The Mid-Twentieth Century Baby Boom and the Role of Social Influence. An Agent-Based Modelling Approach

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The Mid-Twentieth Century Baby Boom and the Role of Social Influence

An Agent-Based Modelling Approach

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ABSTRACT

Around the middle of the 20th century, most Western countries experienced a surge in birth rates, called the Baby Boom. This boom was unexpected at the time and the underlying mechanisms are still not entirely clear. It was characterized by high levels of inter- and intra-country variability in fertility, as some regions even experienced fertility decline during the Boom. In this paper, we suggest that social influence processes, propelling a shift towards two-child families, might have played an important role in the observed changes in fertility. Interactions in social networks can lead new types of childbearing behaviour to diffuse widely and thereby induce changes in fertility at the macro level. The emergence and diffusion of a two-child norm resulted in homogenization of fertility behaviour across regions. Overall, this led to a reduction of childlessness and thus an increase of fertility, as more people aspired to have at least two children. Yet, in those regions where larger family sizes were still common, the two-child norm contributed to a fertility decline. To explore the role of social influence with analytical rigor, we make use of agent-based computational modelling. We explicate the underlying behavioural assumptions in a formal model and assess their implications by submitting this model to computational simulation experiments. We use Belgium as a case study, since it exhibited large variability in fertility in a relatively small population during the Baby Boom years. We use census data to generate realistic starting conditions and to empirically validate the outcomes that our model generates. Our results show that the proposed mechanism could explain an important part of the variability of fertility trends during the Baby Boom era.

Keywords: Baby Boom, Fertility, Social influence, Social networks, Agent-based modelling, Norm diffusion

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1 INTRODUCTION

Around the middle of the 20th century, the fertility decline that many Western countries had been experiencing since the second half of the 19th century was interrupted by the Baby Boom, a temporary surge in birth rates. The demographic transition, the move from high to low levels of both mortality and fertility, was briefly interrupted, before birth rates and fertility levels decreased again in the 1970s and 1980s. Surprisingly little is known about the social mechanisms behind the Baby Boom. Classical explanations focussing on the optimism and economic boom after the Second World War have been found lacking, as they seem to tell only part of the story (Van Bavel & Reher, 2013). In this paper, we explore another driver of the Baby Boom. Building on the observation that it was during the Baby Boom era that the two-child family became more widely adopted in many Western countries (Brée, 2017; Frejka, 2008b; Van Bavel et al., 2018) we suggest that the emergence and diffusion of a two-child family norm might have been one of the main drivers of the fertility increase. We explore this mechanism with an agent-based model, using Belgium as an example. This context is particularly attractive for our purposes, because Belgium is a small country that nevertheless showed substantive variability in fertility across regions during the Baby Boom era. As would be the case anywhere, there are factors specific to Belgium that may have played a role in shaping fertility patterns over time, but we believe that the overall mechanism that we propose is quite generally applicable, also in other countries.

Our argument starts from the notion that people do not make family decisions in isolation from others. Instead, they learn from the information they gather from those who are close to them (spatially and socially), for example about contraception or the costs of childrearing, and they are influenced by what their friends or neighbours are doing and by what is expected of them. When new information is introduced or existing social norms shift, social influence instigates a diffusion process that can lead to large-scale changes on the macro level. This social aspect is often seen as crucial for understanding the rise of the two-child family (Montgomery & Casterline, 1996). In this paper, we couple this diffusion mechanism with the insight that different starting levels of nuptiality and fertility at the beginning of the Baby Boom era resulted in different outcomes with regards to fertility across countries and regions (Van Bavel et al., 2018; Van Bavel & Reher, 2013). More specifically, we argue that the homogenization process that resulted from the diffusion of the two-child norm led to both *increasing* fertility in regions where the fertility transition had already proceeded a long way and *decreasing* fertility in regions where the transition was still in an early stage. In the first type of region, fertility increased, because fewer people remained childlessness or had just one child, while fertility decreased in the second type of region, due to a shift from larger family sizes to two child families. Crucially, given that the first type of region was more numerous across countries, the diffusion of a two-child family norm led to an overall increase in fertility and thereby contributed to the Baby Boom.

It is difficult to explore how the diffusion of social norms through social influence processes could explain fertility trends with conventional statistical tools. This problem is aggravated by the fact that there is only limited historical data available. To address this problem, we use agent-based computational modelling to study the role of social influence during the Baby Boom. With this approach, we implement our assumptions about people's fertility behaviour and social influence processes in a computational model, which we then submit to systematic simulation experiments. In these experiments, we assess different 'what-if' scenarios, that allow us to theoretically assess the implications of different assumptions (Grow & Van Bavel, 2018). This makes it possible to study the complex process of fertility decision-making, which involves linkages between micro-level interactions and macro-level outcomes. To calibrate and validate our model, we use retrospective Belgian census data of 1981 and 2001 as model input, and compare the cohort completed fertility rates that the model generates with the empirical fertility rates observed in the same census.

In what follows, we first describe the theoretical background of our argument. Next, we present and discuss the empirically observed fertility and family size trends during the Baby Boom in Belgium. We then present our agent-based computational model to study the proposed mechanism in detail. Finally, we report and discuss the results of our simulations.

2 THEORETICAL BACKGROUND

Scholars commonly agree that the increase in fertility rates during the Baby Boom was characterized by an interplay between shifts in fertility timing and fertility quantum (Bean, 1983; Bongaarts, 2008; Ryder, 1980; Van Bavel et al., 2018). On the one hand, there was an acceleration of the shift to earlier transition into parenthood. On the other hand, there was also an increase in the number of children that people had.

Two factors impacting these trends were the so-called marriage boom (Hajnal, 1953) and an associated increase in overall marital fertility (Van Bavel & Reher, 2013). Around 1950, more people married at a younger age than at any point in the past two centuries, making it truly "the golden age of marriage" (Coontz, 2005). At the same time, the contraceptive pill had yet to make an appearance and even though there were advances in the use of other contraceptive methods (Rusterholz, 2015), marriage and fertility were still very closely connected during this period (Coale, 1977). Thus, not only did people have children at an earlier age due to the declining age at first marriage, more people marrying meant that more people had children. Moreover, marital fertility rates too were on the rise in most regions (Van Bavel & Reher, 2013). People were thus more inclined to get married, and once married, were more inclined to have children as well. However, while the rise in nuptiality seems to have been fairly universal among countries that experienced the Baby Boom, increases in marital fertility occurred mainly in countries where this rate had been exceptionally low during the interwar period (Van Bavel & Reher, 2013). In fact, within countries, some regions actually experienced declining rather than increasing marital fertility rates during the Baby Boom era (Gauvreau & Laplante, 2015, 2016).

Although we know these proximate causes of the Baby Boom, we know very little about the social mechanisms behind them. Classical explanations focus on the optimism and the economic boom after the Second World War in the 1950s and 1960s as driving factors (Doepke, Hazan, & Maoz, 2007; Easterlin, 1987; Greenwood, Seshadri, & Vandenbroucke, 2005; Macunovich, 1998; Sánchez-Barricarte, 2018; Van Bavel & Reher, 2013). However, research has recently shown that such changes in socio-economic factors fall short of explaining the observed intra- and inter-country variability in fertility trends during the Baby Boom (Albanesi & Olivetti, 2014; Sandström, 2014). For example, the recovery of fertility started already during – and sometimes even before – the war in many countries (Van Bavel & Reher, 2013), which contradicts the idea that the Baby Boom was a post-war phenomenon.

What we do know is that over the course of the 20th century, the two-child family became a well-established norm (Frejka, 2008a; Sobotka & Beaujouan, 2014). The roots of this trend go back to the 19th century fertility transition (David & Sanderson, 1987), but it was during the Baby Boom era that the two-child family became more widely adopted in many Western countries (Brée, 2017; Frejka, 2008b; Van Bavel et al., 2018). Based on scarce qualitative studies, it seems plausible that during the Baby Boom era, the idea of having a family with precisely two children attained a normative character (Duvoisin, 2017; Hilevych & Rusterholz, 2018). This entailed both a stronger imperative to get married and start a family and a more restrictive norm on stopping after two children, or at least an increasing social stigma on larger family sizes. In the decades that preceded the Baby Boom, childlessness, even within marriage, was rising, a phenomenon in which some have seen a precursor to the "modern lifestyle" in the last decades of the 20th century (Brée, Eggerickx, & Sanderson, 2017; Duvoisin, Burgnard, & Oris, 2016; Morgan, 1991; Van Bavel & Kok, 2010). Yet, it seems that by the end of the 1930s, parenthood and family life experienced a renaissance while alternative life trajectories were dismissed (Hülsken, 2010; Koropeckyj-Cox, Pienta, & Brown, 2007). Limiting family size on the other hand was hardly new, but developments in contraceptives (Barrusse, 2014; Rusterholz, 2015) and increasing costs of childrearing (Duvoisin, 2017; Hilevych & Rusterholz, 2018; Rusterholz, 2017) might have resulted in a strengthening of the norm to not have more than two children. In any case, more and more people were having two children and understanding the rise of the two-child family might therefore contribute to our understanding of the mechanisms that have brought about the Baby Boom itself.

Earlier research has shown that considering social influence occurring in structured social networks can help to explain historical trends in fertility behaviour (Diaz, Fent, Prskawetz, & Bernardi, 2011; González-Bailón & Murphy, 2013; Klüsener, Dribe, & Scalone, 2019; Klüsener, Scalone, & Dribe, 2017). Indeed, social influence processes are becoming increasingly central to demographic explanations of contemporary family formation patterns. The basic assumption of fertility theories based on social influence is that individual fertility behaviour depends on the fertility behaviour of other members of the population, in particular of those to which individuals have personal contact (Bernardi & Klärner, 2014; Prskawetz, 2017; Rossier & Bernardi, 2009).

