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Searching Turing Instabilities in the Abrams-Strogatz Model

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Abstract. The aim of this thesis is to search for Turing instabilities in Abrams-Strogatz language competition model. The theoretical part of this thesis provides an overview of complex systems, explains the nature of Turing patterns and the conditions for pattern formation, describes the aspects of language dynamics and Abrams-Strogatz model. In the practical part of the thesis, the original Abrams-Strogatz model is extended with spatial parameter and using stability analysis Turing instabilities are investigated in the spatial model.
CERCS research specialisation: P170 Computer science, numerical analysis, systems, control
Keywords: complex systems, patterns, endangered languages, statistical physics, dynamic systems

Turingi ebastabiilsuse otsimine Abrams-Strogatzi mudelis
Bakalaureusetöö
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Lühikokkuvõte. Bakalaureusetöö eesmärk on otsida Turingi ebastabiilsusi Abrams-Strogatzi keeltevahelise konkurentsi mudeli puhul. Töö teoreetiline osa annab ülevaate komplekssüsteemidest, selgitab Turingi mustrite olemust ja nende tekkeks vajalikke nõudeid, kirjeldab keeltevahelise konkurentsi dünaamikat ja Abrams-Strogatzi mudelit. Töö praktilises osas laiendatakse originaalset Abrams-Strogatzi mudelit ruumilise parameetriga ning uuritakse stabiilsus analüüsi abiga Turingi ebastabiilsuse eksisteerimist ruumilises Abrams-Strogatzi mudelis.
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Märksõnad: komplekssüsteemid, mustrid, ohustatud keeled, statistiline füüsika, dünaamilised süsteemid

Contents

1 Introduction

The world consists of extremely complex systems that change in time. The growth of an organism, global climate, telecommunication infrastructures, social interactions inside society or the universe itself - these systems consist of many components that interact with each other and form a unified whole. Studying these systems classically the approach has been based on reduction: breaking the otherwise incomprehensible system down to its simplest pieces and then describing the whole system through the properties of the components. The collective behavior can lead to some intrinsically unpredictable properties that cannot be inferred from the individual properties of components. [1] Or importantly, as Aristotle has put it: "The whole is greater than the sum of its parts" [2].

The concept of complexity is very vague and various authors have defined it in different ways. However, some typical characteristics are featured in most of the proposed definitions. One of them concerns the location of complexity on the borderline between order and disorder. Namely, complex systems are to some degree predictable and structured, but in the same time chaotic and uncontrollable. This is caused by the interdependence of the components. The parts can function almost autonomously, but to some extent, they still depend on each other; they are separate, but connected via their interactions [3]. The other unifying principle of complex systems is the idea of emergence: connections between simple low-level subunits cause the emergence of higher-level functionalities or structures. While each component is goal-oriented, trying to maximize its own individual benefit, they also follow the cause-and-effect logic. The local actions of one subunit affect the surrounding environment and therefore trigger further actions of other neighboring components. Such interactions set in motion a chain of activity that spreads across the system and finally results in the unanticipated global properties. [4, 1]

Studying complex systems has helped to understand more about indirect impacts and the relations between causes and effects. [3] In linear systems the response is proportional to the cause making the system easily predictable and resistant to changes. Instead, non-linear systems are very dynamic because the components interact with each other non-linearly. [5] The system acts as a loop: the effects or outputs of one action are fed back into the system as causes or inputs of another action [6]. Non-linear systems are also very sensitive to parameter values. Even small changes in initial configuration or some perturbation caused by external factors can lead to significant or even unpredictable changes in the behavior of the system. [1] The unpredictable final outcome due to the sensitive dependence on initial conditions is a characteristic feature of chaos. A hint of a smile can change the course of a billion-dollar negotiation or a wave of a butterfly in Brazil cause a devastating hurricane in Texas. [6] Thus, chaos and complexity might seem very similar, but the two theories are actually rather contradictory. Theory of chaos observes the processes where simple rules and systems result in complicated and random structures. Complex theory, on the other hand, searches the underlying rules beneath simplicity and order that emerge from the behavior of complex structures. [4]

Due to the dependence on initial configurations, a large number of interactions, sensibility to external factors, unpredictable emerging properties and non-linear characteristics the behavior of a complex system cannot be revealed by considering a few variables or just applying probability theory. For these reasons, different modeling techniques followed by computer simulations are used to study the behavior of complex systems. Very often modeling a complex system is based on nonlinear differential equations, agent-based networks, and stochastic models. Simulations can rely for example on the numerical calculus and Monte Carlo methods as well as cellular automata. Trying different initial conditions and adding random perturbations to the simulation run gives an overview of the possible behaviors the system can exhibit. While the selection of configurations has still a huge impact on the outcome, it has been noted that the results tend to converge into a relatively small set of distinct pattern types. This trend is an effect of self-organizing nature that complex systems possess. To cope better with various perturbations and changes in the environment the system tries to organize itself and reach some kind of order. The recurring patterns are useful for scientists to develop a statistical overview of the most likely outcomes and also gain insight into the specific factors that promote a specific result. [1]

Although the study of complex systems is still relatively young it already stretches the boundaries of traditional science and provides new ways to think about the universe. It creates bridges across different fields in science and accelerates the flow of general scientific knowledge. [2] For example, researchers get closer to explaining many sociological aspects: the decision making, social interactions, the consequences of policies and human behavior in general [7]. But complex systems and also pattern formation are applicable in nearly every field of science. The structure of the universe, stock market movements or diagnosis of diseases are just a few examples where the theory of complex systems has the potential to bring a revolutionary breakthrough. The present thesis focuses on language competition, i.e complexity theory applied in the field of linguistics.

