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Sociophysics

Models and Aspects of Language Competition

Yiwen Yang

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Supervisor: Dr. Tim Evans

Theoretical Physics Group,
Imperial College London

Abstract

The application of physics had expanded into new territories over the past century, as statistical physics flourished and it became possible to describe a large class of natural phenomena through the study of criticality and phase transitions. It became clear that the approaches from physics may grant quantitative perspectives to research in other scientific disciplines. Existing theories, mathematical tools and analysis techniques from physics lend well to formulate quantitative descriptions of more exotic systems. Such interdisciplinary exchanges continues to deepen our understanding of the natural and human societies. The field of sociophysics received increasing attention over the past few decades. I explain the justifications and relevance of physics behind the conception of the field of study, and examine some models with a focus on language competition models.

Statement of Contribution

I hereby affirm that this thesis has been composed in its entirety from my own work, using my own words. I promise that where necessary, I have cited or given credit to the original authors whose work I have referenced in support to the thesis. Except where explicitly stated, all figures within this work have been produced by myself with the help of standard computing software such as `Mathematica` or `Python`. All computational numerical work were carried out using scripts and programmes that were written independently by myself using standard software packages, and run on my personal laptop.

Yiwen Yang

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1 Introduction

After millennia of development and change in science, physics has concretely established itself as a vital component in our description of the universe. Physics is the fundamental study of the natural world, which means that much of the development of other technical subjects have been inextricably linked to it. This comes naturally as physics is a subject which values quantitative approaches at its core; physics applies analytical methods using the language of mathematics, thereby enabling rigorous and logical statements for theories in technical fields.

Over the past century, interdisciplinary fields at the interface between physics and other subjects have experienced comparable growth to more traditional fields of physics[1]. From traditional intersections such as biophysics and geophysics[2], to the more exotic subjects such as econophysics and sociophysics, which originate in humanity sciences[3], physics as a discipline has transcended its age-old confines of solely dealing with matter and energy. An integral driving force of this development is the advances in computational physics. The availability of computation power and large scale data for research has enabled a vastly different way of studying these high complexity topics[4]. Statistical analysis of data illustrates trends and patterns of many dynamical systems in the real world, which are studied by physicists who construct models to explain these phenomena. The access to computers enables numerical modelling methods for modern sciences in the 21st century, which were not possible for centuries prior.

In this work, we focus on reviewing the field of sociophysics and discuss its philosophical origins, principles, potential, and progress. We examine several language competition models to demonstrate the possibilities of sociophysics and their relevance in understanding the complex dynamics of human societies.

1.1 Origin of Sociophysics

Despite the rapid progress in sociophysics during the recent decades, the study of human societies with the tools of physics and mathematics is not a recent idea. The seeds of sociophysics were sown long before the advent of modern physics. The seventeenth century English philosopher Thomas Hobbes was deeply fascinated with the rationalist process of understanding the world through logic and deduction, an approach to learning and discovery that would soon become a driving force for the Scientific Revolution. In his magnum opus of political philosophy, *Leviathan*, Hobbes constructed a logical argument for why the human system of governance was a natural occurrence arising from human nature and interactions. In his thesis, he compared humans to intricate machines which were complex yet still obey the same laws of motion as any other ordinary object, and thus their dynamics could be studied and predicted using principles similar to those governing mechanical systems. In the titular metaphor, the whole society, the Leviathan, displayed a vastly different behaviour to that of the individual actors, the humans. This idea is similarly recognised in modern physics: in the famous words of theoretical physicist Philip Anderson, "More Is Different"[5]; the dynamics that emerges from a system composed of a large number of interacting bodies is vastly different from the dynamics of the individuals. The work of Hobbes lacked in rigour of its details, as his arguments were not based on any established scientific disciplines, yet his idea of understanding societies via the

actions of its constituents would persevere and become part of the founding principles of sociophysics.

The nineteenth century philosopher Auguste Comte suggested in his book series[6] that human societies could be described and understood through a similar approach to the scientific method, via the cycle of theory and experimental verification. He also valued the idea that quantitative reasoning should be the guide to humanity's decision making processes. Most importantly, he noticed the possibility in establishing the study of human societies as a theory similar to other natural sciences like chemistry and physics. Comte viewed sociophysics (or sociology, as he later renamed the study) as a natural extension of the existing physical sciences. He thought of it as an ultimate theory that stems from the collective knowledge of all other scientific theories describing nature. The nigh impossible complexities of human society, all to be coalesced into one coherent theory.

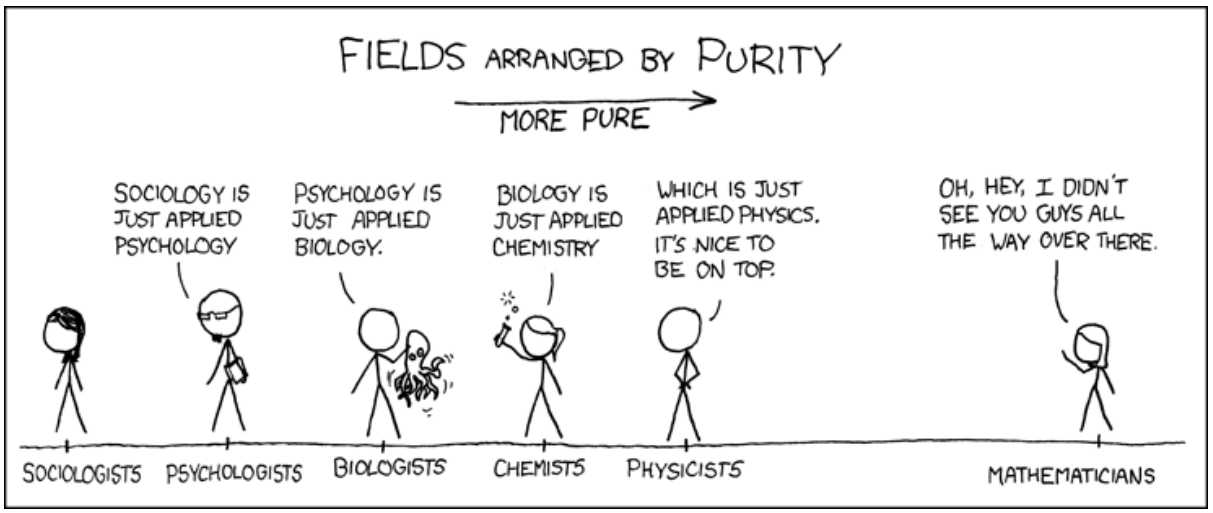


Figure 1: The hierarchy of sciences, not so different to Comte's original vision. Every science is built on top of existing theories of another science. But in reality it is not so compartmentalised, modern science supports exchange of ideas across disciplines. Furthermore, because of the complexities of interacting systems, one could not simply extrapolate the dynamics of a larger scale system from understanding its fundamental constituents. Source: *xkcd comics* `https://xkcd.com/435/`

Perhaps it was this grand ambition of an ultimate theory for societies that caused Comte to disagree with the ideas of his contemporary, Adolphe Quetelet, in developing sociophysics[7]. Quetelet was a statistician who studied, among other things, human populations with statistical methods. While Quetelet conducted his statistical studies, Comte did not believe that the theory of societies could be uncovered by studying statistics alone. Despite Comte's disapproval, statistics would become the basis of modern studies of sociophysics, as they provide the necessary empirical results to verify many theories. Sociophysics theories on the other hand could only reasonably make predictions in a statistical sense. Through statistics the theory-experiment cycle of the scientific method was made possible, and the foundations of sociophysics were laid by the use of statistics over the centuries of sociology studies.

In hindsight it is obvious that statistics plays a key role in describing large scale phenomena such as social behaviours and trends; however, it took significant time before statistics was treated with proper attention as part of a formal theory. A lot of philoso-

phers and physicists at the time, Comte for example, were rather fixated on the idea of determinism in physical laws, which stood unopposed for years. The upheaval of deterministic philosophy arrived with the discovery of quantum effects and the consequent development of quantum mechanics. The foundations of determinism was challenged, and it became apparent that probability and statistics had a vital role in the fundamental laws of nature.

Ettore Majorana noted in an article[8], which was only disclosed after his disappearance, that the laws of physics reformed by quantum mechanics necessitated a probabilistic description down to the irreducible elements. An analogy was drawn between statistical laws of physics and those of social science, where a statistical picture was required due to the inherent complexity of the agents involved. It may not be the direct influence of Majorana, since the article was never published, but certainly the shift in paradigm away from determinism led the scientific community to reevaluate the importance of statistics and probability in modern epistemology. The use of statistics is no longer an admission of the imperfections of human methods of observation and measurement, but rather a tool to describe nature in its fundamental aspect.

Sophisticated modelling attempts began with Serge Galam, one of the influential modern sociophysicists[9]. Galam advocated fervently for the development of interdisciplinary physics when statistical physics and the physics of phase transitions were starting to be understood rigorously. It took a long time before the sociology and physics communities to acknowledge his call, and a major factor was the reluctance of either parties to engage with literature from the other. However, after several publications by Galam and other independent authors, interest in the subject grew throughout the late nineties and at the start of the millennium. Many of the innovative and seminal work within sociophysics were developed during those few decades.

1.2 The Physics Analogy

Incorporation of statistics is essential to the study of human societal patterns and behaviours, but sociophysics is far from the only field where statistics has been extensively put to use. Statistical mechanics is a contemporary field of physics founded on classical thermodynamics, which enables the description of macroscopic properties of substances in terms of the microscopic properties of its constituents. In the famous Maxwell-Boltzmann distribution for the velocities of particles in an ideal gas,

$$f(v)d^3v = \left(\frac{m}{2\pi kT}\right)^{\frac{3}{2}} \exp\Big(-\frac{mv^2}{2kT}\Big)d^3v, \tag{1.1}$$

there is an implicit connection between the microscopic properties of particles, masses m and velocities v, and the macroscopic property, temperature T, of the entire body of gas. This is a celebrated result from classical thermodynamics, and it relies on a statistical description of the system at hand in the form of a probability distribution for properties of its microscopic constituents. The theory of statistical mechanics successfully generalises the translation between micro- and macro-scopic properties for other states of matter, and through later developments, to quantum mechanical descriptions of matter.

This connection between micro- and macro-scopic quantities is exactly what allows fields such as condensed matter physics to flourish, or even be possible to conduct meaningful studies at all. The analogy with social physics is then a natural extension of the

ideas of statistical mechanics: if it is possible to describe properties of interacting systems involving a large number ($\sim 10^{23}$) of particles, then with a proper set of assumptions it should be possible to do the same for human societies. In the analogy, society is the macroscopic system composed of a large number of individual agents that interact via some nontrivial mechanism.

The difference to keep in mind with this analogy is that even though human societies are formed with a much lower number of independent agents compared to e.g. condensed matter systems, as the agents are much more complex fundamentally. It is no longer valid to describe the microscopic properties with only mass and velocity, but other intrinsic properties are also required to model the complex human-human interactions. Unlike in field theory, there are no consensus or mathematical constraints on the precise form of these intrinsic properties. They are model dependent and may be scalars, vectors, matrices, or anything else that could construct a plausible and consistent theory. A key challenge for sociophysics is to identify a suitable form of the intrinsic properties that does not trivialise the underlying complex nature of the agents, yet still admits quantitative analysis.

In essence, sociophysics is the study of mathematical theories that describe the structures and interactions present within human societies, often inspired by underlying analogies with statistical physics. A set of assumptions is often used to simplify the system so the theories can be analysed with a more manageable set of parameters. The information from the theory ultimately condenses into some statistically measurable quantity that can be interpreted in relation to the system of interest within the society.

1.3 Modelling Methods

There are often many ways of approaching the theoretical study of a physical system. Courtesy of the established analytical techniques in physics from centuries of studying the natural world, there are a suite of mathematical tools readily available to sociophysicists.

A natural description of human society is a system which consists of a large number of independent agents that are available to interact with the surrounding environment. As a consequence of the interactions, the agents may attempt to change some aspect of themselves to accommodate their existence within the society. This is quite a reduction of the complex human experience, but an attempt to describe every aspect at once would be an unrealistic endeavour, much like the study of interactions in fundamental physics. Models which directly realise this description are Agent-Based Models (ABM), which are often implemented as numerical simulations with a probabilistic updating rule. The increase in computational power of consumer computers in the recent decades have enabled many opportunities to analyse sociophysics models in this way.

While ABMs reflect the intuitive understanding of societies as a collection of individuals, physicists often prefer models with a more rigorous mathematical framework so more analytical approaches may be taken. Mean field approximations help express ABMs in terms of macroscopic dynamics by taking the average of relevant quantities over all agents; the interactions and evolution of agents are translated to the dynamics of the macroscopic quantities. This is achieved by analysing the model equations directly, approximating a numerical simulation where the number of agents approach infinity, and agents interact with all other agents simultaneously, so any local effects of the model

are averaged out. One could also start directly with a macroscopic dynamics model, which describes macroscopic quantities using a set of differential equations. In this form, the models can be analysed using the approaches in dynamical systems such as stability analysis.

Neither of the models is entirely superior to the other. In macroscopic dynamical models, it is straightforward extract the statistical quantities as they are already explicitly part of the model, and the differential equations allow physicists to use their analytical insight on understanding the dynamics of the systems. On the other hand, ABMs are arguably more accurate to real societies by modelling individuals instead of the system as a whole. Even though the macroscopic model could be thought of as the large N limit of the number of interacting agents, in the limit the two types of models may have different predictions regarding the same systems[10], and it is the sociophysicists' responsibility to assess and reconcile such differences.