In this view, peoples' beliefs and behaviours concerning fertility are interdependent and are shaped by social interaction that occurs in social network structures. There has been an increasing interest in the exact nature of the underlying mechanisms (Bernardi & Klärner, 2014; Kohler, 2001; Lois, 2016; Montgomery & Casterline, 1996). Bernardi and Klärner (2014) distinguish four different mechanisms. People may change their fertility behaviour based on information they receive from observing and interacting with others (*social* *learning*), because they conform to what others expect from them (*social pressure*), because they mimic the behaviour of others (*contagion*) and because of the resources available to them in their social network (*social support*). As we have discussed above, qualitative literature stresses the normative character of the two-child family, which implies that this particular fertility behaviour has spread partly because of social expectations, which create subjective pressures that affect people's fertility decisions. However, social contagion can explain better why people might copy fertility behaviour of people to whom they have no direct personal contact (e.g., people who are prominent in the media), and who therefore are unlikely to create direct social pressure. Social learning could also have played a role by diffusing information on economic possibilities and constraints that lead people to form two-child families. Although these different mechanisms differ substantively from each other, the demarcations between them are not clear-cut. Indeed, empirically, the result is the same, the more people around a given person exhibit a certain kind of behaviour, the higher the chance that this person will adopt it as well. Of course, this is a strong simplification of social reality, but it serves our current purposes well enough, especially considering that we want to avoid too much complexity in our model.

Thus, a person's fertility behaviour is often influenced by the behaviour of other individuals, but some people can be more important in this process than others. The set of relevant others (i.e., those who have significant impact on an individual's fertility decisions) is typically circumscribed by distance in both physical and social space (Wong, Pattison, & Robins, 2006). Spatial proximity still strongly affects the structure of social networks, even though improvements in communication technology and transportation have somewhat diminished its significance (Mok & Wellman, 2007). Those who live in closer physical proximity of each other are more likely to interact with each other on a regular basis and are thus more likely to influence each other. At the same time, people's social characteristics also affects their network contacts. There is a strong tendency for people to associate with those who are similar to them in central socio-demographic characteristics such as age, education, occupation, religious affiliation and political orientation (McPherson, Smith-Lovin, & Cook, 2002). Within these spatially and socially circumscribed networks, the actual structure of the local network can also affect fertility behaviour (Keim, Klärner, & Bernardi, 2009). For example, denser local networks (meaning that there are many interactions among a given set of individuals) is associated with more social influence (Bernardi & Klärner, 2014; H. Kohler, Behrman, & Watkins, 2001; Mönkediek & Bras, 2016). Social class is found to be related to the importance of spatial proximity (Klüsener et al., 2019), for instance the adoption of fertility control by the elite seems to be constrained to a much lesser degree by spatial distance compared to other groups. Given the role that spatial and social proximity play in shaping social networks, we consider these dimensions in the simulation model that we describe below.

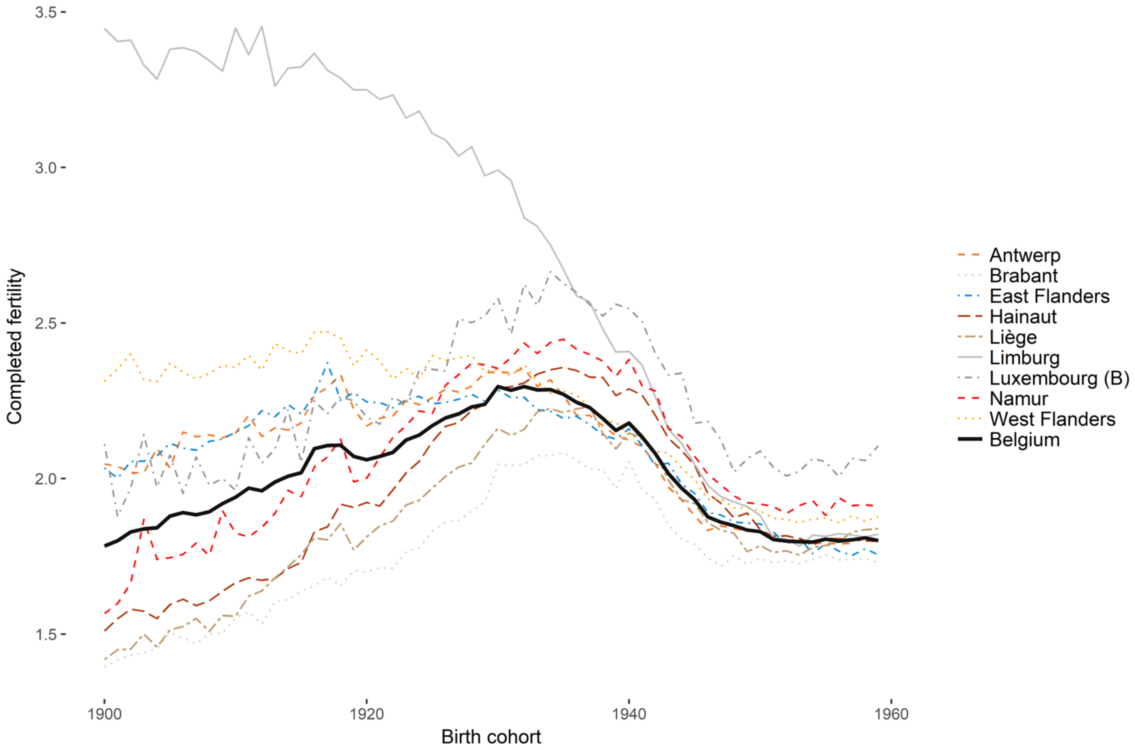
3 EMPIRICAL CONTEXT

The surge in birth rates and the associated recovery of fertility in Belgium started around 1935 and, while temporarily interrupted by the first years of the Second World War, continued until 1964. After this, a steady decline began that brought fertility back to its pre-war level in the 1970s. In general, the intensity of the Baby Boom in Belgium was lower than in other countries, in particular compared to the United States or Canada, but to a lesser extent also compared to France and the Netherlands (Van Bavel & Reher, 2013). Yet, Van Bavel and Reher (2013) have shown that the temporal pattern in the Belgian case was rather typical. The turnaround started earliest in the Nordic countries, that is, in mid-1933 in Denmark and Finland, mid-1934 in Sweden, and by the end of 1935 in Norway. In Belgium, the decline of fertility stopped in 1935, similar to France, England and Wales. The fact that the turning point in the total fertility rate in Belgium, as well as other countries, was well before the war is an important indication that the common interpretation of the Baby Boom as the result of post-war optimism and the economic boom of the 1950s and 1960s is insufficient. In some cases, the recovery of fertility was interrupted when the war broke out. Apart from Belgium, this was also the case in France in 1940, for example, following the declaration of war in September 1939. After 1942, fertility began rising rapidly in many countries, including Belgium.

In the remainder of this paper, we focus on cohort completed fertility rates, as they are indicative of the changes in the quantum of fertility, which arguably was the most interesting change in fertility behaviour of the Baby Boom era. Figure 1, based on Belgian census data of 1981 and 2001, illustrates the substantive increase in cohort completed fertility in Belgium as a whole (bold black line), for generations born between 1900 and 1960. These cohorts reached their twenties during the Baby Boom era and are thus the generations that produced most of the Baby Boom. Women born in the early 1930s had on average almost 0.5 children more than women born at the turn of the century (1.86 vs. 2.29). In fact, each birth cohort between 1900, when cohort fertility was well below replacement levels (Van Bavel, 2010), and 1930, when it reached its peak of about 2.3 children per woman, had higher fertility than the one preceding it. The only exceptions are women born right after the First World War (i.e., shortly after 1918), who reached their reproductive years during the first years of the Second World War.

To illustrate differences between regions, Figure 1 also shows cohort completed fertility for each of the nine Belgian provinces separately. In the provinces in the early industrialised south of Belgium, in French speaking Wallonia, including Liège, Belgian Luxembourg, Hainaut and Namur, the increase in cohort fertility was substantive. In the more rural provinces of the north of Belgium, in Dutch speaking Flanders, including Antwerp, East- and West-Flanders, Brabant and Limburg, however, there was no clear increase in fertility. In one province (Limburg), there was even a rather steep decline. If good economic circumstances were the driving force behind the Baby Boom, one would expect a different picture, namely more of a boom in economically thriving Flanders, and much less so in stagnating Wallonia, where the traditional coal industry went from crisis to crisis in the "grey" 1950s (Cassiers, De Villé, & Solar, 1996).

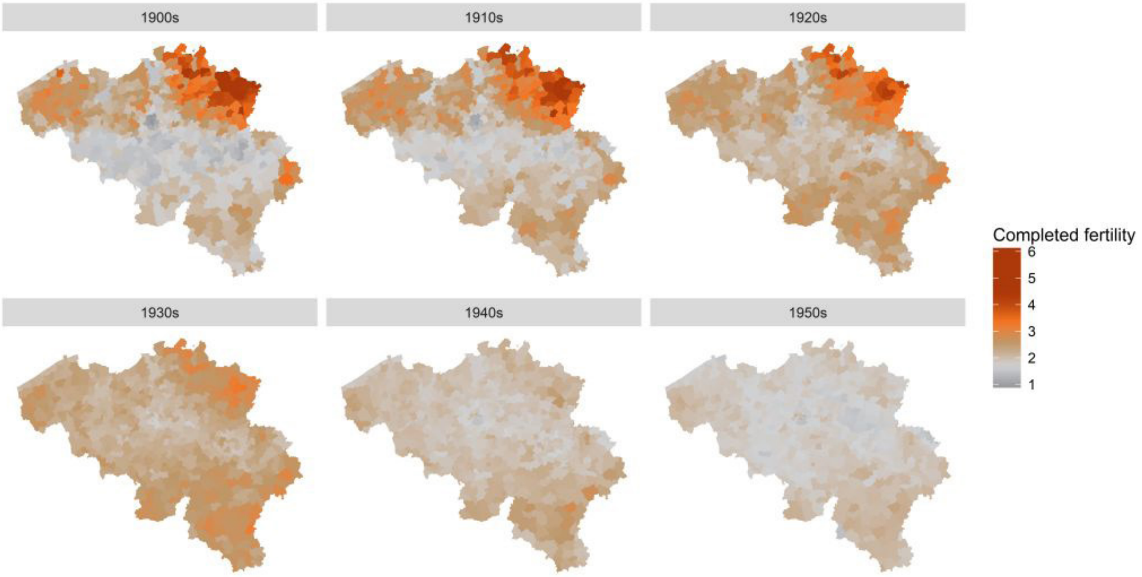
Figure 1 *Cohort completed fertility rates of women born between 1900 and 1960 by province, Belgium*



Source: Belgian censuses of 1981 and 2001, own calculations.