The linguists try to answer various questions concerning the complex concept of language, from the process of learning a language to the evolutionary journey of the whole language. An important component of the evolution of a language is the language competition. Various language competition models have been proposed in order to predict the extinction rates of languages, cultures, and religions as well as the general dynamics leading to the success of one or other language. In the language competition models, the speakers form a network of connected agents who are interacting with each other and switching between languages. The final result in the rivalry for speakers is determined by a combination of factors affecting the behavior of the whole society. Mutable parameters such as geography, social trends, prestige, concentration, etc determine the final outcome.

In the present thesis, language competition and extinction are being analyzed from the perspective of complex systems focusing on the emergent patterns. The focus of Section 2 is to introduce the theory of Turing patterns and give an overview of the research done in this field. First, the formation of the theory itself, the importance of reaction-diffusion systems and diffusion-driven instability are discussed. Then a set of examples and the history of the theory is briefly reviewed. The next part gives a more detailed overview of the structure and the dynamics of Turing systems. The section is concluded with the introduction to stability analysis and finally, general conditions for diffusion-driven instability are presented. In Section 3 the general aspects of language dynamics and types of models are discussed. The concept of language competition is introduced and different models are reviewed. Following the description of Abrams-Strogatz model, its structure and applications. In Section 4 the original Abrams-Strogatz model is extended with a spatial parameter. The new model and the effects of the spatial parameter are discussed. The following part presents the steps for linear stability analysis and carries out the analysis for the new spatial model. At the end of the section, the results through numerical simulations and the conclusion of the analysis are presented. Finally, in Section 5 the main ideas and results of this thesis are reviewed.

2 Theory of Turing patterns

2.1 Pattern formation

The growth from one single egg cell into a living and functioning organism has been investigated for centuries, but some parts of this process have still remained unexplained. The development of an organism starts with the activation of genes which all contain blueprints for the structure under construction. Although genes have the major guidelines, they are too small to contain all of the detailed information — it is identified that an adult human consists of tens of trillions of cells (10^{13}), whereas DNA itself has only 3 billion base pairs (3×10^9) [8]. So it is logical to ask, what are the mechanisms that turn these DNA provided guidelines into a detailed structure. [8]

Among others also Alan Mathison Turing (1912-1954) tried to answer this question. Turing was a famous English mathematician mostly known for his influential work in computer science, artificial intelligence and cryptology [9]. With his mathematical background, he looked at the problem from a different perspective and suggested that a simple mathematical model could solve the problem of the natural mechanisms of growth. Turing proposed that the process of morphogenesis is explained with a system of chemical substances always diffusing and reacting with each other. The action and production of those substances, which he called morphogens, is first activated by genes. As a result of the reaction-diffusion behavior, the concentration of morphogens will vary in different places and therefore generate various spatial patterns. Turing suggested that the concentration patterns are guidelines for the developing cells (illustrated in Figure 1). The cells respond to the concentration of morphogens and differentiate accordingly which in the end leads to the detailed and complex structure of an organism. [8] [10]

Examining the development of a fertilized egg, Turing came to the question of how can one symmetrical cell over time evolve into a completely asymmetrical organism. Something must interfere with the fertilized egg in a stable, symmetrical state and under those deviations, the system becomes unstable resulting in a symmetry-breaking. As an innovative idea, Turing proposed diffusion driven instability. Diffusion is a process of particles moving from an area of higher concentration to one of lower concentration reaching equilibrium. It is commonly thought as a stabilizing process leading to a homogeneous solution (an ice cube dispersing into a hot tea). However, Turing proved that when solution consists of two chemicals with

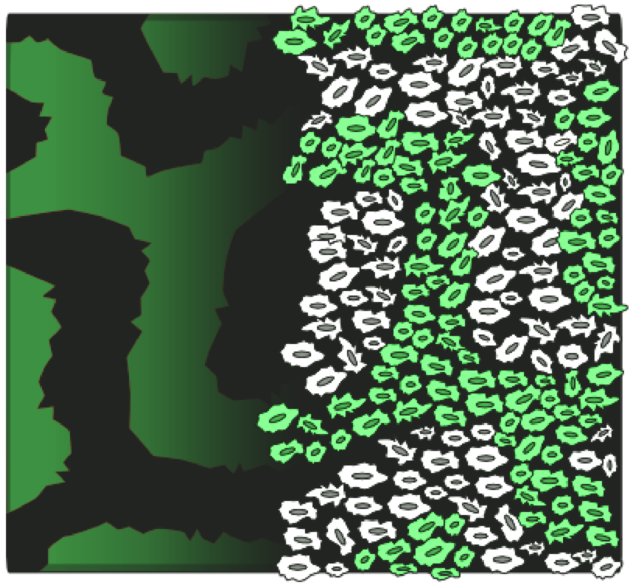

Figure 1: The morphogens lay down the pattern. [11]

different diffusion rates it could lead to an inhomogeneous state. For example activator-inhibitor relationship, where the reaction rate of the inhibitor chemical is faster than the activator's, it may result in spatial variations of concentrations. The diffusion would carry the asymmetry throughout the solution and therefore generate chemical patterns. To keep the system away from equilibrium the chemicals causing the deviations must be fed to the system continuously. Otherwise, the system returns to a homogeneous state and the patterns will vanish. [8, 12]

The most outstanding feature of Turing's diffusion driven instability is that it is governed by the intrinsic parameters whilst the initial conditions and external factors play only a small role in pattern formation. This is a remarkable difference compared to other instabilities that are found in systems out of equilibrium. In Turing systems, the characteristics of the chemicals involved will determine which type of pattern will occur and the initial conditions just affect the position of the pattern. This idea is illustrated by the fact that although all tigers have stripes, the exact pattern differs individually. [8, 12]