1.4 Outline

In this section, we reviewed the historical perspective behind the development of sociophysics and its fundamental principles. We also provided a quick summary for the typical types of models used for systems that sociophysics is interested in. The outline for the rest of the paper is as follows.

In Section 2, we introduce and go through in detail the analysis of a few models that describe language competition, an indispensable part in shaping human societies. In Section 3, we expand one of the analytical macroscopic models by translating it into an ABM and explore some more features of the model that are not readily accessible within the dynamical systems framework. Finally, in Section 4, we will summarise the contents of this essay and provide pointers towards other subject areas available within the vast field of sociophysics.

2 Language Competition Dynamics

A unique feature of human societies is the sophistication in our method of communication, where we can convey complex ideas through languages in writing and in speech. More interesting still, human languages are not static objects; languages that are used within human populations evolve over time. Language evolution takes place at a much faster pace in contrast to biological evolution, albeit still at a longer timescale compared to average human lifetimes[11]. There are clear evidences of language evolution in human literature and written records e.g. Middle English to (Early-)Modern English, and even more recently in the spread of neologisms. To the sociophycisists, there are information readily available to construct and verify models about various features of language evolution.

Much like biological species, languages do not simply coexist within a closed system. The number of speakers of languages grow and wane as the speakers interact within the society. In the contemporary human society, languages are becoming extinct at a rate of about one every forty days, and the rate is expected to continue to accelerate[12]. In the interest of preserving human heritage as well as providing a perfect testing ground for

sociophysical theories, the dynamics of language competition and extinction has been a key interest of study for sociophysicists.

In this chapter we examine two of the influential macroscopic models for describing language competition dynamics, the Abrams-Strogatz model and the Nowak Model. The analysis involved mostly pen and paper work, which altogether were carried out over the course of a few weeks, plus some numerical integration within `Mathematica` where exact results were not possible.

2.1 Abrams-Strogatz Model

A simple nonlinear dynamics model for language competition was formulated by Abrams and Strogatz[13], which described the competition between the populations of speakers of two different languages. The Abrams-Strogatz (AS) model is a macroscopic dynamics model that models the average population as supposed to the individuals within them. This can be seen as a mean field approximation of some microscopic model where any agent can interact with any other agent instantaneously at every timestep, and the number of agents approaches infinity.

The original AS model has two populations that speak two different languages, with population numbers x and y respectively. In the most general form, the dynamics of the two populations is governed by the equations

$$\begin{aligned} \frac{dx}{dt} &= -P_{xy}x + P_{yx}y \\ \frac{dy}{dt} &= P_{xy}x - P_{yx}y, \end{aligned} \tag{2.1}$$

where P_{xy} denotes the probability of the population x to be converted to population y, and analogously from y to x for P_{yx}. Abrams and Strogatz proposed the constraints that $P_{xy}|_{y=0} = P_{yx}|_{x=0} = 0$, based on the idea that no population should be converted to using an extinct language. Additionally P_{xy} and P_{yx} should be a monotonically increasing function of y and x respectively, which is a reasonable assumption considering we do not have any further intuition on how the dynamics should manifest. The AS model chooses, arbitrarily,

$$P_{xy} = s_y y^a \qquad\qquad P_{yx} = s_x x^a, \tag{2.2}$$

where s_y and s_x are arbitrary constants of proportionality, and a is a model parameter that roughly encodes how well a population converts its opposition to their language. To get a better intuition on the parameters at this stage, we require some further assumptions for the AS model.

After substituting Equation 2.2 into the AS model, we reduce the number of parameters by a redefinition $\tau \equiv (s_x + s_y)t$, which changes the time scale but allows us to define a new parameter $s \equiv s_x/(s_x + s_y) \in [0, 1]$, such that the AS model may be rewritten as

$$\begin{aligned} \dot{x} \equiv \frac{dx}{d\tau} &= -(1-s)y^a x + s x^a y \\ \dot{y} \equiv \frac{dy}{d\tau} &= (1-s)y^a x - s x^a y. \end{aligned} \tag{2.3}$$

We note that the two equations sum to zero, so there is always a net zero change in population of the whole system. Therefore it is always possible to rescale the population variables such that $x + y = 1$. The two equations therefore encode exactly the same dynamics, which is governed by the single differential equation

$$\dot{x} = sx^a(1-x) - (1-s)(1-x)^a x. \tag{2.4}$$

Here the parameter s is a measure of the relative status of the language spoken by population x, and likewise $1-s$ for population $y \equiv 1-x$. A higher status parameter favours the conversion from the opposing population to itself and vice versa. The parameter a performs a similar function, but describes more nonlinear tendencies. A larger value of a produces smaller transition probabilities until the population becomes a majority, and a small a produces high transition probabilities except at very low population fractions; the parameter essentially measures how quickly the system goes to a state where one population dominates completely. Sometimes a is called the volatility parameter[14], where counterintuitively a system with large a is less volatile than one with a small a.
Furthermore, there exists a $\mathbb{Z}_2$ symmetry in Equation 2.4 by exchanging $x \leftrightarrow 1-x$ and $s \leftrightarrow 1-s$. This symmetry manifests itself as we find solutions to the system, and may be used as a sanity check.

A limiting case of the AS model is when $a = 1$, then the equations reduce to

$$\dot{x} = (2s-1)x(1-x), \tag{2.5}$$

which is simply the logistics equation that already has a long history associated with population growth with saturation[15]. The logistics equation has already been covered in many literature modelling ecological systems, including in linguistic systems[16], so we do not focus on this limiting case here. On the other hand, $a = 0$ gives an uninteresting linear differential equation and does not contribute much to understanding the dynamical system. Hence we are left with two cases $0 < a < 1$ and $a > 1$, which we now discuss.

2.1.1 Model Analysis

As a standard procedure of analysing nonlinear differential equations, we look at the equilibrium solutions for the equation and their stability. That is, we start by solving for x in the condition

$$\dot{x} = 0 = sx^a(1-x) - (1-s)(1-x)^a x. \tag{2.6}$$

There are two obvious solutions, $x = 0$ and $x = 1$. There is an additional solution $x = x_*$ upon rearrangement, such that it is the solution to the algebraic equation

$$\frac{x_*}{1-x_*} = \left(\frac{1}{s} - 1\right)^{\frac{1}{a-1}}. \tag{2.7}$$

Again, the solutions manifest a $\mathbb{Z}_2$ symmetry where $x = 0$ and $x = 1$ are mapped into each other while $x = x_*$ is invariant.

For linear stability analysis, we linearise the system 2.4 around an equilibrium solution, $x = \bar{x} + \delta\tilde{x}$, where $\delta\tilde{x}$ is an infinitesimal perturbation around the equilibrium. Then

expanding the system to linear order in the perturbation, we find

$$\begin{aligned}
\dot{x} &= s(\bar{x}+\delta\tilde{x})^a(1-\bar{x}-\delta\tilde{x}) - (1-s)(1-\bar{x}-\delta\tilde{x})^a(\bar{x}+\delta\tilde{x}) \\
&= s\bar{x}^a\left(1+a\frac{\delta\tilde{x}}{\bar{x}}+\cdots\right)(1-\bar{x}-\delta\tilde{x}) - (1-s)(1-\bar{x})^a\left(1-a\frac{\delta\tilde{x}}{1-\bar{x}}+\cdots\right)(\bar{x}+\delta\tilde{x}) \\
&\approx s\bar{x}^a(1-\bar{x}) - s\bar{x}^a\left(1-a\frac{1-\bar{x}}{\bar{x}}\right)\delta\tilde{x} - (1-s)(1-\bar{x})^a\bar{x} - (1-s)(1-\bar{x})^a\left(1-a\frac{\bar{x}}{1-\bar{x}}\right)\delta\tilde{x} \\
&= \left[s\bar{x}^a\Big(a\Big(\frac{1}{\bar{x}}-1\Big)-1\Big) + (1-s)(1-\bar{x})^a\Big(a\Big(\frac{1}{1-\bar{x}}-1\Big)-1\Big)\right]\delta\tilde{x}. \qquad (2.8)
\end{aligned}$$

We have used the binomial expansion from the first line to the second, using the assumption that the perturbation is infinitesimal. From the third line to the fourth we used the fact that $\bar{x}$ is an equilibrium solution and obeys 2.6, so the nonperturbative terms vanish. Finally, assume the dynamical behaviour of the perturbation is solely exponential, so the perturbation can be decomposed as $\delta\tilde{x} = e^{\Gamma t}\delta x$, with a characteristic growth rate Γ and a time independent δx. With this ansatz we rearrange the linearised equation into

$$\begin{aligned}
&\left\{\left[s\bar{x}^a\Big(a\Big(\frac{1}{\bar{x}}-1\Big)-1\Big) + (1-s)(1-\bar{x})^a\Big(a\Big(\frac{1}{1-\bar{x}}-1\Big)-1\Big)\right] - \Gamma\right\}e^{\Gamma t}\delta x = 0. \\
&\quad\Longrightarrow\quad \Gamma = \left\{\left[s\bar{x}^a\Big(a\Big(\frac{1}{\bar{x}}-1\Big)-1\Big) + (1-s)(1-\bar{x})^a\Big(a\Big(\frac{1}{1-\bar{x}}-1\Big)-1\Big)\right]. \qquad (2.9)
\end{aligned}$$

The stability of the solution is given by the growth rate $\Gamma = \Gamma(a,s)$. A positive Γ leads to an unstable solution and a negative Γ leads to a stable solution. For the simple $x=0$, $x=1$ solutions it is straight forward to see that

$$\Gamma|_{\bar{x}=1} = \begin{cases} -s, & a>1 \\ \infty, & 0<a<1 \end{cases} \qquad \Gamma|_{\bar{x}=0} = \begin{cases} -(1-s), & a>1 \\ \infty, & 0<a<1 \end{cases} \qquad (2.10)$$

recalling that $s\in[0,1]$, for $a>1$ both $x=0$ and $x=1$ solutions are stable, but become unstable in the regime $0<a<1$.

Next we examine the last equilibrium solution $\bar{x}=x_*$ which satisfies Equation 2.7. Substituting into Equation 2.9 and simplifying yields

$$\begin{aligned}
\Gamma|_{\bar{x}=x_*} &= (1-s)(1-x_*)^a\frac{x_*}{1-x_*}\left[\frac{s}{1-s}\Big(\frac{x_*}{1-x_*}\Big)^{a-1}\left(a\left(\frac{1}{x_*}-1\right)-1\right)\right. \\
&\qquad\qquad \left. + \frac{1-x_*}{x_*}\left(a\left(\frac{1}{1-x_*}-1\right)-1\right)\right] \\
&= (1-s)(1-x_*)^{a-1}\big[a(1-x_*) - x_* + a(1-(1-x_*)) - (1-x_*)\big] \\
&= (1-s)(1-x_*)^{a-1}(a-1), \qquad (2.11)
\end{aligned}$$

where from the first to second line we used Equation 2.7.
The first two factors in $\Gamma|_{\bar{x}=x_*}$ are both positive definite, so the stability of the system depends solely on the $a-1$ factor. Hence, the equilibrium behaves as

$$\Gamma|_{\bar{x}=x_*}\begin{cases} >0, & a>1 \quad \text{unstable} \\ <0, & 0<a<1 \quad \text{stable} \end{cases} \qquad (2.12)$$

There are two different regimes of stability to consider. For a low volatility system with $a > 1$, the only stable equilibrium solutions are at $\bar{x} = 1$ and $\bar{x} = 0$. Therefore the system will almost always tend to a state where one population ends up extinct, except for the edge case where the system starts exactly on the unstable equilibrium with no further perturbations. For a high volatility system with $0 < a < 1$ the stability switches for the equilibrium solutions, and only the x_* equilibrium is stable. In this regime the system tends towards a coexistence state with both populations occupying a nonzero fraction of the total population, with the exact fractions dependent on the model parameters a and s.

The AS model equations can be integrated directly with the help of `Mathematica`, which we use to confirm our equilibrium and stability analysis results. This involves about an afternoon of work, where I got `Mathematica` to numerically solve the model equations with an array of initial conditions and a range of model parameters. Figure 2 shows the trajectories of population x for a select number of parameter values and a range of initial conditions. The coexistence equilibrium x_* is marked for checking against analytical results. It is straight forward to verify that $x_* = 0.5$ for $s = 0.5$ in Equation 2.7, and is otherwise dependent on the value of parameter a. We see that the coexistence equilibrium is unstable for $a = 1.3 > 1$, but becomes stable and attractive for $a = 0.7 < 1$.

2.1.2 Further Discussion

Abrams and Strogatz fitted the model by regression to some real world data on the decline of minority language populations. They found a roughly constant $a = 1.31 \pm 0.25$ across different samples[13], but a more recent analysis puts tension on their estimated values and suggests new values that have drastically different qualitative behaviour[11]. In addition, the parameter a is a dimensionless mathematical model parameter and is difficult to determine outside of empirical methods. We should note the model is supposed to be minimal and unavoidably has some problems when it comes to modelling real world systems. There are no mechanisms in the AS model to implement the existence of bilingual populations in the system, which certainly exist in the real world.