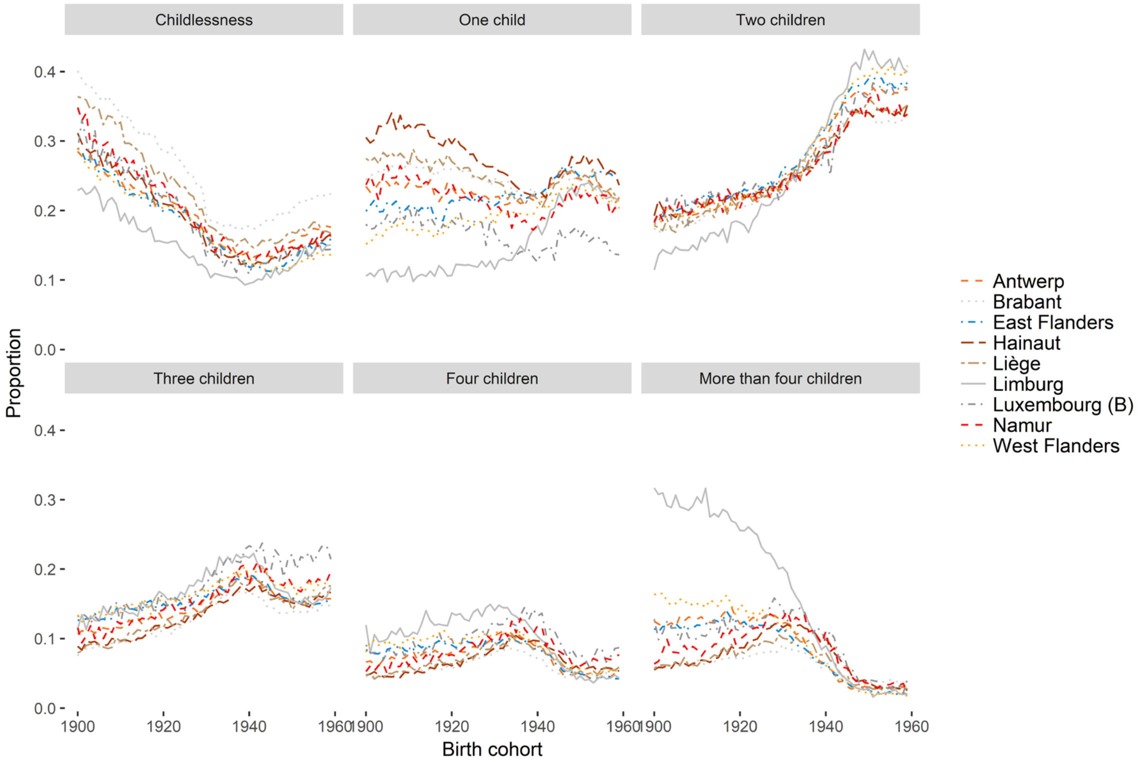
Figure 2 completes the picture by showing cohort completed fertility levels for each of the 633 municipalities in their geographical locations. This illustrates best how regional fertility patterns were becoming more alike over time. Among the oldest cohorts, born in the 1900s, regions differed greatly in fertility. In the north-east, Limburg stands out, but one can easily identify the language border between the north and the south, the larger cities in Flanders (Brussels, Antwerp and Ghent) where fertility was relatively low, the heavily industrialised area in Wallonia and the more rural areas in the northwest and southeast. Among the cohorts of the 1930s, much of the differences had already disappeared. When we look beyond the Baby Boom producing cohorts, the trend of homogenization becomes even clearer. Among the generations born in the 1950s, almost all municipalities had cohort fertility levels between 1.5 and 1.8.

Figure 2 *Cohort completed fertility rates of women born between 1900 and 1960 by municipality, Belgium*



Source: Belgian censuses of 1981 and 2001, own calculations.

Figure 3 *Proportion of childless women, women with two, three, four, and four or more live births, cohorts 1900-1960, by province, Belgium*



Source: Belgian censuses of 1981 and 2001, own calculations.

What family size trends are behind these fertility rates? Figure 3 confirms that the two-child family was on the rise among the cohorts producing the Baby Boom. Among the cohorts born in the 1930s, women with two children became the most prevalent, at the expense of both childless women and larger families with four or more children. In the youngest cohorts, almost one in three women had exactly two children, while childlessness was reduced to less than 15%. The establishment of the two-child family as the dominating family size is remarkably consistent in all provinces. While Limburg was very different from the other provinces among the oldest cohorts, by the generation born at the end of the 1930s, most of these differences had disappeared. Of course, for Limburg, the shift to two-child families meant a sharp drop in the proportion of large families. In other areas, the increase in the number of two-child families was almost completely driven by the reduction of childlessness and to a lesser extent the reduction of families with just one child. In some provinces, especially in Luxembourg, Namur and Hainaut, large families became a bit more common among the first half of the Baby Boom cohorts, but in most regions, the proportion of large families was lower among the members of the youngest cohorts than among the members of the oldest cohorts.

In general, in regions where the fertility transition was further along and in which the proportion of large families was already substantively reduced, the shift from high levels of childlessness to two-child families meant an *increase in fertility*. In regions where the fertility transition was less advanced, the shift from larger families to two-child families implied a *decrease in fertility*. The end result is a situation in which regions are more homogenous in their fertility levels, and in which two-child families dominate. This suggests that the diffusion of a two-child norm could indeed explain part of the observed variation in fertility patterns during the Baby Boom.

4 MODELLING THE BABY BOOM

4.1 Model basics

To theoretically explore the mechanism that we propose, we make use of agent-based computational modelling.[1] We investigate the spatial and educational diffusion of a two-child norm and the resulting fertility behaviour of the Belgian population during the Baby Boom era. For this, we combine insights from two papers that also employ agent-based modelling, one in the context of the 19th century fertility transition (Klüsener et al., 2017) and one in the context of the contemporary fertility decline (Diaz et al., 2011). From the work of Klüsener et al. (2017), we adopt a simple yet effective implementation of the diffusion of new ideas concerning fertility, without having to explicitly model social network structures. One limitation of this model is that it only models the diffusion of new fertility-related ideas, but not their effect on fertility, which is in the focus of our work. To address this issue, we additionally build on the work of Diaz et al. (2011), who modelled actual fertility outcomes. These two elements of our model mirror the duality in the mechanism that we propose: the diffusion of the two-child norm leads to a spatial homogenization of family size, which in turn explains contrasting trends in fertility behaviour given different fertility starting conditions.

To limit the complexity of our model, it deals with females only. A woman – or agent in our model – is influenced by people in her environment. This environment has a socio-structural dimension, which is reflected in our model by including education in defining the set of relevant others for each agent (i.e. the set of people who influence her fertility behaviour, see details below), and a spatial dimension. The spatial dimension is particularly salient in historical populations, where the speed of information exchange was not yet revolutionized by modern means of communication and transportation. The advent of mass media, in the first place the radio and the expansion of transportation networks, might have given people a wider "view" of fertility behaviour, but arguably the direct interactions within people's own spatially structured networks remained the most important source of information (Mok & Wellman, 2007; Skyrms, 2004). Therefore, we expect the most important determinant of who counts as relevant others for a given agent to be the area of her residence, one of the 46 arrondissements in Belgium. However, to reflect the expanding possibilities of communication and transportation, the model also takes into account influence from outside the agent's own area. We hypothesize that especially the elite, here identified as the highly educated living in urbanized areas, can have farther reaching influence, as they are more likely to broadcast their behaviour through mass media.

The basic structure of the model, then, is as follows (see Figure 4). Each simulation run starts with 10,000 female agents who have certain demographic characteristics, based on actual observed distributions from the census of 1981. We model the fertility behaviour of our agents in each year in two steps. In the first step, we address the diffusion of the two-child norm, and in the second step, we address actual fertility outcomes. The proportion of two-child norm adherers in the group of relevant others for each agent determines the

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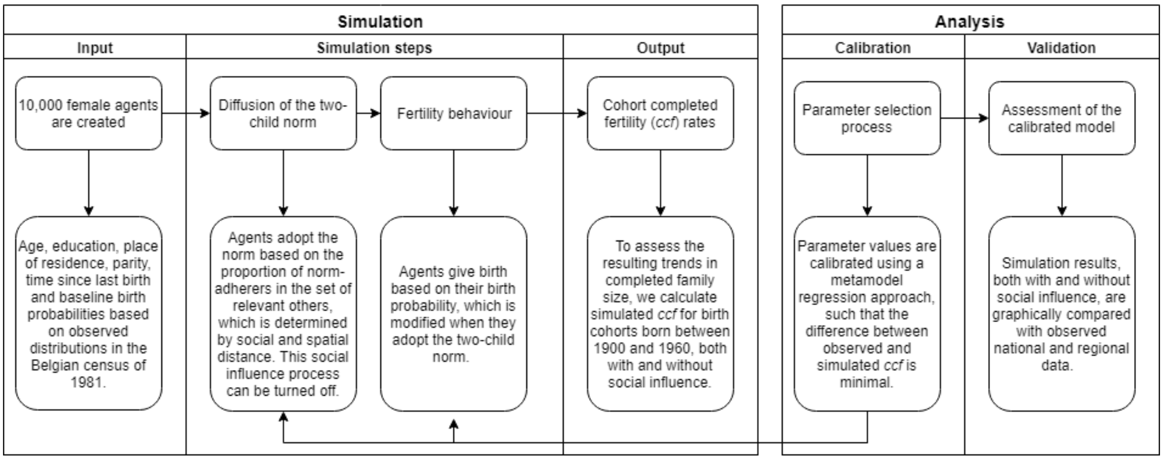
[1] We have implemented the model in NetLogo, version 6.0.4 (Wilensky, 1999). The code and all input files necessary to reproduce our results can be obtained upon request.

likelihood that this agent will also adopt the norm. The more people in the set of relevant others have already adopted the norm, the more likely it becomes that the focal agent will also adopt it. To get the diffusion process started, some agents will already adhere to the norm at the start of the simulation. Agents give birth to children based on observed birth probabilities, but these probabilities change if an agent adopts the two-child norm. After running the simulation, we calculate the main outcome of interest, which are cohort completed fertility rates. To calibrate the model, we compare the results with the observed cohort completed fertility rates from the census of 1981 and 2001. In what follows, we describe the model in greater detail.