2.2 History and examples

Turing published his ideas in 1952 in his article "The Chemical Basis of Morphogenesis" [13]. At first, not much attention was paid to his theory because there were insufficient resources and knowledge for demonstrating the patterns in reality. The chemical reactions often occur very quickly making it difficult to determine the patterns. During 1980s mathematicians, chemists and biologists did numerical simulations, mathematical analysis, and experiments to study Turing's ideas until in the 1990s they were finally able to show experimentally the patterns. [12] The first evidence of Turing patterns was presented by De Kepper and group when they stumbled upon them almost accidentally while working on oscillatory chemical reactions [14]. Although interest in Turing's theory of diffusion-driven instability has grown since then, the major part of the research has focused only on the pattern and model types and their significance in the development of an organism. The topic of controlling the patterns and their formation is studied less. [12]

Generating patterns in the lab and showing theoretically how the formation process works don't necessarily prove that the patterns actually exist in nature. The definite connection between Turing systems and biology is still missing. One of the first evidence suggesting that the link exists, was on the work of Shigeru Kondo and Rihito Asai in 1995 [15]. They studied the formation of the stripes of the angelfish and were able to show that it can be perfectly mimicked by Turing models. The angelfish have unusual characteristics, their stripes continue to grow in time with the development of the fish rather than being established during embryogenesis. The scientists were able to match the computer simulations to the pattern changes in the real fish and imitate the exact branching of the angelfish stripes (Figure 2). The overall idea behind modeling animal coat patterns is that morphogens lay down the pathway on which the melanocytes start producing pigment. However, the morphogens involved in this haven't been identified yet, making it merely a theory. [14, 8]

As Luciano Marcon and James Sharpe note that "One of the most important questions in the field is the identity of the Turing molecules" [16]. They conclude that for many theories, even when evidence for some of the key molecules exists, then multiple questions are still left unanswered [16]. The most recent development in the field is the work of Xavier Diego, James Sharpe and colleagues [17]. The group has expanded Turing's theory with a new topological approach which simplifies the process of determining the

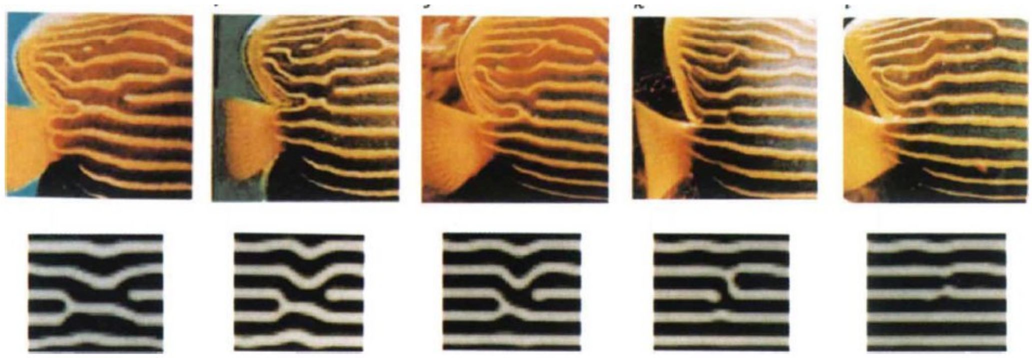

Figure 2: The pattern changes in angelfish (top) are mimicked by the simulation of Turing system (bottom). [15]

required parameters for a Turing system. The new theory is useful for both theoreticians and experimental groups working with biological cells and trying to implement Turing networks in them. Even further, if the experimental groups are successful in making biological cells develop patterns, the long-awaited answer, to whether biological systems can actually be explained by Turing's theory of morphogenesis, will be revealed. [11]

Although Turing models have a very simple and generic nature, they are able to describe extremely complex mechanisms and explain some fundamental ideas of natural systems. They are very robust against random noise, as are most of the systems in nature. In addition to mimicking animal patterns, Turing systems have been applied to explain a variety of biological aspects and structures. Multiple organs of the human body show a similarity to three-dimensional Turing structures, for example, arteries, lungs, cerebral cortex, etc. Being a universal model for self-organization, Turing's theory of pattern formation is definitely not limited to only biology and chemistry but can be used in social sciences, economics, physics, ecology, material sciences, etc. The formation of sand dunes or the constellations of galaxies, termites building their nests, desertification, demographic changes, criminal hotspots or language dynamics in societies — they all show signs of being Turing systems. The difficulty is how to differentiate between a real pattern and a random arrangement that occurs. Before any conclusions about Turing patterns can be made, the model must be studied and analyzed mathematically. [8]

2.3 Turing system

The most general Turing system can be defined with two nonlinear partial differential equations [10]:

$$\begin{aligned} \frac{\partial U}{\partial t} &= D_U \bigtriangledown^2 U + f(U,V), \\ \frac{\partial V}{\partial t} &= D_V \bigtriangledown^2 V + g(U,V) \end{aligned} \tag{2.1}$$

The reaction-diffusion system consists of two main parts. The diffusion part of the equation describes the spreading of the chemical while the amount of the chemical remains the same. The particles which are positioned in a high concentration area move to a lower concentration area. The reaction part of the system at the same time equalizes the two concentrations, describing the production and degeneration of the chemicals. [18] In the above equations there are four factors: $\frac{\partial U}{\partial t}$ and $\frac{\partial V}{\partial t}$ are the concentration rates, U and V mark the inhibitor and activator chemicals, D_U and D_V the diffusion coefficients and nonlinear functions f and g describe the system dynamics. The activator chemical is autocatalytic, increasing the production of itself and also the inhibitor chemical. At the same time, the inhibitor chemical suppresses the production of both. The Turing instability occurs when the balance in the fight over domain space breaks due to the difference in diffusion coefficients. More precisely when the inhibitor chemical has a larger diffusion coefficient than that of the activator chemical. This can be explained by imagining an inhibitor-activator pair. Slightly increasing the activator chemical concentration, it also increases the inhibitor chemical at the nearby points. In the case where inhibitor diffuses faster due to the larger coefficient, it then suppresses the activator chemical and its concentration lowers at neighboring points. Which in turn reduces the production of inhibitor chemical there. So the diffusion carries the disturbance throughout the domain resulting in patterns. [18]