There have been many extensions to the AS model. The Minett-Wang (MW) model[17] incorporates a bilingual population, which serves as a buffer with different transition rates to and from the monolingual populations. This leads to possible asymmetric behaviour, in contrast to the AS model which is fully symmetric between the two populations. The problem with the MW model is the fact that there are no stable equilibrium states with any bilingual population, and all individuals end up as monolinguals, which is inconsistent with observations.
The Mira-Paredes model[18] is a similar extension to the AS model which includes some degree of mutual intelligibility between the monolingual populations in addition to a bilingual population, resulting in stable equilibria with nonzero bilingual populations. The model is fitted to historical data for Hispanic languages in Galicia. The problem with this model is that mutual intelligibility between populations may not always be assumed, and the stable bilingual population configuration is specific to languages with a high degree of mutual intelligibility.

There are also a number of agent-based models inspired by the AS model. These models typically result in more varied dynamical behaviours than the more deterministic AS model. Reviews and examples of agent-based language competition models can be

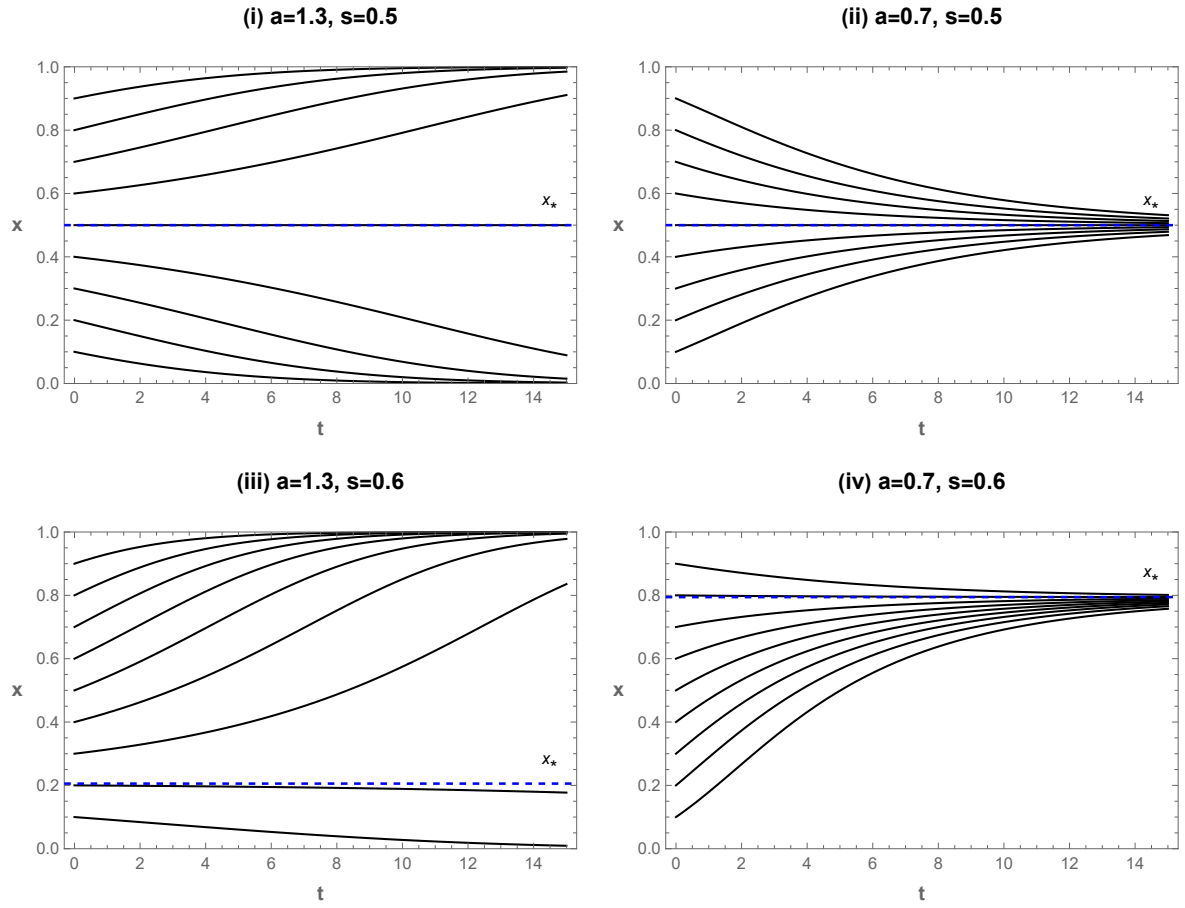


Figure 2: Solutions to the AS model equations for selected parameter values. The coexistence equilibrium solution x_* is denoted by a dashed blue line. The initial values are chosen to be $x = 0.1$ to $x = 0.9$, equally spaced. For (i) and (iii) with $a > 1$, the coexistence equilibrium is unstable and the system moves away from it to $x = 1$ or $x = 0$ depending on the initial conditions. For (ii) and (iv) the coexistence equilibrium is stable and attracts all initial states of the system. For $a > 1$, the coexistence equilibrium position decreases with an increase in s but for $0 < a < 1$ the coexistence equilibrium increases instead with an increase in s.

found in various literature[2,17,19]. We cover in detail one implementation of the microscopic AS model in Section 3

2.2 Evolutionary Dynamics Model

A key feature of languages in the real world that we would like to model is the coexistence of multiple languages over long timescales, without the inevitable extinction of all but one dominant language. An alternative model for language competition in which this arises naturally is the evolutionary dynamics model created by Nowak and collaborators around the 2000s[20]. One application of Nowak's model was to determine evolutionary properties of different language learning strategies and the mechanism of language acquisition, and how one coherent language emerges within a population from a constrained set of possible grammars[21]. This model, however, is quite general and also provides an apt description for competing language variations and their dynamical behaviours.

The principle of evolutionary dynamics is to incorporate the mechanism of Darwinian evolution, i.e. survival of the fittest, into the dynamical behaviour of the model. Development in areas of mathematics such as evolutionary game theory have led great progress in formulating a rigorous theory of evolutionary dynamics. The theory has seen applications from population genetics to social dynamics and medicine. A detailed account of the theory and its applications can be found in Nowak's review[22].

The general principle of evolutionary dynamics is as follows. The system is divided into several populations, whereby some interaction mechanism dictates the fitness of a population. The reproductive success of a population is then proportional to the fitness. This generates equations of motion that describe how populations evolve depending on model parameters and initial conditions. The key point is that since the mathematical theory is agnostic to the exact physical manifestation of the populations it is describing, it can be applied to e.g. human and bacteria populations alike. It is applicable even to more abstract populations with variation in traits such as natural languages, which we will discuss in this section.

The model equations were provided by Nowak et al. in their original paper, as well as a few of the key equations we provide here; however, the exact derivation of the equations were not provided in detail in the paper and required thorough working with the model equations. The analytical on paper and numerical work from `Mathematica` were done and checked over a week. The exact formulation of the model has also been modified by myself to better suit the thesis.

2.2.1 Model Equations

We consider a language with a discrete set of possible languages $L_1, \ldots, L_n$ and correspondingly a population divided into n subpopulations $x_i, i = 1, \ldots, n$, such that the population x_i uses the language L_i. We do not consider here the existence of bilingual populations. Note that there are different ways to define what a language is in term of this model. Nowak's original paper[20] described a language L_i as one possible set of associations between a list of objects and a list of words explicitly constructed in the form of matrices. Here, however, we take the approach from a later paper[23]. We do not care how the L_i manifest themselves, except that there is an $n \times n$ compatibility matrix A_{ij} such that the probability that a sentence from speaker of L_i can be understood by a speaker of L_j. From this definition it is reasonable to assume that $A_{ii} = 1$ and $0 \leq A_{ij} < 1$. Note that in general we can have $A_{ij} \neq A_{ji}$ asymmetric, and there is no further restrictions on the form of the compatibility matrix. This means the model has a huge number of degrees of freedom in parameter space, which is why the model in this form is impractical for analytical approaches.

The payoff function $F(L_i, L_j) \equiv \frac{1}{2}(A_{ij} + A_{ji})$, which can be interpreted as the average success in communication between languages L_i and L_j, is used to define the fitness of a population:

$$f_i = \sum_j x_j F(L_j, L_i). \tag{2.13}$$

The fitness f_i is a measure for the reproductive success of the population x_i.

In the reproduction process, we introduce the inheritance matrix Q_{ij} that quantifies the accuracy at which a language is learned when passing down to the next generation.

Q_{ij} denotes the probability that a child of L_i speakers learns by mistake the language L_j. Recall that a language in this case delimits minor differences in expression that might cause difficulties in communication. In reality this learning mistake may correspond to, for example, minor pronunciation differences in words. Finally, by definition Q_{ij} is (the transpose of) a stochastic matrix, since any child should learn one of the languages in the complete set L_i; the inheritance matrix satisfies $\sum_j Q_{ij} = 1$. Similarly, there are no further inherent restrictions on the form of Q_{ij} so there remains a huge degree of freedom in the parameter space.

Before we motivate the dynamical equations for the model, we impose a few more constraints on the population, to make the model more analytically tractable:

(P1) The subpopulation variables can always be normalised by the total population, so we define them as proportions of population, $\sum_i x_i = 1$.
(P2) The total population over time is assumed to be constant, $\sum_i \dot{x}_i = 0$, where the dot denotes time derivative.

Thus the dynamical equations for the population can be written down as

$$\dot{x}_i = \sum_j x_j f_j Q_{ji} - \phi x_i. \tag{2.14}$$

where $\phi \equiv \sum_i f_i x_i$ is the expectation value of fitness across the entire population. The purpose of the second term is to impose condition 2 from above:

$$\begin{aligned} \sum_i \dot{x}_i &= \sum_j x_j f_j \sum_i Q_{ji} - \phi \sum_i x_i \\ &= \sum_j x_j f_j - \phi = 0, \end{aligned} \tag{2.15}$$

where we have used the fact that Q_{ij} is stochastic and condition (P1). These equations describe the macroscopic evolution of the population proportions, with no reference to the exact form of interaction between individuals speaking different languages.

This is a set of n coupled first order nonlinear differential equations, where the nonlinearity is hidden in the variables f_i and ϕ. It is difficult to solve this equation analytically, and some numerical results were presented by Nowak et al. in their foundational paper of the model[20]. For any useful analytical results to be obtained, a few more assumptions are required.

2.2.2 Symmetric Nowak Model

In literatures that study this system of equations, a common approach is to assume some degree of symmetry in the parameters of the system and exploit that symmetry to arrive at some analytical solution[24,21]. Here we demonstrate how that approach simplifies our dynamical system.

Consider the case $A_{ij} = a, \forall i \neq j$ so all off-diagonal elements of A_{ij} are equal to some constant, while $A_{ii} = 1$ is still true for all diagonal elements. Hence we can write

elementwise $A_{ij} = \delta_{ij}(1-a) + a$, where δ_{ij} is the Kronecker delta function. Then fitness function for the subpopulation x_i becomes

$$\begin{aligned} f_i &= \frac{1}{2}\sum_j (A_{ij} + A_{ji})x_j = \sum_j A_{ij}x_j \\ &= \sum_j (\delta_{ij}(1-a) + a)x_j = (1-a)x_i + a\sum_j x_j \\ &= (1-a)x_i + a, \end{aligned} \tag{2.16}$$

where in the last step we used condition (P1). Next consider a similar condition for the inheritance matrix, $Q_{ii} = q, Q_{ij} = \frac{1}{n-1}(1-q) \equiv u, \forall j \neq i$. The form of the off diagonal elements is restricted by the stochastic property of Q. These two assumptions on the comprehension and inheritance matrices drastically reduce the complexity of the dynamics, since now only 2 parameters a and q are required to specify the model.

One could interpret these assumptions as introducing a permutation symmetry S_n into the system, where now we describe n equivalent languages in competition with each other. Without *a priori* knowledge on the specifics of the languages, it is reasonable to assume that no languages is inherently different from others.

To proceed, the equations of motion may be simplified with these assumptions:

$$\begin{aligned} \dot{x}_i &= \sum_j x_j f_j Q_{ji} - \phi x_i \\ &= (f_i Q_{ii} - \phi)x_i + \sum_{j\neq i} x_j f_j Q_{ji} \\ &= \big[((1-a)x_i + a)q - \sum_j x_j((1-a)x_j + a)\big]x_i + \sum_{j\neq i} x_j((1-a)x_j + a)u \\ &= (1-a)qx_i^2 + aqx_i - (1-a)\big(x_i^3 - \sum_{j\neq i} x_j^2 x_i\big) - ax_i + (1-a)u\sum_{j\neq i} x_j^2 + au(1-x_i) \\ &= (1-a)\big[-x_i^3 + qx_i^2 + \sum_{j\neq i} x_j^2(u - x_i)\big] - au(nx_i - 1), \end{aligned} \tag{2.17}$$

where going to the fourth line we used the relation $\sum_{j\neq i} x_j = 1 - x_i$ from (P1); going to the fifth line we used $1 - q = (n-1)u$. The nonlinearity of the dynamics is explicit in this new form of the equations.

2.2.3 Equilibrium Solutions

One typical approach for this type of equation is to find equilibrium solutions of the system to learn about the behaviour of fixed points. An equilibrium solution is a point in configuration space $p \in \mathbb{R}^n$ where $\dot{x}_i = 0$. There are different families of solutions, each corresponding to a number of dominant populations with the rest present as minority populations[24]. Detailed analysis of the possibilities becomes quite involved so here we proceed using an ansatz with only 1 dominant population.