Figure 4 *Outline of the modelling process*



4.2 Model details

The model consists of exclusively female agents, indexed by *i*, who can be described by their year of birth (b_i, with the range 1900 to 1999), age (a_i, measured in years in the range 0 to 100), educational level (e_i, with the states "low", "middle" and "high"), area of living (m_i, one of 46 arrondissements), whether or not they live in an urbanized area (u_i, determined by the observed proportion of people living in municipalities with a population over 50,000), parity (p_i) and time since last birth (t_i, measured in years, see Table 1 for more details). Moreover, agents have either adopted the two-child norm N or have not adopted it, which is indicated by dummy variable n_i. By interacting with each other, agents exhibit some behaviour: adopting the norm or not, which in turns affects the likelihood of having (additional) offspring.

The model proceeds in discrete time steps and each step represents one calendar year, indexed by y. Each simulation run starts right before the onset of the Baby Boom in Belgium, in 1935, and continues for 65 simulation years (i.e., until 2000), so that we can examine the simulated completed fertility levels of cohorts born between 1900 and 1960. In this, we assume that fertility for women older than 40 is negligible. In each year, agents decide whether or not to adopt the two-child norm. Next, they may or may not give birth to a child, who, if female, becomes a new agent in the model.

Table 1 *Agent-level variables and model parameters, possible states in brackets*

Agent-level variables	
b_i	Birth year of the agent [1900-1999]
a_i	Age of the agent [0-100]
m_i	NIS-code referring to the area/district of residence of the agent [10000-99999]
u_i	Indicating whether the agent lives in an urbanized area or not [0 or 1]
e_i	Educational level of the agent [1 = low, i.e. at most primary or lower secondary school; 2 = middle, i.e. higher secondary; 3 = high, i.e. tertiary education]
p_i	Parity of the agent [1-12]
t_i	Time since last birth of the agent measured in years [1-5]
n_i	Indicating whether the agent has adopted the norm [0 or 1]
Model parameters	
α	Determines the relative weight in agent *i*'s norm adoption of people who are educationally similar to agent *i* [0-1]
β	Determines the relative weight in agent *i*'s norm adoption of people who live in the same area as agent *i* [0-1]
γ	Determines the relation between parity and the birth probability multiplier defined in Eq.s 2, 3 and 4 [1-5]
δ	Determines the relative weight in agent *i*'s norm adoption of the vanguard elite [0-1]
ε	Determines the initial number of norm adherers in urban centres [0-1]
PN_{max}	Determines the maximum probability of adopting the norm [0-1]

In our diffusion model, an agent will adopt the two-child norm depending on the share of people in her social network who are already adhering to this norm. We assume that agents form their childbearing intentions during their fertile years, here conventionally defined in the range age 15 to age 45, although they can carry on influencing others until they reach the age of 65. To keep the model as simple as possible, we decided to not fully incorporate mortality, after having ascertained that this does not make a substantive difference to our results. The probability that a given agent *i* will adopt the norm *N* in year *y* ($P(n_{i,y} = 1)$) is influenced by the shares of norm-adhering people in different subgroups of others relevant to the agent, weighted by a set of parameters. First of all, this probability is influenced by the share of norm-adhering people among those who have the same educational attainment and who are living in the same area ($SN_{e_j=e_i,m_j=m_i,y}$) and by the share of norm-adhering people among people with a different educational level within the same area ($SN_{e_j \neq e_i,m_j=m_i,y}$). The relative weight of the influence from educationally similar and dissimilar people is determined by the weight parameter α and its complement 1 – α, respectively. If α is close to 1, educationally similar people will have maximal influence and dissimilar people will have almost no influence, but if α is close to 0, the exact opposite is the case (see Table 1 for a complete overview of all the parameters in the model). The share of norm-adhering people in the population in *other* areas ($SN_{m_j \neq m_i,y}$) also has a potential influence, and the relative weight of the influence of the agents living in the same area compared to that of those living in other areas is determined by the weight parameter β and its complement 1 – β. If β is close to 1, people who live in the same area as the focal agent will have maximum influence whereas people in other areas will have almost no influence; the opposite is the case when β is close to 0. Moreover, we can give potential vanguard groups, i.e. people having above average education (higher than lower secondary) and living in urbanized areas, a larger weight with the help of parameter δ. The total impact of agents living in other areas is a weighted average of the share of norm adherers among agents outside the agent's own area belonging to the vanguard group $SN_{e_j>1,m_j \neq m_i,u_j=1,y}$ and the share of norm adherers among all other agents outside the agent's own area $SN_{u_j=1 \wedge e_j=1 \vee u_j=0,m_j \neq m_i,y}$.

So, more technically, and largely following Klüsener et al. (2017), the probability of adopting the norm is defined as

$$P(n_{i,y} = 1) = \left[\begin{array}{c} \left[SN_{e_j=e_i,m_j=m_i,y} \cdot \alpha + SN_{e_j \neq e_i,m_j=m_i,y} \cdot (1-\alpha)\right] \cdot \beta + \\ \left[SN_{e_j>1,m_j \neq m_i,u_j=1,y} \cdot \delta + SN_{u_j=1 \wedge e_j=1 \vee u_j=0,m_j \neq m_i,y} \cdot (1-\delta)\right] \cdot (1-\beta) \end{array} \right] \cdot PN_{max}. \quad (1)$$

Thus, the chance of adopting the norm $P(n_{i,y}=1)$ is a weighted average of the shares of norm-adherers in the different subsets of relevant others defined above. These shares are calculated simultaneously for all agents at the beginning of each simulation year, so that agents who start adhering to the norm in a given year have no influence on the behaviour of other agents in the same year. The resulting average is multiplied by a maximum chance of adoption PN_{max}, which serves as a speed limiter on the diffusion process. This parameter has both a technical and a more substantial purpose. On the one hand, it allows us to map the diffusion process on different time scales. For example, if we were to decrease the size of the time steps in the simulation from one year to six months, PN_{max} would have to be calibrated differently, but any changes in the other parameters would be the result of more fine-grained simulation process and not of the smaller time steps in themselves. On the other hand, PN_{max} is reflective of the actual speed with which ideas and norms may diffuse throughout a population, based on people's propensity to adopt new norms.

After all $P(N_{i,y} = 1)$'s have been calculated, for each agent between the ages 15 and 45 who has not adopted the norm N yet a random number between 0 and 1 is drawn from a uniform distribution, as to introduce stochasticity in the model. When this number is lower than $P(N_{i,y}=1)$, the respective agent will start to adhere to the norm (i.e., $n_{i,y}$ changes from 0 to 1). Our focus on the age range 15 to 45 reflects the typical period during which women are fertile.

Conversely, people can also change their mind about the number of children they aim to have. In each year, there is a probability $P(N_{i,y} = 0)$ that an agent who already was adhering to the norm in the previous year ($n_{i,y-1} = 1$), deviates from the two-child norm, so that $n_{i,y} = 0$ (in subsequent years, they may adopt the norm again). We determine $P(N_{i,y} = 0)$ by multiplying a constant with PN_{max}. Note that with this approach, the chance of norm defection is proportional to the speed of norm adoption. That is, if agents have a higher propensity to adopt new norms, they are also more likely to drop them again. In our simulation experiment, we have fixed the value of the constant to be .05, based on exploratory experimentation with the model.

To get the diffusion process started, some agents need to have already adopted the two-child norm at the beginning of our simulation. As discussed above, the empirical evidence suggests that some individuals already adhered to the two-child norm at the start of the period that we considered. We assume that having precisely two children as a normative ideal was really novel in the middle of the 1930s, and was first adopted by medium and highly educated people in urbanized centres (as defined above). We randomly select a number of the members of this group as "seeds", who have adopted the norm already. The number of seeds is determined by the parameter ε. If ε is set to 0.02, for example, two per cent of those highly educated urban dwellers have already adopted the norm at the start of the simulation.

To model actual fertility outcomes, we let agents procreate. For this, we combine a baseline of birth probabilities that we derive from empirically observed data (which we describe in more detail below) with a multiplier effect of the two-child norm (Diaz et al., 2011). More precisely, we calculate the adjusted birth probability $P(B_{i,y})$ of an agent in simulation year y based on two factors. The first factor is the empirically observed average birth probability $\overline{P(B_{e_i,m_i,p_i,a_i,t_i})}$ in 1935 (i.e., the year in which the simulation starts), given the education, area, parity, age, and time since the previous birth. The second factor is the multiplier MP_{n_i,p_i} that adjusts this baseline birth probably, depending on whether the agent has adopted the two-child norm or not, and which is subject to parameter γ and the parity of the agent p_i. Technically, we define $P(B_{i,y})$ as:

$$P(B_{i,y}) = \overline{P(B_{e_i,m_i,p_i,a_i,t_i})} \cdot MP_{n_i,p_i}, \qquad (2)$$

with

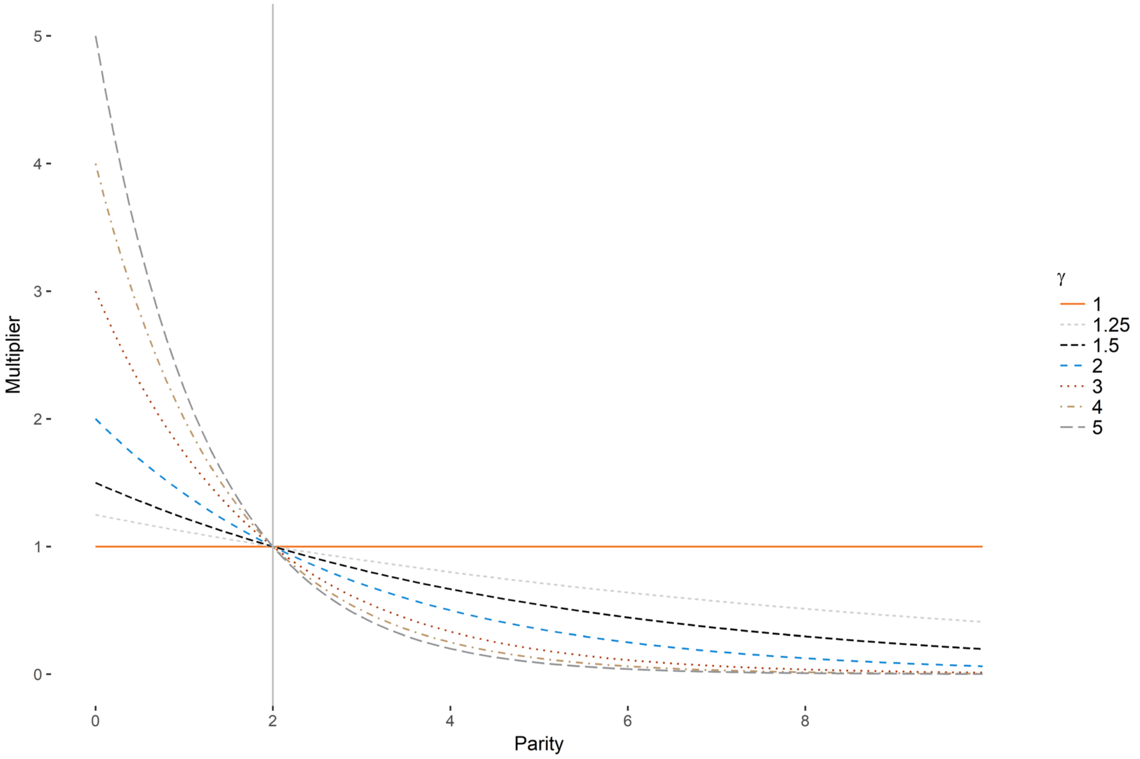
$$MP_{n_i,p_i} = \gamma \cdot e^{-\frac{\log \gamma}{2} p_i} \quad when\ n_i = 1, \qquad (3)$$

