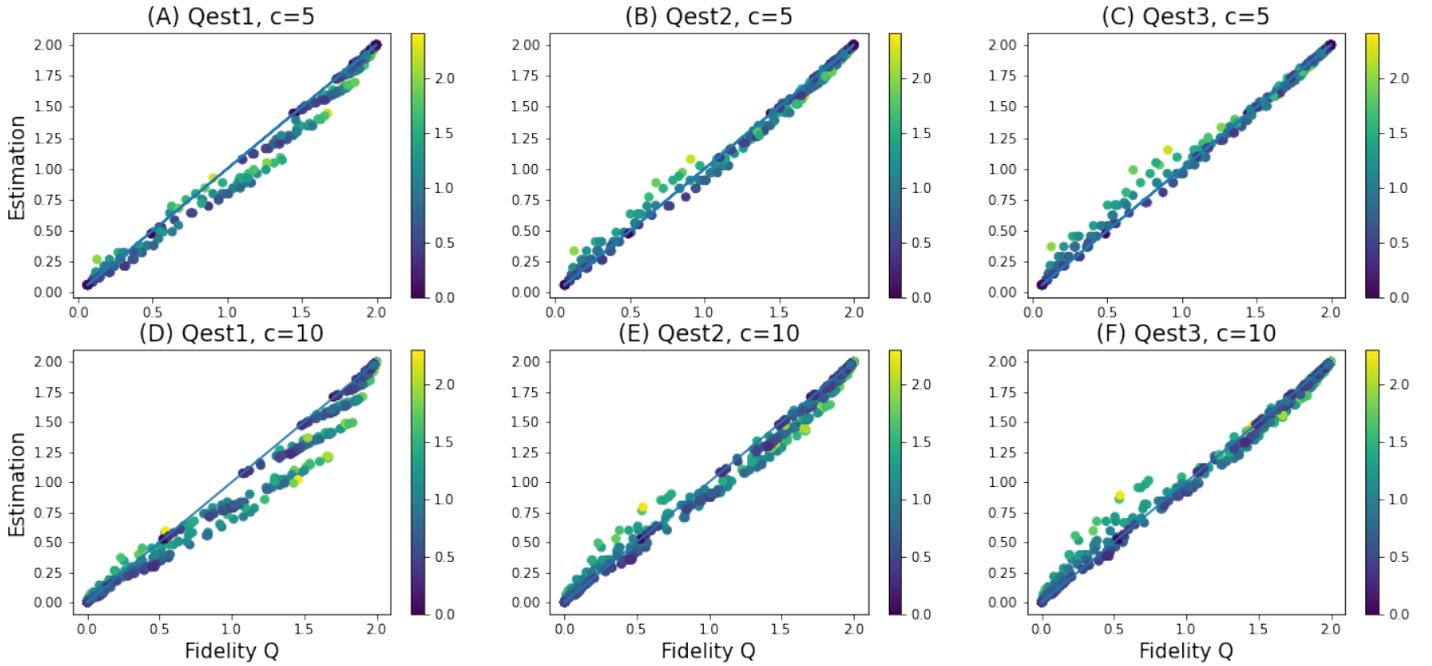


Figure 15: Results from estimations of the fidelity value using the mean and the minimum value in the heterogeneous vector. The performance is shown through plots with the true value on the X axis, where coinciding with the blue equality line would mean perfect agreement. The different columns show the different estimators, in the order defined above. Each estimator is tested for two different complexities, $c = 5$ in first row and $c = 10$ in the second.

Figure 15 (A) and (D) show that a balance between Q_{mean} and Q_{min} , as proposed in Qest1 results in a general underestimation of the true value which was expected due to the larger impact of low instance populations. Remaining figures show that as the weight increases on the Q_{mean} term, the lower fidelity values begin to become overestimated, in figures (C) and (F) quite greatly so. Of the three proposed estimators, claim Qest2 would be best for it seems to have the best balance between the overestimation for the low values and a underestimation of the higher. In appendix, further results show that for increased threshold θ and asymmetry $p < 0.5$, the estimations seems to serve a better accuracy than the base case, and again best for Qest2. With respect to the great facilitation that an estimation using only mean and min would provide for analysis, we judge the results of Qest2 to be good enough to use as an analytical tool, for qualitative analysis especially.

7.4 On the question of transmission or loss

The early question of how one should interpret fidelity values remains in the air. What does unit fidelity ($Q = 1$) really mean for the institution? Does the adaptive region of transmission $1 < Q \leq 2$, secure transmission? How well do values in the critical region of $0/leQ \leq 1$ reflect the risk of institution loss, in terms of probability? The variance has given some guidance in the ambiguity of unit fidelity, where the variance in some of these cases drops near zero indicating a true unit outcome, whilst higher variance values at unit fidelity indicate mixed outcomes, including all values 0,1,2 with a unity average. However, because the variance is an absolute value of the deviation, and because of the equidistance of the possible outcome values, further interpretation of variance values is limited without further analysis. Comparing and analysing obtained fidelity and variance results could likely provide some more detailed rules

of thumb. For example, when comparing different valued cases and their characteristics one could probably find which variance values indicate a mixture of only two closest outcome values and which variance values indicate a mixture of all three outcome values. Also, thanking the cumulativity and the small number of *three* possible outcomes, one could look for informative relations between direction of change (or derivative) of fidelity values and corresponding variance.

While encouraging this exploration, I leave above proposals beyond the scope of this study, instead this section will look at how well low fidelity values reflect the risk of no transmission, and how well high fidelity values secure transmission. We derive the probability of transmission under the binomial assumption, and compare this with corresponding fidelity function.

The probability of transmission for the homogeneous case is derived as follows, using again the formula of joint probability of overlapping events $P(A \cup B) = P(A) + P(B) - P(A \cap B)$, and above notations and derivations. Recall 'X', 'Y' and 'XY', describe the cases of the institution reaching daughter cell D_x , D_y and both, respectively. N is the instance population for all c tradition types, p is the symmetry and θ the threshold.

$$\begin{aligned} P(\text{transmission}) &= P('X') + P('Y') - P('XY') = \\ &= (1 - F_{\text{Bin}}(\theta - 1, N, p))^c + (1 - F_{\text{Bin}}(\theta - 1, N, 1 - p))^c + \\ &\quad + \max\left(0, 1 - F_{\text{Bin}}(\theta - 1, N, p) - F_{\text{Bin}}(\theta - 1, N, 1 - p)\right)^c \end{aligned}$$

A perfect reflection of the transmission probability would be an overlapping of the two curves in the region $0 \leq q$, so that the (cumulative) probability reaches one as the the fidelity function crosses 1. The fidelity will always be higher or equal to the to the transmission probability since it involves the same possible outcomes only one is doubly weighted. The regions when the fidelity becomes higher than the probability is when the probability of double transmission has become non-zero and starts contributing to the fidelity value. The regions when fidelity has crossed unity while transmission not yet has reached unit probability, are regions in which the fidelity needs to be considered with some caution. Since it includes a non-zero risk of institution loss although fidelity is higher than unity. The regions under unit fidelity which overreaches the probability are also considered as *regions of caution*, since the fidelity then has the appearance of a probability value but is in fact the real one at all. Basically, all regions where fidelity over represents probability of transmission, we refer to as *regions of cautions*.

