The Slow Spread of Environmentally Friendly Action

An agent-based model simulation of social networks

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Preface

Madrid. A sizzling summer day warms up the attic flat as I concentrate on the thesis. I hear the whirring sound of my computer, running hot, while simulating one of many interactions. Only then, I notice the thermometer next to me. It shows 32 degrees. It is a day in April, although it feels like July. Not only will it be the hottest and driest April ever measured in Madrid, but most likely the hottest May as well. It is then, when I ask myself the exact same question I ask in this thesis. Why is change so slow? How much warmer does it have to get for people to realise the urgency? How many more awful weather records have to be broken for people to act? Through my study of sociology, I learned that the micro and macro levels are inherently interconnected. Individual actions and systemic changes are interconnected social processes that are influenced by actions of others. Reason enough, to study how individual action can bring change to the whole system. While individual actions are not sufficient to tackle the climate crisis alone, it is a desperately needed start. It is time to get things rolling. It is time to act.

Abstract

The adoptation of environmentally friendly behaviour is rather slow, although the climate crisis is pressing. This thesis aims to understand the slow adoption of environmentally friendly behaviour, specifically focusing on vegetarianism and veganism, by employing social network analysis. By simulating interactions within an agent-based model, the study explores different mechanisms that hinder the diffusion of these behaviours. The research findings highlight the significance of the complexity of the contagion in shaping the speed and extent of the diffusion process. While minimally complex contagions are able to infect half of the network on average, vegetarianism and veganism do not spread, due to their complexity. Additionally, the initial number of vegetarians/vegans was found to be the main driver of infection speed, besides inter-connectedness. The study also explores the possibility of a social tipping point, a critical threshold at which the diffusion process accelerates or reaches a critical mass. However, the research did not observe a tipping point in the adoption of vegetarianism and veganism. By examining the slow adoption of vegetarianism and veganism as a complex contagion, this research contributes to the comprehension of concrete network effect. The findings provide valuable insights for designing interventions and strategies to promote the widespread adoption of vegetarianism, veganism, and other environmentally friendly practices.

Keywords

climate action, network analysis, agent-based model, diffusion process, tipping point

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1. Introduction

Modern vegetarianism emerged in the 19th century in Europe and North America, as the first organisation dedicated to promoting a meatless diet, was founded in the UK in 1847. Since then the proportion of vegetarians increased from under 1 percent to around 4.5% in the UK (Steward et al. 2021). While in some countries the diffusion of vegetarianism is quicker, Sweden currently having 6% vegetarians (Motrøen 2020), it is slower in others, with Spain having only 1,4% vegetarians (Latern 2021). Veganism is even less represented, with just 4% of the population in Sweden and 0.8% in Spain practicing it[1]. Although, data availability is limited what makes it difficult to compare numbers over time as they differ from survey to survey (Leitzmann 2014), it is clear that vegetarians let alone vegans are still a small minority in Europe (ProVeg 2021). Given how long the idea of vegetarianism has been around, this brings up the question how the slow spread can be explained. Generally, environmentally friendly change seems slow, although the climate crisis is a pressing threat of humanity. In 2018, the UN launched the ActNow campaign, which provides a list of 10 recommended actions or behavioural changes designed to reduce an individual's carbon footprint (UN 2023). For instance, behavioural changes, such as turning vegetarian or even vegan could reduce one's personal food related green house gases emission by 190 percent respectively 250 percent or in absolute numbers 1,560kgCO_2e a year (Scarborough et al. 2014). However, despite the campaign's efforts, minimal progress has been observed for the majority of the action points, indicating a slow rate of change. Air travel is almost back to pre-covid levels and expected to rise even further (IATA 2023), food waste per person is still very high in Europe (Scherhaufer et al. 2018) and even household energy usage remains at a high level (Aydin & Brounen 2019). An interesting exception to this pattern is the widespread adoption of electric cars, which has seen a significant increase in recent years (Eurostat 2023). However, unlike other environmentally friendly actions that often require a change in behaviour, the transition to electric cars primarily involves a change in technology rather than individual behaviour.

Recently, the concept of social tipping points has gained attention as a means to expedite efforts in addressing climate change (Sharpe & Lenton 2021, Winkelmann 2022, Meldrum et al. 2023, Bentley et al. 2014). The argument is that in complex systems, including human societies, change often occurs in a non-linear fashion. In other words, there may not be a direct cause-and-effect

[1] Although vegans are technically vegetarians at the same time, the here displayed percentages are not included in the previously mentioned share of vegetarians. The previous references apply here as well.

relationship, as small perturbations can sometimes result in disproportionately large changes. This ‘tipping point’ phenomenon is taken from the complex dynamics of climate change, where a slow and steady increase in global temperatures can eventually lead to catastrophic consequences if we reach a tipping point (Lenton 2011, Armstrong McKay et al. 2022), and applied to the complex dynamics of social systems. A social tipping point is defined as a moment or threshold at which a small change in behaviour or attitude can cause a large and rapid shift in the behaviour or attitudes of a large group of people, leading to a significant social change. It is a point at which a new behaviour or norm becomes the dominant one in a society. Although the evidence for these social tipping points is more scarce, they have been identified in the past (Centola et al. 2018, Wiedermann et al. 2020, Juhola et al. 2022) and found to be connected to a dedicated minority of 25%. Hence, to add to the academic debate, a secondary objective of this thesis is to explore the existence of tipping points in the adoption of vegetarianism/veganism.

1.1 Aim and Research questions

This thesis seeks to explain the slow behavioural change through the lens of social network analysis. By asserting that individual actions are influenced by the actions of others, the main objective of this thesis is to identify the social mechanisms that contribute to the slow adoption of environmentally friendly behaviour. Specifically, this thesis uses vegetarianism and veganism as a proxy for environmentally friendly behaviour and employs an agent-based model to manipulate and simulate different network parameters, in order to elucidate the patterns of slow diffusion. The adoption of vegetarianism and veganism is assumed to act like a contagion, ‘infecting’ other individuals when interacting with vegetarians or vegans. However, multiple reinforcing signals from peers are assumed to be needed for a successful ‘infection’ of an individual, defining them as a complex contagion. Furthermore this thesis argues that adopting a vegetarian diet represents a behaviour that is in competition with other contagions i.e. behaviours, such as non-meat-free diets or beliefs. Considering both vegetarianism and veganism allows to draw conclusions on two similar processes that differ in complexity. Veganism is a more complex contagion in the sense, that it requires more reinforcement from peers, compared to vegetarianism which is more easily adopted. This allows to examine the effect of how complexity potentially hinders diffusion. Besides complexity, other network parameters, such as intra- and inter-connectedness of groups are assumed to have an effect on the diffusion process and are therefore in the scope of this thesis. Additionally, the proportion of hardliners, i.e., agents that never become ‘infected’ is hypothesised to reduce the ability of a contagion to spread, due to less available connections that serve as bridges to other susceptible individuals (Centola 2018: 45). While identifying key parameters that have a significant impact on diffusion, potential tipping points of parameters are carefully observed. Hence, the thesis aims to achieve two objective and is concerned with the following research questions:

i. How can the slow spread of vegetarianism and veganism be explained through the lens of social network analysis?
ii. Drawing on these conclusions, can a potential social tipping point be identified?

The following hypotheses will be examined derived from the theory and previous research:
H1: A high proportion of hardliners limits the diffusion process for highly complex contagions.
H2: The more densely the networks are linked among themselves the less able the contagion is to spread.
H3: The more densely the networks are linked between each other the more able is the contagion to spread.
H4: A general tipping point that involves a dedicated minority around 25 percent cannot be identified.

This paper is structured into four main parts, first in the theory part, it will be discussed how contagious diseases, news, and rumour spread through a social network of individuals. Therefore the concepts of simple contagions, and the distinction between strong and weak ties is introduced. Following up, it is argued that ideas and behaviours do not spread in the same way, introducing the concept of complex contagions. Next, it is reasoned for, that two competing contagions have to be considered when modelling the diffusion process of vegetarianism and veganism. The theory paragraph ends with the description of the threshold model used in this thesis and a discourse on tipping points. The second part, methodology, is concerned with the agent-based model (ABM) that is being built to simulate the actions and interactions of autonomous agents to explain the diffusion process. This part consists of a justification for the model choice and the used parameters in the model. Third, the results from the simulations obtained by different model settings are being presented and key mechanisms identified. Lastly, the discussion focuses on interpreting the results and proposing an empirically calibrated agent-based model for a more accurate description of the phenomenon, as it is important to note that the scope of this thesis is not to (and cannot) provide a precise and exhaustive depiction of the identified phenomenon, but rather to identify and examine the key mechanisms involved.

2. Theory & Previous Research

2.1 Spreading processes

It marked the beginning of a dark era when the Black Death was forcibly introduced into Europe in 1346. Corpses, infected with the deadly and highly contagious virus Yersinia Pestis, were thrown in a high arc with the help of catapults into the besieged city of Caffa. The perfidious war strategy of the Tatars - rather a desperate idea than a sophisticated plan as the black death raged among them, decimating their army daily - was to catapult their own corpses on throwing machines into the city of Caffa. The calculation of the besiegers, that everyone should perish from the unbearable stench worked out. However, the rotting corpses not only brought the stench to the city but also the virus, poisoning the air and the water supply. While the majority of the inhabitants succumbed to the disease or weakened surrendered to the Tartars, other plague-infected inhabitants of Caffa fled by sailing ships to Genoa, Venice and other Mediterranean cities. Once the plague successfully infected these cities it quickly began to cascade across Europe.The more cities it hit the faster the wave front propagated. In 1349, the virus had reached every city in Spain, Italy, as well as Paris, London and Frankfurt. The virus had traveled from town to town, infecting person after person. In the words of Gabriele de' Mussi, a chronicler from Piacenza, Italy, who became an eyewitness to the plague outbreak in Caffa: "Moreover one infected man could carry the poison to others, and infect people and places with the disease by look alone. No one knew, or could discover, a means of defense" (Horrox 1994, as cited in Wheelis 2002: 973). By 1351, one-third of Europes population had died (Benedictow 2021: 867-870).

It is up to debate if Caffa was the starting point for the catastrophic plague epidemic. While the story of the biological attack is plausible, it might not had a decisive role in the spread of plague to Europe (Wheelis 2002: 974). While hygienic standards changed which make transmission less likely, nowadays diseases do not waste time traveling by land or sea. Air travel became widely available and it reduced the time immensely that a contagious disease needs to spread from one part of the world to another. While the Black Plague took years to conquer Europe, in 2020 the COVID-19 pandemic spread through the world in a matter of weeks, due to better and faster transportation systems. In fact the contagion process happened so quickly that it cannot only be explained with more efficient transportation but also with changes in human networks.

In the middle ages most people lived within small communities where everyone knew everyone else throughout their whole life. Migration and travel outside the community was rare. It was a society with community networks determined by geography, low tech transportation and strong ties. Strong ties refer to the close, intimate, and enduring relationships between individuals who share deep emotional bonds, common experiences, and a high degree of mutual trust and reciprocity (Granovetter 1973: 1361, Centola & Macy 2007: 703). They are characterised by frequent and regular interactions, and shared values, beliefs, and interests (ibid.). For a contagious disease it is very inefficient to spread through strong ties as they have a high level of redundancy (Centola 2018: 24). Redundancy is caused by the overlapping structure of strong ties. Because strong ties are the ties that one has to its inner social circle, made up by close friends and family, most of them already know and interact with each other and their friends' friends, as humans have a tendency towards transitivity, meaning that two individuals who are strongly tied to a third person are very likely to also be tied to each other (Feld 1981: 1022, Granovetter 1973: 1363). A contagious disease then bounces to and in between already infected or recovered people, slowing down the diffusion process.

In todays societies with high tech transportation available, people not only move quickly across cities and countries, but also meet other people at conferences, classes, or on vacation with whom they never or just rarely interacted with before. Today, migration and travel outside the initial community is typical. This hints towards the answer of why the corona virus spread so much quicker. In his famous article "The Strength of Weak Ties" (1973) Granovetter argued that: "whatever is to be diffused can reach a larger number of people, and traverse greater social distance […] when passed through weak ties rather than strong" (Granovetter 1973: 1366). The strengths of weak ties are that they connect people across different communities and provide access to new information and resources that are not available within an individual's own social circle. They serve as bridges between different clusters of strong ties, making us more likely to hear about new information from them. Granovetter's famous argument is that, we are more likely to hear about a job vacancy from weak ties due to the redundancy of strong ties. It only takes a second-degree cousin to spread the news about a lucrative job. The same holds true for other simple contagions.

2.1.1 Simple contagions

Simple contagions can spread quickly and efficiently through human networks provided that enough weak ties allow the contagion to jump between clusters of strong ties. For simple contagions only a single source of exposure is needed. In the case of the Black Plague and COVID-19 a single individual was enough to infect their peers. Other examples for simple contagions besides news and diseases are rumours and to a certain extent memes[2]. Overall, the key to the success of simple contagions is the social structure of the population in combination with high levels of contact between individuals and high levels of contagiousness. With the idea that every person is only a few social connections (weak ties) away from each other (Milgram 1967), a simple contagion can quickly infect the whole network. The vocabulary of network science is heavily influenced by epidemical research as many models have been build and proposed to understand the spread of diseases. Sociologist could then draw upon the existing knowledge and assumed that diffuse process of social contagions functioned like contagious diseases making it convenient to work with existing models (Gladwell 2000: 7). In summery, simple contagions spread easily and fast across a network because it only needs a single individual to potentially infect the whole network. Weak ties can accelerate the diffusion process even more as they allow the virus to spread efficiently to other groups of individuals. Complex contagions, however, work differently as they need multiple sources of exposure. The idea of becoming vegetarian does not seem to spread like a virus. Even if the Tartars would have catapulted vegetarians into the city, this would have certainly not persuaded people to become vegetarian themselves. While the information about vegetarianism and veganism can spread quickly as a simple contagion, the behaviour does not.