and

$$MP_{n_i,p_i} = 1 \qquad\qquad when\ n_i = 0. \qquad (4)$$

If the agent has adopted the two-child norm (i.e., if $n_i = 1$), the multiplier is a function of the agent's parity p_i (Eq. 3), so that it increases the agent's birth probability $P(B_{i,y})$ when she has a parity lower than 2 and it decreases the birth probability when she has a parity higher than 2. If the agent has not adopted the two-child norm (i.e., if $n_i = 0$), the multiplier equals 1 regardless of the agent's parity (Eq. 4). Thus, only agents who have adopted the norm experience adjusted birth probabilities. The relation between the agent's parity and the birth probability multiplier is assumed to be non-linear, because of the skewness of the parity distribution. Figure 4 shows this relation given several possible values of parameter γ, which can range from 1, indicating no effect of the two-child norm, to 5, indicating a very strong effect. Even higher values result in agents controlling their fertility almost perfectly, which is not realistic. Thus, as Figure 5 illustrates, the value of γ allows us to control the strength with which norm adoption affects fertility behaviour. The larger γ, the stronger the "pull" towards two children for agents at parity 0 or 1, and the stronger the deterrent for agents already at parity 2 or higher. Note also that with this approach, the observed birth probabilities at the beginning of the simulation period serve as a baseline and a proxy for the birth probabilities we may have expected to observe in the absence of the two-child norm, *ceteris paribus.*

Figure 5 *Relation between agent's parity and birth probability multiplier (MP_{n_i,p_i}), given parameter γ*



Once the adjusted birth probability $P(B_{i,y})$ has been calculated for all agents in the age range 15 to 45, we again draw a random number in the range 0 to 1 for each of these agents and compare this value against $P(B_{i,y})$ to determine whether or not a child is born. If the child is female, which is determined based on the observed yearly sex-ratios at birth, she is added to the model as a new agent. She gets assigned her ultimate educational attainment, based on the observed educational distribution of her cohort and area. After 65 simulation years, the model output consists of all the agents and their final parity levels. From these, we can calculate completed cohort fertility rates, which is the variable of interest.

4.3 Input data, outcome measures, and experimental setup

As input data for the model, we use age, educational attainment, parity distributions and birth probabilities calculated from Belgian census data of 1981 (Willaert & Deboosere, 2008). Given that our data is retrospective, we cannot use other, time-varying social indicators, such as occupation. Furthermore, since we do not have access to information on internal migration, we cannot really assess its impact, either on the social influence process itself or on our ability to analyse spatial patterns of the Baby Boom based on census information. Also, in combination with the fact that there is a social gradient in mortality (Gadeyne & Deboosere, 2002), some bias due to selection effects with regards to mortality is unavoidable. However, previous research has established the usability of the census data for reconstructing cohort completed fertility rates (Nomes & Van Bavel, 2016; Van Bavel, 2013). Moreover, since we focus on cohort trends and not on birth rates or period fertility rates, we do not use actual cohort sizes in our simulations. Mortality is therefore of a somewhat lesser concern, although the selectivity issue remains. This is likely to especially concern women among the oldest cohorts, who reached higher parities, and thus potentially had higher mortality risks, and who might consequently be underrepresented in the census data, resulting in underestimations of higher parity birth probabilities. Moreover, external migration and underreporting might also introduce a certain amount of bias in the data.

We use district ("arrondissement") level geographical data (NUTS 3), because using municipalities would demand a very large number of agents, so that running the model repeatedly would take a lot of time. The model is initiated with 10,000 agents to make sure all 43 districts are well covered. The agents are distributed over the areas proportionally to the observed number of inhabitants in each arrondissement in 1935. Using finer grained spatial information would lead to more detailed spatial patterns, but we do not expect that the results would be very different from those presented below. Hence, the added value of using finer grained spatial information would be very limited, and the computational cost would be high, as we would need to add a lot of extra agents and simulation runs to achieve statistically stable results for smaller municipalities.

We calculate the baseline average yearly probability $\overline{P(B_{e_\iota,m_\iota,p_\iota,a_\iota,t_\iota})}$ that a woman, given her location, education, age, parity and time since last birth, gives birth for the years 1935 and 1936. We use the average of two years, because this reduces the effects of random fluctuations. We calculate the yearly probabilities needed in the model as follows, assuming that the probability of childbirth is equally distributed over the two years:

$$\overline{P(B_{e_\iota,m_\iota,p_\iota,a_{\iota,},t_\iota})} = 1 - \sqrt{1 - P(B_{e_i,m_i,p_i,a_{i,},t_i,y=1935\,|1936})}. \qquad (5)$$

Regarding outcome variables, we are mainly interested in cohort completed fertility rates (*ccf*), nationally and by province, and cohort parity distributions. To calibrate the model, we compare the simulated national cohort completed fertility rates with the empirically observed fertility rates based on our census data, by calculating the sum of the squared residuals (i.e. the differences between the empirically observed cohort completed fertility rates and the simulated cohort completed fertility rates). We refer to the sum of these residuals as *DEV*, which is defined as

$$DEV = \sum_{c=1900}^{1960} (ccf_{c,obs} - ccf_{c,sim})^2. \qquad (6)$$

This measure calculates for each cohort (*c*) of women born between 1900 and 1960 the squared difference between the empirically observed and the simulated completed fertility (both at the national level), and then sums these deviations across cohorts. Hence, the smaller *DEV* for a given simulation run, the better the simulation outcomes approximate the empirical data. To find the best fit, we have to find the parameterization that minimizes this deviation measure.

To find the best-fitting combination of parameter values (i.e. the combination that yields the smallest average value of *DEV* across simulation runs), we use a regression metamodel (Grow, 2017). With this approach, the simulation model is run several times, while its parameters are systematically varied across runs. For each run, the value of *DEV* and of the corresponding model parameters is recorded. After all runs have been completed, an ordinary least squares regression model is estimated, in which the different *DEV* values across the different simulation runs are regressed on the corresponding values of the different model parameters. The result is a regression equation in which for each parameter of the simulation model there is one regression coefficient that indicates how the average value of *DEV* changes in response to changes in the respective parameter. It is possible to also consider interactions between different model parameters, as well as potential non-linearity in the effects that a given parameter may have on model fit. The final equation can be used to analytically determine the parameter combination that is likely to yield the lowest average difference between model outputs and empirical data (i.e. the lowest average value of *DEV*).

Our use of a regression metamodel has the advantage that we can determine the parameter combination that is likely to create the best fit with the empirical data without having to explore every possible parameter combination. Instead, we need to run the simulation model only a limited number of times, based on an appropriate experimental design. Here, we opted for an inscribed central composite design, which enabled us to explore possible interactions between different model parameters, as well as possible nonlinearities in the effects that the different parameters have on model fit (for details see Grow (2017)). More specifically, since the relation between parameter γ and the birth probability multiplier is of a non-linear nature, it seems likely that γ may have a non-linear (quadratic) effect on the model fit as well. Such non-linearity can best be explored with inscribed central composite design. With this design, the different parameter combinations at which the simulation model are run are chosen so that non-linear (i.e., quadratic) effects for all model parameters can be included, and also all possible two-way interactions between all model parameters can be explored. Given the six parameters whose values can vary in our model (i.e. α, β, γ, δ, ε and PN_{max}), we had to run the model for 81 different parameter combinations to generate a central composite design. The exact values used in each of these design points in our simulation experiment are given in Appendix 1 and a detailed explanation of how the design points for a central composite design are chosen is given in Grow

(2017). Given the stochastic nature of the simulation process, we conducted 50 independent simulation runs for each of the 81 parameter combinations (leading to a total of 4050 runs) and averaged the resulting *DEV* values for each set of 50 simulation runs (i.e. for each parameter combination, there is only one average *DEV* value that is based on 50 independent simulation runs that all used the same parameterization).[2] The full results of our regression metamodel (including the estimated main effects for all model parameters, as well as all possible quadratic effects and all possible two-way interactions) can be found in Appendix 3.

In the results section, we present comparisons of simulations with and without social influence, as to gauge the merits of the mechanism we are interested in. Technically, the model that contains social influence is the complete model, as described in this section. In the version without social influence, we set parameter γ, which determines the relation between parity and the birth probability multiplier, to 1, so that the diffusion of the two-child norm has no influence on fertility at all, and all the other parameters become obsolete. This results in a model in which agents continue to have children in accordance with the observed birth probabilities of 1935 and 1936. However, the changing educational and spatial composition of the population will still affect the aggregated fertility trends.

5 RESULTS

Figure 6 shows the results of the fully calibrated model and Table 2 shows the full parameterization. We consider two versions of the model, one with social influence ($\gamma = 1.7761$) and one without social influence ($\gamma = 1$), in comparison to the empirically observed fertility. When we 'turn off' the effect of social influence, the fertility levels are exclusively based on the birth probabilities of 1935 and 1936, which remain fixed during the whole period for all agents. In this version of the model, fertility decreases almost monotonously over time, to a level of about 1.25 among the cohort born in 1960. The reason for this is that period fertility rates in 1935 and 1936 were very low and cohort fertility therefore decreases substantively when the birth probabilities are kept constant at these levels. Thus, if people would have kept having children in the 1940s and 1950s at the same rate as they did in the middle of the 1930s, cohort completed fertility would have turned out very low. Moreover, over time, the share of highly educated women, who have lower fertility rates than low or medium educated women, has increased, which also contributes to the decrease in fertility.