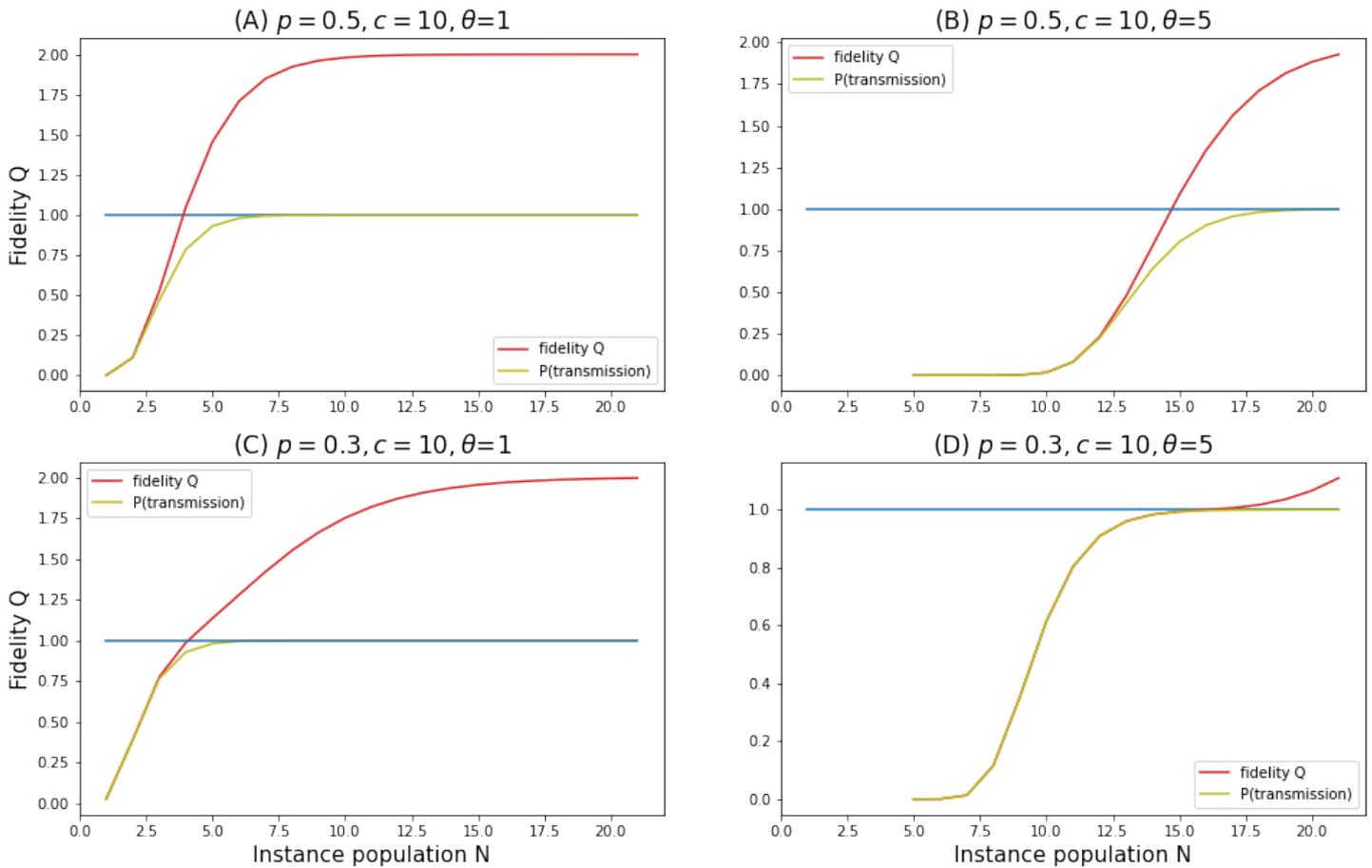


Figure 16: Shows institutional fidelity for homogeneous instance populations plotted as a function of N together with the corresponding function of transmission probability. The parameters of the sub-figures are indicated in the titles. The blue line on the constant value of one is plotted for visual aid.

Figure 16 shows that such regions of caution indeed do exist, for some parameter values more than others, indicating that symmetrical splits have greater such reasons. The figure implies that the deviations do not begin until transmission probability has reached or crossed 0.5, and that the fidelity does not cross over unity before transmission probability has reached or crossed 0.75.

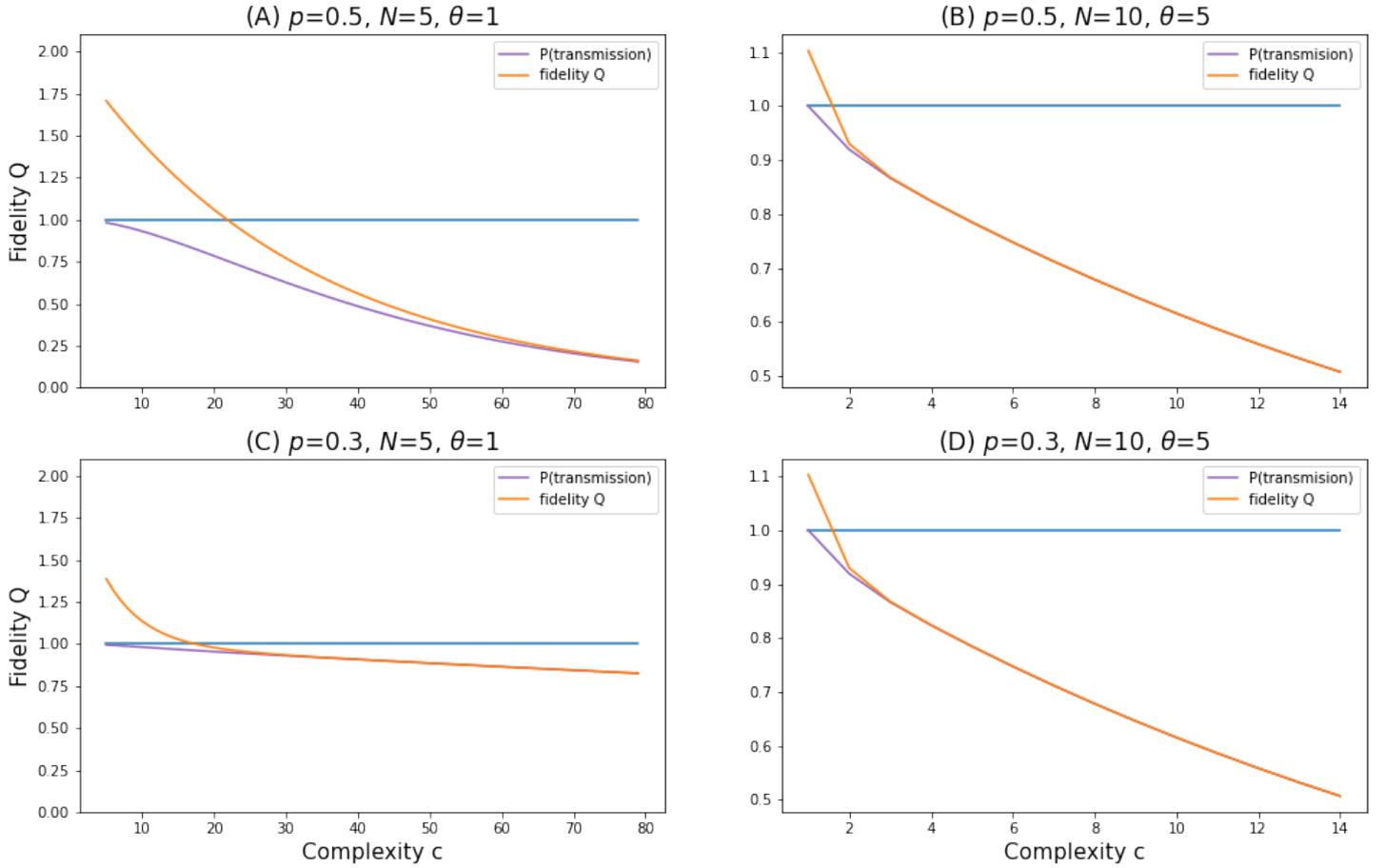


Figure 17: Institutional fidelity for homogeneous instance populations plotted as a function of the complexity c , together with the corresponding function of transmission probability. The parameters of the sub figures are indicated in the titles. The blue line on the value of one is plotted for visual aid. Note the differences of ranges in both x and y axis for every sub-figure

Figure 17 with functions of complexity show broader regions of caution, likely because of the slower fidelity change for the complexity parameter than for the variable N_t . Figure does show that deviation begins at lower values, but again the fidelity for all tested cases does not cross unity before the probability has reached 0.75. Further, the figures show in the worst cases, that the probability has reached unity by when fidelity reaches 1.75. For the better cases, which are asymmetrical ones, the fidelity leaves the region of caution earlier, by 1.5 in 17(C). For high θ and c the asymmetrical case 16(D) shows perfect overlap.

One concludes that for fidelity, as we have defined it, a value of unity or higher does not necessarily mean guaranteed (in the probabilistic sense) transmission, although in some cases it does. The 'if' will depend on the parameter of the studied case, where higher thresholds and asymmetry cases have shown better correspondence to transmission rate. This is in agreement with the results of figure 9 and 10 where existence of near zero variance regions were identified for cases with higher asymmetry, which implies non occurrence of double transmission in the low region and vice versa which should indeed result in better overlap with the probability curve. The figures imply a general region of which the fidelity will indeed give good loss risk

implications. For the lower region $q \leq 0.5$ is shown to overlap the transmission probability for all tested parameters. A unit fidelity or above is shown to imply a transmission probability of at least 0.75. And finally it seems a fidelity of 1.75 or above will guarantee transmission for all parameter cases.

7.5 The effect of agent carriers

Up until this point, the simulations have been prone to the same assumptions upon which the binomial theory was derived, including the assumption of one instance per agent. This assumption is far from the only assumption made in this study, but it is one that was made inside an already complete setup of the other assumptions, solely for the sake of theoretical derivation. It is thus an assumption that is easily lifted without changing any building stones. This is done in the next part of the study, where the simulations move on to the more general setting a community of multi-traditional able agents.

A comment for the following section, the agent carrier population numbers of different cases will almost always be implicit, because the impact of aIpA and instance populations are chosen as the central ones. But the agent carrier population can always be approximately calculated by multiplying the mean instance populations by c , and dividing this by the mean number of instances per agent, $N_a \sim \frac{\bar{N} \cdot c}{aIpA}$.