The exact forms of functions f and g depend on the particular system and the function parameters vary accordingly. Whereas the parameters play the key role in pattern selection it is clear that different Turing models generate different patterns. Most common patterns are linear and radial structures, for example, stripes and spots in 2D space (Figure 3). Although the function parameters govern the pattern selection, the most notable part of the Turing system is that the pattern generation itself does not depend on the initial configuration. The time-independent spatial patterns appear when particular conditions within the system are satisfied. [8, 10]

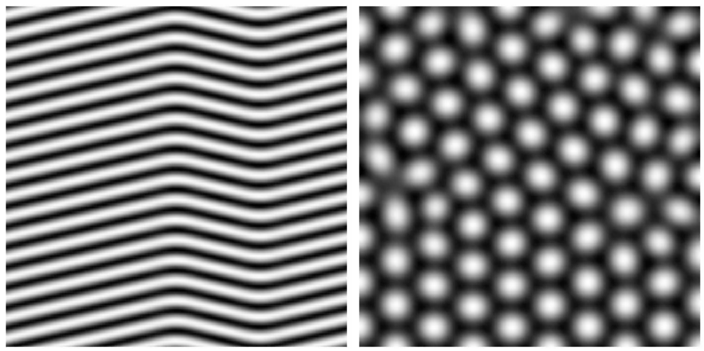

Figure 3: Chemical concentration patterns obtained from numerical simulations [19]

2.4 General conditions for diffusion-driven instability

To predict the pattern formation in systems, linear stability analysis is used. Linear stability analysis examines how the system in a stationary state responds to small perturbations over time. As the name implies, the method ignores the higher order terms and is limited to giving linear information. Therefore the results of the analysis cannot be used to describe the full dynamics of the nonlinear system. However, it is effective in detecting instabilities and thus pattern formation in reaction-diffusion systems. Later, a nonlinear analysis is carried out to study the pattern selection and structure. [8] In the present thesis in the section 4.2 linear stability analysis is applied to a spatial language competition model.

The concept of diffusion-driven instability means that the system is stable to perturbations in its homogeneous steady state, but when diffusion is introduced through spatial perturbations the system becomes unstable. For the diffusion-driven instability of a steady state, it is important that the state is spatially dependent, meaning that in the absence of spatial variations it is linearly stable. From the linear analysis of the homogeneous steady state, the initial conditions for the diffusion-driven instability and for the generation of spatial patterns have been derived (specific steps can be found for example in Ref. [20]). Accordingly, the following inequalities must apply [20]

$$\begin{aligned} f_U + g_V &< 0 \\ f_U g_V - f_V g_U &> 0 \\ D_V f_U + D_U g_V > 2\sqrt{D_U D_V}\sqrt{(f_U g_V - f_V g_U)} &> 0. \end{aligned} \tag{2.2}$$

In the above conditions, the subscripts denote the partial derivatives of the functions f and g, with respect to the marked variable; d is the ratio of the diffusion coefficients. The functions are evaluated at the stationary state. From the conditions (2.2) it follows that f_U and g_V must be with opposite signs. Other model specific functions and parameter values can be derived from these initial conditions. [20]

3 Overview of Language dynamics

3.1 Development of different language competition models

Just like biological species, over time the new languages are born, they evolve and eventually some of them become extinct. In the 21st century, the world has reached a time when this natural process of extinction has greatly accelerated and 90% of the around 6000 languages currently spoken are in danger of dying out. Languages are a big part of the cultural diversity of the world, they define and affect the characteristics of different cultures and societies. In turn, the survival of a language is influenced by numerous factors, including geographical, historical, socioeconomic, demographics, etc. [21]

To preserve the endangered languages and cultures, the first step is finding the key factors behind language shift. Language shift is a process where speakers give up the use of one language in favor of another one [22]. Once knowing the driving factors, one can use the tools of physics, mathematics, statistics to create accurate models of language competition. On the one hand, the models should give insight into how the linguistic field is changing, but on the other hand, it is still difficult to identify the "goodness" of a model, in the context of contemporary world where outcomes are yet to be unknown. Considering that the world is constantly changing, the models must improve also. For example, as a result of globalization and social media, the significance of geographical or social factors is no longer the same. It is important that "For language dynamic models to stay relevant, they must be able to handle real-world changing scenarios, and to adapt, when current modeling frameworks mis-predict" [23].

In the field of language competition, two main types of families of models are represented by microscopic and macroscopic models. The macroscopic models describe the population size or density, treating the language as an object with a specific number of speakers. The population can be assumed to be homogeneous, evenly dispersed in a fixed area, where all individuals interact with one another (models usually described by ordinary differential equations) or distributed in space in some way (described by partial differential equations). The focus of language competition dynamics is on the change of the number of speakers, while the internal structure of the language (syntax, grammar and their changes) is ignored. On the other hand, the microscopic models monitor each speaker, their interactions with the others, and the individual transitions. Microscopic models can describe languages spoken across a network of speakers, letting each person to be connected to a certain number of other speakers. All these models are generally studied using computer simulations, employing Monte Carlo algorithms for their stochastic parts [21, 24].