From the symmetry of the original system, assume that after choosing a dominant population there will still be an unbroken permutation symmetry among the minority

populations, which have identical dynamics. Because of the S_n symmetry assume, without loss of generality, that the equilibrium solution takes the form

$$x_1 = X, \qquad x_j = \frac{1-X}{n-1}, j = 2, \ldots, n. \tag{2.18}$$

Substituting the ansatz into Equation 2.17 yields n equations for X. But $n-1$ of those equations are redundant since condition (P2) implies $\dot{x}_1 = -\sum_{j=2}^{n} \dot{x}_j$. Our ansatz had the minority populations obeying the same dynamics, so if the LHS is zero then all $n-1$ other equations are trivially satisfied. Thus it is sufficient to find the equilibrium solution for x_1 alone. To do so, we solve the equation

$$-X^3 + qX^2 + \frac{(1-X)^2}{n-1}\left(\frac{1-q}{n-1} - X\right) - \frac{a(1-q)(nX-1)}{(1-a)(n-1)} = 0. \tag{2.19}$$

This is an algebraic equation for X which can be solved straightforwardly with computer algebra packages such as `Mathematica`. There are three solutions for the cubic equation,

$$X_0 = \frac{1}{n}, \tag{2.20}$$

$$X_\pm = \frac{1}{2(n-1)}\big((1+(n-2)q) \pm \sqrt{D}\big), \tag{2.21}$$

where

$$D = (1+(n-2)q)^2 - \frac{4(1+a(n-2))(n-1)(1-q)}{(1-a)}. \tag{2.22}$$

The symmetric equilibrium solution X_0 corresponds to the state where all subpopulations are equal in proportion and there is no dominant population. This solution is independent of a and q, therefore it exists for all model parameters. From the symmetry of the equations of motion, it is not surprising that such a solution exists.

The asymmetric equilibrium solutions are much more interesting. In the absence of any inheritance inaccuracies, $q = 1$, the solutions are $X_+ = 1$ and $X_- = 0$. The former solution corresponds to a state where there is only one surviving population, and all minority languages have gone extinct. This is similar to the default equilibrium state for the AS models. The latter solution corresponds to the disappearance of one population and a symmetric configuration for the rest. This solution will be shown later to be unstable.

In order for the asymmetric solution to exist, we require the equilibrium population $X_\pm$ to be real. This imposes the condition $D \geq 0$ which can be solved for conditions on q or a. Figure 3 shows the behaviour of D across a range of model parameters. In general for a fixed a solutions exist only above a certain value of $q = q_*$, at which point there actually exists a bifurcation. A quick calculation of $\frac{dD}{dq}$ shows that D is a monotonically increasing function of q, which means the equilibrium points $X_\pm$ grow increasingly distant as q increases.

Some further analytical results could be obtained by looking at the system in the large $n \gg 1/a \approx 1/q$ limit. In this limit 2.21 becomes

$$\begin{aligned} X_\pm &\to \frac{1}{2n}\left(nq \pm \sqrt{(nq)^2 - \frac{4an^2(1-q)}{1-a}}\right) \\ &= \frac{q}{2}\left(1 \pm \sqrt{1 - \frac{4a}{1-a}\frac{1-q}{q^2}}\right). \end{aligned} \tag{2.23}$$

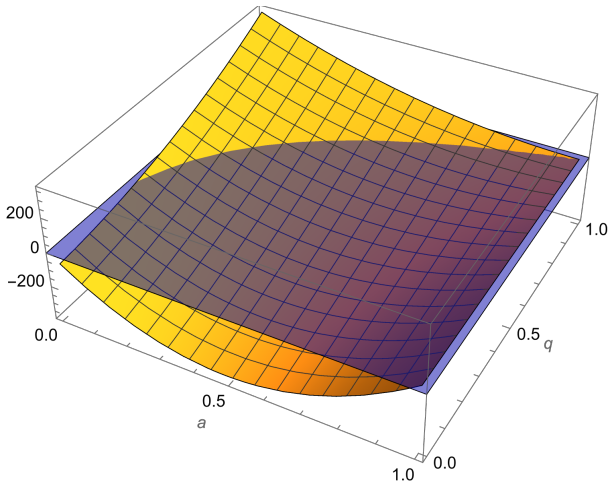


Figure 3: Plot of values of D with $n = 20$ for $0 \leq a \leq 1$ and $0 \leq q \leq 1$. The surface $D = 0$ is marked in blue. D is a monotonically in q but has a more complicated form in a, going from quadratic for low q to monotonically decreasing for large q. Real equilibrium solutions for the system in Equation 2.17 only exist for $D \geq 0$.

An approximate value for q_* can be solved for in this regime

$$1 - \frac{4a}{1-a}\frac{1-q_*}{q_*^2} = 0$$
$$\implies q_* = 2\frac{\sqrt{a}}{\sqrt{a}+1}, \tag{2.24}$$

which approaches 1 as $a \to 1$, as illustrated in Figure 3. In this limit neither the equilibrium population nor the critical q_* depend on the model parameter n.

2.2.4 Stability Analysis

The existence of multiple equilibrium solutions for certain parts of the parameter space suggests looking at the stability of these solutions to better understand the dynamics. A standard way to approach stability analysis for nonlinear systems is to linearise the system near the equilibrium solutions and analyse the linear system instead[23].

Expand around the solutions with

$$x_1 = X + \tilde{y}_1 \qquad\qquad x_j = \frac{1-X}{n-1} + \tilde{y}_j,\ j = 2, \ldots, n. \tag{2.25}$$

Substitute this expansion into Equation 2.17 and ignoring terms quadratic and above in $\tilde{y}_i$ yields, for the first equation,

$$\dot{x}_1 = (1-a)\left[-3X^3\tilde{y}_1 + 2qX\tilde{y}_1 - \frac{(1-X)^2}{n-1}\tilde{y}_1 + 2\frac{1-X}{n-1}(u-X)\sum_{j>1}\tilde{y}_j \right] - aun\tilde{y}_1, \tag{2.26}$$

where we have used the fact that X is a solution of the equilibrium system and satisfies Equation 2.19 to eliminate the constant terms. Next assume that the only time dependence of the perturbations $\tilde{y}_i$ around the equilibrium are exponential, $\tilde{y}_i = e^{\Gamma t}y_i$, where

Γ is the growth rate of the perturbation and y_i now time independent initial conditions for the linearised system. Then with some rearrangement the linearised equation can be written as

$$\alpha y_1 + \beta \sum_{j>1} y_j = 0, \tag{2.27}$$

where

$$\alpha = 3X^3 - 2qX + \frac{(1-X)^2}{n-1} + \frac{\Gamma}{1-a} + \frac{a(1-q)n}{(1-a)(n-1)}, \quad \beta = 2\frac{(1-X)(X-u)}{n-1}.$$

A similar albeit longer calculation for the other equations yields

$$\gamma y_j + \delta \sum_{\substack{l \neq j \\ l>1}} y_l + \varepsilon y_1 = 0, \tag{2.28}$$

where $j = 2, \ldots, n$ for a total of $n-1$ equations, and coefficients are defined as

$$\gamma = \frac{\Gamma}{1-a} + (n+1)\Big(\frac{1-X}{n-1}\Big)^2 + X^2 - 2q\frac{1-X}{n-1} + \frac{a(1-q)n}{(1-a)(n-1)},$$
$$\delta = 2\frac{(q-X)(1-X)}{(n-1)^2}, \quad \varepsilon = 2X\frac{q-X}{n-1}.$$

These equations can be further simplified using condition (P2), since $\sum_i \dot{x}_i = \Gamma e^{\Gamma t} \sum_i y_i = 0 \implies \sum_i y_i = 0$ if we assume $\Gamma \neq 0$. This gives a useful relation $y_1 = -\sum_{j>1} y_j$. Therefore the linearised system of equations can be written as, from Equation 2.27,

$$(\beta - \alpha) \sum_{j>1} y_j = 0, \tag{2.29}$$

and from Equation 2.28,

$$\gamma y_j - \delta y_j + \delta y_j + \delta \sum_{\substack{l \neq j \\ l>1}} y_l - \varepsilon \sum_{l>1} y_l = 0,$$
$$\implies (\gamma - \delta) y_j + (\delta - \varepsilon) \sum_{l>1} y_l = 0. \tag{2.30}$$

This is now a system linear of equations for perturbations around equilibrium solutions, and can be written in the form of a matrix acting on the vector of perturbations

$$\begin{pmatrix} \beta-\alpha & \ldots & \ldots & \ldots & \beta-\alpha \\ \gamma-\varepsilon & \delta-\varepsilon & \ldots & \ldots & \delta-\varepsilon \\ \delta-\varepsilon & \gamma-\varepsilon & \delta-\varepsilon & \ldots & \delta-\varepsilon \\ \vdots & & \ddots & & \vdots \\ \vdots & & & \ddots & \vdots \\ \delta-\varepsilon & \ldots & \ldots & \delta-\varepsilon & \gamma-\varepsilon \end{pmatrix} \begin{pmatrix} y_2 \\ \vdots \\ \vdots \\ \vdots \\ y_n \end{pmatrix} = \mathbf{0}. \tag{2.31}$$

The matrix, however, is not fully linearly independent. The first row is proportional to the sum of the other $n-1$ rows and hence may be ignored in the analysis of this set of linear equations.

Define $\mathbf{J}$ to be the matrix in Equation 2.31 with first row removed. For any nontrivial solution of these equations to exist (i.e. where $y_i \neq \mathbf{0}$), there must exist an eigenspace with eigenvalue $\lambda_i = 0$. By symmetry of the form of $\mathbf{J}$, the eigenvectors can be easily obtained. One eigenvector is $v_1 = (1, \ldots, 1)^T$, which corresponds to eigenvalue

$$\lambda_1 = (\gamma - \varepsilon) + (n-2)(\delta - \varepsilon).$$

The other eigenvectors need be orthogonal to v_1. One possible choice of basis is to have $(1, 0, \ldots, 0, -1, 0, \ldots, 0)^T$, for -1 occurring in the k th row, giving a total of $n-2$ eigenvectors. This gives an $n-2$ fold degenerate eigenspace with eigenvalue

$$\lambda_2 = \gamma - \delta.$$

The stability of solutions can be determined by substituting in Equations 2.20 and 2.21, then solving $\lambda_1 = 0$ and $\lambda_2 = 0$ for Γ. By definition, $\Gamma > 0$ corresponds to an unstable equilibrium while $\Gamma < 0$ corresponds to a stable one.

For the fully symmetric solution $X_0 = 1/n$ this gives

$$\begin{aligned} 0 = \gamma - \delta &= \frac{\Gamma}{1-a} + \frac{n+2}{n^2} - \frac{2q}{n} + \frac{a(1-q)n}{(1-a)(n-1)} - 2\frac{nq-1}{n^2(n-1)} \\ \implies \Gamma &= \frac{1}{n(n-1)}\big[(n(2q-1)-1)(1-a) - a(1-q)n^2\big]. \end{aligned} \tag{2.32}$$

The other condition $\lambda_1 = 0$ gives the exact same result for Γ, which was confirmed in `Mathematica` by solving the algebraic equation for Γ.
Out of the parameters of the system, the self-inheritance accuracy q is the most relevant for understanding useful dynamics, since it is the parameter that can change over time as a result of social factors; a and n are both intrinsic properties of the languages in the model and should not vary much over time because the evolution of languages themselves are not taken into account.
Γ is linear in q, so simply solve $\Gamma < 0$ for q to find the region in parameter space which give stable equilibria, which yields

$$q < \frac{(1-a)(n+1) + an^2}{2n(1-a) + an^2} \equiv q_0. \tag{2.33}$$

Furthermore, substituting $q = q_0$ into Equation 2.21 we find $X_-|_{q=q_0} = 1/n$. So in fact the fully symmetric equilibrium solution becomes unstable at its intersection with the negative branch of the asymmetric solution.

The same approach could be applied to the asymmetric solutions, but the expression becomes too unwieldy to be written down concisely. Going through the algebra is not particularly enlightening, so again we consult `Mathematica` for the algebra and study the properties of our system graphically. The basic procedure remain the same, except the asymmetric solution is substituted into the conditions $\lambda_1 = 0$ and $\lambda_2 = 0$ then solved for Γ
Figure 4 shows the behaviour of the growth rate Γ of the perturbations. Two differently coloured curves correspond to the Γ for different eigenvectors. There are no asymmetric solutions below $q = q_*$, as expected. The X_+ solutions (solid lines) always have $\Gamma < 0$ and are thus always stable, because all decays will die off exponentially over a characteristic time scale $1/\Gamma$.

The X_- solutions start with one eigenvector unstable and the other stable, but they cross over at $q = q_0$ where the unstable eigenvector becomes stable and vice versa. This means that the negative branch of the asymmetric solution will always be unstable, since in any equilibrium state there will be at least one eigenvector whose perturbations grow exponentially and moves the populations away from the equilibrium state.