2.1.2 Complex contagions

The distinction to simple contagions hinges on the idea that complex contagions such as innovations, ideas or behavioural change require exposes/reinforcements from multiple peers and do not spread through a single person (Centola & Macy 2007). The distinction between ‘multiple exposures’ and 'exposure to multiple sources’ here is crucial (ibid.: 707). As not every simple contagion has a transmission probability of 1, it might take multiple exposures for the contagion to spread. However, even for very small probabilities, for any $P > 0$, it is possible that the contagion spreads after just a single encounter (ibid.). On the contrary, complex contagions require multiple sources of activation, a single source is per definition never enough, as they are either costly, risky, or involve some degree of complementarity. Four mechanisms are known that explain why complex contagions require exposure to multiple sources of activation and therefore differ from simple contagions. *Strategic complementarity.* The value of a behaviour increases with the number of others who adopt it (Centola 2018: 38). Especially in the early stage of an innovation or a collective

[2] Certain more controversial or political memes need more reinforcement making them a complex contagion.

action such as a social movement the costs and benefits for investing often depend on the number of prior contributors (Centola & Macy 2007: 708). C*redibility.* If a behaviour or belief is perceived as credible, individuals are more likely to believe that it will have the desired outcome, and therefore more likely to adopt it. The credibility of a contagion, for example of a message, becomes higher if it consistence across multiple sources, which makes it less likely that it is just a fanciful invention of the informant (ibid.). *Legitimacy.* While credibility refers to the extent to which a piece of information or a behaviour is perceived as reliable or trustworthy, legitimacy refers to the extent to which a behaviour or belief is perceived as conforming to prevailing norms and values. If a behaviour or belief is perceived as legitimate, meaning that more individuals adopt it, other individuals are more likely to perceive it as socially acceptable, and therefore more likely to adopt it (Centola 2018: 38). *Emotional contagion.* An individual may be more likely to adopt a behaviour or belief promoted through emotional contagion if they witness it in the context of a close friendship or social group, rather than from a stranger or acquaintance as well as the "excitement associated with adopting a behaviour increases with the number of others who adopt it" (Centola 2018: 39).

When only a few people have adopted vegetarianism or veganism, strategic complementarity, credibility, and legitimacy is most likely limited, making it challenging for the contagion to spread widely due to opposing i.e. countervailing influence (Centola 2021: 325). For instance, the legitimacy of vegetarianism or veganism as a socially acceptable behaviour may be undermined when it is not widely practiced. Individuals may feel hesitant to adopt a behaviour that deviates from the prevailing norms and values if they perceive it as uncommon or unconventional. The same idea applies to the other mechanisms as well. Complexity arises from these mechanisms. Therefore, this thesis argues that vegetarianism and veganism are a highly complex contagions requiring even more than two reinforcements, contrary to minimal complex contagions. Generally, to understand the slow diffusion through the lease of social network analysis, it is crucial to consider the role of complexity and carefully analyse its implications.

2.1.3 Countervailing Influence

Each network peer that has not adopted the complex contagion is sending out countervailing influence to every other. This countervailing influence has to be accounted for when building a diffusion model for vegetarianism/veganism. As acting environmental friendly usually involves some costs, an agent might initially refrain from adapting the behaviour. Becoming vegetarian or even vegan, involves learning a new shopping behaviour as well as potentially giving up on former favourite dishes. Furthermore, the lack of social support and marginalisation of an individual's vegetarian/vegan efforts by others can pose significant challenges and threats to the success and sustainability of the dietary choice. For example, if the individual is the only one in their social circle or living environment who follows a vegetarian/vegan diet, they may feel socially isolated and excluded from shared meals or events. This goes along with moral disengagement; if the individual feels that their efforts to adopt a vegetarian/vegan diet are not being supported or respected by those around them, they may be more likely to disengage from their moral beliefs and revert back to their previous dietary habits, as marginalisation and lack of support from others can also lead to reduced motivation to maintain the diet, as the individual may feel that their efforts are not making a difference or are not valued by those around them. Thus, it is likely that an individual knows about the environmental benefits from a government campaign but does not adopt the behaviour until she/he receives encouragement and reinforcement from friends and family members who also became vegetarian, or stops the behaviour due to lacking support (cf. Centola 2018: 77).

Most complex contagions like vegetarianism/veganism require the agent to stay infected. For instance, the use of condoms it requires the individual to stay infected, to remain effective rather than being a one-and-done complex contagion like vasectomy (Centola 2018: 20). Similarly, consistent application of vegetarianism/veganism is the most effective. Countervailing influence thus has two roles, not only prevents individuals on becoming infected, it can also influence individuals to abandon a newly adapted behaviour. If not enough peers adopt the new behaviour, activated agents might give up on that idea as well. When studying the diffusion process of vegetarianism and veganism the possibility that individuals become uninfected again has to be considered. Subsequently, to combine this circumstance with countervailing influence, this thesis argues for countervailing complex contagions (ccc).

When researchers study diffusion processes of diseases, innovation or behavioural changes, the focus is typically on a single contagion and its propagation through a network (Klovdahl 1985, Beaman et al. 2021, Centola 2018). However, in an ‘open system’ as mentioned before, multiple processes are happening at the same time. Just like multiple COVID-19 mutations are in competition to each other, it can be argued for a similar situation regarding social contagions. Relaxing the assumption of a single contagion and allowing another contagion in the model can help to understand the slow spread of environmental friendly behaviour, as it can be assumed that multiple processes are present. In order to research conflicting behaviours or norms (Centola et al.

2005) multiple contagions need to be considered. Agents might not only be exposed to countervailing influence by neighbours rejecting the behaviour but to a ccc as well. Just like a party member of a specific party is also always exposed to different ideas and behaviours from other parties, an individual is likely to be exposed to different behaviours, norms, i.e., ccc's. Sticking to the example before, in the United States the explicit choice for condom-less sex has become a ccc against safer-sex promoting partner intimacy and social identity within the community for some individuals (Dean 2009). During COVID-19 propagating the dangerousness of vaccines has become a ccc against covid measures promoting natural immunity and healthy lifestyle choices (Centola 2021 329, 330). Climate activists see themselves confronted with countervailing beliefs, fatalism or sheer convenience (Costello et al. 2011, Mayer & Smith 2019). Rapid changes in norms or behaviour might even be the cause opposing norms sometimes, as the choice of people who see themselves as victims of fast-changing norms have either the possibility to adjust to the new behaviour, or question the attack and to create an alternative worldview, one that feels better (O'Neil 2022: 113). Especially if people come in contact with a new behaviour observed by a group of people that the individual does not identify this, this oppositional behaviour can be triggered (Centola 2021: 330). A ccc competing against vegetarian/vegan might manifest in the form of social norms and cultural traditions that prioritise meat consumption as a source of protein and nutrition. This could lead to a societal perception that vegetarianism is a restrictive or incomplete dietary choice. Additionally, the prevalence of fast food and convenience-oriented diets that often rely on meat-based products could further reinforce the notion that vegetarianism is inconvenient or difficult to sustain. Furthermore, vegetarians may encounter countervailing beliefs that challenge their dietary choice. For instance, some individuals may argue that humans are natural carnivores and require meat in their diet, or that vegetarianism is a less healthy or less sustainable dietary choice. Such counter beliefs can be discouraging and may cause vegetarians to doubt their decision.

Finally, the ccc against vegetarianism/veganism may involve counter-actions, such as individuals or organisations promoting meat consumption or criticising vegetarianism. For example, food companies may market meat-based products more aggressively than vegans options, or individuals may mock or criticise vegetarians for their dietary choices. The listed examples should demonstrate it is not only countervailing influence at work that prevents individuals to become or stay infected, but a ccc that is counters the 'initial' contagion and provides an alternative to the new norm or behaviour. This paradigm, that multiple complex contagions compete with each other, is guiding this research how behaviour spreads in a network.

Although the focus in this thesis is the spread of vegetarianism/veganism it serves as a proxy for acting environmental friendly versus acting not environmental friendly functioning as the ccc. Other actions such as using public transportation instead of driving a car, taking the train instead of prioritising air travel, or recycling vs no recycling are other examples that are noteworthy when it comes to environmental friendly action. For people that are vegetarian or vegan countervailing beliefs or behaviours pose a complex contagion, and vice versa. It must be emphasised that the aim of this paper is not to speculate on different motivations that lead to different actions, but to propose a general model of two competing complex contagions to research how behavioural changes spread across networks in that case. Even though vegetarian is used as the main example, it should be understood as a symbolic illustrations of the concept - environmental friendly action versus non-environmental friendly action[3].

2.2 Threshold model

Sociologists study dynamics and phenomena that are fundamentally rooted in social interaction. This is because social interaction can give rise to collective phenomena that cannot be solely attributed to the individual characteristics of the people involved (Durkheim 1982). The classic example of this is Coleman's boat (Coleman 1986), which illustrates the link between individual actions and the emergence of macro-level phenomena. This fact that actions of agents are part of a two-folded process has often wrongly been understood as necessitating two different types of explanations (Hedström 2005, Hedström 2021, Mondani & Swedberg 2022); firstly, we need provide an intentional explanation for the reasons behind individuals' micro-level actions. Secondly, we must provide a causal explanation for the macro-level outcomes that result from their actions.

However, since we scarcely ever know the reason that motivated the behaviour of another individual, intentional explanations cannot be used appropriately. One might actually get convinced by friends to act environmental-friendly, while another just acts because of peer pressure (Calvó-Armengol & Jackson 2010) or social norms (Elster 2011). Given the lack of knowledge regarding both the individual’s relevant mental states at the time of acting and the mental states → action relationship, it is advisable to refrain from relying on causal explanations that lack solid empirical backing. Assumptions not only need to be logically consistent but they must have empirical

[3] Since the motives for turning vegetarian/vegan or the according ccc are unknown, it is to be noted that both contagions could serve as a container for the listed examples. It doesn't matter whether the adaptation of a vegetarian diet is actually environmentally friendly, as long as two opposing behaviours can be identified.

implications to preserve testability (Raub et al. 2022: 6). Whereas basing assumptions on mental states therefore prevents testability. Instead, analytical sociology should not be concerned with the *why* (individuals react as they do, in the intentional sense) but on the *how* (individuals react) (Hedström 2021: 500). To understand individual actions it should be focused on what can be actually observed - action - and relate them to the actions of others with whom they interact, as even the decision to divorce seems to be no exception to this rule[4]. By emphasising actions as building blocks of social mechanisms, the explanation of individual behaviour becomes less of a concern which allows to shift the attention towards the social dynamics in which the actions of embedded individuals give rise to macro-level consequences (Kroneberg & Tutic 2021: 187). This paradigm is reflected in this work and guided the construction of the contagion model as a threshold model.

The threshold model developed by Granovetter (1978) is concerned how the aggregation of individual preferences cause (collective) action. Since complex contagions require multiple sources of activation, the thresholds equals the number of activated people an individual needs to observe before deciding to join in. How strong an individual is interested in the outcome determines the number of others required to trigger their activation. Granovetter's original assumption was that actors were rational, and their thresholds corresponded to the costs and benefits of participation to a social movement. However, this argument can also be applied to other used cases[5] as well as emotional and normative cascades among individuals who vary in excitability (Granovetter 1978: 1436-37, Granovetter & Soong 1983: 167) to account for emotional contagions. The threshold model is designed in a way that allows cascades with the option of assigning every individual a different threshold. This leads to the conclusion that small random variations in the distribution of thresholds can have big effects for the diffusion of a behaviour. He demonstrated this dynamics using two groups, each consisting of 100 members. The first group had a uniform threshold distribution [0,1,2, ..., 99], while the second group was identical, except that there was no member with a threshold of 1 [0,2,2,3, ..., 99] (Granovetter 1978: 1425). Despite the two groups having almost the same average threshold, the diffusion process cascades throughout every individual in the first group, where the individual with a threshold of 0 serves as the initiator, activating the individual with a threshold of 1, who then activates the individual with a threshold of 2, and so on.

[4] Åberg (2011: 358-359) suggests that the marital status of significant others influences an individual’s decision to divorce. Her findings indicate that social interactions play a crucial role in understanding divorce, with the marital status of an individual's coworkers exerting a strong influence on their likelihood of divorce. The primary discovery is that divorce spreads like a contagion.

[5] Granovetter proposes 8 different examples: such as strikes, joining a party, voting, diffusion of innovations, or leaving social occasions (Granovetter 1973: 1424).

On the other hand, in the second group, this domino effect is blocked, leaving only the initiator activated while the rest remain unactivated.