The general method of generating agent communities and the simulation of the splits were described in section 6.3.

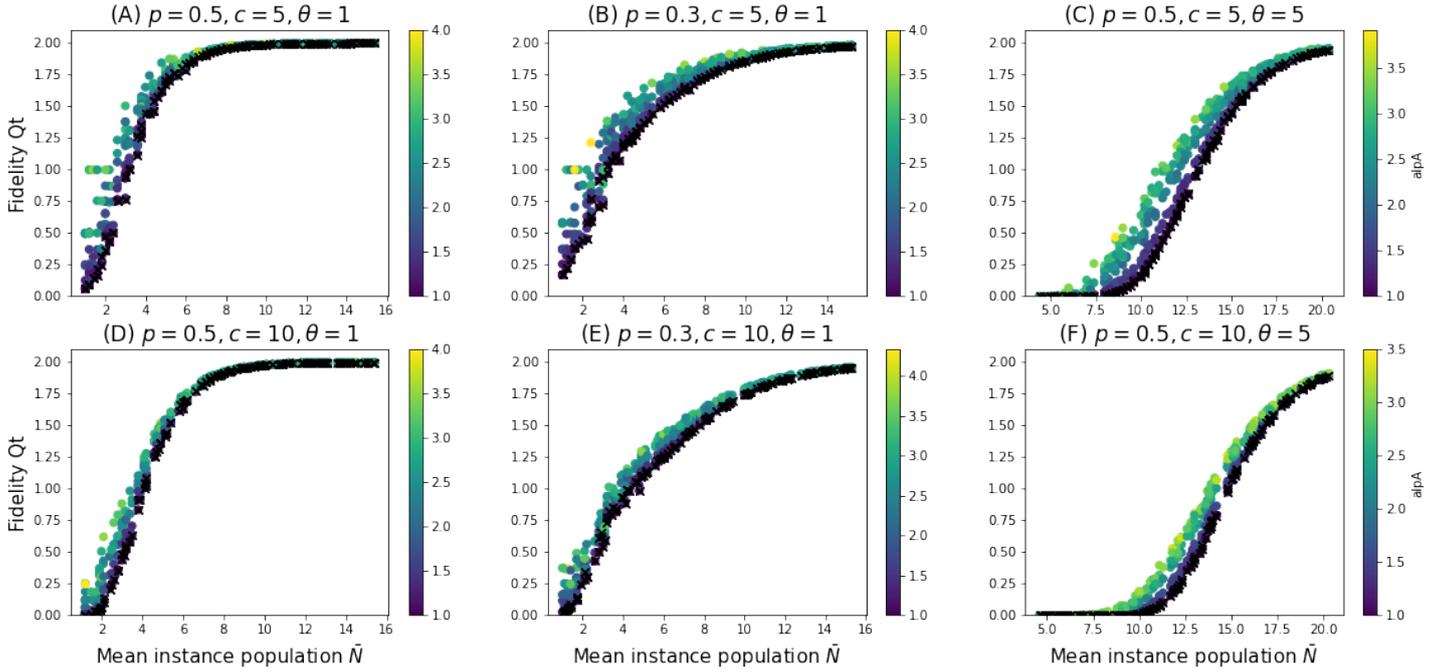


Figure 18: Institutional fidelity as a function of mean instance population \bar{N} , results from simulations with agents are shown as dotted points, each dotted point represents a unique community for which the split was repeated 10000 times. For each dotted point, there is a black 'x' point on the theoretical Q value of that given instance vector. The colours represent $aIpA$ in that community, values are seen in the colour bars to the right of each sub figure. Each sub figure shows the function for a different set of parameters symmetry p , complexity c and threshold θ .

All sub-figures show that as the number of aIpA starts to increase in the community, deviations emerge from the values expected from theory. The darkest points, that is the points with a majority number of single instance agents, show overlap to theory. This confirms the assumption that at low densities the presence of agents is negligible. But already as density starts to approach 2, the simulated values start to lift above the theoretical, and for higher densities still the deviation upward seems to only increase. The deviation exclusively upward is understood, since the case of one instance per agent is the most difficult case for institutional transmission. In the case of one instance per agent, each instance moves alone, and thus can as likely end up with several of its own kind, as with several of different kinds, (if they are as populated in the mother community). In the case of higher $aIpA$ however, the instances do not move alone but thanks to their agent carrier along with other instances, and these instances are guaranteed to be all of different types. So a higher $aIpA$ will increase the probability that an arbitrary group of instances reaching a daughter community, are of different tradition types, which increases the chances of institutional transmission, since this requires presence of all types.

(A) and (B) show the highest deviating points, right at the start for the lowest mean instance populations \bar{N} . Imagine the case of such low instance populations, for small institutions $c = 5$, and a minimum threshold. If agents carry three or four instances each, one agent carries a *great* chunk of the institution alone. This dramatically increases the chances for transmission, which is almost zero without that help. For corresponding cases with increased complexity, (D) and (E), the deviations from theory are not as large, although they are also largest in this low

population region. This is expected since three or four instances per agent of larger institution is a less significant chunk. The higher complexity cases $c=10$ over all show lower deviations and probably all for that same reason. Higher threshold cases show high deviations but also appear more systematic ones, where distinct curves of near-constant number of instances per agent, can almost be seen. Comparing to the asymmetric cases of $\theta = 1$ there seems to be overlaps in deviations of different aIpA . We do note high concentration of randomly created points in the figures makes it hard to look for systematic trends in the errors, since theoretic points themselves, deviate from any specific curve. Also the varying concentration of points in different regions makes it harder to visualise any potential curves. The overall high concentration of random points does however help to visually indicate that the deviating values in all sub figures, do in fact seem to stay within certain proximity of the theoretical curves, and that the region of proximity seems to follow the main shapes derived by theory, for all different parameters.

Next we show the corresponding plot but for the fidelity variance.

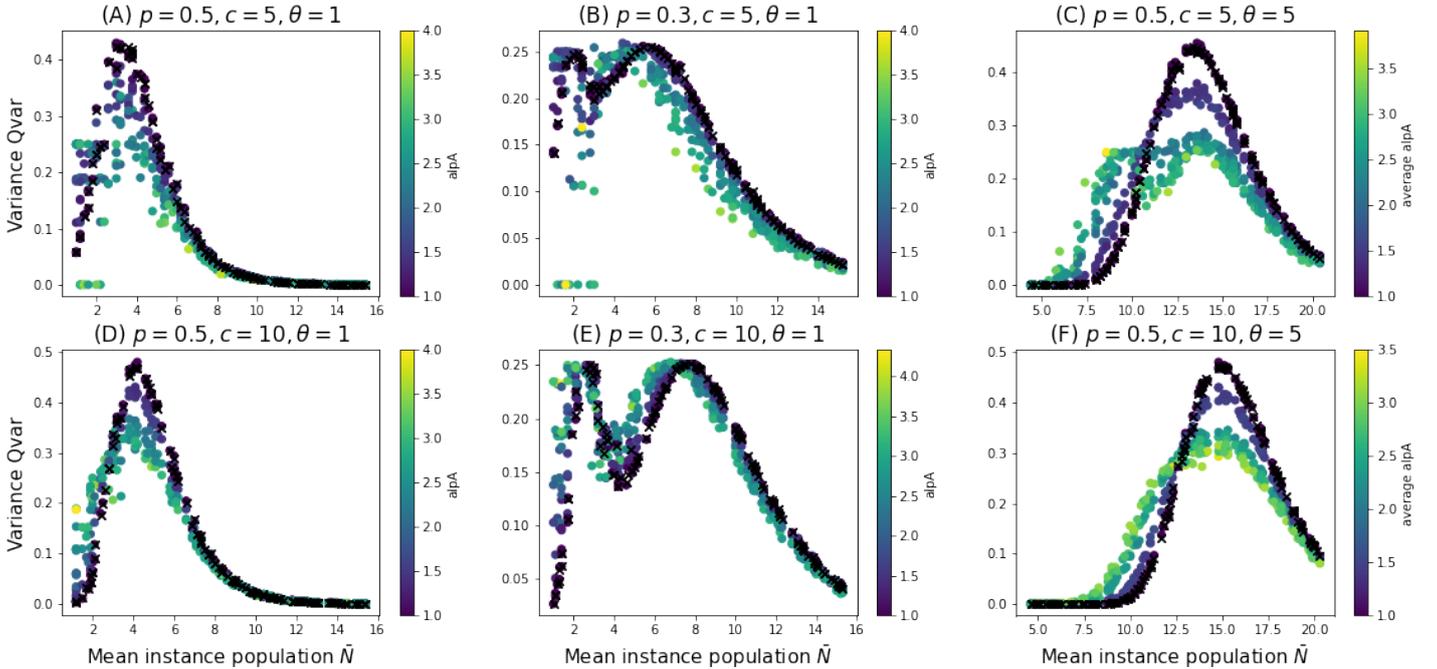


Figure 19: Fidelity variance as a function of mean instance population \bar{N} , results from simulations with agents are shown as dotted points, each dotted point represents a unique community for which the split was repeated 10000 times. For each dotted point, there is a black x-ed point on the theoretical Q value of that given instance vector. The colours represent average number of agents in that community, values are seen in the colour bars to the right of each sub-figure. Each sub-figure shows the function for a different set of parameters symmetry p , complexity c and threshold θ .