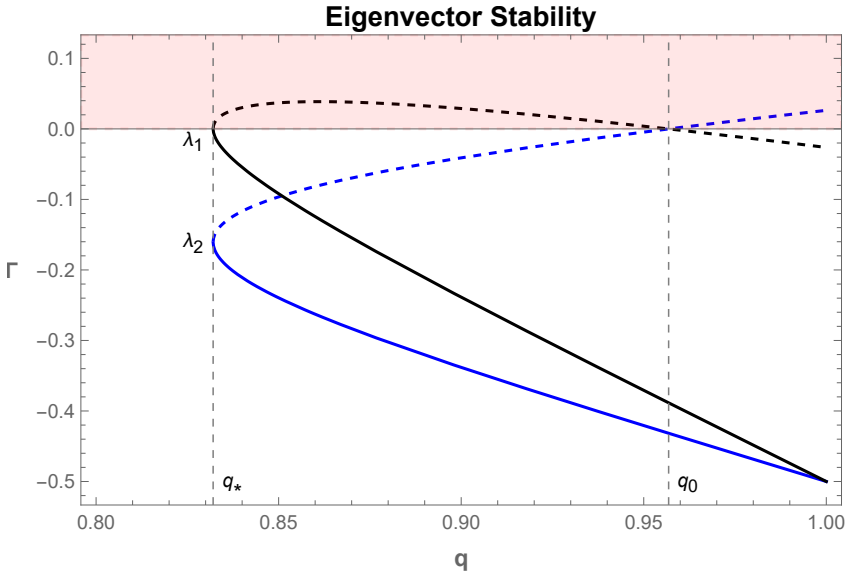


Figure 4: Plot of the growth rate Γ of the perturbations against values of the self-inheritance accuracy parameter q. Parameters used for the plot are $a = 0.5$ and $n = 20$. The solid lines are obtained from X_+ solutions and dashed lines from X_- solutions. The black curve shows Γ for the eigenvector with eigenvalue λ_1 and the blue curve for eigenvectors with eigenvalue λ_2. The red shaded region denotes where $\Gamma > 0$ and hence where perturbations become unstable. The special values q_*, where the asymmetric solutions begin to exist, and q_0, where the asymmetric solution X_- intersects the symmetric solution X_0, are also marked on the plot.

2.2.5 Further Discussion

The dependence of the equilibrium populations on q is shown in Figure 5, taking into account the stability of the solutions as discussed in the previous section. The asymmetric equilibrium X_- equilibrium is always unstable, and the X_+ equilibrium is always stable. The symmetric equilibrium X_0 crosses over from stable to unstable at the intersection $q = q_0$ with the X_- branch. The figures have been given for a specific set of model parameters, but the general trend and features of the equilibrium solutions do not change with values of $0 \leq a < 1$ and $n > 2$.
This particular analysis of the model relies upon the symmetry of the comprehension and inheritance matrices A and Q to make simplifying assumptions. Therefore, there will be other equilibrium solutions for asymmetric configurations of model parameters which have been ignored for this discussion, but more details can be found in the references provided within this section. Here we will assume that the parameters stay in the symmetric Nowak model regime, to a good approximation.

The general behaviour is that below a critical $q < q_*$, there is only one stable equilibrium solution and any initial value of populations x_i will settle down to the fully symmetric

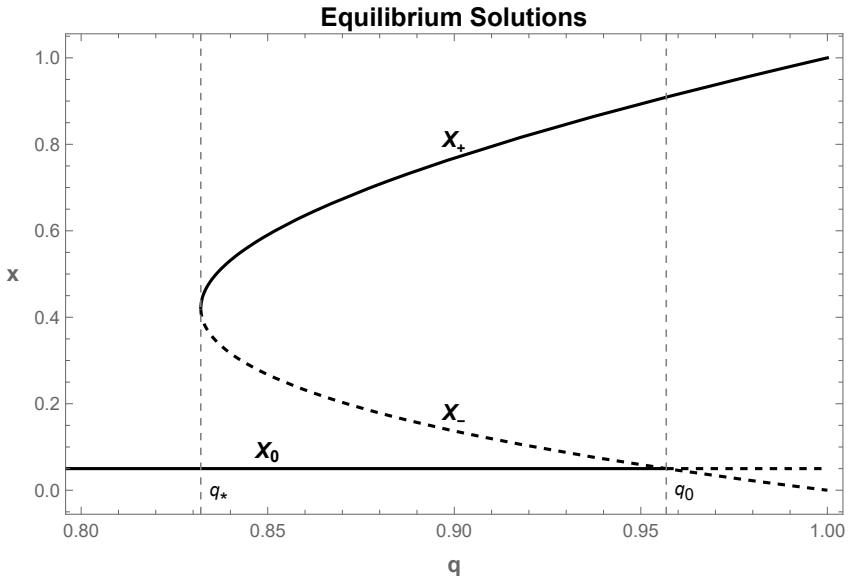


Figure 5: Plot of the equilibrium solutions of the original system in Equation 2.14. Parameters are $a = 0.5$ and $n = 20$. The equilibrium population x is plotted against the self-inheritance accuracy parameter q. X_0 is the fully symmetric equilibrium where all populations share the same proportion of the total population. $X_\pm$ are the asymmetric equilibria where there is one dominant population with proportion x. The dashed lines denote unstable solutions, as determined within this section. Special values q_* and q_0 are marked on the plot. The solid line of the X_0 solution extends all the way down to $q = 0$, which is not shown in order to highlight the more interesting behaviour at large q.

solution $x_i = 1/n,\ \forall i = 1, \ldots, n$. For the region $q_* \leq q < q_0$ there exist two stable equilibrium states, X_+ and X_0. The state in which the system ends up depends on the initial conditions. From the stability analysis prior, there are two types of eigenvectors for perturbations on the X_- equilibrium solution. The eigenvector $v_1 = (1, \ldots, 1)^T$ corresponds to the eigenvalue λ_1 and is unstable for $q_* \leq q < q_0$. Recall that for any perturbation vector we assume the total population stays constant, so implicitly x_1, the dominant population, experiences unstable perturbations on the X_- branch. It either grows towards the majority-minority equilibrium or the symmetric equilibrium. The other eigenvectors v_2 as given prior are stable within this parameter range, for perturbations that are essentially reshuffling of populations within the minority groups.

As the parameter grows to $q \geq q_0$, the X_0 equilibrium loses stability and the two eigenvectors for the X_- branch switch roles; however, in this regime the X_- solution implies that the assumed dominant population is proportionately less than the other populations. In this case the solution no longer has a valid physical interpretation and we assume that the system never ends up in this state. Then the system essentially has one stable equilibrium at the X_+ solution in this regime.

The equilibrium analysis gives us some insight into the qualitative behaviour of the system. From an assumption of a symmetric set of parameters, the model exhibits a sort of phase transition behaviour starting at $q = q_*$ that takes the system from a disordered state with n languages (speakers) in equal proportions to a more ordered state with a single dominant language. Importantly the dominance of one language does not necessarily lead to the extinction of all other languages, and for most values of the inheritance accuracy

parameter q the equilibrium state has a non-zero population for the minorities.

Note that in our analysis we assume without loss of generality that one particular population x_1 ends up as the dominant one, but due to symmetry the same solution exists for any of the other populations. Therefore there are in fact n equivalent equilibrium states with a dominant language, and which one the system ends up in depends on the initial conditions.

In the Nowak model that we have presented in this section, the emergence of language is explained as a natural result of evolutionary dynamics. In particular, languages and their interactions are modelled akin to biological species, which evolve by natural selection subject to a fitness parameter. With a quantitative mathematical model we are able to study the evolution and competition within systems consisting of multiple languages. From studying the equilibria of the dynamical model equations and their stability, we gain intuition on the qualitative behaviour of the system, which can help verify the model in the physical world.

An area suitable to apply the model is in language shift. Mitchener suggests as example the shift from Old English to Middle English to be a case that can be suitably modelled with a evolutionary dynamics model[24]. There are more cases in history involving language shifts that possibly admit a qualitative description using this model.
Following the introduction of another language into a monolingual population, either by increased social exposure or by education policies, the q parameter decreases as a speaker population maybe converted to some other closely related language. If the parameter does not decrease far enough, then the population distribution will stay near the original equilibrium state of having a single dominant language unless subjected to a large perturbation; if q decreases past the critical q_*, then the original stable equilibrium disappears and the system ends up in the disordered state with equal populations of speakers across all languages.
Both of these situations can be observed in real life language distributions. From a recent study, the distribution of French and Dutch speakers in Belgium reflect that of the X_+ equilibrium; the distribution of Spanish and Catalan speakers in Catalonia reflect that of the X_0 equilibrium[25]. While the evolutionary dynamics model does not capture any sophisticated details in spatial distribution, complex social structure or bilingual populations, it can regardless provide a perspective on why these types of distributions might occur naturally as they are stable equilibria of dynamical systems.

Unfortunately, quantitative predictions and tests of the model prove to be difficult due to the ambiguity in definition of the parameters[26]. The model parameters a and q are tricky to quantify, not to mention that they are parameterising a simplified symmetric case of the matrices A and Q. As mentioned previously in this section, the precise definition of a language in terms of the model is not clear and there is no exact method of determining whether two languages are different, so the dimension n of the model is also not clear.

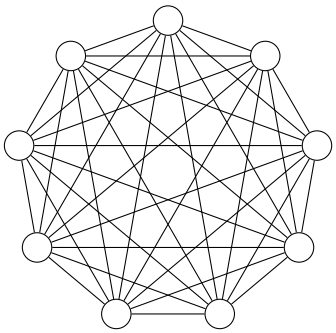
Further contemporary studies on evolution dynamics of languages involve, e.g. using more formal bifurcation theory[24] and introducing learning strategies so there is a dependence $q = q(a)$ in the parameters[23] for more accurate modelling. There is also work that uses evolution dynamics to explain the natural emergence of words and syntax[27], which is not directly related to language competitions but nonetheless demonstrates the greater scope of applications of the theory.

3 Microscopic Models

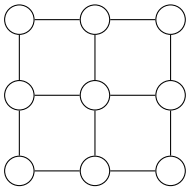
Agent based models are essential to constructing sociophysics theories. In ABMs, the dynamics in the system is delegated to the behaviour of the individual agents. The most effective way to implement ABMs are through numerical simulations, where agents are placed on some underlying topology and the agents' intrinsic values are updated iteratively through a set of rules. The dynamics of the system are studied by extracting relevant macroscopic variables from the population of agents. Numerical simulation of ABMs have become more accessible than ever for study thanks to the increase in computing power of commercial computers, so sociophysicists can run simulations at reasonable scales even on their laptops.

There are a few important aspects to consider in the designs of numerical simulations for ABMs. The topology on which the model is simulated significantly affects the dynamics. The topology of a model is often phrased in the language of complex networks, which we will not cover in detail here; a comprehensive review of complex networks is available in literature[28] and there have been investigations into the effect of social network structures on language evolution[29].

We consider models which implement two simple network types: fully connected networks and regular networks. In an ABM on a fully connected network, every agent is capable of interacting with every other agent, so the agent updates its own properties based on the combined information from the whole population. When there are a large number of agents, the fully connected network approximates macroscopic models.
A regular network ABM is one where every agent has an equal number of neighbours that they can interact with. This is often realised as a 2D lattice which is a regular network with four neighbours. On regular networks, every agent only sees their immediate neighbours which causes interesting local effects to become manifest. Lattices also better reflect how real life societies behave, as humans have a limited mobility range that restricts their social interactions to close neighbours. Though in reality social networks may be more accurately modelled by more sophisticated complex network structures.



(a) Fully connected network



(b) Regular network

Figure 6: Two networks with $N = 9$ nodes, or agents in an ABM. The structure of the two types of networks are vastly different. In a fully connected network (a) every agent can interact directly with every other agent, but in a regular network (b) only those who are neighbours can interact.

Another important consideration in setting up ABMs is the iterated evolution rules of the agents, which constitutes the details of the model. The cellular automaton (CA) mod-

els, popularised by Conway's Game of Life[30], involve identical individual agents on a 2D lattice which obey a set of simple rules that change their state after every timestep. The CA models are used to study complex phenomena which arise from simple constituents which are unaware of the global state of the system[31].
As an alternative, a common approach to numerical simulations in physics is the Monte Carlo (MC) method of random sampling. In MC simulations, random variables are used to obtain a state of the system which is part of a statistical distribution. With enough runs of the simulation one may recover information about macroscopic properties or features of the system. The Ising model is a well-known example where MC simulations have been successful in describing the physical system. Compared to CAs which are deterministic, MC sampling is intrinsically random, and is more suitable in capturing the randomness of the agents which compose human societies. Indeed, the Ising model has been adapted to model human opinion dynamics[32], where binary opinions are chosen as the analogue of up/down spins of electrons in ferromagnets.

In this section we consider a MC model for language competition, using a microscopic Abrams-Strogatz model that is based on the AS model discussed in Section 2.1. The simulation was written in one sitting, but further analysis of the results required extra quantities that need be computed from the simulations using suitable algorithms. Writing extra code to carry out the analysis and visualise the results took up most of the project time.

3.1 Microscopic AS Model

Monte Carlo methods have been applied to study the AS model and its variants before[19,33]. Here we make a similar attempt to study the AS model as an ABM using numerical simulations. The model proceeds as follows.

1. Start with an $N \times N$ square lattice filled randomly with an initial proportion x_i of speakers of one language.
2. At every timestep, select $N \times N$ random cells on the lattice to be updated
3. For every cell, sample the density either
   (a) locally, by computing the density of speakers in the four neighbouring cells, or
   (b) globally, by computing the density of speakers over the entire lattice.
4. Compute the transition probability $p_{yx} = sx^a$ or $p_{xy} = (1-s)y^a$ depending on whether the cell was aligned with population y or x, respectively. s and a are model parameters corresponding to relative status and volatility of the two languages, similar to the macroscopic AS model.
5. Roll a random number and change the cell to the opposite alignment if the number is less than the transition probability p.
6. Repeat from step 2 until the required timesteps are reached.