One of the first macroscopic models was introduced in 2003 by Abrams and Strogatz [25], who developed a simple model where all speakers are monolinguals and the language dynamics is defined by the status (later known as prestige) parameter. The majority of language dynamics models that have been introduced afterward extend the Abrams-Strogatz model to improve certain aspects. For example, the Minett and Wang [26] model also includes bilinguals. Patriarca and Leppänen [27] extended the model with a spatial parameter and later Patriarca and Heinsalu [28] studied the effects of barriers and boundaries between the regions of different language groups. Mira and Paredes [29] added a new parameter describing the similarity of the two competing languages. Some most influential microscopic models were put forward by Schulze and Stauffer [30], who studied some versions of their models embedded in a network structure.

The classical models first predicted that the competition between two languages always ends in one language dominating over the other. Yet the idea that the extinction of one language is inevitable, in the context of bilingualism, doesn't fit today's reality anymore. Instead, newer models consider the possibility that bilingualism doesn't always lead to monolingualism. Coexistence of languages opened a new direction in the studies of language competition: investigating under which conditions languages are able to survive together, which factors govern the coexistence and how the speakers distribute in a common area.

The coexistence of different languages is often accompanied by patterns, i.e. languages survive when mainly concentrated in specific geographical regions. In this respect, Ref. [27] describes two languages which can live in equilibrium because of a barrier dividing the simulation box into two regions, each language being favored in one of the two regions. Kandler describes language segregation as a consequence of inhomogeneity of the dynamical parameters [31], such as the transition rate. Coexistence of languages in space in a fragmented landscape is possible – without patterns — due to other mechanisms, e.g. to volatilities $a < 1$ [32] or to a resilient behavior of the individuals in changing their status, as in the generalized two-options Naming Game model with parameter β [33, 34].

Recently, much attention has also been given to models predicting language coexistence, possibly accompanied by the Turing mechanism. In fact, in some cases, the spatial distribution of speakers could be interpreted as Turing patterns. For instance, Turing pattern in groups of speakers connected through a network was reported in Ref. [35] and spatial patterns were obtained in the study of a variant of the model of Pinasco and Romanelli (see Ref. [23]). It is therefore natural to check whether such kind of pattern arises in other language competition models.

3.2 Abrams-Strogatz model

As mentioned, one of the first mathematical models of language competition was proposed by Abrams and Strogatz. The model describes the struggle for speakers between two languages. At any time a speaker of language one can instantly switch to language two and vice versa; there are no transition states in the switch. The driving force for individuals to change their language is the attractiveness of a language. It is defined by the number of speakers together with the status of the language (a combination of socioeconomic factors, e.g. the language prestige and usefulness). [28]

The scheme for the Abrams-Strogatz model is illustrated in Figure 4 and the model can be swritten as follows:

$$\begin{aligned} \frac{\partial N_U}{\partial t} &= k_{VU} N_U^\alpha N_V - k_{UV} N_U N_V^\alpha \\ && . \\ \frac{\partial N_V}{\partial t} &= -k_{VU} N_U^\alpha N_V + k_{UV} N_U N_V^\alpha \end{aligned} \tag{3.1}$$

Here N_U and N_V are fractions of speakers of the two linguistic groups. The constant α determines the volatility of a language (choosing the other language over the current one) and $k_{UV}, k_{VU} \in (0,1)$ are such that $k_{UV}+k_{VU} = 1$ and they represent, respectively, the status (or attractiveness) of language V and U. [36] The status and volatility of a language are determined by fitting the model to the empirical data of some specific area's population speaking the language [24]. The value $\alpha = 1.31 \pm 0.25$ was suggested in Ref. [37].

The model has three equilibrium states: for $a > 1$, two states are stable, in which the entire population speaks one of the two languages and the other language has become extinct ($N_U \neq N_V$), while in the third stable

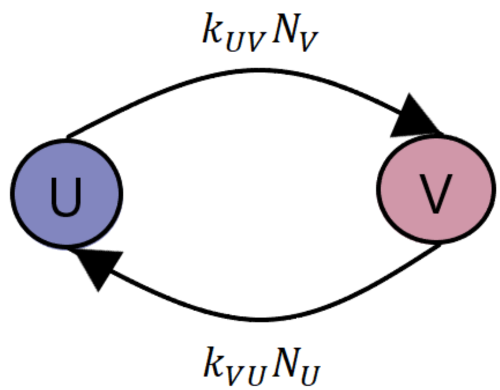

Figure 4: General scheme for the Abrams-Strogatz model with two languages U and V with statuses k_{UV} and k_{VU} and fractions of speakers N_U and N_V.

state both languages have a number of speakers larger than zero but it is unstable. Therefore, for $a > 1$ the model predicts the absolute dominance of one language and the extinction of the other language [24], shown in Figure 5. In the high volatility regimes, where $\alpha < 1$ and language switching is frequent, the coexistence of languages is possible: the first two equilibrium states become unstable, while the third unstable point becomes stable [38]. Different states are reached depending on the initial population sizes N_U and N_V, volatility parameter α and both language's statuses k_{UV} and k_{VU} [28].

Like for most models of real-world scenarios, a few assumptions have been made to gain this simplified model. The model doesn't consider the evolution of languages during its timeline and solely describes the evolution of the population size of the two linguistic groups. It is therefore similar to a population dynamics model of two biological species [28]. One of the most important assumptions is the uniform social and spatial structure of the population. The model considers only the competition between two languages in the same geographical area with similar resources. So the speakers are interacting with each other constantly, creating a highly connected population [21, 40].