Table 2 *Parameterization of the full model*

Parameter	**Calibrated value**
α	0.3959
β	0.5005
γ	1.7761 (with social influence); 1 (without social influence)
δ	0.4836
ε	0.1108
PN_{max}	0.4415

The full model – in which social influence is turned on – performs very well in reproducing the upswing of cohort fertility levels, although the match between simulated and observed fertility levels is not perfect. As Figure 6 illustrates, just as observed empirically, fertility increases from cohorts born in the 1900s to cohorts born in the 1930s, after which fertility decreases again. The model slightly underestimates the peak in fertility among those born in the 1930s, but the overall trend is qualitatively very similar. This suggests that social influence processes could potentially explain a substantive part of the changes in cohort total

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[2] Given the stochastic nature of the simulation model, the simulation outputs might vary substantially between independent runs. Hence, the larger the number of runs over which outcomes are averaged, the more reliably we can describe the central tendency in model outcomes. Based on an exploratory analysis, we determined that 50 simulation runs were sufficient to generate reliable results, so that there was no added value to using a larger number of runs.

fertility during the Baby Boom. Somewhat unexpectedly, the model also reproduces part of the fall of fertility among cohorts born after 1935, which were not in the focus of its development. For example, the model does not consider the introduction of the contraceptive pill in the second half of the 1960s, and neither the rapid changes in nuptiality in the 1970s, which are usually associated with the second demographic transition (Lesthaeghe & Neels, 2002). The model is nonetheless able to reproduce the turnaround and one central reason for this is the interplay between norm diffusion and changes in the educational composition of the population. The initial increase in fertility is due to the fact that the initial diffusion of the norm to have two children induces many women to actually have children. Once the norm has diffused widely, fertility reaches a plateau, typically among cohorts born in the 1930s. After this, the share of highly educated women tends to increase rapidly and this has a fertility decreasing effect, given that more educated women have lower fertility rates than less educated women.

Figure 6 *Simulation result of the calibrated model with and without social influence, compared with the observed fertility trend*

Figure 7 shows the simulation results by province. When we turn on social influence, we see that the model copes with the differences between provinces fairly well. The increase of fertility in Antwerp, Brabant, East-Flanders and Liège is reproduced quite accurately. In the case of Hainaut, Namur and Luxembourg there is a slight underestimation, due to the fact that there was, as we have seen in Figure 3, a minor increase in higher parities there that the model cannot reproduce. For the provinces of Limburg and West-Flanders, the decrease of fertility is also predicted correctly. The introduction of the two-child norm increases fertility in provinces where fertility was low and childlessness was high. It drives fertility further down in provinces where it was still relatively high, and large families were still fairly common. In these provinces, the difference between the simulation results with and without social influence are much smaller. The long-term trend that was already implicitly present in the baseline birth probabilities of the 1930s is here in line with the trend produced by the introduction and diffusion of the two-child norm. In the other provinces, where a Baby Boom was observed, the two-child norm diffusion causes a reversal of the earlier downward trend.

In a number of provinces, there is an overestimation of fertility levels among the younger cohorts, as we have seen at the national level in Figure 6. All in all, the model deals well with the regional variation, it succeeds in reproducing both the Baby Boom and the baby bust, but it misses part of that increase of fertility, and it misses part of the decrease in fertility later on.

Figure 7 *Simulation results of the calibrated model with and without social influence, compared with the observed fertility trend by province*

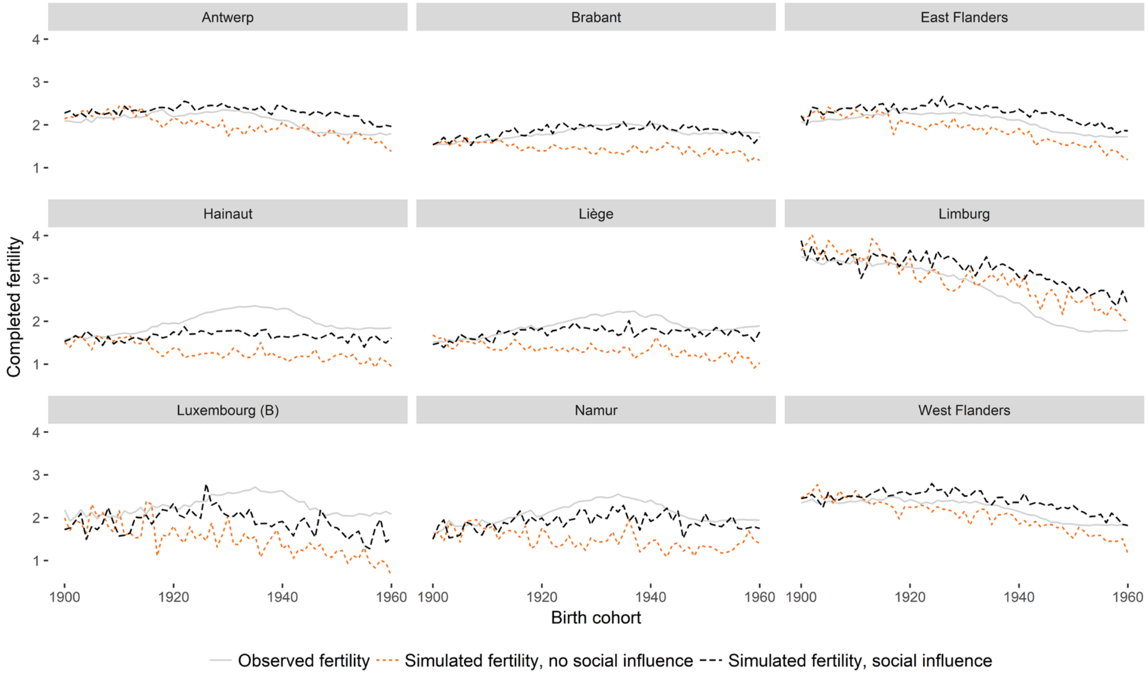
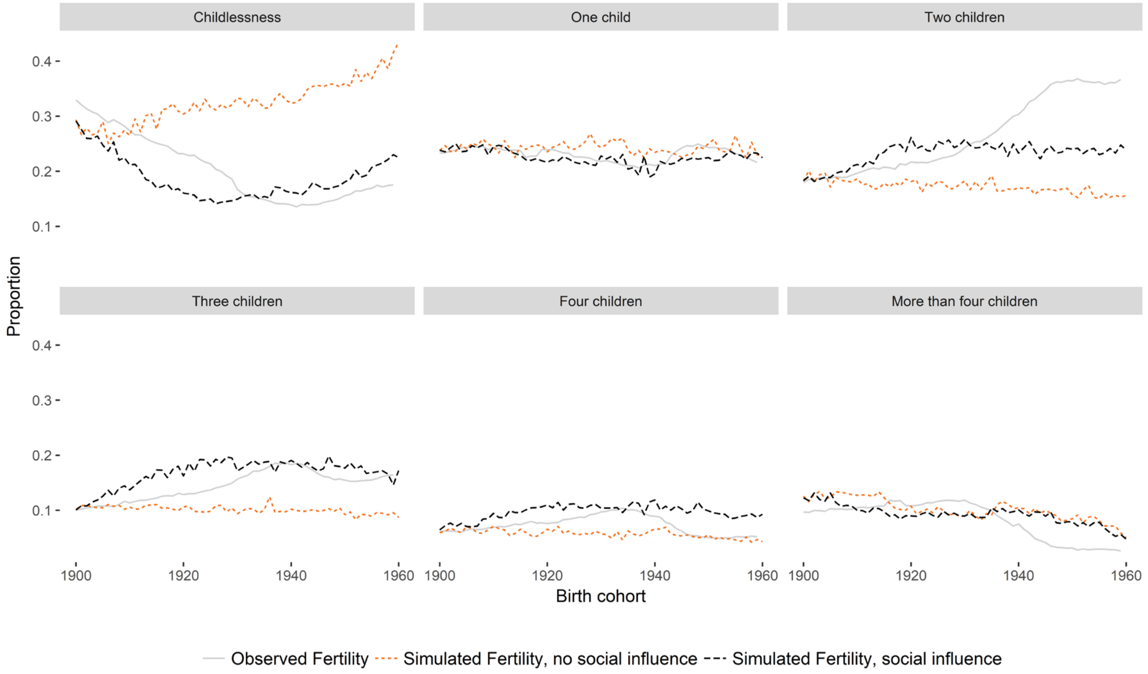


Figure 8 *Parity distribution by birth cohort of the calibrated model with and without social influence, compared with the observed trends by province*



In Figure 8, we show the parity distributions that we obtained from the simulation model and compare them with the empirically observed distributions. Overall, the simulation with social influence fits the observed data quite well, and it especially does well with reproducing the decrease in childlessness among older cohorts, and the turnaround of this trend among the younger cohorts. However, the rise of the two-child family is not entirely captured. While many agents in our simulation indeed reach parity two because of the introduction of the two-child norm, they continue to have more children more often than people did in reality, especially among the younger cohorts. It seems that our model, while capturing the overall fertility trends rather well, somewhat oversimplifies the family size limiting trends. To a large extent, the overestimation of the higher parities might be due to the fact that the model ignores the introduction of the contraceptive pill, as it allowed younger cohorts to limit their family size more effectively.

For parities higher than four, the model produces a downward trend. We indeed observed a sharp decrease in one province (Limburg), but there was an increase in several provinces, resulting in a modest overall increase. A contributor to this discrepancy could be that the baseline birth probabilities that the model uses, underestimate higher parities, due to underrepresentation of high parity mothers in the census because of mortality selectivity and underreporting (Van Bavel, 2013). It has been shown that in modern population, a high parity negatively affects mortality (Le Bourg, 2007). If people among the oldest cohorts who had a lot of children indeed had a higher chance of dying before the time of the census, then they are underrepresented, and birth probabilities for people already at higher parities would be off.

6 SENSITIVITY ANALYSIS

To test the robustness of our results, we assessed to what extent the results depend on certain key aspects of the model. First of all, we consider the starting conditions of the diffusion process. Second, we tested two alternative relations between birth probability multiplier MP_{n_i,p_i} and agents' parity. We fully calibrated all of these alternative models, the results of which can be found in Appendix 2.