In principle, the update rule is a good approximation to the AS model locally. When the sampling is taken to be global in step 3, the results should resemble those from the macroscopic analysis. There are a few caveats with this particular implementation of the microscopic AS model.

One technicality with the simulation is that we have chosen to use asynchronous random updates, where $N \times N$ random cells are chosen at every timestep to be updated sequentially. An alternative is regular updating where cells are updated in a fixed order, usually corresponding to the index order of the cells in computer memory. The two different update styles had been found to give tangible but minute effects on the results[33], so we only consider one update style here. Additionally, the whole grid maybe updated via synchronous updates where all cells are updated simultaneously, but this can be very memory intensive and is impractical for this project.

In lattice simulations, periodic boundary conditions (PBCs) are often used to exclude the consideration of edge effects. With PBCs a 2D lattice wraps around east-west and north-south so e.g. the neighbour of the easternmost cell is the westernmost cell, effectively simulating the system on a torus. PBCs also simplify the computation of correlation functions, which will be discussed in a later section, due to the isotropy of the lattice.

The simulations presented here were all produced with custom `Python` code written independently by myself using mainly the `numpy` and `matplotlib` libraries. Regarding the timescale of the simulations, each run with a 100×100 lattice over $t = 100$ timesteps takes on average half a minute to run on my laptop. Some of the results involve averaged values over ten runs, which can take up to ten minutes to run depending on the model parameters.

3.1.1 Simulation Results

We first verify the validity of the simulation by verifying some of the expected behaviours. Figure 7 shows the evolution of population density x averaged over ten runs. Over the same number of timesteps, we observe a much steeper change in x for the global compared to the local sampling rules. For global sampling, the results agree with features of the macroscopic analysis, c.f. Figure 2. In particular, initial populations $x_i > 0.5$ are attracted to the population $x = 1$ while $x_i < 0.5$ are attracted to $x = 0$. The unstable equilibrium solution $x = 0.5$ is stable for all times in the macroscopic case, but it spontaneously decays for Monte Carlo simulations due to the statistical perturbations shifting the population away from the equilibrium state. However, the equilibrium decays into $x = 1$ and $x = 0$ with equal probabilities, so the statistical average the solution still agrees with the macroscopic analysis, as shown in the figure.

Different sampling rules lead to significant differences in decay timescales of the system. For global sampling it takes most initial values of x_i about $t = 20$ timesteps to reach one of the equilibrium states, while for local sampling it takes much longer, only reaching equilibrium after $t = \mathcal{O}(100)$ (not shown in figure). For the rest of this section we will focus on using local sampling rules as they reveal new features of the model.

An interesting case to study is when the two languages in the system are asymmetric, i.e. $s \neq 0.5$. According to the macroscopic analysis, there will be some critical population x_* that the x population will evolve monotonically towards or away from, depending on the value of the a parameter. However, the microscopic AS model does not fully agree with these predictions. Figure 8 shows the evolution of a population x with inferior status for a few initial conditions. The decay profiles roughly follow exponentials, which are straight lines on the log-linear axes. The slope becomes less steep for larger initial

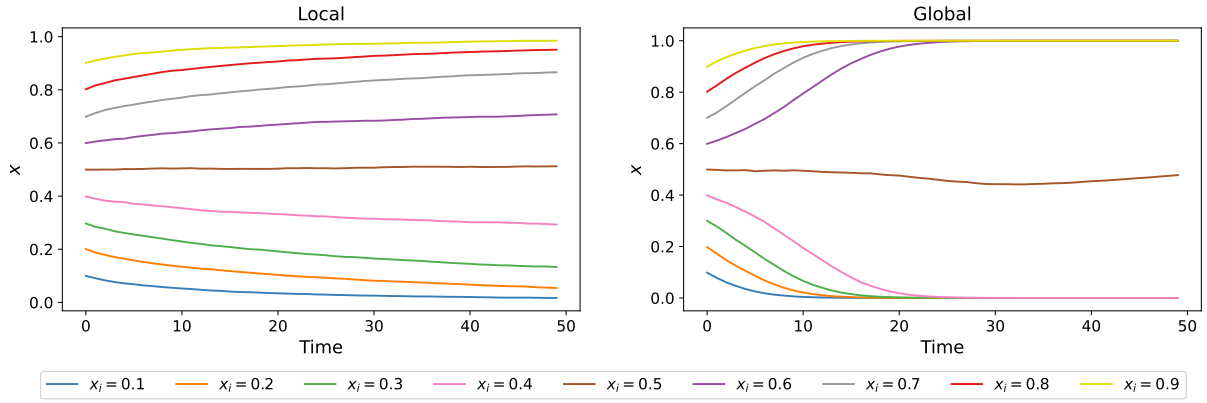


Figure 7: Time evolution of the population x in an MC simulation of the microscopic AS model with parameters $s = 0.5, a = 1.3$ without PBCs. A set of initial populations x_i between 0 and 1 are simulated. Results shown are averaged over ten independent runs. The time scale has been cut off at $t = 50$ to help see the shape of the curves in the global case. Left figure shows the simulation run with local sampling rules and right figure with global sampling rules. Local sampling leads to a much longer time to reach equilibrium. Global sampling leads to qualitative behaviour that resembles the macroscopic analysis in Figure 2.

populations, which corresponds to slower exponential decay rates. Straight lines are fitted to the log-linear plots to find exact values of the exponential decay rates. The fits are done with a generic linear regression fit from `numpy`, with weights to adjust for exponentially decreasing values of the data.

For most samples the evolution strays away from the exponential at the start and final parts of the curves. The starting behaviour for a few initial conditions can be seen more clearly on the right panel of the figure. This is possibly due to the coarsening effect on an initially random lattice, where agents rapidly seek to reach consensus in their immediate neighbourhood. The data deviates from the exponential towards the end of the curve. It is not clear why exactly this behaviour arises and more runs could help by improving the statistics of the current data. A possible explanation is that due to the random update rules in this implementation of the model, it is more difficult to choose the last few cells of a language, so it takes extra timesteps to fully eliminate the population. This hypothesis can be easily tested by modifying the model to use regular update rules, but was not done here due to time considerations.

The model parameters mean that x is the population with an inferior status, so unless it starts at a majority it will almost certainly be eliminated. However, the superior status population $y = 1 - x$ is not fully eliminated except for very large initial x populations. In the simulation only $x = 0.9$ came close to the elimination of the superior population. In the right panel of Figure 8, for $x_i = 0.7$ there is an initial increase in population corresponding to the coarsening effect, but the population reaches a maximum at $t \sim 100$ and begins to decrease exponentially. This is assumed to continue until the initial majority population x is eliminated. For $x_i = 0.8$ the turnaround takes much longer and the system remains in a metastable state for longer than the simulation was run.

An alternative perspective on the dynamics of this system is available through another variable. The interface density ρ is defined as the density of neighbouring cell pairs which have opposite alignments and is commonly used to analyse phase transitions in Ising-like

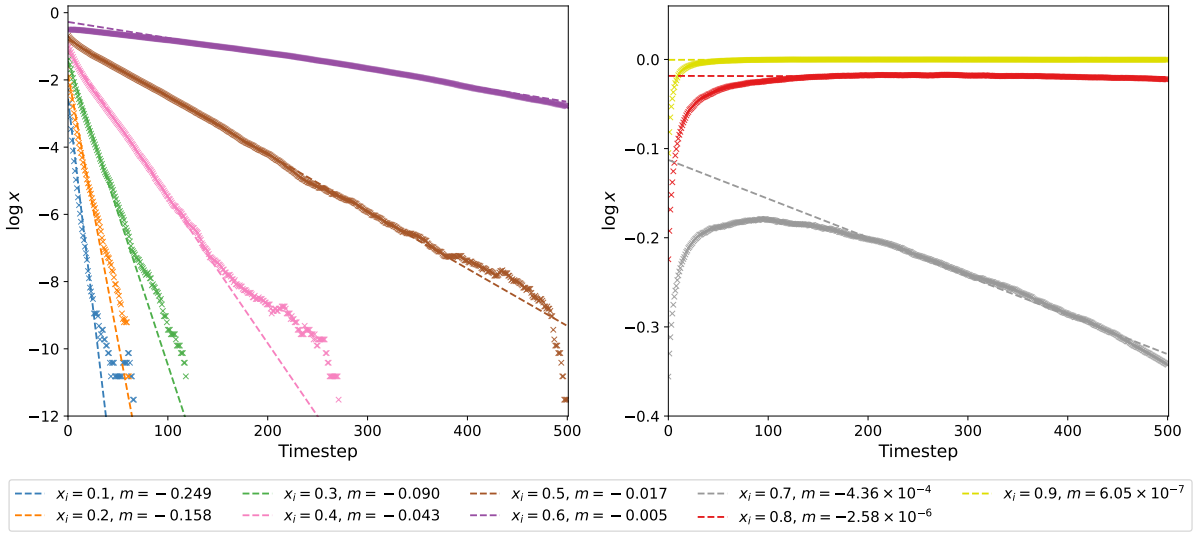


Figure 8: Plots of the population of x over 500 timesteps from one run of the simulation with model parameters $s = 0.4, a = 3.0$ in a log-linear plot. Note the different axes between the left and right plots. Most of the population curves follow exponentials, with deviations at the start and end. Straight lines are fitted to the population curves to obtain the slopes and hence decay rates of the exponentials.

sociophysics models[34]. The interface density is maximum when the lattice is completely random with an equal occurrence of both populations, in which case $\rho = 0.5$ for the case of two populations. When the lattice is homogeneous $\rho = 0$ as there are no longer any interfaces. Essentially, ρ is larger when the system is more disordered.

Figure 9 shows two distinct trends in evolution of the interface density. The left panel shows densities which decrease exponentially, after an initial coarsening stage which rapidly decreases interface densities. This behaviour is consistent with the exponential decrease found in the population evolution plot. The right panel plots show interface density evolution for large initial x populations, which similarly goes through a coarsening stage but ends in a plateau. For $x_i = 0.8$ and $x_i = 0.9$ this is consistent with them reaching a metastable state with varying proportions of the superior population y. The plateau for $x_i = 0.7$ continues even after the population enters the exponential decay phase in Figure 8. A possible explanation is because in the initial conditions where x is at an initial majority, the superior population y only exists in small pockets. When the pockets expand uniformly, there are no drastic changes to the shapes of these clusters since they are initially too spread apart to merge. If the simulation was run for longer, an exponential decay might be observed for the curves in the right panel.

Both the population and the interface density are measurements which describe global properties of the lattice. While interface density does capture some feature of the population clusters, it does not quantify any length scales that arise in the model. A standard quantity used for studying length scales in Ising models are correlation functions, which can similarly be applied to the microscopic AS model. This will also help understand the behaviour of the model for different volatility parameters a.

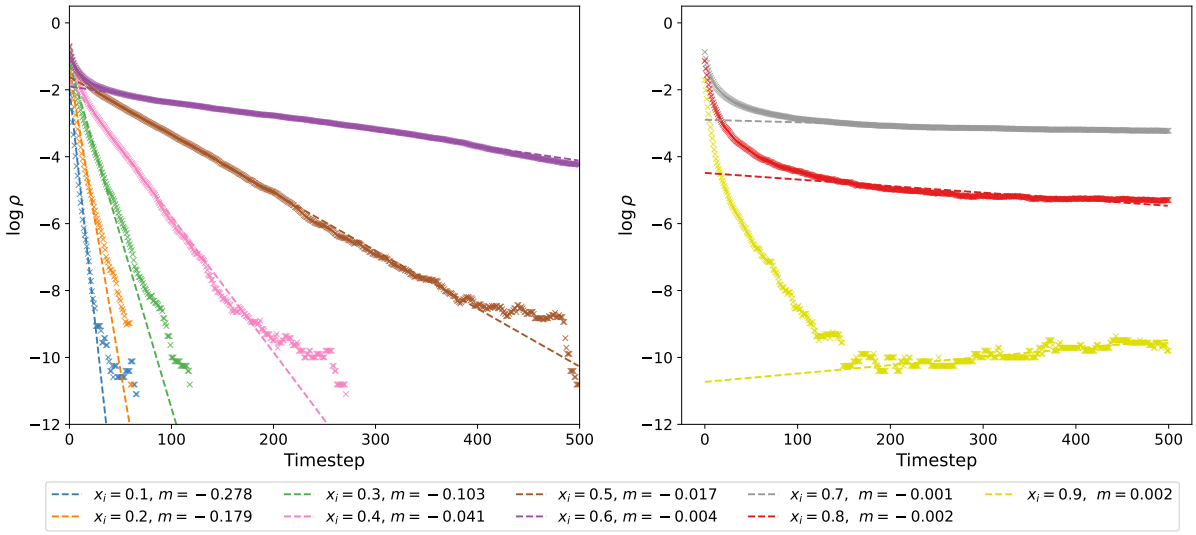


Figure 9: Plots of the interface density over 500 timesteps from the same run as in Figure 8. There are two distinct shapes of the curves which are shown in separate plots. Straight line fits are also done on the log-linear axis to find the exponential decay rates. Note the initial interface density is maximum for $x_i = 0.5$ and decreases for $x_i > 0.5$, which can be seen in the right panel.