In the variance curves for $\text{aIpA} > 1$, there are clearer indications that the deviations of higher aIpA might be occurring as *transformations* of the curves derived from theory. We note though on what appears as an interesting exception in (C) $p = 0.5$ $c = 5$ and $\theta = 5$, where for high enough aIpA s, the shape seems to have changed dramatically, and introduced what could be a new minima. Also (F) shows indications of something like (C). The figures indicate for different parameters, quite different kinds of transformations. Interestingly enough, the asymmetrical

cases (B) and (E) are the ones that most indicate translation, whilst in the fidelity figures 18 these cases do not show the same indication. Instead, in the fidelity figures it is cases 18(C) and 18(F), that mostly indicate translation. We make a daring suggestion that maybe the shapes of the theoretical curves such as steepness or concavity can serve as better indicators than the parameters themselves, either for the visibility of the transformations, or for the transformations themselves. We finally note also on the difference that the deviations of the variance have no particular sign, while the fidelity deviations do.

Next we show the progression of the deviation, of the theory from the agent simulations, and do for this simulations of two particular $\alpha p A = 2, 4$. This was done for the base case $p = 0.5$, $\theta = 1$, for three different complexities $c = 5, 7, 10$. Again, randomly generated instance vectors were created for each mean with range kept mostly on 0 or 1, meaning homogeneous or only slightly heterogeneous instance vectors.

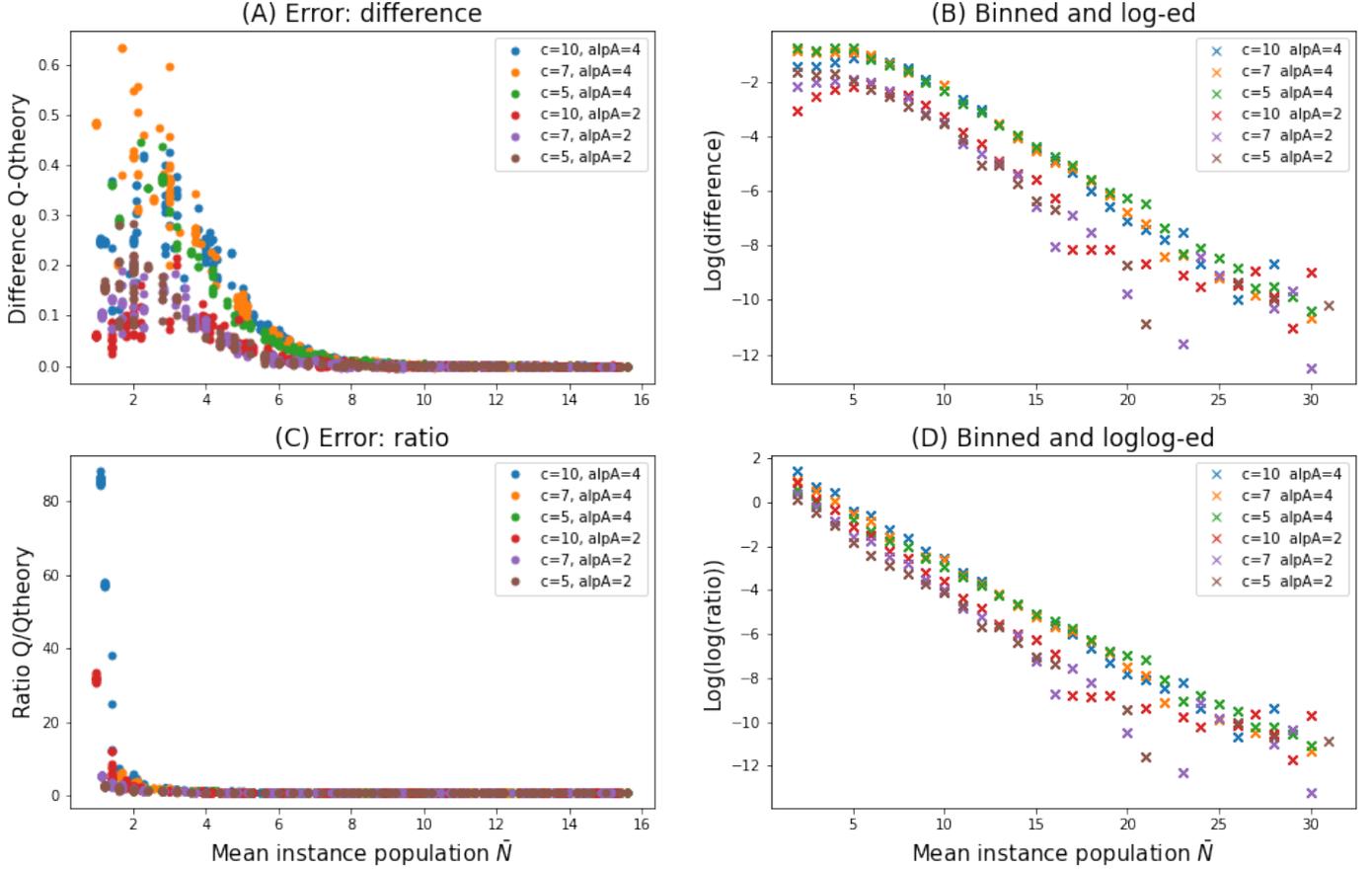


Figure 20: Plotting the error of predicted theoretical values from the simulation outcomes, as a function of instance population. In (A) the error is presented as a difference, $Q-Q_{theory}$, that is the absolute increase of the error as mean instance population \bar{N} increases. In (B) the mean values are sorted into bin values of size 0.5, and the results presented as a logarithm of the difference. In (C) the errors are plotted as a ratio Q/Q_{theory} , that is the factor with which the simulated results have increased from prediction. In (D) the mean values are again binned into intervals of size 0.5, and the factor is log-ed two times. Note that the x axis is for the binned plots (B) and (D), indicate the bin index and not the instance population mean. The mean interval is then around half of the bin index, since each bin has the size of 0.5.

The figure shows the deviation of theory in the base case, analysed in different ways. The increase in the deviation for decreasing instance populations appears highly exponential. The ratio figures (C) and (D) reveal however, that it is not the ratio of deviation that exponentially increases (for decreasing instance population), it is the *exponent of the exponent* of the deviation that exponentially increases. This truly means an explosion of deviation from theory, when increasing alpA for low populated traditions. Again, although maybe not to this extent, the dramatic increase in the deviation factor, for decreasing instance populations, was expected. This is because of the theoretical predictions are almost zero, while the simulated are not. Figures (C) and (D) shows the deviation factor being highest for the higher complexity $c = 10$, for both densities, 2 and 4 instances per agent, while the absolute deviation is shown on average highest in (B), for the lowest complexity $c=5$, as was also seen in previous figure 18. In (B) the curves show the absolute deviation to be ordered primarily by density, showing the group of all

complexities with $\text{aIpA} = 4$ to be higher than the entire group of $\text{aIpA} = 2$. Inside these groups the deviation is higher for lower complexities. In (D), the deviation ratio is shown highest for the highest complexity $c = 10$ for both aIpA , at start. But their lines also indicate the steepest decay, as the instance populations increase (and thus the fidelity values too). The lines in (D) indicate some sort of crossing of all complexity lines, for both aIpA s separately, but both at bin index around 13, which with $\text{binsize} = 0.5$, which represents the mean instance population \bar{N} value of around 6.

No opinion is given of which way of analysing the deviations would be better, the different ways show to reveal distinct interesting patterns. In all cases the questions that arise about the deviations are many, and call for deeper and more rigorous exploration. Recall there are other ways of testing deviations that might be better, such as for example relative errors, or functional transformations.

We proceed to study deviation functions for some other parameter cases, first for symmetric splits with higher $\theta = 5$, and next for asymmetrical splits $p = 0.3$ and the higher $\theta = 5$.