2.3 Adjustments to the threshold model

The original threshold model has some rather unrealistic assumption that need to be addressed before adapting it. First, it predicts that either no-one or the entire population eventually becomes activated (Wiedermann et al. 2020: 2). However, individuals' personal preferences, norms (Elster 2009), or opportunities (Hedström 2005: 40), can restrict their behaviour, making it unlikely that everyone adapts a vegetarian/vegan lifestyle, regardless of how many others have already became one. This issue is resolved by defining a group of agents as hardliners that are immune to peer-influence and never change their initial behaviour. Since it is argued for ccc's, hardliners are assumed to exist in both groups of vegetarians/vegans as well as non-vegetarians/vegans. Further, the proportion of hardliners is likely to depend on the country and contagion, so it will be programmed as an adjustable parameter. For concerned complex contagions in this thesis a high proportion of hardliners could become a critical bottleneck, as certain agents are not available for infection, possibly preventing a cascade diffusion process, leading to the first hypothesis **H1**. Second, another assumption of the basic model is that agents will certainly act once their threshold is reached. To relax this assumption, a small amount of randomness in the agents behaviour i.e. their threshold is allowed, which has been shown to also make the model less sensitive to random perturbations and therefore more predictable (Macy & Evtushenko 2020). In addition to this, the effect of a stochastic threshold utilising a cumulative logistic function will be examined.

Second, Granovetter's model assumes that everyone has the same influence on everyone. This assumption is altered by coupling the different functionality of absolute and fractional thresholds[6] to the idea that the influence of agents varies depending on the strength of their ties. Strong ties are more influential because their opinions and actions are trusted and valued by the other end. They provide social support, advice, and guidance that can have a significant impact on an individual's decision-making process. Therefore, it is argued that strong ties influence other individuals in an absolute manner. Absolute thresholds reflect situations in which an individual is persuaded by a

[6] Granovetter circumvents this distinction between absolute and fractional thresholds by defining the number of agents to 100.

fixed amount of peers, regardless of any countervailing influences[7]. In contrast, weak ties tend to be more superficial, with fewer shared experiences and a lower level of emotional investment. Weak ties are less likely to be able to overcome countervailing influences. Due to this, it is argued that weak ties, on the other hand, influence others in a fractional threshold manner. A couple of weak-tie adopters in a sea of non-adopters do not provide much confidence that others should adopt too, especially if the adaption is costly (Centola 2018: 55)[8]. By giving more weight to the actions of strong ties, the model is better able to capture the influence of clusters within the network.

Third, the phenomenon of homophily has to be accounted for. The well-established concept in sociology refers to the tendency of individuals to form social connections with others who are similar to them in some way, such as in their beliefs, attitudes, behaviours, or appearance (Simmel 1955, McPherson et al. 2001). This can result in the formation of clusters or subgroups within a larger social network, where individuals who share certain characteristics are more likely to be connected to each other than to individuals who do not share those characteristics. This clustering effect can create pockets of high adoption rates in certain areas of the network, which can then spread to other parts of the network through the redundancy of connections, as individuals are more likely to adopt a new behaviour or idea when they receive consistent messages from multiple sources, rather than just one. In a fully connected network a complex contagion has little chance of spreading (Watts 2002) due to missing redundancy and high countervailing influence (Centola 2018: 77). The more likeminded people an individual is connected to, the more ties it needs to persuade him to act differently, and even if she/he becomes activated the remaining ties will make sure that he abandons the new action. In their study, DiMaggio and Garip (2011) employ a computational model to examine the diffusion of a practice within a network. By manipulating the degree of homophily in network formation, the authors find that as the bias towards homophily increases, the divergence in adoption patterns becomes more pronounced among groups categorised by income, education, and race. Based on this, hypothesis **H2** is derived. Contrary, the more inter-connected the clusters are (the less homophily), the more likely that agents get introduced to other actions/behaviours and the more likely they adopt as well, leading to **H3**. However, inter-connectedness also brings the risk that individuals become infected by a ccc.

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[7] If the absolute threshold is set to four, then four vegetarian/ vegan neighbours will be enough to trigger a change, even the individual is connected to many other non-vegetarian/vegan neighbours. This assumes that people ignore the non-adopters.

[8] If the fractional threshold is set to 0.5 and the agent has 10 neighbours, 5 vegetarian/vegan neighbours trigger a change. However if the agent has 100 neighbours, 50 opposing neighbours are needed to make an agent adopt.

Lastly, it has to be considered that societies are dynamic and constantly changing representing an open system. Compositions of social groups and networks can change over time, as individuals enter or leave for various reasons (Hedström 2005: 77, 80), such as moving to a new city or changing jobs, etc. For this reason, a function has to be added to the model, that simulates this phenomenon.

2.4 Tipping points

Social tipping points work in conjunction with the threshold model. A small change might trigger a cascade, establishing a new behaviour or norm. In the context of vegetarianism and veganism, a social tipping point could occur when a critical mass of the population becomes vegetarian/vegan, leading to a shift in social norms and increased adoption of plant-based diets. Experimental evidence suggests a tipping point of a dedicated minority of 25% to overturn established conventions (Centola et al. 2018). In this experiment participants were randomly assigned to one of 10 online groups of 20 to 30 people. Each round, members of each group were paired at random and simultaneously assigned names to a pictured object, with rewards for coordination and penalties for failure. Once a convention was established, the incentives strongly encouraged coordination. After each round, participants were reassigned to a new partner. Eventually, all players consistently coordinated on the same naming behaviour. A small number of players were then introduced to each group to attempt to overturn the established convention. Populations with a committed minority of at least 25% were significantly more likely to succeed in overturning the dominant convention than those with a minority below 25%. In one case, increasing the size of the committed minority by just one person resulted in a successful transition from the old convention to the new (ibid.: 1118). The critical size around 25% of a dedicated minority at which the system undergoes a rapid change is consistent with results from a random graph network, and has been discussed with respect to the Pareto principle (Wiedermann et al. 2020, Pareto 1971). However, the emphasis here is on *dedicated* minority. It is assumed that only the minority is dedicated and refuse to change their behaviour. However, as previously theorised it cannot be ruled out that a minority of the majority also actively advocates a meat-based diet, acting as hardliners. Additionally, it seems unlikely to identify a universal tipping point regardless of the complexity of the contagion. In the conducted experiment a behavioural change did not involve any radical change. This considered might relativise the tipping point that has been found, as social change processes might not be instances of tipping, after all (Milkoret 2022). “[S]eeing the world through tipping-point glasses” (ibid.: 6) must be avoided to ensure an open-minded research. Thus, while leaving the possibility open, to identify a tipping point, it is hypothesised (**H4**) that a general tipping point related to a dedicated minority of 25 percent cannot only be identified.

2.5 Previous research

Most research regarding environmentally friendly action and vegetarianism/veganism focuses on the individual motives for adaption. Analysis that move beyond descriptive and correlational statistical techniques remain scarce, a systematic literature review finds (Salehi et al. 2023). However, early research already hinted at the importance of the social network as a determinant for environmental action (Jaeger et al. 1993). Knowledge about climate change and sociodemographic characteristics turned out to be much weaker predictors of environmental commitment than being embedded in a social network that is emphasising problems of climatic change (ibid.). Embeddedness in such network clusters can be observed online (Pilař et al. 2022), however studies that specify concrete network effect of being embedded in vegetarian/vegan social network are lacking (Judge et al. 2021: 8). A critical review regarding norm changes for climate action identified five network determinants, that are decisive for how and whether a norm will spread within a given context. These determinants include the level of heterogeneity in preferences, beliefs, and adherence to social norms, the structure of the social network, the clustering of preferences within certain groups, the presence of anti-coordination incentives due to in-group/out-group dynamics, and the initial targeting of specific members of society through interventions (Constantino et al. 2022). The interplay of these factors ultimately is assumed to determine the extent and success of norm diffusion. The simulation model presented in this study takes these factors into account in order to address the research gap and explore their impact on the diffusion of vegetarianism and veganism.

3. Data and Methods

Agent-based modelling (ABM) is a computational modelling technique that enables the study of complex systems by simulating the behaviour of individual agents and their interactions within a larger system. ABMs have become increasingly popular in various fields, including sociology (Bianchi & Squazzoni 2015) as they allow researchers to study social phenomena from a bottom-up perspective, as outcomes of the actions of interacting actors (Hedström 2005: 118).

The use of ABMs has several advantages over traditional methods: first, ABMs allow researchers to study complex systems and phenomena that are difficult to study with traditional methods due to the ability to capture emergent behaviour, nonlinear relationships, and feedback loops that are inherent in complex systems. Second, ABMs enable researchers to conduct experiments in a controlled environment, allowing them to manipulate variables and observe the effects on the system. Finally, ABMs can provide insights into the emergence of macro-level patterns and outcomes from the interactions of individual agents, which is often difficult to observe in real-world settings (El-Sayed et al. 2012). Therefore, the use of ABM simulations in this study provides a powerful tool to test hypotheses and gain insights into the dynamics of the spread of vegetarian and vegan contagion. Simulated data is necessary because it is infeasible to manipulate and control network properties in real-world situations. Gathering network data is challenging since observing networks requires identifying and surveying a large number of individuals. Additionally, even with complete network data, manipulating network parameters to research the effect of different aspects of the network structure would require multiple complete network datasets. Using simulated data enables controlled experiments and allows researchers to vary the parameters of the simulation to examine how changes in the network structure or other factors affect network behaviour. Furthermore, simulations can generate data similar to real-world networks, allowing to study phenomena they would not otherwise be hard to observe.

3.1 Networks

Three types of networks are usually considered when modelling social systems: Random graphs, small-world networks and scale-free networks. In random graph networks, edges between nodes are formed randomly, with each pair of nodes having an equal probability of being connected (Erdös & Rényi 1960). Small-world networks are characterised by a combination of local clustering and short average path lengths, where most nodes are connected to their immediate neighbours, but a few long-range connections (Watts & Strogatz 1998). Scale-free networks are characterised by a few highly connected nodes, known as hubs, and many sparsely connected nodes, following a power-law distribution (Barbasi & Albert 1999). The network structure, i.e., the way individuals are connected and able to interact with each other, is crucial as it directly affects and determines how a contagion can spread through a network. (Chwe 1999, Centola 2018). Since, scale-free networks have been proposed to better capture the features of real-world systems (Wiedermann et al. 2020: 8, Centola 2018: 49) they are used in this simulation model.

Scale-free networks are a type of complex network that exhibit a power-law distribution of node degrees. The power-law determines that the frequency of nodes with degree k is proportional to k^(-γ), where γ is a constant that characterises the distribution (ibid.: 510). The algorithm starts with a small number of nodes, and at each time step, a new node is added to the network. The new node is connected to k existing nodes, where k is a parameter of the algorithm (Figure 1). The probability that a new node is connected to an existing node is proportional to the degree of the existing node. In other words, nodes with a high degree have a higher probability of being connected to the new node than nodes with a low degree. This results in a preferential attachment mechanism, where nodes with a high degree become more likely to receive new connections, and the network grows in a self-organizing manner. These high-degree nodes are referred to as hubs. This is the main difference to the previously introduced network models, based on the argument that most real networks exhibit preferential attachment (ibid: 511).

A real-life example of preferential attachment in scale-free networks can be observed in the social network of people attending conferences or social events. New conference attendees are more likely to be introduced to well-known and influential figures such as keynote speakers, organisers or established members of the community. As a result, the probability that a new attendee will form a connection with an influential individual is much higher than that they will form a connection with other less-known attendees[9]. However, empirical social networks are not expected to be as significantly skewed as Barabási and Albert initially proposed. They are at best weakly scale free (Broido & Clauset 2019). Other examples of networks that were found to have scale-free properties i.e. preferential attachment are social media networks such as Twitter, or Facebook (Aparicio et al. 2015, Ugander et al. 2011) - a few individuals (celebrities, influencers, public figures) have a large

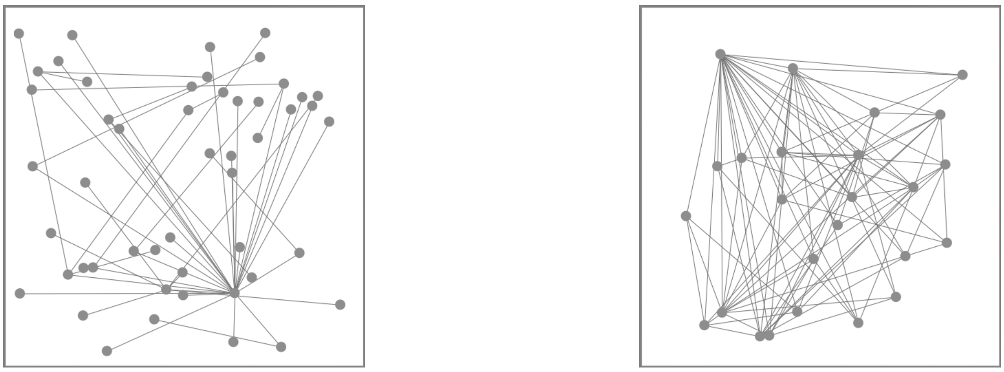

Figure 1: Visualisation of 2 scale-free networks with different k-degree: 50 nodes, 1 edge (left) and 25 nodes with 4 edges (right)

[9] Compare Barbasi & Albert (1999) with a similar example, stating that new actors are more likely to be linked to already established and better-known actors.

number of followers, while the majority have fewer connections - and even in and sexual contact networks (Liljeros et al. 2001). Therefore, it is believed that the scale-free model still offers significant insights, particularly regarding the influence that highly connected individuals can exert on the propagation of social contagions.

3.2 Simulation Model

The simulation model is built upon the following assumptions. Assumption 1 assumes that the spread of vegetarianism and veganism functions as a complex contagion competing with other countervailing complex contagions. Assumption 2 assumes that weak ties have a weaker influence on agents and therefore spread based on a fractional threshold and that strong ties have a stronger influence on agents and therefore spread based on an absolute threshold. Lastly, assumptions 3 assumes that the spread of social contagions can be adequately represented in a scale-free network. The agent-based model used in this thesis has been build in NetLogo 6.3.0 (Wilensky 1999). NetLogo is an agent-based modelling software that was developed by Northwestern University in the late 1990s. It is a free, open-source programming language and integrated development environment that allows users to create and run ABMs. NetLogo is used in a variety of fields, such as social science, biology, economics, and environmental science, to study complex systems and emergent behaviour. The code for the used model can be found in the appendix or online where it is available to download[10].