The main application of Abrams-Strogatz model is to predict how the use of languages will evolve in time. It also acts as an alert system pointing out when a language starts to be in danger of extinction, so different measures can be used to prevent it from happening. Playing through different scenarios by tuning the parameters in the equations and simulating the evolution

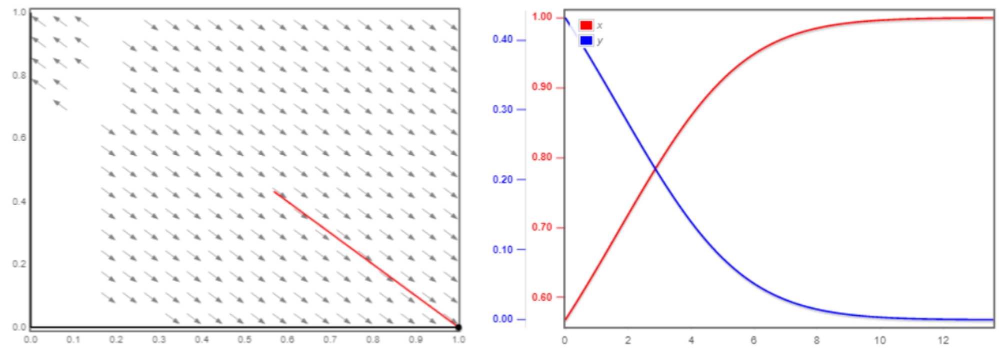

Figure 5: The behaviour of Abrams-Strogatz model described by equation (3.1) with parameters $k_{UV} = 0.8, k_{VU} = 0.5, \alpha = 1.3$ and initial conditions $N_U = 0.568, N_V = 0.432$. The model predicts the dominance of language U and the extinction of language V. The figure is made using slope and direction fields generator [39].

process, helps to see the various outcomes. Finally, one can reach the best solution and find the desired parameter values for that. The tuned model can then be applied in reality by using the means of education, policy-making, advertising, technology, laws, etc. [21] In addition, it was later shown that Equation (3.1) can be applied to model other competitions as well, for example, competition between various cultural traits, particularly the decrease in religious affiliation [36].

In their study, Abrams and Strogatz used historical data to test their model against declining languages such as Welsh, Scots Gaelic, and Quechua. Although most of the data was taken from public census figures, Abrams also visited Peru to collect data and interview the people himself. They concluded that it is possible to preserve an endangered language. Abrams gave an example of French language almost disappearing in Quebec 35 years ago, which was then saved with the help of government passing laws and adopting policies to favor and in some cases even require the use of French [41]. Later, there have been many case studies using Abrams-Strogatz model and also comparing it to the other models. For example Sutantawibul et al. [24] used three different models (Abrams-Strogatz [25], Castelló [42], Mira and Paredes [29]) to compare the outcomes of language competition in Catalonia (Catalan and Spanish), Houston (Spanish and English), Brussels (Dutch and French), Spain (Euskera and Spanish) and Canada (French and

English). But the complications of acquiring parameter values from empirical data still remain, especially in many cases lacking direct competition data.

4 Results for the spatial model

4.1 Extending the original Abrams-Strogatz model in space

The original Abrams-Strogatz model (3.1), where volatility $\alpha \geq 1$, predicts that one or the other language prevails. But this is not the case in many real situations and it is clear that the model neglects various factors that may affect the final outcome. One of the missing factors from the original model (3.1) is the space parameter. Adding the space dimensions to Abrams-Strogatz model can change the result of the system decidedly. It can lead to the coexistence of the languages where both are more concentrated in different parts of the domain. [43] In this section the original Abrams-Strogatz model (3.1) is extended with the spatial parameter that introduces the spreading of the language in space. To take the dependence of space into account a reaction-diffusion system is used for investigation. The stability analysis is carried out to examine the coexistence of two languages with two different diffusion coefficients and to determine the necessary conditions for Turing patterns.

Equations (4.1) are formally equivalent to Equations (3.1) defining the Turing system:

$$\begin{aligned} \frac{\partial N_U}{\partial t} &= D_U \bigtriangledown^2 N_U \underbrace{-k_{UV} N_U N_V^{\alpha} + k_{VU} N_V N_U^{\alpha}}_{f} \\ \frac{\partial N_V}{\partial t} &= D_V \bigtriangledown^2 N_V \underbrace{+k_{UV} N_U N_V^{\alpha} - k_{VU} N_V N_U^{\alpha}}_{g} . \end{aligned} \tag{4.1}$$

The spatial model divides similarly the fixed population of speakers into two groups: the speakers of language U and the speakers of language V. In the Abrams-Strogatz model, there are no bilinguals included nor an intermediate state in the switch from language U to language V. As described in section 2.3, the Turing system usually consists of two nonlinear partial differential equations. In the Equations (4.1) the speakers of the two languages are marked with N_U and N_V. Scalars D_U and D_V mark the space-dependent diffusion coefficients and for the analysis $D_V \neq D_V$ is chosen. The constants k_{UV} and k_{VU} describe accordingly the shift from language U to V and V to

U. Parameter $\alpha > 0$ is a scalar defining the system dynamics. To determine whether Turing patterns exist in this reaction-diffusion system and under what conditions, the system will be studied through the use of linear stability analysis.

4.2 Linear stability analysis of the spatial Abrams-Strogatz model

Linear stability analysis reveals the behavior of the system around its stationary states. Therefore the first step in the analysis is finding the homogeneous stationary states (N_{U_0}, N_{V_0}) of the system. This can be done by assigning the reaction kinetics to zero, i.e $f(N_U, N_V) = g(N_U, N_V) = 0$. Since the system consists of two symmetrical equations it has two symmetrical stationary states as well:

$$\begin{cases} N_{U_0} = 0 \\ N_{V_0} = c \end{cases} \qquad \begin{cases} N_{U_0} = c \\ N_{V_0} = 0 \end{cases}$$

Because of the symmetrical behavior, solely the stability of the first stationary state is analyzed. The idea of the stability analysis is to introduce a small wave-like spatially non-uniform perturbation to the system at its stationary state and then study the response of the system. If over time the perturbation converges to zero and the system moves back to the stationary state then the state is considered stable. Otherwise, if the perturbation amplifies and the system initially close to the stationary state starts to move farther away, then patterns will occur.