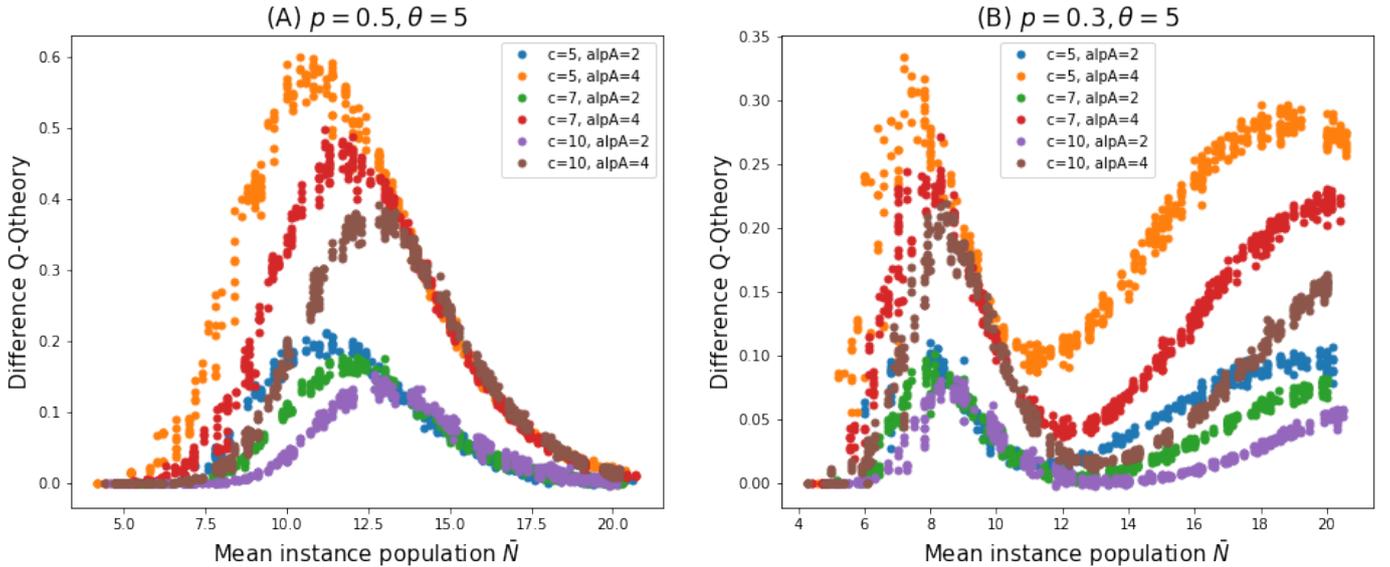


Figure 21: Deviations of theory from simulations, as the difference (Q - Q theory) shown for case $p = 0.5, \theta = 5$ in (A), and $p = 0.3, \theta = 5$ in (B), as functions of mean instance populations \bar{N} . Colours indicate different complexities $c = 5, 7, 10$, and $\text{aIpA} = 2, 4$.

Figure shows new very different progressions of the deviation, (A) and (B) are different both from each other and from the base case. The deviations no longer seem to be overall of exponential decay for growing instance populations. The deviations now show more complex dynamics, with peaks and dips for different regions of mean instance populations. We can relate the region of zero deviation at low mean instance populations, to the region of zero fidelity that we have seen emerges from higher threshold values. See the zero regions in 18(E) and (F), which we conclude are largely unaffected by higher numbers of aIpA . Then the left side of the emerging peaks of deviations seem to coincide with steep growth of fidelity values, specifically the convex region. The right (downward) side of the peak, corresponds to the concave part of the steep curve in 18, and shows again exponential decay almost independent of complexity, which reminds of the base case which we note is concave more or less from start.

For the asymmetrical (B) with $\theta = 5$, we have no comparison in 18, however we can refer to the trends found in earlier figure 12(D) with this same parameter configuration but for $\text{aIpA} = 1$.

Also there, there had emerged a flat zero fidelity region for the lowest instance populations, due to the high threshold $\theta = 5$, although somewhat briefer, around half the extent in the asymmetrical case than that of the symmetrical case. This is shown to be reflected in the deviations, followed by a steep growth and peak, again as in (B) for a region of steep convex fidelity growth. The steep dip that follows reflects the plateau region in 12(D). The plateau is then followed by a convex growth in fidelity, although somewhat slower, and the deviations here remind of the deviations of convex fidelity growth also in 21(A).

We state that also these results shows indications of a relation between convex growth in the theoretical curve and translative deviations from the simulated curves. And between concave growth in the theoretical curve, and exponential decay of the deviations from the simulated curves.

Now move on to the final results which are two more examples of comparing fidelity functions from simulations of higher aIpA to binomial theory, this time as functions of complexity. The figures below recreate a part of the early theoretical complexity plots in figures 9(A) and 10(A), also the case of mean instance population $\bar{N} = 6$. This time the instance vectors are kept completely homogeneous, that is, a vector of sixes of increasing length c . This is done again for three different symmetries $p = 0.5, 0.3, 0.2$, and for thresholds $\theta = 1, 4$.

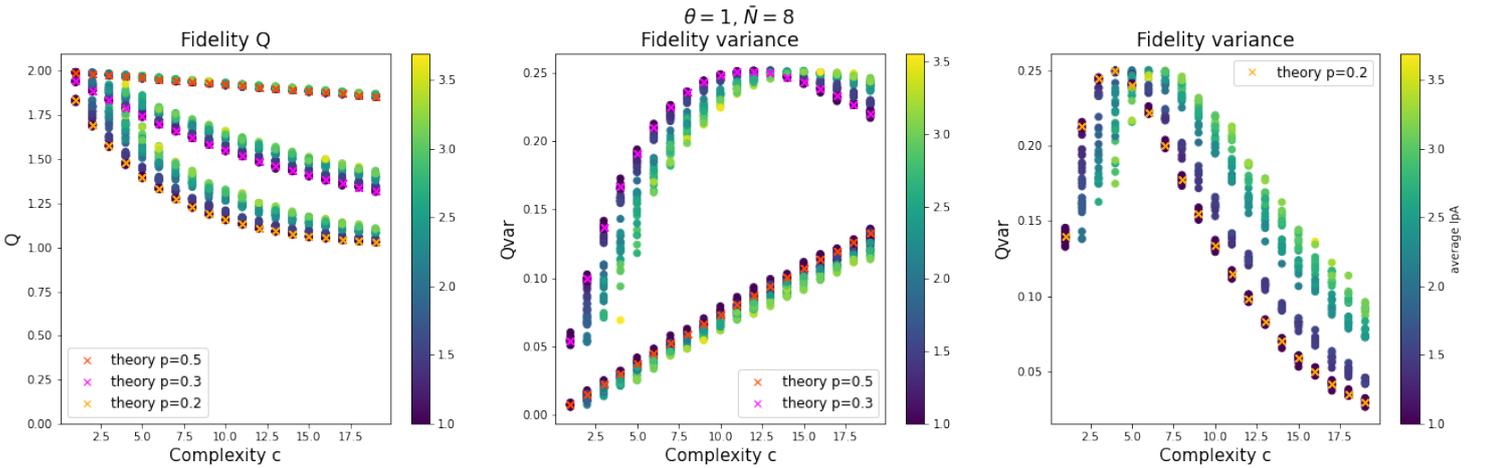


Figure 22: $\theta = 1$. In (A) the fidelity as a function of complexity for threshold value $\theta = 1$ and instance populations of $N = 6$ for all traditions. Each dot shows the average fidelity outcome from 10 000 simulated splits of a randomly created agent community where instances were given to agents of varying density, average indicated in the colour bar to the right. 'x' dots represent the theoretical values of the fidelity for the homogeneous instance population of institution of size c . (B) and (C) show the corresponding variance points, separated into two figures for better visibility