The aim of the simulation model is to simulate the diffusion of vegetarianism and veganism within a social network. The model seeks to understand how individuals' adoption of vegetarianism and veganism spreads and influences others within the network to identify determinants that can explain the rather slow spread. It operates by simulating the interactions and influence dynamics of agents within two scale-free networks based on the Barabasi-Albert algorithm. The networks are initially unconnected[11] and consists of two types of agents: green agents representing the green contagion (vegetarianism/veganism), and grey agents representing the ccc (opposition to vegetarianism/veganism). The agents are connected through links that represent the relationships between them. Links can consists of strong-tie links and weak-tie links. For this reason, the Louvain algorithm

[10] Further explanation of the model can be found under the tabs "Code" and "Info", respectively. Explanatory comments in the code added by the authors (starting with ";"). It is available here: http://modelingcommons.org/browse/one_model/7196.

[11] In this way it is ensured that green and grey agents are clustered together, accounting for homophily. Additionally, it allows to control how interconnected green and grey agents are.

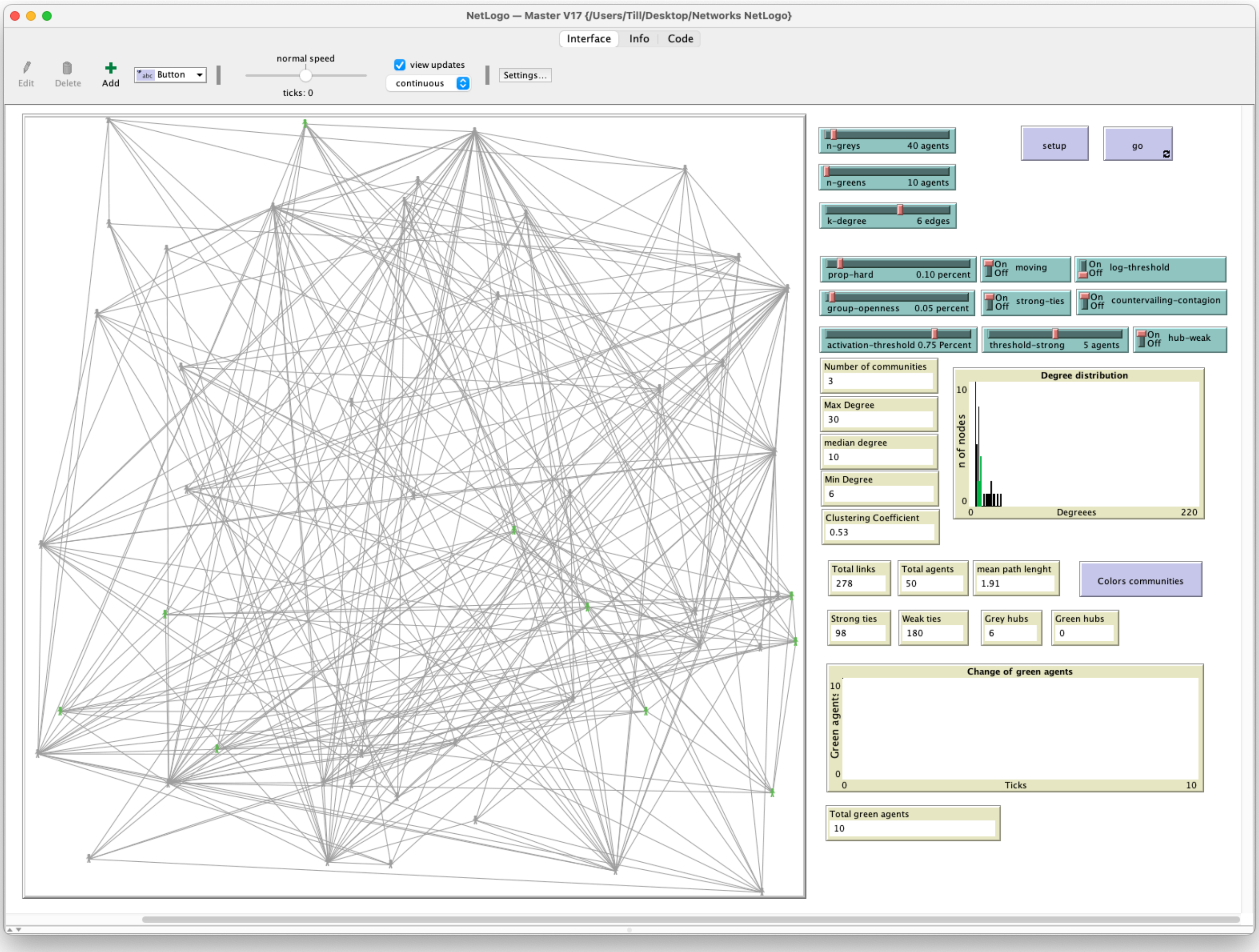

Figure 2: Screenshot of model interface, with generated networks of 40 grey and 10 green agents.

(Blondel et al. 2008) is applied to identify community structures within the networks. It is based on the modularity optimisation method, which seeks to partition a network into groups of agents that are more densely connected with each other than with agents in other groups. Strong ties are links connecting agents within the same Louvain community, while weak ties are links connecting agents across different communities[12]. The concept of using two colours is simplifying the interaction process by reducing it to a simple colour change if the agent is connected to enough other agents of opposing colour i.e. if the threshold is reached. If the number of weak ties with an opposing colour reaches the fractional threshold, the agent may change its colour with a chance of 20% for every interaction (model tick). For every additional weak tie link that exceeds the threshold the chance increases 20% up to 100%[13]. The same logic applies to strong ties with the difference that strong tie

[12] The algorithm has been criticised for the reason that it may identify communities that are badly connected (Traag et al. 2019), but since the proposed alternative has not yet been implemented into NetLogo, the Louvain algorithm will be used.

[13] This increase in chance is based on the idea of Macy & Evtushenko (2020) that small amount of randomness in individual behavior can make the model more predictable. For strong ties the chance increase is set to 25%.

thresholds are absolute and not fractional[14]. In other words, agents can be persuaded to change colours either by their weak-tie links or by their strong-tie links. This categorisation allows for a differentiation between the influences of strong and weak ties in the model. Other parameters alter the interactions further or determine overall network conditions.

It is important to carefully consider the level of complexity when designing an ABM, that is needed to answer the research question. Simpler models are often better models, as they allow researchers to understand the underlying mechanisms driving the system and to test hypotheses in a more controlled and focused way (Laver 2020: 116-118). Adding too many parameters can make the model unwieldy and difficult to analyse, while leaving out important interactions can lead to inaccurate or incomplete results (Sun et al. 2016). ABMs are particularly susceptible to this trade-off because they involve modelling the behaviour of individual agents and their interactions with each other. Therefore, it is important to strike a balance between including enough details to capture the behaviour of individual agents while keeping the model simple enough to understand the emergent behaviour of the system.
Moreover, simplicity in ABMs allows for easy manipulation of parameters to test various scenarios and hypotheses. The ability to test multiple scenarios and analyse the outcomes in a simplified model is a valuable tool in research and decision-making processes. As a result, as tempting as it might be to include as many parameters as possible in an ABM to make it more realistic, it is important to balance complexity and simplicity to ensure that the model accurately captures the essential dynamics of the system being modelled. This consideration has substantially lead the design on the simulation model, breaking it down to 5 essential parameters.

3.3 Parameters

The following parameters are part of the model and can be adjusted accordingly to study the effects of different settings on the diffusion process in the network:

- n-greys / n-greens (2-500): determines the number of grey and green agents in their network.
- k-degree (1-10): sets the minimum degree (number of links) each agent has when introduced into the network.
- prop-hard (0-1): determines the proportion of hardliners in each network. Hardliners influence other agents but stick to their own colour.

[14] For a detailed explanation of the difference between fractional and absolute thresholds, see Centola 2018: 49-51.

- group-openness (0-1): determines the chance of each node to create a link with another node of the other network. If set to 0, both networks co-exist next to each other with no links in-between. If set to 1, a node is linked to every node of the other network.
- moving (on-off): if switched on, there is a 1 percent chance that a random link will be selected and deleted. Additionally, there is a 1 percent chance that a random agent will be prompted to create a link to another agent. The newly created link has a two-thirds chance of being a weak tie and a one-third chance of being a strong tie. This is because new ties are likely to connect different groups and be long distance ties.
- strong-ties (on-off): if switched on, agents that have strong ties links to other agents can exert influence on one another based on the threshold-strong. Conversely, if the switch is disabled, nodes will only change colours based on their weak ties' competitive influence.
- countervailing-contagion (on-off): if switched on, countervailing complex contagions are allowed, enabling grey agents to infect green agents. Conversely, if the switch is disabled, only grey agents can turn green, but not vice versa.
- log-threshold (on-off): if switched on, a stochastic threshold for weak ties is enabled. The logistic function equation is f(x) = 1 / (1 + e^(-nw - (at * n)*5), where nw represents the number of weak tie peers, and at the activation-threshold, and n represents the total number of network peers. This enables nodes to activate with a small chance even if their threshold is not yet reached.
- hub-weak (on-off): if switched on, all links of the network's hubs will transform into weak ties. Hubs are identified as nodes having the maximum number of edges in the network, minus ten. This modification aims to explore the significance of hubs in greater depth.
- activation-threshold (0-1): this parameter sets the fractional activation threshold for weak ties.
- threshold-strong (1-10): this parameter sets the absolute activation threshold for strong ties.

Before turning to the results, it has to be noted that if not stated otherwise, for robust evidence, every setting is simulated at least 100 times. A setting is defined as a certain set of parameters. Additionally most simulations are capped to 1000 iterations for the reason that after this time most simulations reached a stable phase making further computation unnecessary. Although some rather unlikely settings will be simulated to identify the overall functionality of a parameter, the premises of every simulated setting is to be feasible. For this reason rather low numbers of initially green agents are chosen when experiments are conducted, as the proportion of vegetarians and vegans is to be estimated to be around 1-10 percent in most countries.

4. Results

4.1 Thresholds

Table 1 presents an overview of the diffusion process, varying threshold levels for strong ties while holding all other parameters constant. The simulation consisted of 200 grey agents and 20 green agents, with 100 repetitions and a maximum of 1000 iterations. The agents' median degree ranged from 7 to 11. The threshold for weak ties remained constant at a relatively high value of 0.75. Simulations with a logarithmic threshold for weak ties yielded in very similar results, and due to the fact that the non-logarithmic threshold contains random factor as well, these settings were preferred due to lower complexity and lower computation time. The other parameters were set to moderate levels.[15] The results indicate that when the threshold is very low i.e. when only two strong-tie agents with opposing colour are needed to trigger a colour change, the contagion is able to spread throughout the network, with only 3 out of 100 repetitions resulting in 0 green agents. However, for higher thresholds, the contagion tends to 'fail' to spread, resulting in 0 green agents in almost every repetition. The stark increase in runs that ended with 0 green agents once the threshold increased from 2 to 3 is surprising. Additionally surprising, is that a turning point can be observed after the threshold levels exceeds 5, leading to less runs that ended up with 0 green agents. However, this decrease in 'failed' runs, is to be explained not due to successful spreading, but rather because the increasingly complex counter contagion was unable to infect the initial green agents either.

Table 1: Summary of simulation runs that resulted in 0 green agents for different strong-tie thresholds (200 grey agents, 20 green (10%))

Threshold	**2**	**3**	**4**	**5**	**6**	**7**	**8**
runs with 0 green agents in %	3	68	99	99	92	76	44

For further investigations, the same simulations were run in a larger network comprising 500 grey agents and 25 green agents (Figure 3). Just as before, lower thresholds enabled the green contagion to infect large parts of the network, with no instances of failure when the threshold is set to the lowest value. As thresholds increase, the median number[16] of green agents significantly decreases. While a few outliers may infect a substantial portion of the network, including the entire network in

[15] The other parameters are set to be: prop-hard (0.0), group-openness (0.05), k-degree (6), moving (on), strong-ties (on), hub-weak (on), log-threshold (off), countervailing-contagion (on). These parameter settings are based on logical reasoning and previous experience with the model.

[16] The median is preferred, as it provides less biased results in case a single outlier run compared to the mean.

rare cases, the majority of simulations end with less than 50 green agents after 1000 iterations for medium threshold levels. For the highest threshold levels, all but one run result in 0 green agents after 1000 iterations, indicating no spreading occurs. Overall, as the threshold increases the diffusion of green agents becomes less extensive. Considering this thesis assumes the vegetarian and vegan contagions as complex contagions with high thresholds, subsequent further simulations will employ a threshold level of 5 referring to the vegetarian contagion and 8 for the vegan contagion. The threshold level also applied equally to the respective counter contagion.