In the context of spatial Abrams-Strogatz model, introducing perturbations to the system one obtains $N_U = N_{U_0} + dw$ and $N_V = N_{V_0} + dw$. More precisely, studying only the first stationary state, $N_U = dw$ and $N_V = c + dw$, where perturbation dw can be written as [8]

$$dw(x,t) = \sum_j c_j e^{\lambda_j t} e^{-ik_j \cdot x} \tag{4.2}$$

The wave modes k_j govern the spatial part of the solution and the eigenvalues λ_j the temporal part [8]. Substituting this into the initial Equations

(4.1) (more detailed description can be found in [12]) leads to the eigenvalue problem

$$|A - Dk_j^2 - \lambda_j I| = 0 \tag{4.3}$$

for each wave mode k_j. The matrix A consists of the partial derivatives of functions f, g with respect to N_U and N_V

$$A = \begin{pmatrix} f_{N_U} & f_{N_V} \\ g_{N_U} & g_{N_V} \end{pmatrix}_{(N_{U_0}, N_{V_0})}. \tag{4.4}$$

Evaluating partial derivatives

$$\begin{cases} f_{N_U}(N_{U_0}, N_{V_0}) = -k_{UV} N_{V_0}^{\alpha} + \alpha k_{VU} N_{V_0} N_{U_0}^{\alpha-1} \\ \\ f_{N_V}(N_{U_0}, N_{V_0}) = -\alpha k_{UV} N_{U_0} N_{V_0}^{\alpha-1} + k_{VU} N_{U_0}^{\alpha} \\ \\ g_{N_U}(N_{U_0}, N_{V_0}) = k_{UV} N_{V_0}^{\alpha} - \alpha k_{VU} N_{V_0} N_{U_0}^{\alpha-1} \\ \\ g_{N_V}(N_{U_0}, N_{V_0}) = \alpha k_{UV} N_{U_0} N_{V_0}^{\alpha-1} - k_{VU} N_{U_0}^{\alpha} \end{cases}$$

at the stationary state $(0, c)$ and substituting to (4.4), the matrix A can be written as

$$A = \begin{pmatrix} -k_{UV} c^{\alpha} & 0 \\ \\ k_{UV} c^{\alpha} & 0 \end{pmatrix}. \tag{4.5}$$

The matrix I in the eigenvalue problem (4.3) is an identity matrix and the matrix D consists of diffusion coefficients:

$$I = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \qquad D = \begin{pmatrix} D_U & 0 \\ 0 & D_V \end{pmatrix}. \tag{4.6}$$

After applying everything to (4.3), it leads to the determinant

$$\left| \begin{pmatrix} -k_{UV} c^{\alpha} - D_U k_j^2 - \lambda_j & 0 \\ \\ k_{UV} c^{\alpha} & -D_V k_j^2 - \lambda_j \end{pmatrix} \right| \tag{4.7}$$

and thus to the characteristic polynomial of the system (4.1)

$$c^\alpha k_j^2 k_{UV} D_V + c^\alpha k_{UV}\lambda_j + k_j^4 D_U D_V + k_j^2 D_U \lambda_j + k_j^2 D_V \lambda_j + \lambda_j^2 = 0. \quad (4.8)$$

Solving the characteristic equation for each wave mode k_j gives two dispersion relations $\lambda_1(k)$ and $\lambda_2(k)$ that satisfy the equation. Since the growing modes have the form of $We^{ikr}e^{\lambda(k)t}$, where W marks the amplitude and $\lambda(k)$ the growth rate, it can be seen that the solutions with negative growth rate will converge to zero when $t \to \infty$ and thus remain stable. The solutions with positive growth rate, however, will grow exponentially resulting in the formation of patterns. Thus the eigenvalues of (4.8) help to determine the stability of the system and predict the parameter values that lead to the Turing instability. [8]

Solving characteristic polynomial (4.8) one obtains two values

$$\begin{cases} \lambda_1 = -k_{UV}c^\alpha - D_U k_j^2 \\ \lambda_2 = -k_j^2 D_V \end{cases} \quad (4.9)$$

The second solution λ_2 is negative because the coefficients D_U, D_V are always positive. Also the first solution, in which the parameters α, c, and the rate constant k_{UV} have positive values, cannot lead to an instability to occur.

Checking the stability conditions (2.2), it is revealed that the linear stability of the stationary state is not spatially dependent. In the case of spatial Abrams-Strogatz model $f = -g$ and therefore $f_{N_U} = -g_{N_U}$ and $f_{N_V} = -g_{N_V}$. Applying these changes to the second condition in (2.2) it can be seen that $f_{N_U}g_{N_V} - f_{N_V}g_{N_U} \equiv 0$ by writing

$$\begin{aligned} f_{N_U}g_{N_V} - f_{N_V}g_{N_U} &= -g_{N_U}g_{N_V} + g_{N_V}g_{N_U} = \\ &= \alpha k_{UV}^2 N_{U_0} N_{V_0}^{2\alpha-1} - k_{UV}k_{VU}N_{U_0}N_{U_0}^\alpha N_{V_0}^\alpha - \\ &-\alpha^2 k_{UV}k_{VU}N_{U_0}^{2\alpha-1}N_{V_0}^{2\alpha-1} + \alpha k_{VU}^2 N_{U_0}^{2\alpha-1}N_{U_0} - \\ &-\alpha k_{UV}^2 N_{U_0}N_{V_0}^{2\alpha-1} + k_{UV}k_{VU}N_{U_0}N_{U_0}^\alpha N_{V_0}^\alpha + \\ &+\alpha^2 k_{UV}k_{VU}N_{U_0}^{2\alpha-1}N_{V_0}^{2\alpha-1} - \alpha k_{VU}^2 N_{U_0}^{2\alpha-1}N_{U_0} = 0\,. \end{aligned} \quad (4.10)$$

For Turing instability to occur, one needs that $f_{N_U}g_{N_V} - f_{N_V}g_{N_U} > 0$. So it can be concluded that for the spatial Turing model, and for all models defined by a dynamics where $f = -g$, the patterns do not occur since the general conditions for diffusion-driven instability (2.2) are not met. The numerical simulations illustrated in Fig. 6, show the stability of the model without patterns.