$$\theta = 4, \bar{N} = 8$$

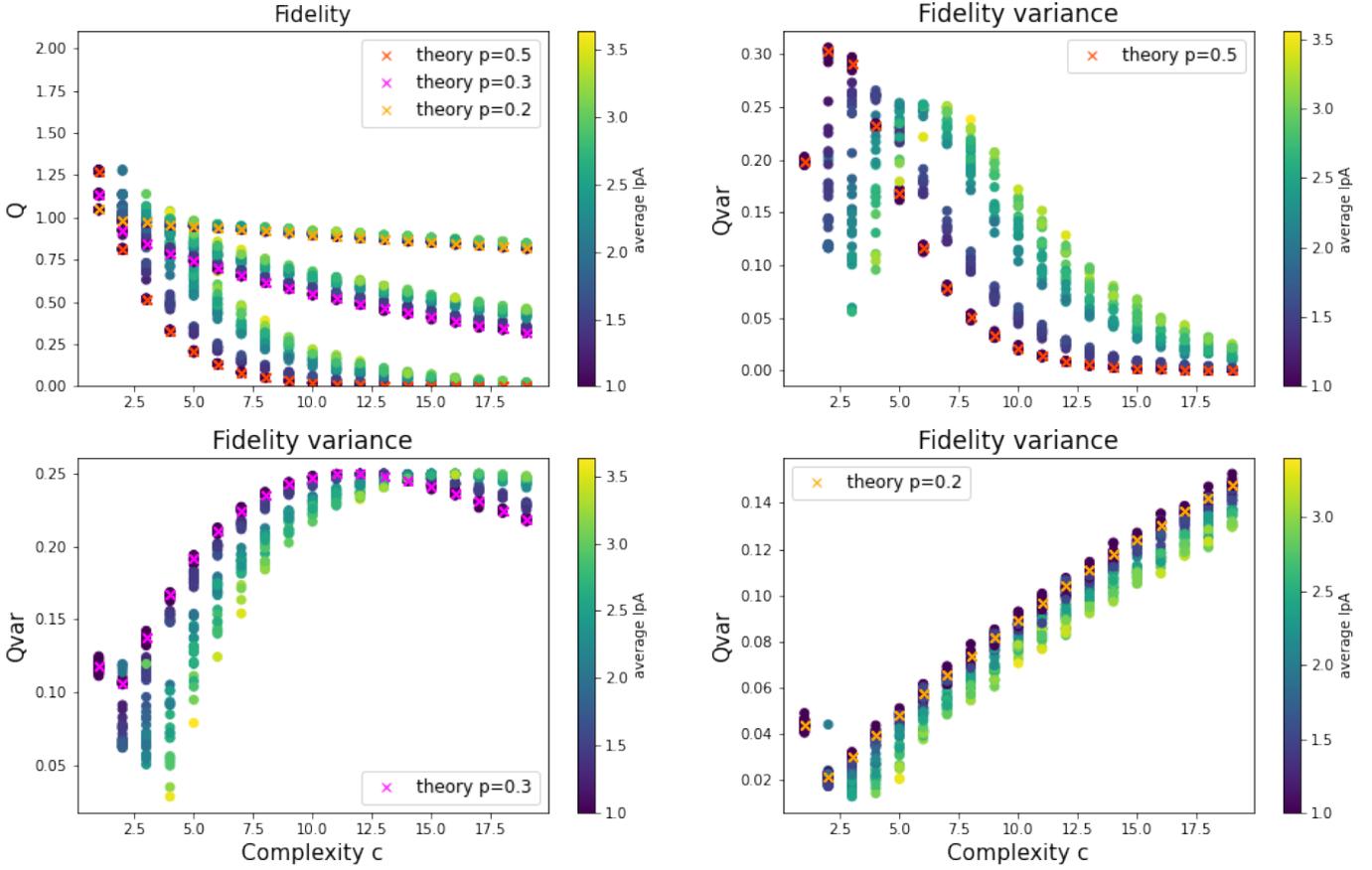


Figure 23: $\theta = 4$, In (A) the fidelity as a function of complexity for threshold value $\theta = 1$ and instance populations of $N=6$ for all traditions. Each dot shows the average fidelity outcome from 10 000 simulated splits of a randomly created agent community where instances were given to agents of varying density, average indicated in the colour bar to the right. 'x' dots represent the theoretical values of the fidelity for the homogeneous instance population of institution of size c . (B) and (C) and (D) show the corresponding variance points, separated into two figures for better visibility

We see simulated fidelity function for threshold $\theta = 1$ shows largest deviations for the most asymmetrical splits $p = 0.2$, whilst for $\theta = 5$ the largest deviations are seen for the symmetrical split $p = 0.5$. We note that the curves of high deviations resemble each other, and the curves of low deviations resemble each other. These results support the idea that deviations depend less on parameter values and more on the shape of the theoretical curves. Same seems to be indicated from the variance curves, where the steep peaked curves deviate more regardless of parameters, and the more linear shapes deviate less. Further the figures indicate that deviations will decrease for growing complexity, as have the previous and as was expected, although we note, quite slowly.

Overall the simulated results in figures indicate emergence of curves of points with similar aIpAs, and that these curves do quite resemble the ones predicted by theory for the same parameter values. Again simulated curves appear to be stretched or shrunken, or translated versions of the theoretical ones.

Finally, we refer to appendix for some further results, that show that if the instance vector is heterogeneous meaning that some tradition types are rarer than others, even subtle differences on the level of which instances are carried by the same agents, can affect the fidelity. If instances of rarer tradition types, coincide together in the same agent carrier, the fidelity will deviate significantly higher from theory, than if such rare traditions don't coincide. This indicates that even when one manages to find better theoretical predictions of the fidelity of higher number of instances per agent, deviations will be still be found due to details undetectable without adding new parameters to describe the instance-in-agent distribution.

8 Discussion

In the context of the Social Protocell Hypothesis the behaviour of fidelity serves to indicate how well adaptive institutions could survive community splitting, adaptive institutions serving as incipient socients. The model setting in which the theory was derived, with uncorrelated agents carrying single instances of tradition, is arguably a hard setting for institutions to survive splitting, because there is no structure to help the institution. As results indicate, only by letting agents carry more than one tradition –not many, and still uncorrelated– will significantly help fidelity and especially the lowest values of the maladaptive region. Theoretical results show that in many parameter settings even for 'hard case' scenario of $aIpA = 1$, institutions would quite easily survive splitting. For lowest threshold values close to $\theta = 1$, a number lower than 10 instances of each tradition are needed in the community for transmission of institutions to be probable, for complexities as high as $c=10$. Social protocells that allow for institutional complexity while staying adaptive provide good chances for cumulative culture since at points of higher complexity institutions might develop autonomous traits that further increase fidelity. A critical instance number of 10 to achieve relatively high complexity can be counted as fairly small if one assumes social learning is present and a relaxed time frame. On top of that simulated results for higher $aIpA$ cases indicate that the critical instance number gets exponentially smaller once agents are allowed more than one tradition type, (doubly-exponentially smaller, figure 20 implies). Further, the theoretical curves of fidelity as functions of complexity in figure 9 imply that for low thresholds $\theta = 1$, there is room for substantial complexification of institution with relatively little loss of fidelity, again for fairly low instance populations, such as six instances per tradition. We reason on top of that that a process of complexification of institution over generations could also likely lead to increase in the $aIpA$, as this could be over large time scales and also as there are all the more traditions present to learn. As results show, increased $aIpA$ would then further help fidelity of complexifying institutions. Let us also recall that no assumptions have been made about the complexity of the traditions themselves or about the method of spreading of the traditional instances. Thus, fidelity of the spreading method need not necessarily be high, as it is only the *function* of a tradition that all instances need to have in common. This allows for both individual instances and social spreading to maintain a very primitive/maladaptive level while results show they can still serve as part of a complexifying, cumulative, high fidelity institution.

The threshold value was shown to be an impactful parameter, as θ grows it quickly worsens the prognosis for successful transmission in split. Figure 10 for example showed that for $\theta = 4$ potential for complexification is dramatically lower if not gone, for the same low instance populations that figure 9 $\theta = 1$ showed to be sufficient for double transmission. The threshold parameter of the traditions in a community can serve to define several aspects both about the community and about the institution. A high threshold value could for example be the result of a low social learning rate in relation to the death rate in the community, where in

instances are fewer than θ instances die with their agents before they have sufficiently spread to other agents and so the tradition is lost. But a high threshold value could also arise from very elementary/basic tradition types that do not serve the institution unless there are a larger number of agents performing them. We propose that by steering the threshold parameter, one can choose to steer a broad variety of aspects, of mother communities or institutions, and find significant differences in the fidelity.

The fidelity expression also revealed strong effects of the symmetry parameter p . Asymmetric splits were shown to raise fidelity in the lowest values of the maladaptive region and thus better ensure the survival rate for institutions in this region. However asymmetry has a damaging effect on fidelity in and into the adaptive region, results show a firm fixation on unit fidelity for asymmetrical splits and struggles to pass over to the adaptive region. As stated in section 4.4, institutions in settings with unit fidelity are assumed in practice eventually doomed to disappear. In higher threshold cases asymmetry seems to completely remove the chances of double transmission even for high instance populations (referring to the emergence plateau of zero variance, seen in figure 14(D)). For the symmetric splits, results show in contrast that rapid fidelity growth persists into the highest values of the adaptive region. This suggests a variation of potential scenarios where symmetric splitting would more likely have lead to evolution and spreading institutions. This gives great domination potential to the symmetric splits, although asymmetric splits would be a better fit in settings where institutions would be on the verge of disappearing. This fits well with empirical and historical data that state that symmetrical community splitting is most likely the prevalent case Andersson and Törnberg (2019); Moffett (2013).

The derived fidelity expression has shown to serve accurately under the binomial assumption while deviations from theory were found in simulations when the binomial assumption was lifted. The deviations were exclusively above the theoretical fidelity value. This was understood by considering that agents bring larger 'chunks' of an entire institution with them in a split, thus help the fidelity. The larger the $aIpA$ value, the higher the fidelity value rises above theory ($aIpA=1$). Simulated results have largely indicated that the values rise systematically while keeping the shape of the theoretical curve, only somewhat transformed. This indicates that the curve under the binomial assumption $aIpA=1$ does manage to capture the main behaviours of the fidelity curve also for higher $aIpA$. Thus a proposal is that the derived fidelity expression is useful for qualitative study of fidelity and the parameter's behaviours, also for larger cases of $aIpA$.