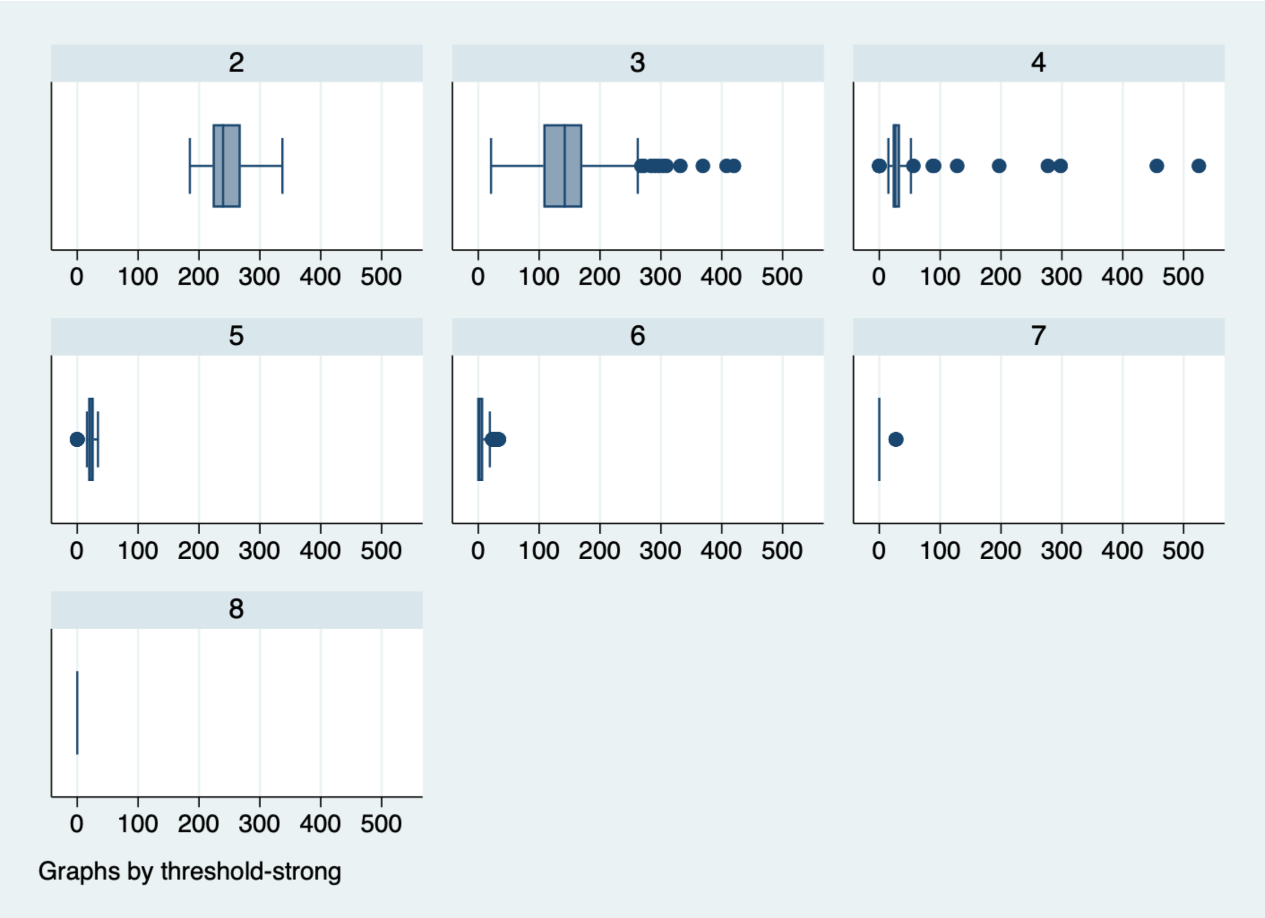

Figure 3: Box plot displaying the range of results for different strong tie-thresholds (500grey, 25 green 5%)

4.2 Hardliners

The previous simulation allowed the possibility that the whole network either becomes fully green or grey. However, as previously theorised, some agents (green, as well as grey) may be immune to influence from their peers, remaining committed to their dietary choices. It is hypothesised that an increase in the proportion of hardliners will make it harder for the green contagion to spread, as the threshold will be harder to reach and the presence of hardliners may act as a barrier to reach certain clusters. However, a higher proportion of hardliners can also prevent the vegetarian/vegan contagion from being completely taken over by the ccc. To explore the impact of these hardliners, the "prop-hard" parameter will be adjusted accordingly. The range of 0.05 to 0.25 will be considered for the "prop-hard" parameter, with increments of 0.05, as higher proportions are deemed unreasonable.

The results from simulations (Table 2), using identical settings as before, indicate that the introduction of hardliner proportions only has a minimal effect. The table displays the median number of green agents for each proportion of hardliners, along with the count of runs that ended with the minimum number of green agents for both the vegetarian (threshold of 5) and the vegan contagions (threshold of 8). Overall, there is no significant difference in the median number of green agents for different hardliner proportions. However, the total number of runs resulting in the minimum number of green agents decreases with higher proportions of hardliners. For the vegetarian contagion, simulations with low proportions of hardliners result in virtually the same median as those with high levels. However, for high proportions, no runs end up with only green hardliners in comparison to 14 percent of runs with a proportion of 0.05. Similarly, for the vegan contagion, an increase in green agents is not observed, as only the number of hardliners is increasing. However, as with the vegetarian contagion, the number of ‘failed’ runs decreases with higher proportions of hardliners. Once the number of green hardliners exceeds the absolute threshold level, the contagion never becomes trapped at its technical minimum. A repeated simulation for the vegan contagion with a hardliner proportion of 0.32 (matching 8 hardliners, i.e., 0.32*25) demonstrates this, as no runs result in the technical minimum of 8 green agents. Therefore, there is insufficient evidence to support hypothesis 1. The presence of a higher proportion of hardliners could not be associated with a significant limitation in the diffusion of the vegetarian or vegan contagion, as the proportion of hardliners generally had only a minor impact on the diffusion process. Moreover, higher settings actually ensured the persistence of the green contagion. For further simulations, a hardliner proportion of 0.1 will be adopted to explore possible interaction effects and because it aligns with a plausible proportion of hardliners.

Table 2: Median number of green agents for different proportions of hardliners, and runs that ended with only green hardliners (5% green agents)

% of hardliners	0.05	0.1	0.15	0.2	0.25
Vegetarian median	24.5	24.5	24	25	24
Vegetarian min	14	9	3	0	0
Vegan median	1	2	3	5	6
Vegan min	99	99	100	86	62

4.3 Intra- & Interconnectedness

Moving forward, the focus will now shift towards exploring the relationship between intra-connectedness and interconnectedness, starting with the investigation of intra-connectedness. By manipulating the number of edges assigned to each node upon its introduction to the network, the impact of intra-connectedness can be examined. Since two initially separate networks are being generated, increasing the k-degree parameter provides agents with more connections to other agents of the same colour. Table 3 displays the median number of green agents at the end of each repetition for degrees ranging from 2 to 10. The absolute thresholds used are 5 for the vegetarian contagion and 8 for the vegan contagion. The table includes results for three scenarios with 15, 25, and 50 initial green agents. The numbers on the left side represent the vegetarian contagion, while the numbers on the right side represent the vegan contagion. For scenarios with very few initial green agents, there is no noticeable difference in the median number of green agents. This observation holds true for both contagions and across different degrees. In all simulations, the vegetarian as well as the vegan contagion ‘fail', leaving only the green hardliner behind. However, upon closer examination of the scatter plot (Figure 6,7 & 8 provided in the appendix), it becomes apparent that although the median values are consistent across all parameters and contagions, a higher degree increases the likelihood of the vegetarian contagion infecting larger portions of the network over the course of the simulation. The disparity between the two contagions becomes more evident when there are 25 initial green agents, representing approximately 5 percent of the proportion of grey agents. In this scenario, the median number of green agents differs significantly between the contagions. While the less complex vegetarian contagion manages to sustain the initial number of green agents and even surpasses it with a degree of 10, the median number of green agents for the vegan contagion remains at two hardliners, regardless of the degree. Once again, while the median stays the same, a closer examination confirms that as the degree of intra-connectedness increases, more repetitions are able to infect larger parts of the network. Moving on to the scenario with 50 initial green agents, accounting for 10% of the initial grey agents, this patterns become even more pronounced. Once more, there is no change for the vegan contagion, but this time the median number of green agents did not drop to the minimum. Similarly, the median rises only by a few agents for the vegetarian contagion but then increases rapidly once the turning point of 10 degrees is reached. By examining the scatter plot, a pattern emerges that is not apparent when solely considering the median. It becomes visible that even the vegan infection exhibits a few outliers for high levels of intra-connectedness. Further, it reveals that although lower degrees are associated with lower median numbers, there is still a slight chance for the entire network to become infected. As intra-connectedness increases, this chance diminishes, but the overall median number of green agents rises.

Table 3: Varying the kdegree and n-greens for the (vegetarian | vegan) contagion

kdegree / n-greens	***15 green agents (3%)***	***25 green agents (5%)***	***50 green agents(10%)***
2	*1 | 1*	*24 | 2*	*38 | 37*
4	*1 | 1*	*24 | 2*	*38 | 37*
6	*1 | 1*	*24 | 2*	*39 | 38*
8	*1 | 1*	*24 | 2*	*41 | 38*
10	*1 | 1*	*27 | 2*	*147 | 38*

The findings indicate that greater intra-connectedness plays a significant role in preserving the vegetarian/vegan contagion. This can be attributed to the increased positive reinforcement that green agents receive from their neighbours, making it more challenging for the ccc to infect them. Contrary to the initial hypothesis, higher intra-connectedness not only hampers the ccc's ability to infect the initial green agents but also promotes the spread of the vegetarian/vegan contagion. Hence, hypothesis 2 was not validated; rather, the findings indicate the contrary. Regarding the slow diffusion of vegetarianism/veganism, it seems that low levels of intra-connectedness may play a role, but they are not the sole determining factor. In many instances, the contagion failed to spread, and significant change only occurred when there was a high initial proportion of green agents. This suggests that other factors beyond intra-connectedness are likely influencing the spread of the contagion.

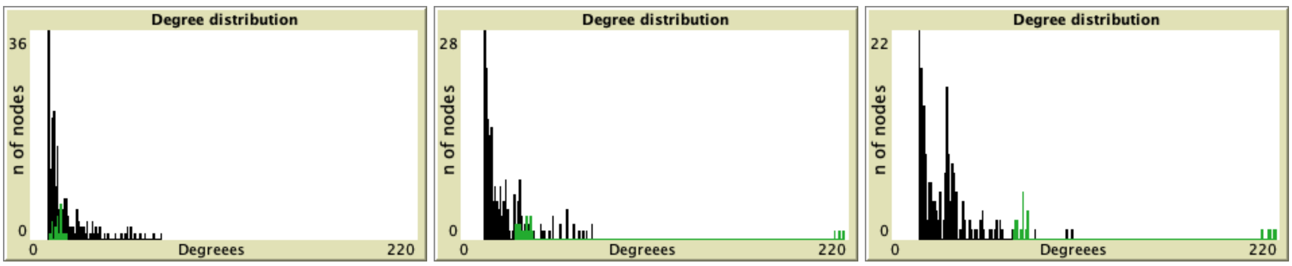

Figure 4: Degree distribution, for group openness = 0.01, 0.1, 0.3 and 200 grey, 20 green agents

To explore the effect of inter-connectedness, simulations were conducted with the same parameters but allowing group-openness to vary. Increasing the group openness causes every grey agent to have more links with green agents and vice versa. Increasing group openness leads to more connections between grey and green agents. In a scenario with 20 green agents and 200 grey agents, and a degree parameter set to 1, a group openness of 1 means that every grey agent is connected to

only one other grey agent, but to 20 green agents. Similarly, every green agent is connected to only one other green agent, but to 200 grey agents. Therefore, However, it is important to approach the adjustment of group openness with caution, as high values can deviate from the assumption that clusters are formed based on homophily. To mitigate this deviation, a k-degree of 10 is set, ensuring that each agent is connected to 10 other agents of the same colour[17]. This helps maintain a balanced level of inter-connectedness while exploring the effects of group openness on the social network.
At the lowest setting of 0.01, green agents have an average median degree of 17 (ranging from 14 to 24), indicating that they are connected to around 10 green agents and 7 grey agents. On the other hand, grey agents have an average median degree of 14 (ranging from 14 to 16), meaning they are connected to 10 grey agents and approximately 4 green agents. In contrast, at the highest setting of 0.3, grey agents have an average median degree of 25 (ranging from 18 to 31), indicating that they are connected to 15 green agents on average. The average median number of green agents for this setting is significantly higher, averaging at 56 (ranging from 30 to 145)[18]. As the group openness increases, it becomes more common for a few green agents to be connected to every grey node, leading to the formation of hubs with an extremely high number of neighbouring nodes. This occurrence is primarily due to the larger number of grey agents present in the network.
Table 4 presents the median number of green agents at the end of each simulation for different group openness settings. When the group openness is set to a very low value of 0.01, there is minimal change in the initial number of green agents. Increasing the group openness to 0.05 results in both the vegetarian and vegan contagions being reduced to only 2 green hardliners. Whereas very low inter-connectedness prevents any significant contagion, slightly higher inter-connectedness allowed the ccc to take over the green agents.

For the vegetarian contagion, the turning point occurs at a group openness of 0.1, resulting in double the number of initial green agents. The median number of green agents continues to double for group openness values of 0.2 and reaches 102 for a group openness of 0.3. For the vegan contagion however, the turning point is only reached at the highest inter-connectedness level. Prior to that, in the majority of repetitions, the contagion fails to spread. However, a closer analysis reveals that change is already imminent for the vegan contagion even before the group openness

[17] Over the course of the simulations this might vary due to the moving command.