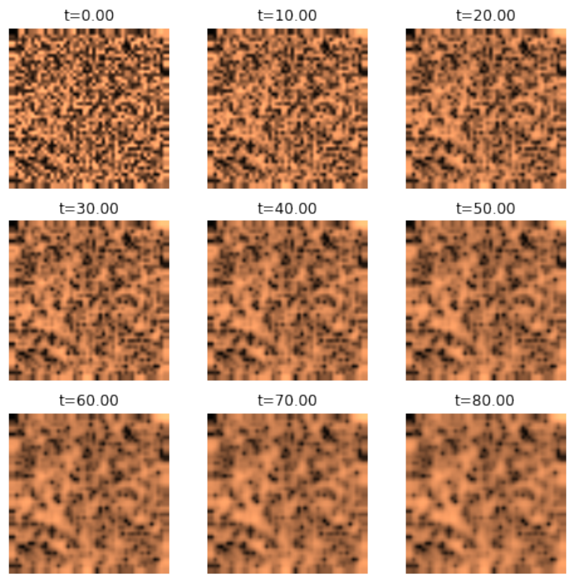

Figure 6: The simulation of the Abrams-Strogatz spatial model. The state of the system is plotted 9 times in 50 x 50 grid based on 90 000 iterations for a time step 0.001. The following parameters are used for the simulation: $\alpha = 0.95, D_U = 0.498, D_V = 0.502, k_{UV} = 0.009, k_{VU} = 0.007$.

5 Conclusion

The studies of Turing patterns and diffusion-driven instability have shown promising results in explaining the details of morphogenesis and the behavior of reaction-diffusion systems. Described by simple mathematical models, the Turing systems are able to explain extremely complex mechanisms. The most notable part of the Turing system is that, unlike other complex systems, its behavior and thus the occurrence of patterns is determined intrinsically and does not depend on the initial configuration. The type and characteristics of patterns can be adjusted by changing only one parameter value in the model. Although the evidence of these patterns can be found in almost every field of science starting from biology and chemistry until social and medical sciences, the definite link between the theory and examples of patterns is yet to be found.

Languages, just like species, are competing against one another and preserving the endangered ones plays an important role in our culturally diverse world. Studying the driving forces for shifting from one language to another, helps to predict the future of a language and its speakers. Recently more attention has been turned to analyzing the specific conditions that result in the coexistence of languages. While multiple languages coexist in a uniform area the spatial distribution of the speakers sometimes forms specific patterns that can be interpreted as Turing patterns.

This thesis presented the background and method for analyzing the occurrence of Turing patterns in spatial models. The conditions for diffusion-driven instabilities were presented and finally, the analysis of Abrams-Strogatz spatial language competition model with two different languages with different diffusion rates was carried out. The results showed that in the spatial Abrams-Strogatz model the Turing patterns do not occur due to the specific form of model dynamics. The general conditions for diffusion-driven instability are not met and over time the model stabilizes itself. To illustrate the findings, numerical simulations of the model were shown.

6 Appendix A

6.1 Jupyter Notebook code

The Jupyter Notebook code used in this thesis for numerical simulations is a modified version of Cyrille Rossant's code from his tutorial of simulating partial differential equations. The code is taken from the book "IPython Interactive Computing and Visualization Cookbook" by the same author. The Jupyter Notebook code uses Python. [44].

```
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline

a = 0.95
D_u = 0.498
D_v = 0.502
k_uv = 0.009
k_vu = 0.007
gridsize = 50
dx = 5
T = 90
dt = 0.001
n = int(T / dt)  # number of iterations
U = np.random.rand(gridsize, gridsize)
V = np.random.rand(gridsize, gridsize)

def compute_laplacian(A):
        A_top = A[0:-2, 1:-1]
        A_center = A[1:-1, 1:-1]
        A_bottom = A[2:, 1:-1]
        A_right = A[1:-1, 2:]
        A_left = A[1:-1, 0:-2]
        return (A_top + A_left + A_bottom + A_right -
                4 * A_center) / (dx**2)

def show_patterns(U, ax = None):
        ax.imshow(U, cmap = plt.cm.copper,
                                interpolation='bilinear',
```

```
                              extent=[-1, 1, -1, 1])
        ax.set_axis_off()

fig, axes = plt.subplots(3, 3, figsize = (8, 8))
step_plot = n // 9

for i in range(n):
        deltaU = compute_laplacian(U)
        deltaV = compute_laplacian(V)

        Uc = U[1:-1, 1:-1]
        Vc = V[1:-1, 1:-1]

        U[1:-1, 1:-1], V[1:-1, 1:-1] = \
                Uc + dt * (D_u * deltaU * Uc \
                        - (k_uv * Uc * Vc**a) \
                        +  (k_vu * Vc * Uc**a)), \
                Vc + dt * (D_v * deltaV * Vc \
                        + (k_vu * Uc * Vc**a) \
                        -  (k_uv * Vc * Uc**a))

        for A in (U, V):
                A[0, :] = A[1, :]
                A[-1, :] = A[-2, :]
                A[:, 0] = A[:, 1]
                A[:, -1] = A[:, -2]

        if i % step_plot == 0 and i < 9 * step_plot:
                ax = axes.flat[i // step_plot]
                show_patterns(U, ax=ax)
                ax.set_title('t=%s' %format(i * dt, '.2f'))
```

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