One would also argue that for more quantitative study in the general case, the proposed fidelity expression could serve as a useful starting point, since the simulated $aIpA > 1$ so often appear to be transformations of the derived $aIpA=1$ curves. While some primary analysis of the deviation of higher $aIpA$ was performed, the methods chosen were shown not optimal for revealing much about the dependencies on $aIpA$. Further study is called for and suggestively a more systematic investigation of the deviated curves is not far away. The aim would be an approximated general fidelity expression, where an $aIpA$ parameter is included for transforming the derived expression to better suit the simulations. From the brief analysis of this study it is proposed that the extent and type of necessary transformations, potentially show dependency on the shape of the $aIpA=1$ curve, where convex and concave regions react differently to the increased $aIpA$. So that perhaps one could transform regionally depending on convexity of the curves.

However this study has not shown, that deriving the true probabilistic expression of fidelity for

general aIpA would not be a better way, than transforming the proposed expression. Although one strongly believes so, one would still do right with some more sophisticated analytical tries than was performed in this study, before ruling that out. Either way, it would be practically rewarding to stay with an expression stochastically built up on binomial distribution functions, because of well established theory of binomial distribution in statistics and stochastic analysis. Binomial distributions are for example frequently handled in Bayesian statistics which could be useful if the model was to be extended to include stochastic parameters. This would allow for example testing for different distributions in the community of the symmetry parameter p . Or variation in the threshold θ parameter for different tradition types.

Finally, the results calls for testing on larger simulations including more agent based community dynamics, pre- and post split. The institution and splitting event need to be put into their context of resource distribution and community survival. In this study the simulations have been only repetitions of the instantaneous events to collect outcome statistics. Only when put into the larger dynamical context, can the expression find its true usefulness.

9 Conclusion

The results of this study show several useful aspects of the derived fidelity expression, both in its presented form in this study, but also in indicated potential for generalisation. The proposed expression has the benefit of being nothing but simple elementary operations of binomial CDF functions, making the expression both easily computable, and a good potential building block for more complex analytical study. On a contextual note, this study aimed to formulate the theoretical expression of institutional fidelity in a very general and accessible community setting, avoiding any pre-assumed structure and organisation, outside of the institutions themselves. The theoretical assumption of aIpA= 1, also happened to result in the most structureless setting of all the other aIpA values. One can defensibly argue that a hominin community as described in literature (Andersson and Törnberg, 2019; Davidson et al., 2021) would need not much more than the presence of an institutionally rewarding resource, and the benefit of time and space, to have obtained the scenarios upon which the theoretical expression of fidelity was derived and showed unquestionably high values. The in cultural terms excessively long time span of millions of years of pre-modern human development, could arguably have provided the time and the space, and the coinciding emergence of carnivore hunting in historical records in this time period, could arguably have provided the reward (Andersson and Czárán, 2022). The final conclusion of this study is thus in support of the SPH, stating that high fidelity community splitting of our most primitive traditions in cooperation might indeed have been the very early and very powerful spark of our culture.

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Figure of q_t vs p

Included is a figure of the fidelity as a function of symmetry p as no such figure was included in the main text.

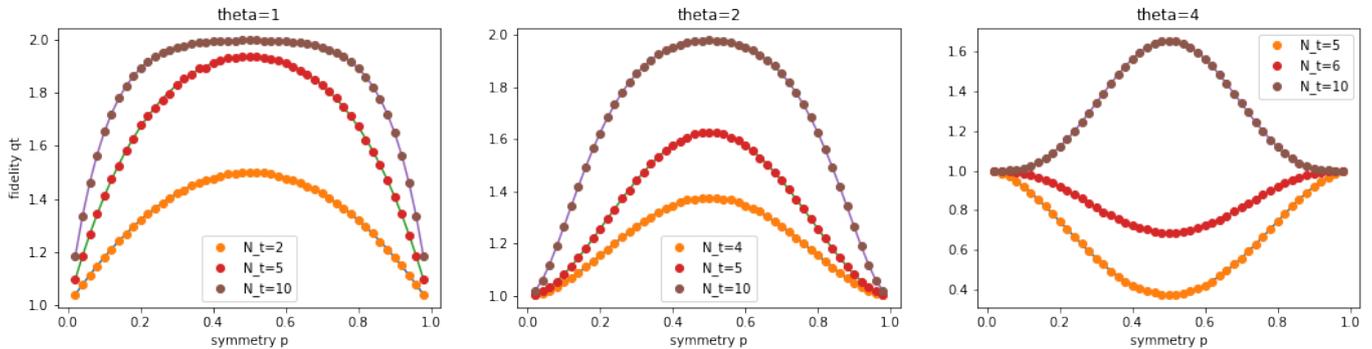


Figure 24: Single tradition fidelity q_t as a function of symmetry parameter p for three different threshold cases and for each, three different instant population cases.

As concluded in the main text, this figure shows that the symmetry parameter has different effects on fidelity depending if fidelity value is above or below unity.

Estimation test for other parameter cases

Included are two more parameter sets for the estimation test of section ??.