[18] The degree levels are fluctuating for every setup. The median is an approximation from 100 repetitions. The average maximum degree for a value of 0.01 was 78 (65-217), and the average minimum was 10 (10-12). For green agents: average maximum; 57 (18-219), average minimum; 12 (10-19). Grey 0.3: average maximum; 148 (76-219), average minimum; 16 (11-21). Green 0.3: average maximum; 213 (77-219), average minimum 46 (15-85).

parameter reaches 0.3. In 10% of vegan simulations with a parameter of 0.2, results show 50 or more green agents, with 4 repetitions even exceeding 100 green agents. In comparison, for the highest setting of inter-connectedness 34 vegan runs result in 50 or more green agents, with 7 even in 150 or more green agents.

The hypothesis H3 regarding inter-connectedness suggested that higher levels of inter-connectedness would facilitate easier spread of the contagion due to the availability of more ties, such as wide bridges. The results confirm this hypothesis, showing that as inter-connectedness increases, the contagion spreads more easily and becomes dominant in the network. Additionally, the higher it is the less variation can be observed. Small levels of interconnectedness lead to limited spreading or even extinction of the green contagion. Similar overall results were observed in simulations with larger networks, except that the negative penalty for a group openness of 0.1 was only observed for the vegan contagion.

Table 4: Median number of green agents (10%) for different settings of group-openness

group-openness	**0.01**	**0.05**	**0.1**	**0.2**	**0.3**
Vegetarian	20	2	39	79	102
Vegan	21	2	2	2	39

4.4 Tipping points

The previous findings indicate that identifying a tipping point for the spread of vegetarianism/veganism largely depends on other parameters besides group size. In one scenario, 25% of initial green agents may be sufficient to infect the entire network, while in another scenario, 25% may never be enough. Therefore, a general conclusion based solely on the proportion of the minority cannot be drawn. The results from the hardliner experiment also do not indicate any tipping points, likely due to the fact that the proportion of hardliners was adjusted for both agent groups. To be consistent with previous research, the following experiment assumes hardliners only exist for green agents. Parameters were chosen for settings that previously exhibited low or negative green agent spreading. The experiments were conducted in a larger network of 500 grey agents (figure 4) and a small network of 200 grey agents and. Figure 5 (and 6 in the appendix) present the results.
The key finding is that no clear tipping points can be identified. For both network sizes, the vegetarian contagion consistently has a reasonable chance of infecting the whole network, even with a low number of initial green agents. The proportion of successful repetitions gradually

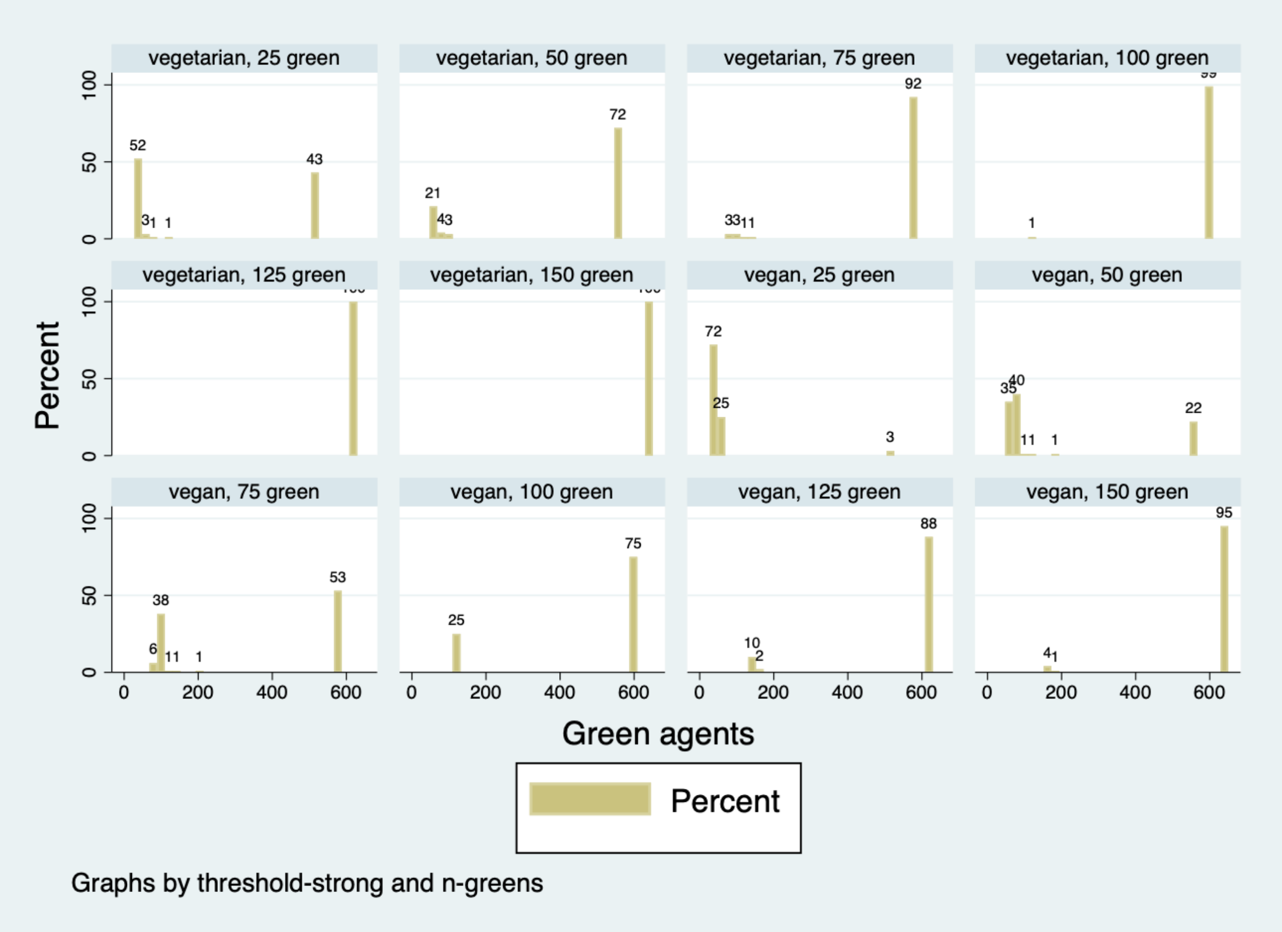

Figure 5: Histogram showing the vegetarian and vegan contagion for different n-green in a network with 500 grey agents with only green hardliners

increases with every change in the number of green agents, without any without any abrupt shifts or tipping points. Moreover, the results are highly influenced by the level of complexity and network size. In the smaller network, green agents are less likely to dominate the network compared to the larger network. For example, when a dedicated minority of 30% of the grey agent proportion is present, only 77% of the runs in the small network are successful in infecting the whole network, whereas the success rate is 100% in the larger network. Similarly, with a dedicated minority of only 5%, one-fifth of all runs succeed in the small network, while more than two-fifths succeed in the larger network. Regarding complexity, a significant difference between the vegetarian and vegan contagion in their spreading dynamics becomes apparent as well. In the small network, only 27% of vegan runs successfully infect the entire network with a dedicated minority of 30% (150 agents), compared to 77% of vegetarian runs. Additionally, while a dedicated minority proportion of 10% (50 agents) is sufficient for 75% of runs to succeed in the vegetarian contagion, a proportion of 20% (100 agents) is needed for the same level of success in the vegan contagion. In conclusion, evidence for hypothesis 4 is found, as no distinct tipping point or relationship with a dedicated minority of

25% can be observed. The absence of abrupt changes and the influence of complexity and network size further support this conclusion.

4.5 Counter-models

Below, a concise summary of counter-models is presented, that explore alternative possibilities to the existing models. In this analysis, four counter-models are considered by deactivating their respective switches in the following order: hub-weak (off), strong-ties (off), moving (off), and countervailing-contagion (off). By deactivating the hub-weak switch, a strong influence of highly connected agents as hubs becomes possible. This counter-model aims to examine whether the presence of strong social connections outgoing from hubs affects the diffusion process. The moving counter-model assumes a scenario in which individuals do not move or change their social connections over time. This counter-model allows us to analyse the impact of stability in social networks on the diffusion of vegetarianism. Lastly, the countervailing-contagion counter-model deactivates the countervailing contagion mechanism. By turning off this switch, we can evaluate the impact of countervailing forces on the diffusion process. It is important to note, that these counter-models are intended to explore alternative perspectives and possibilities within the context of the vegetarian contagion. The according diagrams can be found in the appendix (figure, 9, 10, 11 & 12)[19].

Hub-weak (off): The assumption that the influence of hubs is low is based on the notion that they provide group over-spanning links and are often subject to countervailing influences. However, it can be argued that highly connected individuals serve as role models and exert a strong influence on others through strong ties. Additionally, even hubs have close friends whom they trust and have strong connections with. To explore this counter-model, simulations are conducted allowing hubs to have strong ties, and the results are compared to a model where hubs have weak ties - 'hub-weak true)'. In parallel, another simulation is performed where all hubs are identified and their colour is changed to grey. The outcomes of all four settings are presented in figure 9. Although the change affects only a small number of agents, it can have a significant impact on the overall network structure due to the large number of connections hubs possess. When the influence of hubs is set to allow for strong ties, the diffusion of the vegetarian contagion is lower, and the number of agents

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[19] If not stated otherwise, the settings for the counter models were the following: 20 green agents, 200 grey agent, prop-hard (0.1), group-openness (0.05), k-degree (6), moving (on), strong-ties (on), hub-weak (on), log-threshold (off), countervailing-contagion (on).

infected never surpasses 50. In comparison, 25% of all runs with green hubs result in 50 or more agents when all links connected to hubs are defined as weak. Additionally, setting all hubs as grey agents alters the diffusion process, resulting in more failures and less spreading of the contagion.

- *Strong-ties (off)*: In the current digital age, much communication and interaction occur online through social networks like Reddit or Twitter, where connections tend to be less intimate. A counter-model that considers only weak tie influence can simulate an online environment where strong ties have no influence. To explore the effect of such a setting, an experiment is conducted where agents can only be directly influenced by weak ties. However, strong ties still have passive influence and serve as "offline ties" as the fractional threshold considers all neighbours. The results are compared to a model with 'strong-ties (true)'. The results, as shown in the appendix, reveal that when the strong-ties switch is turned off, the countervailing contagion has a much harder time infecting the initially green agents. This leads to a more balanced distribution, with around 20 green agents. While the contagion struggles to infect other agents, it is also not suppressed by the countervailing contagion. On the other hand, when strong ties are enabled, 99% of all runs end up with only 2 green hardliners, indicating a significant suppression of the contagion.
- *Moving (off):* In a scenario where there is no movement or change in social connections, the social network remains static and stable over time. This can be observed in small towns or rural areas, where the population is relatively small and residents have long-standing relationships with their neighbours. The lack of mobility results in a sense of familiarity and continuity in social connections, leading to a stable social network. To investigate the diffusion process in such a static network, the mechanism that randomly deletes and generates ties is turned off. The results are compared to a model with 'moving (true)' to assess the impact of mobility.

To ensure a fair comparison, the simulation is allowed to run for a longer duration of approximately 10,000 iterations, as the effects of movement take time to manifest and be comparable to a static network. Additionally, to prevent the green contagion from being unable to spread, 5 green hardliners are introduced. The results demonstrate that after 10,000 iterations, the outcomes are very similar for both settings. The median number of green agents remains at 19 for both the static network and the model with movement. Similarly, in both scenarios, a few runs manage to infect nearly the entire network, indicating that the presence of movement how it is modelled here, does not significantly impact the overall diffusion process.

- *Countervailing-contagion (off)*: In this thesis, the influence of opposing forces or competing contagions that can impede the spread of vegetarianism was considered. By deactivating this switch, we can assess the impact of countervailing forces on the diffusion process. A simulation is conducted with a setting where only green agents can infect grey agents, but not vice versa. The results are compared to a model with ‘countervailing-contagion (true)’ to examine the difference. When the countervailing-contagion switch is turned off, the vegetarian contagion is able to infect the entire network in half of the cases (46 out of 100) within a few iterations. The remaining half of the cases show a low level of green agents. Only in one instance did it take around 400 iterations for the contagion to spread throughout the network. In contrast, in the comparison model with countervailing-contagion enabled, 99% of all runs ended up with fewer than 50 green agents. The diffusion pattern without countervailing forces can be described as an ‘all-or-nothing’ pattern, where either the contagion spreads widely or remains at a low level.

5. Discussion

Having described the results, what can be said through the lens of social network analysis about the slow spread of vegetarianism and veganism? Complexity was found to be the most significant factor. Based on the four mechanisms of complex contagions, it has been theorised that vegetarianism and veganism function as complex contagions with high thresholds, requiring significant reinforcement to spread effectively. Observations from the simulation model indicate that as the threshold increases, the green contagion (representing vegetarianism/veganism) spreads slower, infecting fewer people on average. Higher complexity leads to more restricted diffusion, as a larger number of agents need to change their behaviour in order to trigger a cascade. In simulations with high threshold levels, the majority grey contagion (representing non-vegetarianism/veganism) often prevails, as the majority of agents were already predetermined and not neutral. While the simulation results show that spreading stops in small networks for very high thresholds, this effect is not observed in larger networks where the countervailing contagion almost always takes over any available green agents. This finding aligns with real-world data, as vegetarianism and veganism have not spread to the majority of the population in any country, suggesting that these vegetarianism/veganism can accurately be portrayed as contagions with high thresholds. The model's results also correspond to the slow diffusion processes observed in real life.