3.1.2 Correlation Functions

Correlation functions are useful statistical measurements for physical systems which quantifies the level of disorder within a system. For numerical simulations on a 2D lattice such as the one we have done here, the two point correlation functions can be defined analogously to 2D Ising models[35]:

$$C(\mathbf{x}, \mathbf{x}') = \langle S(\mathbf{x}) S(\mathbf{x}') \rangle, \tag{3.1}$$

where $\mathbf{x}$ and $\mathbf{x}'$ in general are four-vectors of discrete points in space and time, though most of the time spatial and temporal correlation functions are calculated separately; $S(\mathbf{x}) = \pm 1$ are spins (in this case they are technically adopters of one of the two languages, but we will refer to them as spins for brevity and to highlight the analogy with the Ising model); the angled brackets $\langle \cdot \rangle$ denote a statistical average. At the extremes, two points are completely correlated if $C = 1$, anticorrelated if $C = -1$, and uncorrelated if $C = 0$.

If we exploit the isotropy of a 2D lattice with periodic boundary conditions and rotational symmetry of the model, the spatial correlation function may be written in terms of radial distances between two points on the lattice

$$C(0, R) = Z^{-1} \sum_{|\vec{r}|=R} \sum_{\vec{x}} S(t, \vec{x}) S(t, \vec{x} + \vec{r}), \qquad Z = \sum_{|\vec{r}|=R} \sum_{\vec{x}} 1, \tag{3.2}$$

where the vectors e.g. $\vec{x}$ are now spatial three vectors, and the distance is defined in terms of the L^1 norm $|\vec{r}| = |r_1| + |r_2|$ to be computationally more adequate for the 2D lattice.

The temporal correlation function is one dimensional by definition, so it does not

require any further reductions in degree of freedom. Explicitly, it is defined as

$$C(T,0) = Z^{-1} \sum_{\vec{x}} S(t,\vec{x}) S(t+T,\vec{x}), \qquad Z = \sum_{\vec{x}} 1. \tag{3.3}$$

Sometimes, one could define population specific correlation functions $C_s(\mathbf{x},\mathbf{x}')$ where the sums in the above equations are taken over position vectors of one fixed population $s = \pm 1$. However, for this analysis we are mostly interested in equilibrium configurations where both populations are symmetric, so this will not be necessary.

Figure 10 shows lattices at the end of the simulations with the same model parameters except a, where we choose three values to illustrate the qualitative differences. The simulations had been run with PBCs to facilitate the computation of correlation functions. The simulations had parameters $x_i = 0.5, s = 0.5$ so they would remain in equilibrium for longer timescales than the simulations were run for, such that we can focus on studying the stable lattice configurations that appear in the AS model. As discussed in Section 2.1, a low volatility parameter $a < 1$ corresponds to high volatility i.e. more disorder in the system, while a high volatility parameter $a > 1$ corresponds to low volatility. This is reflected in the lattice simulations.
For $a = 0.3$ the lattice does not look too different from a completely random lattice configuration. The main difference is that there are some more clusters of one or the other population. As volatility decreases (increasing a), the lattice settles down into more ordered configurations. The $a = 1.0$ case has much larger clusters compared to both random and $a = 0.3$ lattices, but there are still pockets of the opposing population interspersed between large clusters. For $a = 3.0$ the small pockets almost completely disappear, leaving only large contiguous clusters of either population.

We quantify these features through spatial correlation functions, where the existence of large clusters manifests as a longer correlation distance. The code used to compute correlation functions were written independently by myself with standard `numpy` functions. Figure 11 shows the correlation functions computed for the four simulations discussed previously. The zero correlation line is marked on all of the plots, and we define the correlation length λ as the distance at which the correlation first crosses zero, interpolated where necessary. Note that usually correlation lengths are defined in terms of an exponential curve fitted to the curve, but we define it in a different way due to the lack of data. With additional computing resources, running multiple simulations could be useful for eliminating any statistical variation at the tails of the curves.
From the data we have, the random lattice has a correlation length less than one unit distance of the lattice, which means a completely uncorrelated lattice, as expected. With volatility parameter at $a = 0.3$, the correlation length is still quite short at $\lambda = 4.63$, which captures the small clusters that form in the lattice at this volatility parameter. The correlation length continues to increase for $a = 1.0$, but decreases again for $a = 3.0$. From the lattices in Figure 10, the boundaries between the two populations are less clearly defined for the $a = 1.0$ case, which could have led to the large correlation length.

As mentioned above, we also measure the temporal correlation to ascertain how quickly the grid changes over time. Figure 12 shows the temporal correlation function for a range of volatility parameters between $a = 0.3$ and $a = 3.0$. The correlation stays high over longer timescales for larger values a, where the lattice is less prone to rapid changes and large clusters are formed which will stay stable for long times. For smaller a the clusters are small and move around more sporadically, so correlation decreases rapidly

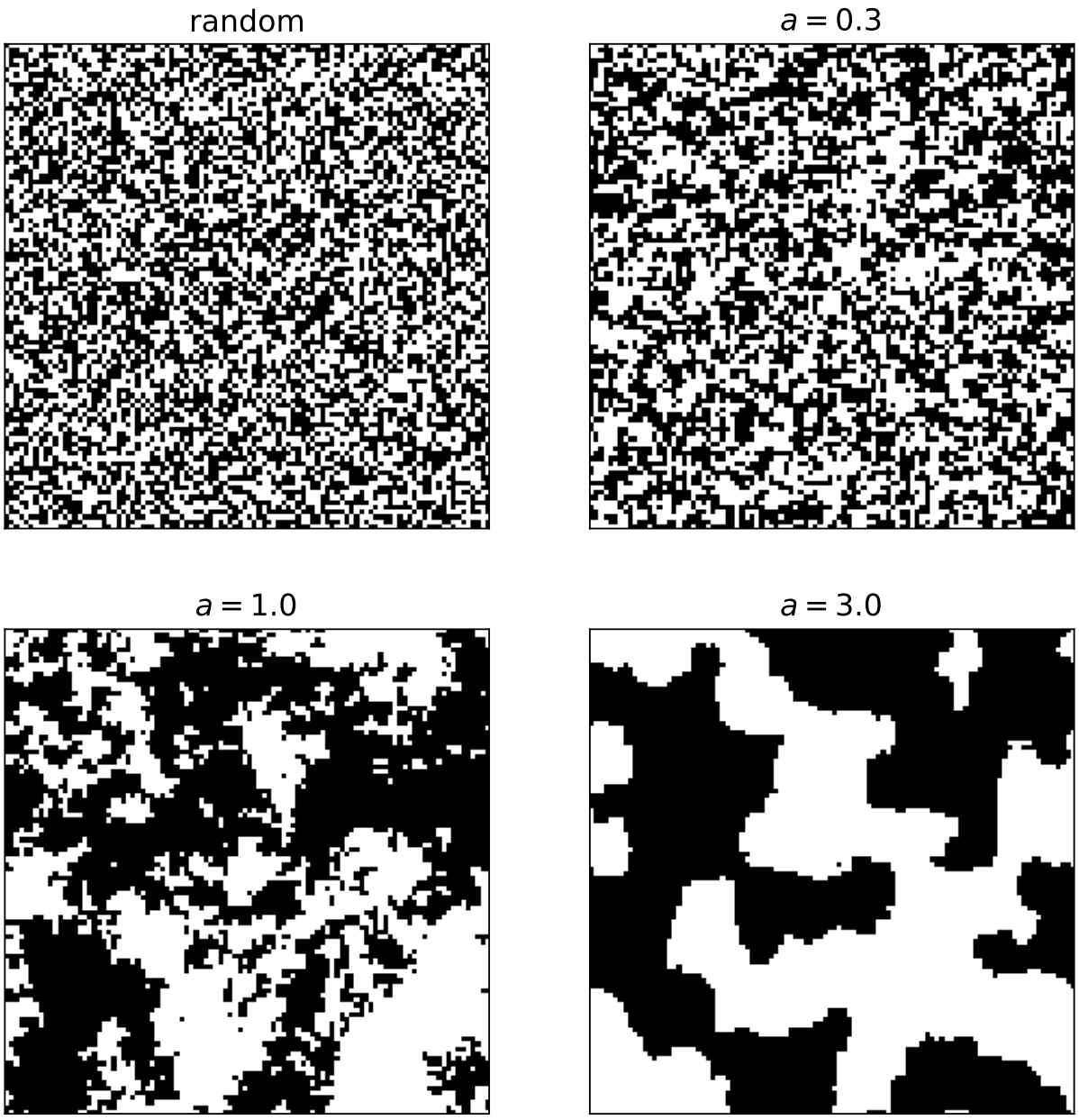


Figure 10: Top left lattice is completely randomly generated with equal probabilities for both populations. The rest are 100×100 lattices at the end of the MC simulation after $t = 500$ timesteps, using the same random number generator seed. All simulations are run with $x_i = 0.5$ and $s = 0.5$, but with different volatility parameter a as displayed in the labels. PBCs are applied for all three of these simulations in preparation for computing correlation functions. Full movie of the simulations can be accessed at: `https://drive.google.com/file/d/1C1tvZTDn2c3zFJoFP_7__0hQYA6lJ-p2/view?usp=sharing` (Google compresses the video with the builtin player so download the video for better quality viewing).

over time. For $a < 1$ the correlation data also becomes quite noisy below $\sim 10^{-2}$. This could be similarly caused by the lattice being more erratic at low a values, with cells flipping back and forth rapidly, so the long time correlations are largely random. Similar to before, these noisy phenomena would be elucidated if more data were available through more runs of the simulation.

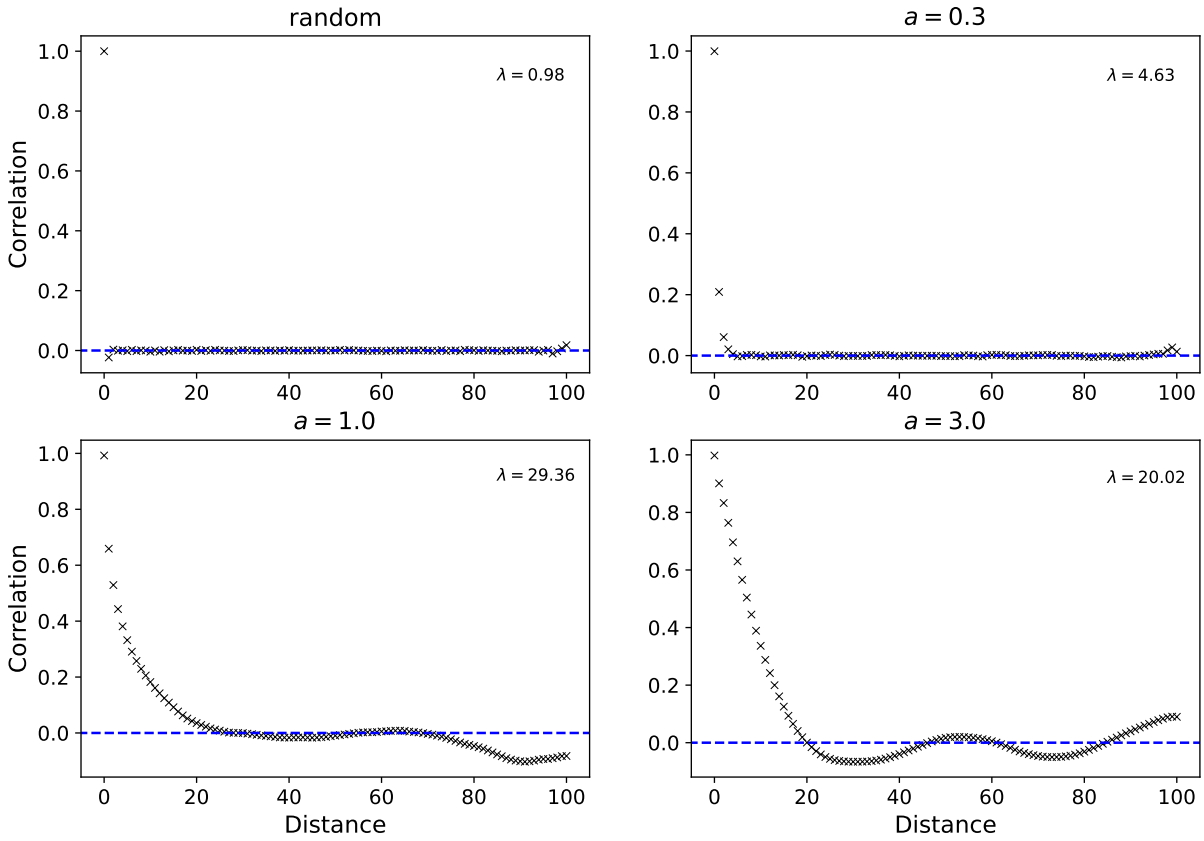


Figure 11: Spatial correlation functions computed for the four final lattice arrangements in Figure 10. The correlation is obtained from one single run so there are likely statistical noise present. The correlation length, distance at which the first zero crossing for correlation, is achieved is shown on each of the plots, along with the zero correlation line.

We define analogously the correlation time τ as the time taken for the temporal correlation to drop below an arbitrary threshold, which we take to be 0.1 here. Together with correlation length we examine the dependence of correlation length/time scales on the volatility parameter a. This is motivated by the Ising model where correlation lengths have an interesting dependence on temperature, and volatility is intuitively an analog of temperature for our system.