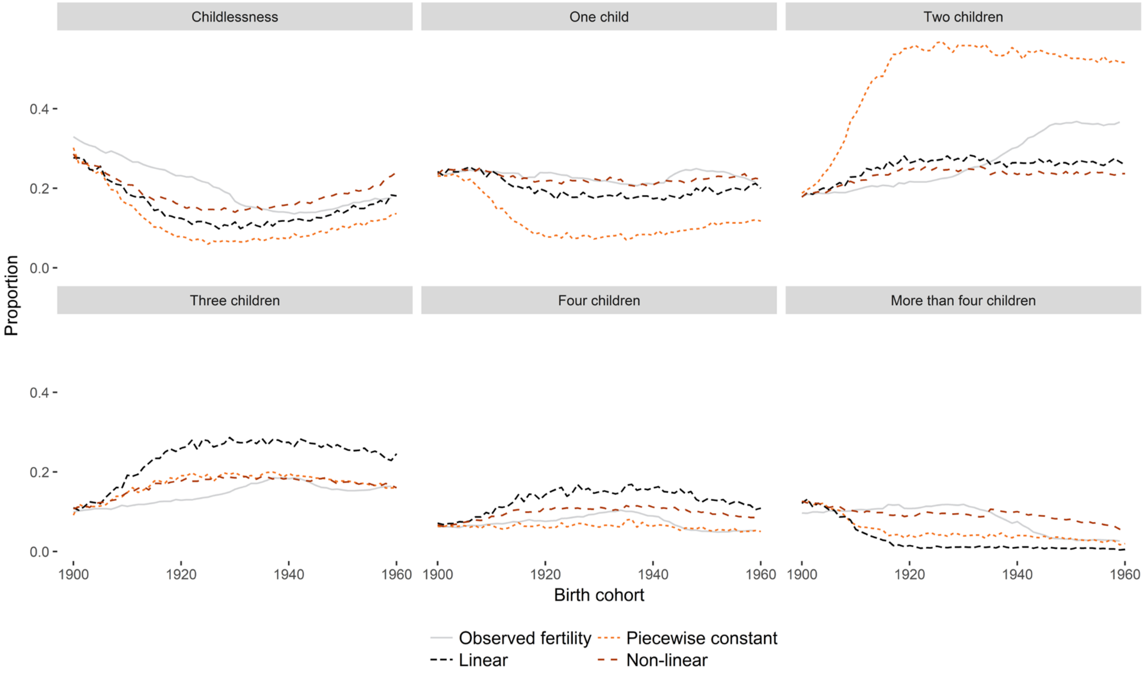
We do not know for sure how adherence to the norm was distributed exactly at the start of our simulations. In the model that underlies the results presented above, we assumed that agents with a high education living in urbanized areas were potential early adopters (we call this Scenario 1 from here on). To assess whether this assumption matters for our argument, we have developed two other scenarios. In the second one (Scenario 2), the share of norm-adherers defined by ε at the start is uniformly distributed over the population. In the third one (Scenario 3), we assume that members of the oldest cohorts (1900-1910) who ended up with two children had already adopted the norm at the start of our simulation. This implies a relatively large number of people who already adhere to the norm from the start of the simulation, ranging from 10% to more than 20% depending on place of residence and educational attainment. Thus, in Scenarios 1 and 2, the proportion of norm-adherers is determined by parameter ε. In Scenario 3, this parameter is dropped, since the proportion is based on actual observed data.

Figure 9 (left panel) shows the simulation result of these alternative scenarios. It is clear that our original model (Scenario 1) performs best in reproducing the observed data. When using a uniform distribution (Scenario 2), the model underestimates the peak in cohort fertility, presumably because it is not so well equipped in dealing with differences between urbanized and rural areas. However, the overall cohort trend and the trend reversal is still there. When using fixed proportions of early norm-adherers based on observed completed fertility (Scenario 3), the model performs considerably worse.

To check whether the model is sensitive to the way we have defined the relation between agents' parity and the birth probability multiplier MP_{n_i,p_i}, we have devised two alternative functions, namely a linear function with a negative slope determined by γ and a piecewise constant function which is equal to γ when the agent's parity is lower than 2 and $1/\gamma$ when it is higher than 2. Note that our linear function is not completely linear, as the birth probability multiplier cannot be smaller than 0. Figure 9 (right panel) shows the result, by which it becomes clear that the exact form of the function does not matter much for the results, and our conclusions hold regardless of which one is used. However, we do find that, even though the overall fertility trend is captured by all functions, the non-linear function as used in our main model is better in reproducing the underlying parity distribution, as Figure 10 shows. The piecewise constant function results in a distribution that is way off the mark, but the non-linear function is also substantively more accurate than the linear function, especially with regards to the higher parities.

Figure 9 *Sensitivity check of starting conditions and the form of the birth probability multiplier function*

Figure 10 *Comparison of the simulated parity distributions by birth cohort for the different forms of the birth probability multiplier function*



7 DISCUSSION AND CONCLUSION

In this paper, we have proposed an agent-based computational model to assess whether the diffusion of a two-child norm might have contributed to shaping the cohort fertility trends observed during the Baby Boom era in Belgium. Our results show that a norm diffusion process based on social influence is able to explain a large part of the observed changes in fertility. To a large extent, the model is able to reproduce observed fertility trends both in provinces which experienced fertility declines and in provinces which experienced fertility increases. Even more, the model is able to partly capture the turnaround in fertility after the Baby Boom, due to the interplay between the decreasing effect of the diffusion of the two-child norm and the gradual shift in the educational distribution. Thus, our model shows that an explanation of the Baby Boom should not only consider individual decision making determining the fertility behaviour of rational actors, but also, and possibly more importantly so, social influence processes in combination with structural changes in the composition of the population. In doing so, this paper moreover adds to growing literature that connects fertility with social networks and social interaction.

In developing our model, we focused on social influence processes that occur in spatially and socially structured networks and that might affect people's fertility behaviour, net of other factors that might impinge on fertility-related decisions. As such, we abstracted from a number of other factors that might have contributed to the Baby Boom. For example, increasing incomes in the 1950s might have broken down barriers to get married and start a family at a relatively young age. By contrast, the rising importance and the associated cost of education might have compelled people to limit their family size to two children. Moreover, these mechanisms might be governed by, or might work through, processes of social influence themselves. If we would include such factors in future work, it would therefore be important to carefully define the actual mechanisms and their interplay with the influence mechanisms that we have considered here.

Furthermore, we make a number of simplifying assumptions that could be relaxed in future research. For example, we do not consider men, who are likely to have an impact on the structure of the social networks of women they partner up with. We also exclude possible selection effects, as people with similar ideational goals with regard to fertility might be more likely to move to certain regions. Yet, two of the arguably most central assumptions are that (1) we impose the two-child norm as an ideal that governs both behaviour concerning starting a family and behaviour concerning family size, and that (2) we assume that birth probabilities of the middle of the 1930s are applicable to the people who do not adhere to this norm for 65 years. Separating the mechanism concerned with transition to parenthood and the mechanism that deals with family size limiting may improve model performance in this regard, but this would come at the cost of a much more complex model. In this paper, we choose to keep the model relatively simple and the way we have defined the relationship between the two-child norm and child-bearing behaviour mirrors the assumption that if the two-child norm is strong, it will strongly affect both starting a family and stopping after two children. This assumption appears plausible, but to date there is little empirical research that directly assesses this relation. Thus, in reality this association may not hold if, for example, stopping after two children is in fact much less affected by the two-child norm than starting a family (Koropeckyj-Cox et al., 2007). The simulated parity distributions show the potential limitations of these assumptions. The model is in fact able to produce the initial increase in three- and four-child families, even though the probability to have a third or a fourth child is decreased, due to the fact that more women have two children and are consequently at risk for having a third child. However, it overestimates those higher parities, at the expense of two-child families. In other words, the model successfully reproduces the increasing number of women who have at least two children, but in our simulations, more women continue to have more children than people did in reality. Part of this can be explained by the absence in our model of a mechanism concerning the introduction of the contraceptive pill, which surely had an impact on the effectiveness of family size limiting starting from the late 1960s.

In this paper, we have furthermore used Belgium as a case study. Belgian census data was used to infuse our model with data on the population distribution and the birth probabilities at the start of the period the model covers. The census data has some important limitations, as it does not allow us to look into characteristics beyond education, such as occupation. The retrospective nature of the data introduces bias due to mortality and we are not able to properly assess migration, which could not only distort our picture of the population in the 1930s, but could in fact be a driving force behind the diffusion process itself. It would be a logical next step to test the model with data from other countries. While many countries have their own particularities in their experience of the Baby Boom, we are confident that the Belgian case is typical enough to allow the model to be easily adapted to other countries, especially other Western European countries, like France, the Netherlands or Sweden (Van Bavel & Reher, 2013). Although the Netherlands, for example, experienced a substantively higher first peak of births and period fertility during the Baby Boom era than Belgium, the cohort trends behind it look very similar to the Belgian ones and this is even more the case for Sweden. However, given that the model is specifically suited to deal with intra-country differences, we believe it is well equipped to handle countries that differ somewhat more from Belgium as well, like the UK, the US or Canada.

Integrating the above factors into our model may yield intriguing new insights that go beyond the ambition of this paper. Nevertheless, despite this need for future research, the results that we have presented here illustrate that the diffusion of a two-child norm could potentially explain a large part of the observed changes in fertility during the Baby Boom era.

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APPENDIX 1: EXPERIMENTAL SCHEDULE FOR THE FULL MODEL

To calibrate the parameters of our simulation model (i.e., to find the parameter combination that maximizes the fit between the simulation outcomes and observed cohort completed fertility rates), we used an optimization method based on a so-called regression metamodel. With this approach, there are three steps in the calibration process. In the first step, a systematic simulation experiment is conducted, in which the simulation model is ran for different combinations of values for its input parameters. In this experiment, both the values of the input parameters and the corresponding outputs are recorded. In the second step, an ordinary least squares regression model is fitted to this data, so that the model outputs are regressed on the corresponding model inputs. In the resulting regression model, it is possible to estimate both the main effect of each input parameter, as well as the effects of possible parameter interactions (e.g., the effect of one parameter might depend on the exact value that is chosen for another parameter in the model) and non-linear effects of the different parameters on the model output. The final regression parameters describe how the output that the model generates changes if one or more of the input parameters change. In the third step, the regression equation is used to analytically find the parameter combination that maximizes the fit between the predicted model outcome and some target value; in our case, this target value is observed completed cohort fertility rates.