However, contrary to the model's results, vegetarianism and veganism do not disappear entirely in reality. To explain this, simulations have been conducted introducing the concept of hardliners. It was found that as long as a sufficient proportion of hardliners exists, surpassing the threshold level, vegetarianism and veganism can persist. Paradoxically, a high proportion of hardliners, although technically limiting the spread within the network, actually helps maintain the contagion. Hardliners, driven by ethical, environmental, or health motivations and possessing strong convictions, play a significant role in sustaining the behaviours.

In comparison, non-vegetarian hardliners who strongly adhere to a meat-based diet and firmly believe in its consumption may also exist, but their proportion is likely lower. This could explain the persistence of vegetarianism and veganism despite their slower spread. Future models could explore the importance of hardliners further by simulating different proportions of hardliners for different clusters or allowing newly infected agents to become hardliners, providing insights into their impact on the diffusion dynamics of these behaviours.

If it is assumed that vegetarianism and veganism are indeed highly complex contagions with a proportion of hardliners, simulations show no significant progressive spread. However, in reality, the proportion of individuals adapting vegetarian and vegan diets is, although slowly, increasing rather than stagnating as portrayed by the model. This suggests that the complexity of these contagions is gradually reduced over time. One possible explanation for this reduction in complexity is the increasing availability of food options. As the number of individuals embracing vegetarian or vegan diets increases, there is a greater demand for plant-based food products. This, in turn, leads to a wider variety of vegetarian and vegan options becoming available in the market. The increased availability of alternative food choices makes it easier for individuals to adopt and sustain a vegetarian or vegan lifestyle, reducing the complexity (strategic complementarity). The same holds true for legitimacy, as the number of individuals adopting vegetarianism and veganism increases, it becomes more socially accepted and perceived as conforming to prevailing norms and values. Additionally, when multiple sources consistently advocate for the benefits of a plant-based diet and provide reliable information about its environmental and health impacts, it enhances the credibility of the message. This makes it more likely that individuals will believe in the positive outcomes associated with vegetarianism and veganism, making them more inclined to adopt these behaviours (credibility).

This effect is demonstrated by the results, underpinning that less complex contagions have the ability to infect a larger number of agents. Furthermore, reducing the threshold level for strong ties even during a simulation run, immediately results in an increase in the number of individuals adopting vegetarian or vegan diets. Conversely, increasing the threshold level again during the simulation, leads to a reduction in the number of individuals adopting the green contagion. Overall, the simulations suggest that as complexity decreases, the spread of vegetarianism and veganism becomes more efficient. Factors such as increased availability of options, enhanced legitimacy, and improved credibility contribute to the reduction of complexity and facilitate the adoption of these behaviours by a larger population. Therefore, as this positive feedback effect is dependent on the number of agents that adopt, the slow spread of vegetarianism/veganism might be caused and explained due to its slow momentum. In other words, paradoxically the slow spread can be explained partly by itself, which is the result of the complexity of vegetarianism and veganism that leads to a slow positive feedback loop.

Generally, changing the weak-tie threshold did not result in any noteworthy changes, except for making the green contagion slightly more prone to failure. This suggests that weak ties may not have a strong influence on an agent's decision to switch colours. However, it is important to note that this conclusion should be taken with caution, as the model already incorporates this premise. In addition to complexity and the proportion of hardliners, other mechanisms such as intra- and inter-connectedness have been shown to affect the diffusion process. Higher intra-connectedness generally made the contagion more stable and less susceptible to random fluctuations. Surprisingly, higher intra-connectedness also enabled the vegetarian contagion to infect more agents, despite the fact that agents had more connections to their own colour. This is because once clusters were infected additional connections provided wide bridges that allowed the contagion to spread further. However, although low levels of intra-connectedness may play a role as a contributing factor, they are not the sole determinant. In most cases, the contagion failed to spread and only resulted in significant change when there was a high initial proportion of green agents. This suggests that while intra-connectedness can facilitate the diffusion process to some extent, other factors such as complexity, the initial number of green agents and inter-connectedness also need to be considered in explaining the limited spread of the contagion.

The initial number of green agents turned out to be a main driving factor of infection speed, as it not only stabilised the green contagion by making it harder for the ccc to take over, but also enabled more runs to infect large parts of the network. When it comes to inter-connectedness, it is important to note that high settings are not commonly observed in real-world networks, as they contradict the assumption of homophily (the tendency for individuals to associate with others who are similar to them). However, simulations have shown that when high inter-connectedness is introduced, it leads to a greater number of green agents in the model. High inter-connectedness enabled vegetarianism to infect large parts of the network although the initial number of green agents was low. Low inter-connectedness on the other hand hindered the vegetarian contagion from spreading, as not enough ties were available to cause a colour change. For the more complex vegan contagion, higher inter-connectedness had less impact, indicating that complexity is still of major concern.

A secondary objective of this thesis was to identify a possible tipping point. The commonly theorised tipping point of a dedicated minority comprising 25% of the population did not seem to apply to the specific settings and parameters used in this study. Furthermore, no other distinct tipping points were observed in the conducted simulations. A tipping point can be defined as a critical threshold where a system undergoes a significant and nonlinear transformation, transitioning from one stable state to another (Milkoreit 2022). In the context of this study, it would signify a moment when the diffusion process shifts from gradual change to a rapid and widespread adoption of the contagion.

Adopting this definition, it has to be noted that the observed changes in the diffusion process for different settings were gradual rather than sudden, even when the model exclusively included green hardliners. Although the main simulations did not reveal an explicit tipping point, an interesting finding emerged when a simulation was conducted without the presence of countervailing complex contagion. In this scenario, the outcome became binary, where either all agents adopted the contagion or none did. The occurrence of this 'all or nothing' pattern in the absence of countervailing contagion suggests the possibility of a different tipping point mechanism at play. Further investigation into the underlying mechanisms and conditions that contribute to this pattern could help uncover a tipping point within the context of this contagion. Overall, while this thesis did not identify a definitive tipping point, it has provided insights into the complexities of the diffusion process and the absence of a clear threshold for rapid and widespread adoption. Instead of fishing for a "chance of creating nonlinear social change in pursuit of sustainability" (Milkoreit 2022: 8), a more fruitful approach could be to investigate measures that reduces the complexity of environmentally friendly action.

The simulation model employed in this study aims to uncover general social network dynamics related to the diffusion of behaviours/actions, rather than being tailored to a specific case. It acknowledges that societies and countries vary in terms of eating culture, politics, the availability of vegetarian/vegan food, and other factors. These differences are accounted for by adjusting model settings, such as complexity and intra- and inter-connectedness. However, it is important to note that the model is primarily theoretical and lacks an empirical foundation. While the parameters are derived from theory, their real-life values may differ. In order to capture the specific characteristics of a particular country, empirical data is needed to calibrate the parameters accordingly. Generally, an empirically-adjusted agent-based model (ECA) could be a valuable tool in bridging the gap between theoretical assumptions and empirical research (Hedström 2005). By incorporating empirical data and observations, an ECA strives to provide a more realistic representation of social phenomena (ibid.). Furthermore, empirical data-driven parameterisation improves the accuracy of the model's assumptions and predictions and enhances the validity of the model by grounding it in empirical evidence (Flache & de Matos Fernandes 2021). However, this thesis study focuses more on theoretical exploration rather than empirical validation. Although an ECA is beneficial in proving a much more accurate prediction of a phenomena it does not necessarily help with understanding the social processes that are at work (Laver 2020: 120). While empirical validation is essential for understanding specific cases and calibrating the model to real-world data, the theoretical exploration provided by this study lays the groundwork for future research and opens up avenues for empirical studies that can further refine and validate the theoretical findings. By combining theoretical insights with empirical observations, researchers can gain a more comprehensive understanding of the complex social processes involved in the diffusion of environmentally friendly behaviours.

Another constraint of this thesis was the limited number of simulated agents. Due to computational limitations, the simulations were conducted with a maximum of 500 grey agents and a maximum of 10 degrees. However, it is important to acknowledge that smaller networks are more susceptible to random fluctuations, and the results obtained may differ in larger networks, with for instance, 100,000 agents (Watts 1999, Centola et al. 2017, Wiedermann et al. 2020). With the advancement of computational power and the growing prevalence of agent-based modelling in sociology, future studies should consider expanding the scale of simulations to better understand the dynamics of larger networks.

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Appendix

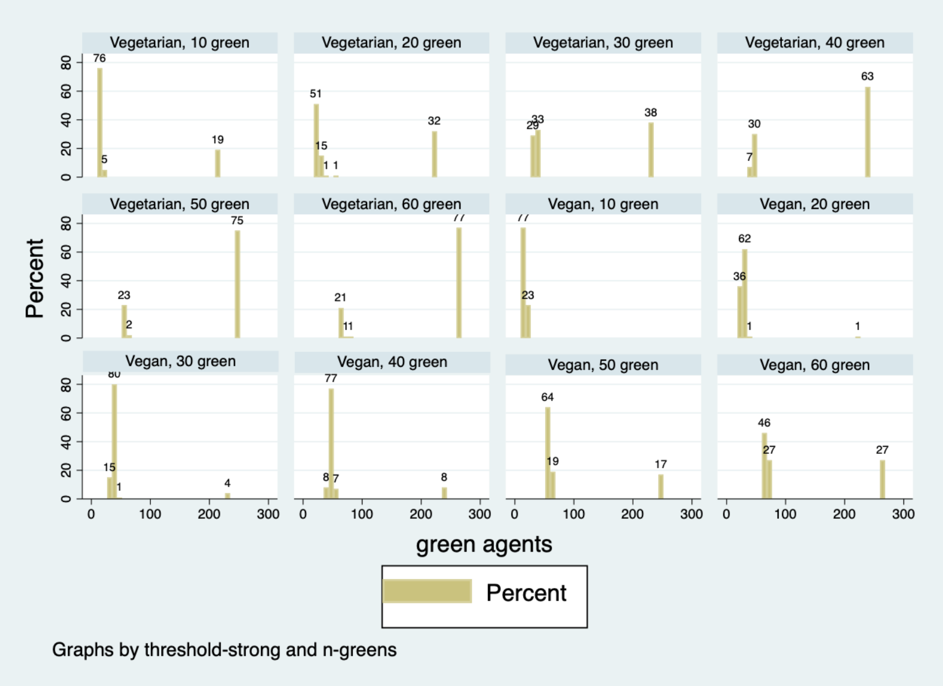

Figure 6: Histogram showing the vegetarian and vegan contagion for different n-green in a network with 200 grey agents with only green hardliners

kdegree: The next three figures are a in-depth analysis of the diffusion pattern for different k-degrees. Each blue dot represents a number of green agents for a specific run and step. (Page 29).

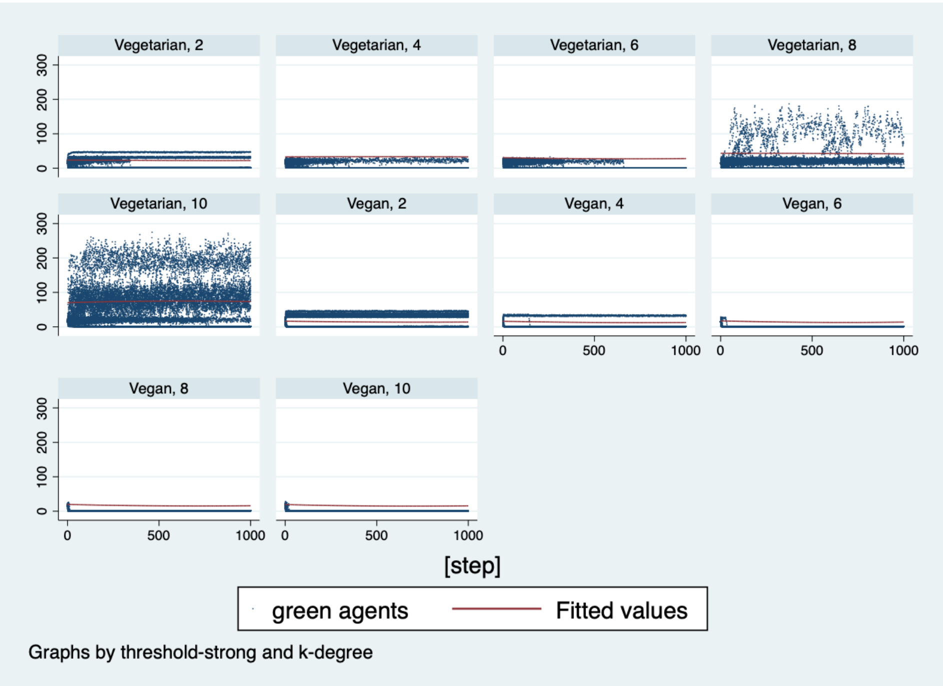

Figure 7: 100 runs for 1000 iterations for vegetarian and vegan contagions varying kdegree, 15 initial green agents

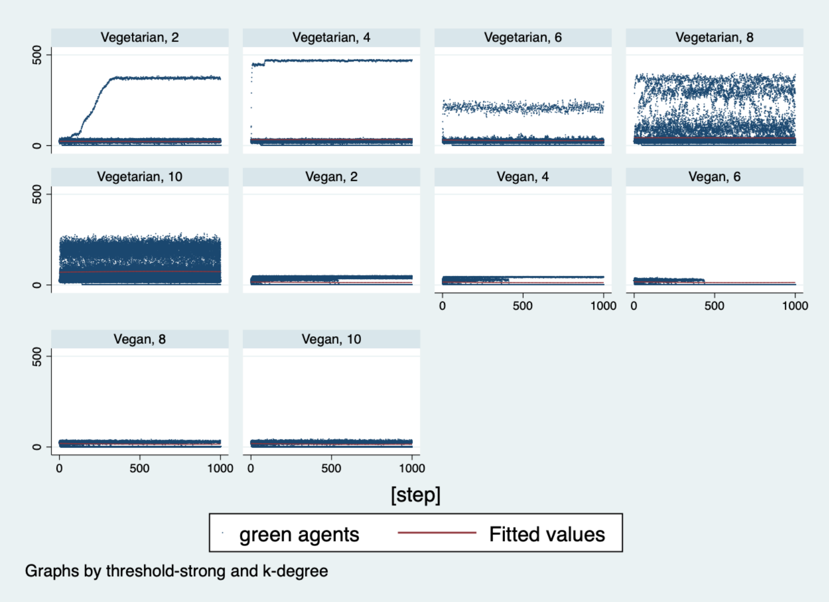

Figure 8: 100 runs for 1000 iterations for vegetarian and vegan contagions varying kdegree, 25 initial green agents