Figure 13 shows both the correlation length and time dependence on a. Because of the unoptimised algorithm used to compute spatial correlations, it takes around a minute to compute the correlation function from one lattice, so only one lattice was used for each of the data points. The correlation length data could be significantly improved if a more efficient algorithm could be implemented. For temporal correlation, the algorithm was much more efficient essentially because time is one dimensional, so better averaged data were available.

The correlation length appears to peak around $a = 1.4$, falling rapidly towards zero for $a < 1$ and a slower fall for $a > 1$. The shape of the a dependence of λ roughly resembles the correlation length divergence at critical temperature in the Ising model. However, due to the uncertainties in the data this behaviour should be confirmed once better data are available. On the other hand, correlation time displays a clear sigmoid shape with a sharp transition at $a = 1$, where we identified, both in the macroscopic

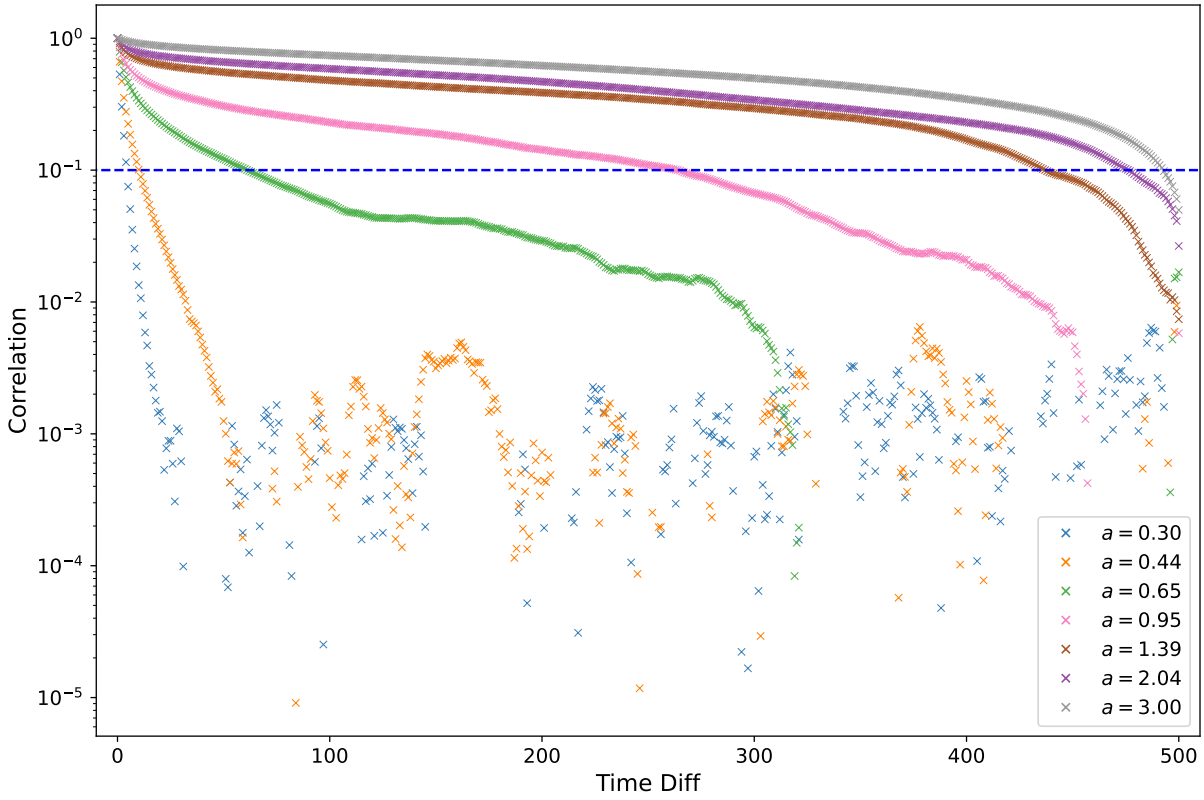


Figure 12: Temporal correlation functions computed for a number of simulations run on the same 100×100 lattice with PBCs, with parameters $x_i = 0.5, s = 0.5$ but for a range of a as shown in the legend. The data is collected over a single run of the simulation for each parameter, so there are quite a lot of statistical noise. The blue dashed line is the constant line where correlation equals 0.1.

analysis and in the simulations, a qualitative difference in the dynamics of the system. This also resembles the transition from order to disorder around the critical temperature in the Ising model, though in that case the correlation length peak also lines up with the critical temperature.

3.1.3 Further Discussion

We have studied the microscopic AS model as an ABM of language competition through MC simulations. The evolution of population densities follow exponentials, but takes place over longer timescales when compared to the macroscopic analysis. Results show that with even a slight advantage in the relative status of one language, it becomes difficult to completely eliminate that language, even if it starts at an initial disadvantage in population. The interface densities similarly follow exponentials when one population takes over, but remains nearly constant for metastable states. There are also interesting dependence of the model dynamics on the volatility parameter, which warrants further studies.

Beyond population densities and correlation functions, another way to quantify the lattice configurations is through directly counting clusters. Cluster sizes and number densities are important quantities used in studying statistical system such as percolation[36].

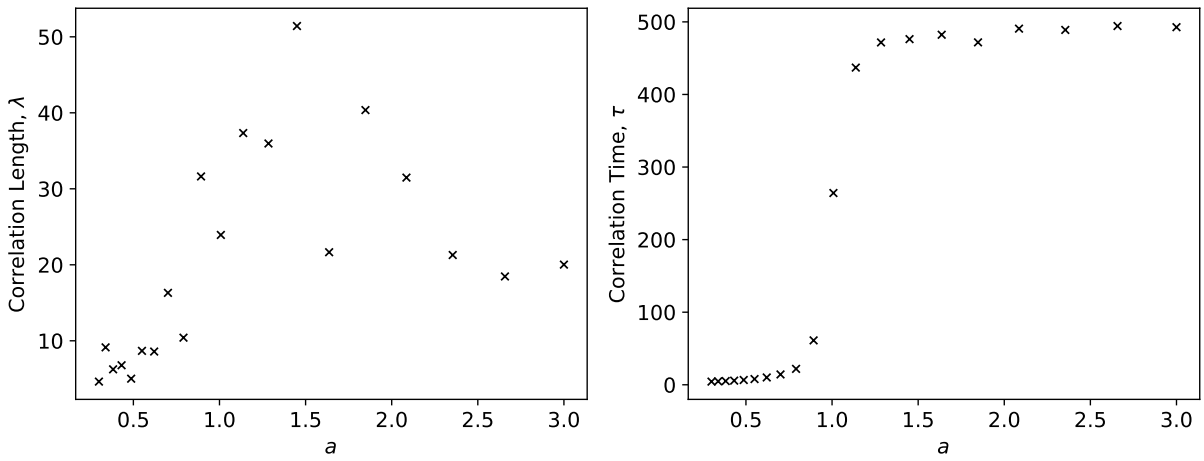


Figure 13: Variation of correlation length/time, as defined in the text, over a range of volatility parameters between $a = 0.3$ and $a = 3$. The correlation length plot has much noisier data because only one run is used for each data point. Correlation length displays a peak at $a \sim 1.4$ and correlation time appears as a sigmoid shaped function in a.

A standard cluster counting algorithm could be implemented on the lattice in the future to further study the properties of the system.

At a practical level, the AS model was originally developed as a model describing language competition. The problem with the macroscopic model, as discussed in Section 2.1.2, is that the volatility parameter a is a dimensionless model parameter that does not have any intuitive physical or sociological interpretation. However, we find here that a has quantifiable effects on the typical length scales in equilibrium state. This means that with more available resources, it is plausible that one could make a fit to real world data, possibly with time series data as well, to extract the model parameters while accounting for features in spatial distributions, which were not considered in the original work by Abrams and Strogatz[13]. A similar study was done recently by Kauhanen et al. on fitting a linguistic temperature for linguistic features over the world[37], though in their case a much more sophisticated stochastic model was used.

It is also worth mentioning that there are many assumptions and limitations in this simple microscopic AS model. No population dynamics have been included, since all interactions happen on a static lattice with a fixed number of agents. In reality these agents would be able to reproduce, whereby the languages they speak are inherited or mutated. The interaction between agents should also have some dependence on the similarity in their languages. The languages here are only categorical with one relative status parameter to encode their differences. There are no reference to the specific features of each language, which can often be quite complex. Caution should be exercised when implementing extra features to sociophysical models such as the AS model. Furthermore, one could consider including geographical information in the regular lattice, or run the model on more sophisticated complex network structures. These additions are useful to more accurately model language competition in real life, but they might also introduce complexities to the model that are not necessarily relevant. It is the responsibility for sociophycisists to make judicious choices on which model details are needed to accurately describe real life systems.

The numerical simulations in this work have been mostly proof of concepts, to demon-

strate that MC simulations are capable of leading to useful conclusions in sociophysics studies. Further work would likely require greater computation power, in order to run the simulations over larger time scales and on larger lattices. The number of agents scales as $\sim N^2$ where N is the length scale of the lattice, so many of the simulations run in this project would scale algebraically without further optimisations. More efficient algorithms and faster computer programs, e.g. in `C++` instead of `Python`, are desirable if larger scale simulations are attempted.

Therefore, while the sociophysical models have been interesting from a physics perspective, it still requires more work to apply them to real world situations and draw meaningful conclusions. The connection between the model parameters and real life data are not yet clear. But the potential is there for these models to provide accurately descriptions for language competition dynamics and hence inspire new ideas on how the trend of language extinction can be stalled or even reversed.

4 Conclusions

Most of this work was dedicated to exploring various dynamical models for language competition, where we explored a few of the influential models in sociophysics literature. In doing so, we saw that physics provides powerful tools, from analytical techniques to quantitative intuition, to analyse sociological systems. Even though the agents in social systems were humans who are capable of exhibiting complex behaviour on their own, it was not entirely hopeless to prescribe models that govern their collective behaviour. Statistical physics and complex systems provided the integral connection between the nature of the individual and the characteristics of the collective.

We examined two analytical models, the Abrams-Strogatz model and the Nowak Evolutionary Dynamics model, for language competition. Both resembled special competition within biological systems, though in this case the human population acts as a proxy through which different languages may compete. Using stability analysis, we found that both systems have dynamical behaviour that explains the coexistence of multiple languages. The Nowak model provided the mechanism to explain how a shift in dominance between languages might occur. We also examined the microscopic AS model as an example of agent based models and an extension to the AS model. We found that the microscopic dynamics exhibit an interesting dependence on the model parameters.

It is not surprising that we find parallels between traditional physical systems and these exotic dynamical systems, where the language of physics can be used to provide insight and grant new perspectives on problems from other fields of science. Physics and mathematics is universal in describing our world, and many complex problems in our world may be reduced by assumption into analytically tractable models. But in doing so we must not forget that sociophysics is not a replacement for sociology, as there are many social dynamics whose full complexities cannot be captured by reductive assumptions imposed by sociophysics. Knowledge from both disciplines should be made compatible through meaningful communications between the scientists working in either fields. Only then may we eventually reach the ultimate theory of sociology as dreamt of by Auguste Comte in his philosophical endeavour.

4.1 Extra Models for Interest

There are many more interesting models in sociophysics which require attention and further development, and due to time constraints it is impractical to cover more models in similar detail to the few which have already been presented. More comprehensive reviews of sociophysical models and their applications are available, among others, in the various works cited throughout this essay[2,38,26].
Here we briefly highlight a few more areas of sociophysical modelling, both in and outside the subject of language dynamics and evolution. This is to provide further support to the claim of the potential of sociophysics as an alternative approach to innovate for the traditionally subjective studies of social sciences.

The Schulze-Stauffer model[39] uses an alternative representation for individual languages in modelling language spread and competition. In their model, individual languages are represented as bitstrings, a sequence of zeros and ones. Starting with a single origin language, populations reproduce iteratively with a mutation probability, which either flips one of the bits within the bitstring or, in one extension of the model, replaces it with one from an arbitrarily defined superior language. The authors found that the emergence of a dominant language is dependent on the mutation probabilities; at a low mutation rate the origin language dominates with a few trailing behind, while at high mutation rates the population size distribution of languages begin to qualitatively resemble real world data.

De Oliveira's model[40] also studies the evolution of an initial ancestor language, but with an additional consideration of spatial effects. The ABM simulation is conducted on a square lattice, where the ancestor language mutates and colonises new locations within the lattice, intended to simulate the spread of human languages on Earth from one common ancestor. The relation between linguistic diversity and the lattice size are found to mirror experimental observations.

The Axelrod model[41] is a model of cultural dynamics, their spread and assimilation. The model realises cultural features in the form of vectors carried by agents, who interact and modify their own cultural vector based on some predetermined rule. This model also leads to regions of dominance of one culture or coexistence of many cultures, depending on the specific parameters of the model.

Social Impact Theory models[42] are a class of opinion dynamics models, which attempt to predict opinion formation in and across communities. These can be thought of as extensions to Ising-like models, which are the simplest opinion dynamics models. The model assumes inhomogeneity in the agents' abilities to form opinions and convince other agents of their opinions. The model exhibits many interesting dynamics such as formation of stable clusters of opinions, metastable states and phase transitions. An extension of the model[43] introduces spatial dynamics where agents migrate and opinions are spread via a field that reacts to the existence and spatial distribution of individual opinions.

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