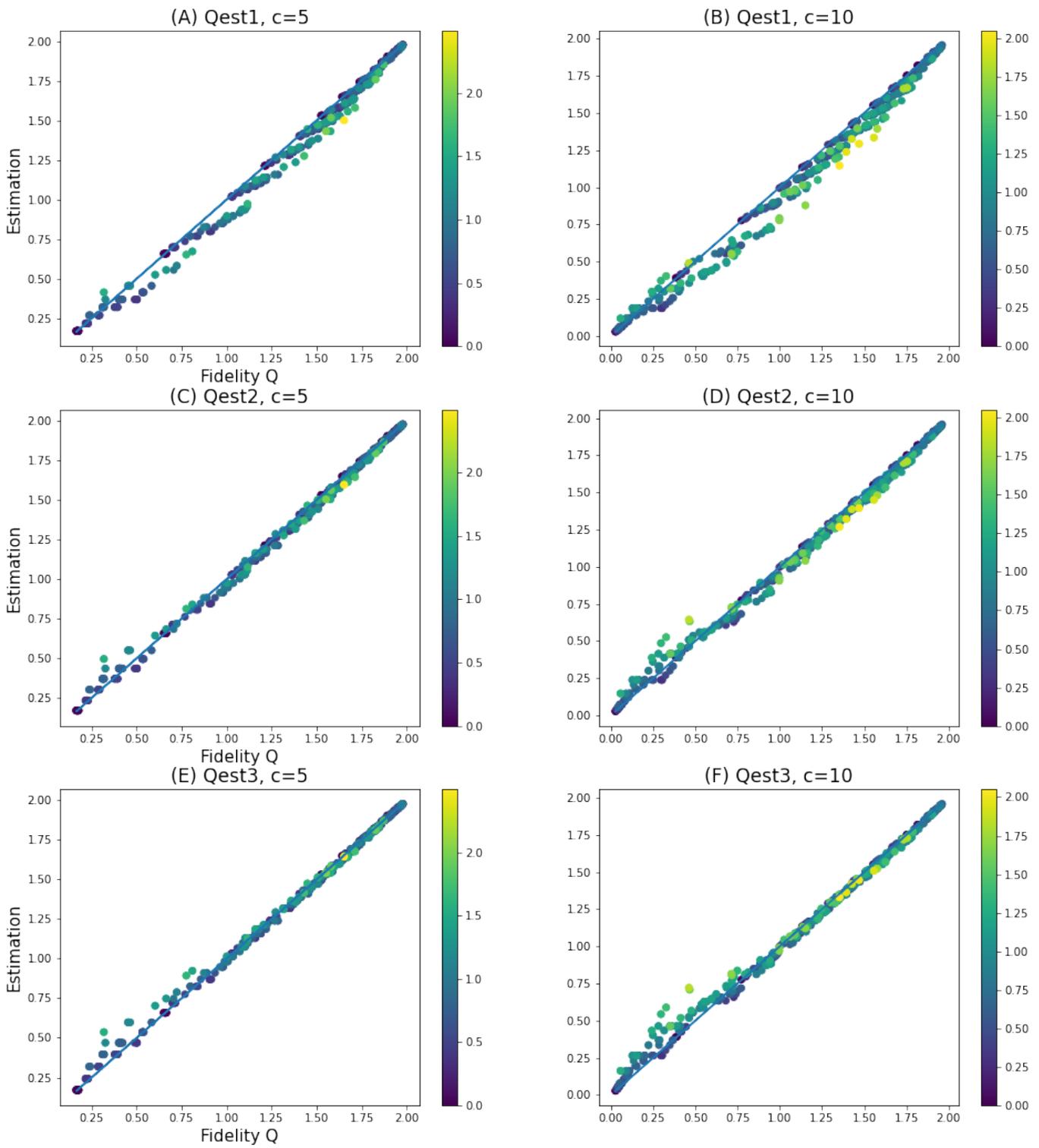


Figure 25: Estimation tests for parameters $p = 0.3$, $\theta = 5$

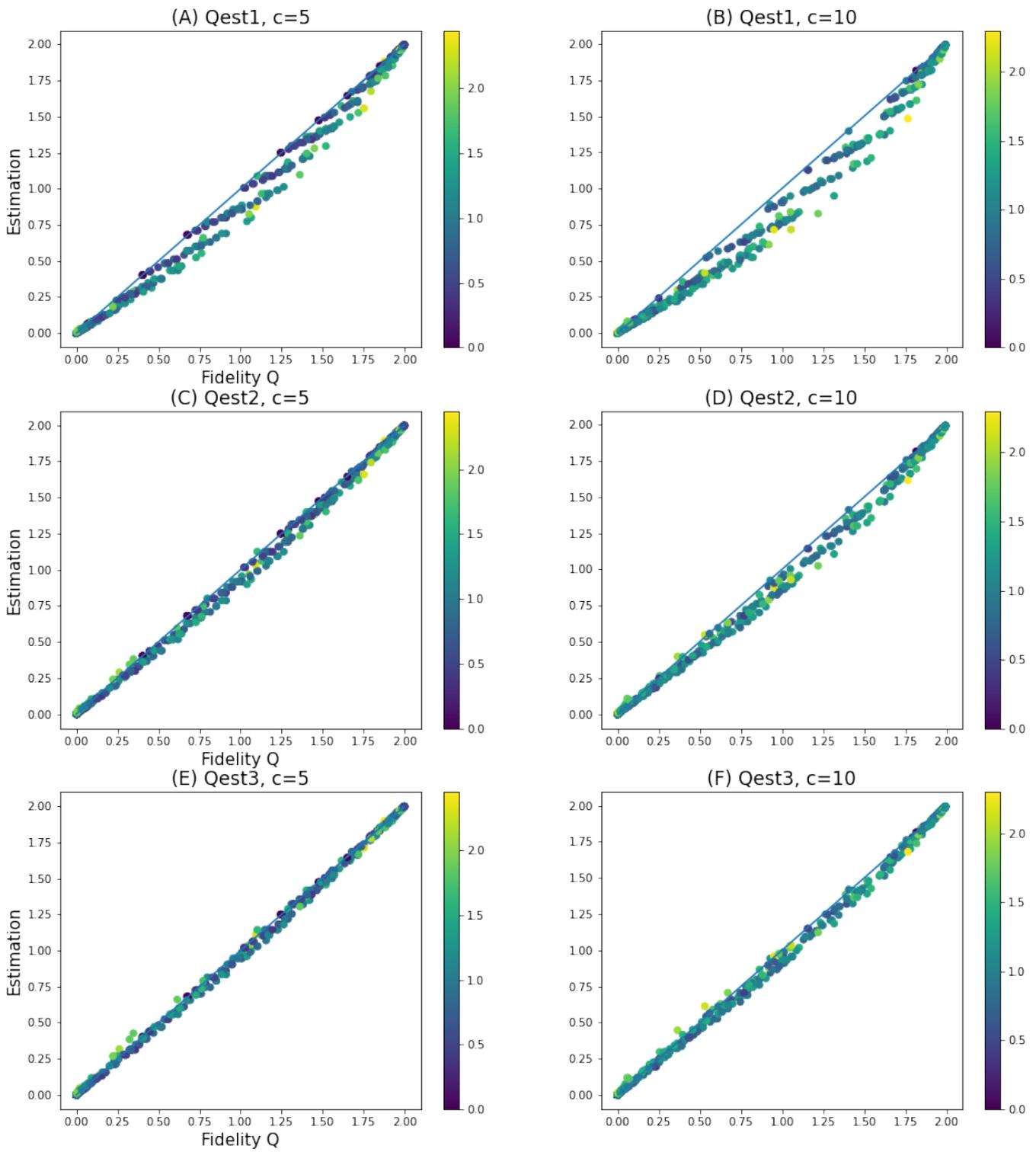


Figure 26: Estimation tests for parameters $p = 0.5$, $\theta = 5$

The figures show better agreement of the estimators with the actual fidelity values than the base case, especially for Q_{est2} and Q_{est3} .

Progression of the convergence of fidelity values

Included are two figures showing the progression of simulated fidelity values for increasing number of runs. The three colors in each subfigure show three different community realisations of 15agents, separated by colors. In all cases in the first figure, the instance vector is homogeneously $N_t=[2,3,4,4,5]$ and for each community realisation the total of 18 instances of five different tradition types. These are randomly distributed amongst the fifteen agents so that five agents have two (different) instances each, and the ten have one.

$N_a=15$ (12+3), Instance-vector=[2, 3, 4, 4, 5], alpA=1.2

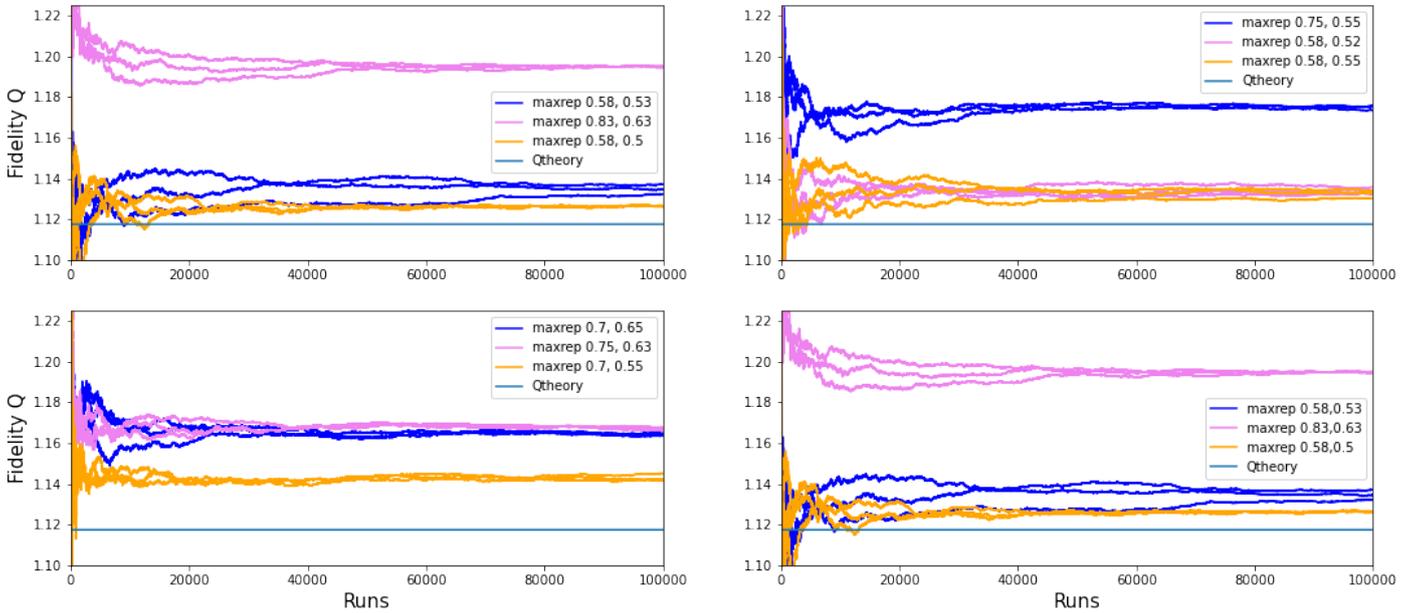


Figure 27: Base Case $p=0.5$, $\theta=1$. $c=5$ with heterogeneous instance vector= $[3,3,4,5,5]$. The measure **maxrep** shown in the legends is explained below

In each sub-figure a different colour represents a new realisation of the community, with the instances distributed amongst the agents randomly as described in section 6.3. In every sub-figure the same colour shows a realisation of the same community repeating 100 000 splits and calculating the average. Thus in total the figure shows twelve different communities, and three realisations of fidelity estimation for each community. The quantities of **maxrep** is unique for each community and represents the two largest *average representations* of each agent in a community. The average of representations of an agent means how much each of its instances represent on average from the total amount of instances of the same tradition type. Thus if an agent has an instance that no other agent has, the representation of that instance will be 1 for that agent. For another agent who has an instance that five other agents have, the representation of this instance for this agent will be $\frac{1}{6}$. This quantity is tested if it can explain the apparent differences that exists in fidelity amongst different communities that share all the parameters studied in this text, including the alpA whose effect has yet to be determined. This figure shows that the chosen limitation of parameters (including alpA) that this study has chosen evidently is not enough for precise results of fidelity estimation, and that there are

interesting dynamics on the level of agent-instance relation, and perhaps even more. One can argue too that the deviations appear to be sometimes bigger than the deviations caused by $\alpha p_A > 1$. This means that more variables could be necessary in future study of the dynamics of agents carrying multiple instances.