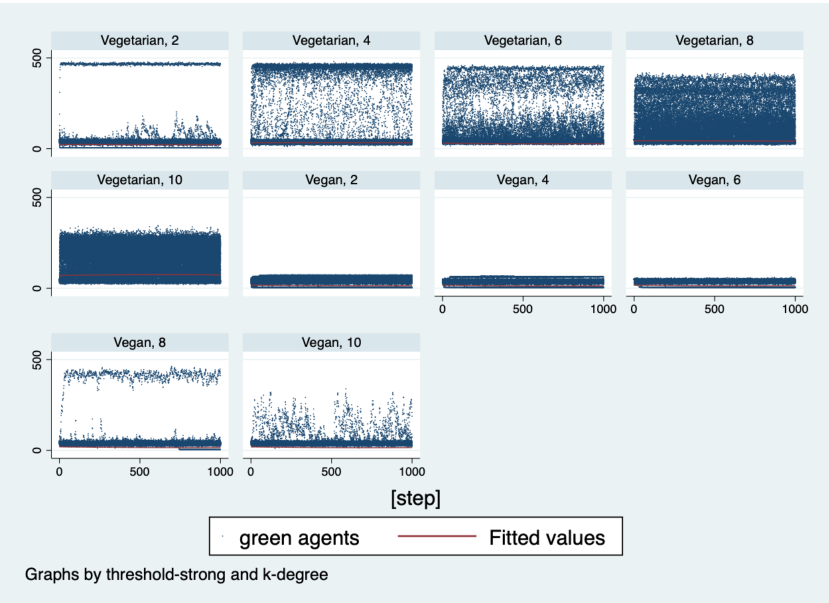

Figure 9: 100 runs for 1000 iterations for vegetarian and vegan contagions varying kdegree, 50 initial green agents

Counter models: The next four figures show the counter models that were referred to on page 33. The histograms show the percentages of runs (y-axis) that ended with a certain number of green agents (x-axis).

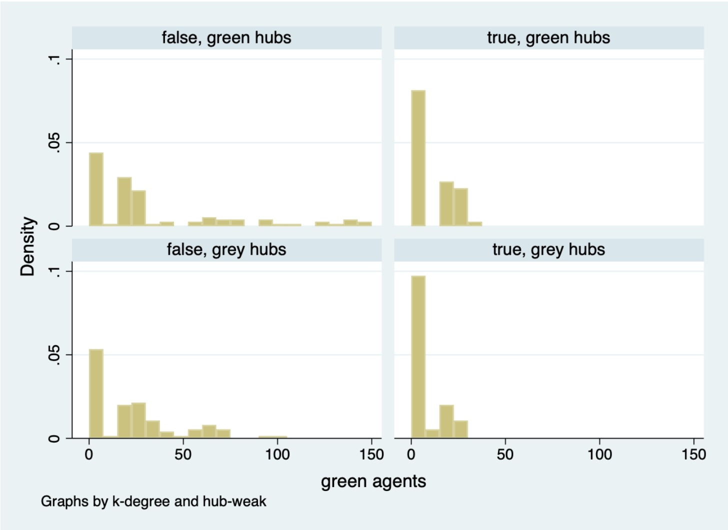

Figure 9: Hub-weak (false/true) diagram with green and grey hubs

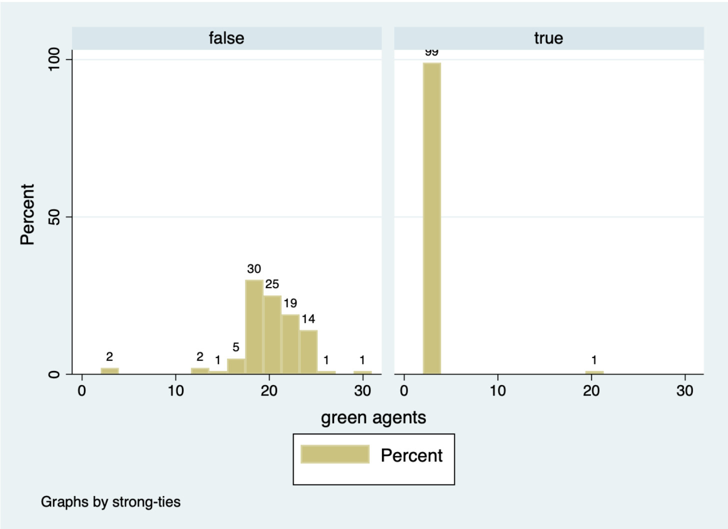

Figure 10: strong-ties (false/true)

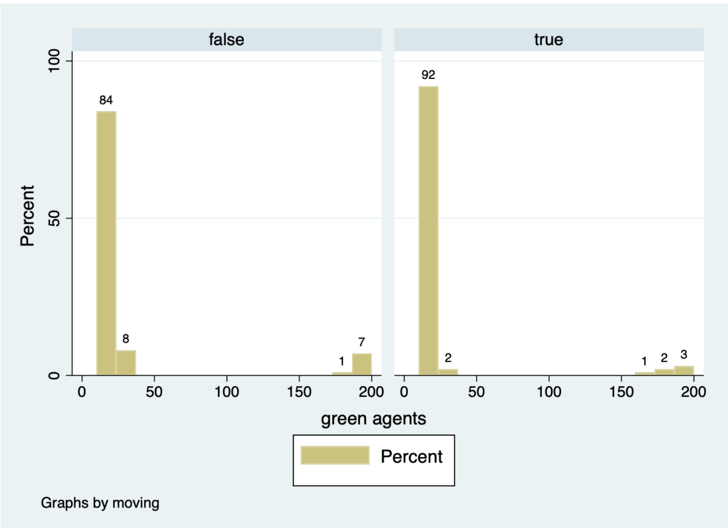

Figure 11: moving(false/true)

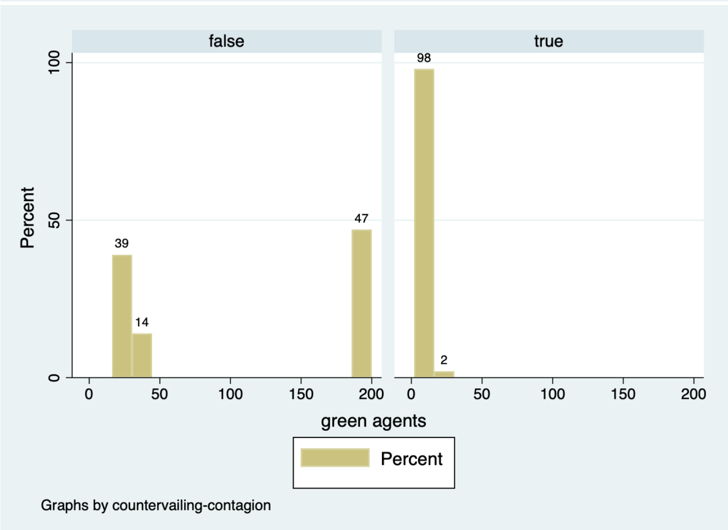

Figure 12: countervailing-contagion (false/true)

Netlogo Model Code

It is recommended to download the model indeed of copy and pasting the code. It can be downloaded here: http://modelingcommons.org/browse/one_model/7196

```
; Using the network extention of Netlogo we will create two preferential-attachment networks and three different kinds of agents
;Green agents, grey agents, and hardliners that never change their opinion
;***************
; SETUP
;***************
extensions [nw]            ; start up the network extension
breed [AgentAs AgentA]                        ; the A breed are grey
breed [AgentBs AgentB]                        ; the B breed are green
breed [hardliners hardliner]
links-own [weight]
turtles-own [community clique]

to setup
  clear-all
  nw:generate-preferential-attachment AgentAs links n-greys k-degree [set color grey]
  nw:generate-preferential-attachment AgentBs links n-greens k-degree [set color green]
    ask AgentBs [ if random-float 1 < group-openness [create-links-with AgentAs]]
    ask AgentAs [ if random-float 1 < group-openness [create-links-with AgentBs]]

 ask turtles [
    set size 1
    set shape "person"
    setxy random-xcor random-ycor ]
    ask patches [set pcolor white]


   ask n-of int(prop-hard * n-greys) AgentAs [set breed hardliners ] ; make "AgentAs" grey hardliners
   ask n-of int(prop-hard * n-greens) AgentBs [set breed hardliners ]  ; make "AgentBs" green hardliners
   ask hardliners [set shape "person"]

  foreach nw:louvain-communities [ [comm] ->                                        ;tell every turtle in what community they are
  ask comm [ set community comm ]
  foreach nw:maximal-cliques [ [cliq] ->                                    ;tell every turtle in what community they are
  ask cliq [ set clique cliq ]
]
]
nw:set-context turtles links
weight-clusters nw:louvain-communities                              ;assign weights to links
reset-ticks
end

to color-communities
  nw:set-context turtles links
  color-clusters nw:louvain-communities
end

;***************
; DYNAMICS
;***************
to go
    if (all? turtles [color = green]) [stop]
    if (all? turtles [color = grey]) [stop]
  if moving [
  move
  ]
  ask turtles [interact]
  tick
```

```
end

to move ;asks a random link to die with a 1% change. And creates a random(!) link from a random agent to any other agent with a 33% chance of it becoming a strong tie
   ask one-of links
  [ if random-float 100 < 1 [die]]
  ask one-of turtles [ if random-float 100 < 1 [create-link-with one-of other turtles [set weight random 3]]]
end

to weight-clusters [ clusters ] ;gives links between clusters weight = 1 (weak tie) and links within clusters weight = 2 (strong tie). Clusters are defined by louvain-communities
  ask links [ set weight 1 ]
  let n length clusters
  let colors ifelse-value (n <= 12)
  [ n-of n remove gray remove white base-colors ]
  [ n-values n [ approximate-hsb (random 255) (255) (100 + random 100) ] ]
   (foreach clusters colors [ [cluster cluster-color] ->
     ask cluster [
       ask my-links [ if member? other-end cluster [ set weight 2 ] ]

     ]
   ])
if hub-weak [
let max-neighbors (Max [count link-neighbors] of turtles)
let hub turtles with [count link-neighbors > max-neighbors - 10]
if any? hub [
  ask hub [
   ask my-links [
     set weight 1
   ]
  ]
]
]
end

to color-clusters [ clusters ]
  ;reset all colors
  ask turtles [ set color gray - 3 ]
  ask links [ set color gray - 3 ]
  let n length clusters
  let colors ifelse-value (n <= 12)
   [ n-of n remove gray remove white base-colors ] ;
   [ n-values n [ approximate-hsb (random 255) (255) (100 + random 100) ] ]
   ; loop through the clusters and colors zipped together
   (foreach clusters colors [ [cluster cluster-color] ->
     ask cluster [ ; for each node in the cluster
       ; give the node the color of its cluster
       set color cluster-color
     ; making links slightly darker
       ask my-links [ if member? other-end cluster [ set color cluster-color - 1 ] ]

     ]
   ])
end

to interact ;aks two times, once to turn grey, once to turn green
    ask one-of turtles [
      let count-total 0
      let count-weak 0
      let count-strong 0

      set count-total count link-neighbors
      let strong (my-links) with [weight = 2]
   if any? strong [
      set count-strong count link-neighbors with [color != [color] of myself]]
      let weak (my-links) with [weight < 2]
```

```
  if any? weak [
    set count-weak count link-neighbors with [color != [color] of myself]]
  ifelse log-threshold [
    let activation-probability 1 / (1 + exp(-(count-weak - (activation-threshold * count-total)) * 5))
    if random-float 1 < activation-probability [
      if breed != hardliners [set color green]]
  ]
  [
      if count-weak >= (count-total * activation-threshold) + (random (6)) [
    if breed != hardliners [set color green]]
  ]
   if strong-ties [   if count-strong >= threshold-strong + random 4 [
   if breed != hardliners [set color green]]                               ]
 ]
 if countervailing-contagion [
   ask one-of turtles [
    let count-total 0
    let count-weak 0
    let count-strong 0
    set count-total count link-neighbors
    let te (my-links) with [weight = 2]
  if any? te [
    set count-strong count link-neighbors with [color != [color] of myself]]
    let weak (my-links) with [weight < 2]
  if any? weak [
    set count-weak count link-neighbors with [color != [color] of myself]]
    ifelse log-threshold [
     let activation-probability 1 / (1 + exp(-(count-weak - (activation-threshold * count-total)) * 5))
     if random-float 1 < activation-probability [
     if breed != hardliners [set color grey]]
  ]
  [
      if count-weak >= (count-total * activation-threshold) + (random (6)) [
     if breed != hardliners [set color grey]]
  ]
  if strong-ties [ if count-strong >= threshold-strong + random 4 [
  if breed != hardliners [set color grey]]
 ]
 ]
 ]
end
```