One way to design the simulation experiment of the first step of such a calibration exercise would be to use a three-level full factorial design, in which all parameters of the simulation model are varied at three levels orthogonally to each other. This approach is usually not feasible, because it often necessitates running the model for a very large number of unique parameter combinations. For example, in our case, we would have had to run the simulation model for $3^6 = 729$ unique parameter combinations, given that we considered six free model parameters. As an alternative, it is possible to use experimental designs that only use a smaller number of unique parameter combinations, but that still make it possible to estimate an ordinary least squares regression model with interactions and non-linear effects. The most common design to estimate a regression metamodel that considers the main effects of all model parameters, as well as all possible two-way interactions between them and additional quadratic effects of the different parameters, is the central composite design. This design starts from a two-level full factorial design, in which all parameters of the simulation model are varied at two levels orthogonally to each other. To this we then add a number of $2k$ star/axial points that lie somewhat outside the borders of the original two-level factorial design (where k is the number of model parameters), and a small number of center runs (which are located exactly in the middle of the borders of the original two-level factorial) that make it possible to estimate non-linear effects. Here, we used 5 center points. For more details on how to create a central composite design see Grow (2017).

Design Point	α	β	γ	δ	ε	PN_{max}
1	0.5	0.5	1	0.5	0.1	0.5
2	0.323223	0.323223	1.96967	0.323223	0.064645	0.393934
3	0.323223	0.323223	1.96967	0.323223	0.135355	0.393934
4	0.323223	0.323223	1.96967	0.676777	0.064645	0.393934
5	0.323223	0.323223	1.96967	0.676777	0.135355	0.393934
6	0.323223	0.323223	1.96967	0.323223	0.064645	0.606066
7	0.323223	0.323223	1.96967	0.323223	0.135355	0.606066

8	0.323223	0.323223	1.96967	0.676777	0.064645	0.606066
9	0.323223	0.323223	1.96967	0.676777	0.135355	0.606066
10	0.323223	0.676777	1.96967	0.323223	0.064645	0.393934
11	0.323223	0.676777	1.96967	0.323223	0.135355	0.393934
12	0.323223	0.676777	1.96967	0.676777	0.064645	0.393934
13	0.323223	0.676777	1.96967	0.676777	0.135355	0.393934
14	0.323223	0.676777	1.96967	0.323223	0.064645	0.606066
15	0.323223	0.676777	1.96967	0.323223	0.135355	0.606066
16	0.323223	0.676777	1.96967	0.676777	0.064645	0.606066
17	0.323223	0.676777	1.96967	0.676777	0.135355	0.606066
18	0.676777	0.323223	1.96967	0.323223	0.064645	0.393934
19	0.676777	0.323223	1.96967	0.323223	0.135355	0.393934
20	0.676777	0.323223	1.96967	0.676777	0.064645	0.393934
21	0.676777	0.323223	1.96967	0.676777	0.135355	0.393934
22	0.676777	0.323223	1.96967	0.323223	0.064645	0.606066
23	0.676777	0.323223	1.96967	0.323223	0.135355	0.606066
24	0.676777	0.323223	1.96967	0.676777	0.064645	0.606066
25	0.676777	0.323223	1.96967	0.676777	0.135355	0.606066
26	0.676777	0.676777	1.96967	0.323223	0.064645	0.393934
27	0.676777	0.676777	1.96967	0.323223	0.135355	0.393934
28	0.676777	0.676777	1.96967	0.676777	0.064645	0.393934
29	0.676777	0.676777	1.96967	0.676777	0.135355	0.393934
30	0.676777	0.676777	1.96967	0.323223	0.064645	0.606066
31	0.676777	0.676777	1.96967	0.323223	0.135355	0.606066
32	0.676777	0.676777	1.96967	0.676777	0.064645	0.606066
33	0.676777	0.676777	1.96967	0.676777	0.135355	0.606066
34	0	0.5	2.5	0.5	0.1	0.5
35	0.5	0	2.5	0.5	0.1	0.5
36	0.5	0.5	2.5	0.5	0	0.5
37	0.5	0.5	2.5	0	0.1	0.5
38	0.5	0.5	2.5	0.5	0.1	0.5
39	0.5	0.5	2.5	0.5	0.1	0.5
40	0.5	0.5	2.5	0.5	0.1	0.5
41	0.5	0.5	2.5	0.5	0.1	0.5
42	0.5	0.5	2.5	0.5	0.1	0.5
43	0.5	0.5	2.5	1	0.1	0.5
44	0.5	0.5	2.5	0.5	0.1	0.2
45	0.5	1	2.5	0.5	0.1	0.5
46	0.5	0.5	2.5	0.5	0.1	0.8
47	0.5	0.5	2.5	0.5	0.2	0.5
48	1	0.5	2.5	0.5	0.1	0.5

49	0.323223	0.323223	3.03033	0.323223	0.064645	0.393934
50	0.323223	0.323223	3.03033	0.323223	0.135355	0.393934
51	0.323223	0.323223	3.03033	0.676777	0.064645	0.393934
52	0.323223	0.323223	3.03033	0.676777	0.135355	0.393934
53	0.323223	0.323223	3.03033	0.323223	0.064645	0.606066
54	0.323223	0.323223	3.03033	0.323223	0.135355	0.606066
55	0.323223	0.323223	3.03033	0.676777	0.064645	0.606066
56	0.323223	0.323223	3.03033	0.676777	0.135355	0.606066
57	0.323223	0.676777	3.03033	0.323223	0.064645	0.393934
58	0.323223	0.676777	3.03033	0.323223	0.135355	0.393934
59	0.323223	0.676777	3.03033	0.676777	0.064645	0.393934
60	0.323223	0.676777	3.03033	0.676777	0.135355	0.393934
61	0.323223	0.676777	3.03033	0.323223	0.064645	0.606066
62	0.323223	0.676777	3.03033	0.323223	0.135355	0.606066
63	0.323223	0.676777	3.03033	0.676777	0.064645	0.606066
64	0.323223	0.676777	3.03033	0.676777	0.135355	0.606066
65	0.676777	0.323223	3.03033	0.323223	0.064645	0.393934
66	0.676777	0.323223	3.03033	0.323223	0.135355	0.393934
67	0.676777	0.323223	3.03033	0.676777	0.064645	0.393934
68	0.676777	0.323223	3.03033	0.676777	0.135355	0.393934
69	0.676777	0.323223	3.03033	0.323223	0.064645	0.606066
70	0.676777	0.323223	3.03033	0.323223	0.135355	0.606066
71	0.676777	0.323223	3.03033	0.676777	0.064645	0.606066
72	0.676777	0.323223	3.03033	0.676777	0.135355	0.606066
73	0.676777	0.676777	3.03033	0.323223	0.064645	0.393934
74	0.676777	0.676777	3.03033	0.323223	0.135355	0.393934
75	0.676777	0.676777	3.03033	0.676777	0.064645	0.393934
76	0.676777	0.676777	3.03033	0.676777	0.135355	0.393934
77	0.676777	0.676777	3.03033	0.323223	0.064645	0.606066
78	0.676777	0.676777	3.03033	0.323223	0.135355	0.606066
79	0.676777	0.676777	3.03033	0.676777	0.064645	0.606066
80	0.676777	0.676777	3.03033	0.676777	0.135355	0.606066
81	0.5	0.5	4	0.5	0.1	0.5

Inscribed central composite design. Alpha value = 2,828427

APPENDIX 2: PARAMETRIZATIONS OF ALL MODELS

Parameter	Full Model	Scenario 2	Scenario 3	Linear function	Piecewise constant function
α	0.3959	0.6512	0.7120	0.5975	0.4651
β	0.5005	0.3314	0.2298	0.5111	0.4701
γ	1.7761	1.4839	1.2122	1.5723	2.6113
δ	0.4836	0.4587	0.4059	0.5453	0.6105
ε	0.1108	0.1280	-	0.1187	0.1090
PN_{max}	0.4415	0.4306	0.5408	0.4288	0.4999

APPENDIX 3: REGRESSION RESULTS FOR THE FULL MODEL

The regression metamodel that we have fitted to validate the model, has a sufficiently high R^2 of 0.91, with lack of fit being insignificant (Grow, 2017). Parameters β and δ do not have a significant effect on the deviation of the model outcome measure (*DEV*). The other parameters do contribute significantly to the *DEV*. γ and ε have quadratic effects, and γ also has significant interaction effects with ε and PN_{max}.

	Estimate	Std. Error	t value	Pr(>ltl)	
Intercept	92.66	9.27	9.99	0.00	***
α	-17.79	7.18	-2.48	0.02	*
β	-0.72	7.18	-0.10	0.92	
γ	131.38	7.18	18.29	< 2.2e-16	***
δ	-13.33	7.18	-1.86	0.07	.
ε	24.27	7.18	3.38	0.00	**
PN_{max}	59.45	7.18	8.28	0.00	***
α: β	-9.90	22.71	-0.44	0.66	
α: γ	-32.93	22.71	-1.45	0.15	
α: δ	-1.46	22.71	-0.06	0.95	
α: ε	-5.08	22.71	-0.22	0.82	
α: PN_{max}	7.20	22.71	0.32	0.75	
β: γ	5.29	22.71	0.23	0.82	
β: δ	2.09	22.71	0.09	0.93	
β: ε	-2.51	22.71	-0.11	0.91	
β: PN_{max}	-8.33	22.71	-0.37	0.72	
γ: δ	-26.17	22.71	-1.15	0.25	
γ: ε	76.83	22.71	3.38	0.00	**
γ: PN_{max}	129.16	22.71	5.69	0.00	***
δ: ε	-2.72	22.71	-0.12	0.90	
δ: PN_{max}	1.33	22.71	0.06	0.95	
ε: PN_{max}	-5.69	22.71	-0.25	0.80	
$\alpha 2$	-9.18	18.97	-0.48	0.63	

$\beta2$	-36.59	18.97	-1.93	0.06	.
$\gamma2$	126.61	18.97	6.67	0.00	***
$\delta2$	-14.40	18.97	-0.76	0.45	
$\varepsilon2$	48.80	18.97	2.57	0.01	*
$PN_{max}2$	-12.94	18.97	-0.68	0.50	

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1. Multiple R-squared: 0.9115, Adjusted R-squared: 0.8664