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Clustering drug-drug interaction networks with energy model layouts: community analysis and drug repurposing

Lucreția Udrescu[1], Laura Sbârcea[1], Alexandru Topîrceanu[2], Alexandru Iovanovici[2], Ludovic Kurunczi[3], Paul Bogdan[4] & Mihai Udrescu[2]

Analyzing drug-drug interactions may unravel previously unknown drug action patterns, leading to the development of new drug discovery tools. We present a new approach to analyzing drug-drug interaction networks, based on clustering and topological community detection techniques that are specific to complex network science. Our methodology uncovers functional drug categories along with the intricate relationships between them. Using modularity-based and energy-model layout community detection algorithms, we link the network clusters to 9 relevant pharmacological properties. Out of the 1141 drugs from the DrugBank 4.1 database, our extensive literature survey and cross-checking with other databases such as Drugs.com, RxList, and DrugBank 4.3 confirm the predicted properties for 85% of the drugs. As such, we argue that network analysis offers a high-level grasp on a wide area of pharmacological aspects, indicating possible unaccounted interactions and missing pharmacological properties that can lead to drug repositioning for the 15% drugs which seem to be inconsistent with the predicted property. Also, by using network centralities, we can rank drugs according to their interaction potential for both simple and complex multi-pathology therapies. Moreover, our clustering approach can be extended for applications such as analyzing drug-target interactions or phenotyping patients in personalized medicine applications.

Drug repositioning or repurposing is an emerging concept that consists of identifying new therapeutic indications for already existing active pharmaceutical ingredients[1]. Over the recent years, repositioning strategies have been intensely investigated, due to the outstanding advances in scientific and technological fields[2,3]. The motivation behind this trend is the fact that, despite the constantly growing resources invested in drug discovery[4], the drug design process is still cumbersome, slow and prone to many errors[5,6]. As a result, the number of new approved bio-active molecules is not increasing anymore[7]; therefore, the pharmaceutical industry is forced to come up with alternative solutions[8]. The fact that the repurposing strategy can be the right answer for current challenges in the pharmaceutical industry is further stressed by a recent report, which states that 20% of the new drugs brought on the market in 2013 are actually repositionings[9]. Another motivation for drug repositioning is that it fits the aims and scopes of personalized and precision medicine[10].

Traditionally, drug repositioning mostly relies on chance and it is achieved by experimentally exploring the link between molecular structure and biological activity[11]. The advent of big data gathering and analysis has spurred the use of computational approaches in many aspects of pharmacology and drug design, including drug repurposing. Indeed, computational models are used to uncover drug interactions which were not discovered during clinical trials[12], or to predict drug safety[13]. Moreover, using in-silico tools creates a visual and intuitive system for representing drug interactions[14], thus helping medical and pharmaceutical practice. In the case of drug repositioning, computational strategies explore the relationships between drug databases on one hand, and genomic, transcriptomic and phenotypic data on the other hand[2]. The computational approaches used to perform

[1]"Victor Babeş" University of Medicine and Pharmacy Timişoara, Faculty of Pharmacy, Timişoara, 300041, Romania. [2]University Politehnica of Timişoara, Department of Computer and Information Technology, Timişoara, 300223, Romania. [3]Institute of Chemistry Timişoara of the Romanian Academy, Timişoara, 300223, Romania. [4]University of Southern California, Ming Hsieh Department of Electrical Engineering, Los Angeles, CA 90089-2563, USA. Correspondence and requests for materials should be addressed to M.U. (email: mudrescu@cs.upt.ro)

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Uncovering the fingerprint of online social networks using a network motif based approach

Alexandru Topirceanu*, Alexandra Duma, Mihai Udrescu

Department of Computers and Information Technology, Politehnica University Timisoara

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ABSTRACT

Complex networks facilitate the understanding of natural and man-made processes and are classified based on the concepts they model: biological, technological, social or semantic. The relevant subgraphs in these networks, called network motifs, are demonstrated to show core aspects of network functionality and can be used to analyze complex networks based on their topological fingerprint. We propose a novel approach of classifying social networks based on their topological aspects using motifs. As such, we define the classifiers for regular, random, small-world and scale-free topologies, and then apply this classification on empirical networks. We then show how our study brings a new perspective on differentiating between online social networks like Facebook, Twitter and Google Plus based on the distribution of network motifs over the fundamental topology classes. Characteristic patterns of motifs are obtained for each of the analyzed online networks and are used to better explain the functional properties behind how people interact online and to define classifiers capable of mapping any online network to a set of topological-communicational properties.

1. Introduction

Complex networks cover an active area of scientific research inspired largely by the empirical study of real-world networks such as communication networks, economical networks and social networks. They are classified into four major types, based on the context which they model: biological networks (e.g., metabolic networks, transcription regulatory networks, protein–protein interaction networks, protein structure networks, neural networks, ecological networks, and natural food chains) [1,15,50], social networks (e.g. friendship networks, citation networks, voter networks, world markets, and political structures) [36,42,50], technological networks (e.g., computer networks, electrical circuits, and road networks) [1], and semantic networks (e.g. word-net [31] and recipe networks [43]). Without exception, all these networks can be represented as graphs, which include a wide variety of subgraphs. One fundamental property of networks are the so-called network motifs, which were introduced by Milo et al. [33]. They represent recurrent and statistically significant subgraphs or patterns in these complex networks. The fact that motifs repeat themselves in specific networks, or even among various networks, is highly correlated with the concepts of evolutionary theory. Each of these subgraphs, defined by a particular pattern of interactions between graph nodes, may reflect a framework in which particular functions are achieved efficiently. Motifs are considered to have a notable importance today because they may reflect underlying functional properties [30]. In light of their ability to uncover structural design principles of complex networks, motifs have been slowly adopted from Systems Biology into the broader perspective of Network Science. Although they foster a deep insight into the functional abilities of a network, their detection is computationally challenging even by current standards.

Particular research has been done in the areas of biology and genetics where motifs are associated with functional roles of transcription regulation networks which control the expression of genes [2]. Experimental studies show how motifs serve as basic building blocks of transcription networks. Another example is the understanding of how some cellular components are conserved across species but others evolve rapidly [54]. A notable study brings forward this new motif-inspired paradigm to uncover drug development strategies that help in the identification of drug target candidates [12]. A similar scientific track to our proposal is presented by Wang et al. in a study focused on detecting important nodes, not through the classic centrality metrics approach, but through specific motif patterns[49].

While conceptually (and functionally), complex networks can represent biological, technological, social or conceptual relationships between entities, we propose a motif-based analysis of networks from the topological perspective. As such, the fundamental topological families are: regular networks, random networks, small-world networks and scale-free networks [50]. Regular [8] and random

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* Corresponding author. at Faculty of Automation and Computers, Politehnica University of Timisoara, Bd. Vasile Parvan 2, 300223, Timisoara, Romania. Tel.: +40 256 123456.

E-mail address: alext@cs.upt.ro (A. Topirceanu).

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Statistical fidelity: a tool to quantify the similarity between multi-variable entities with application in complex networks

Alexandru Topirceanu and Mihai Udrescu

Department of Computer and Information Technology, Politehnica University Timisoara, Timisoara, Romania

ABSTRACT
Complex networks are often characterized by their underlying graph metrics, yet there is no unified computational method for comparing networks to each other. Given that complex networks are entities characterized by a set of known properties, our problem is reduced to quantifying the similarity between the multi-variable entities. To address this issue, we introduce the new statistical fidelity metric, which can compare any types of entities, characterized by specific individual metrics, in order to gauge the similarity of the entities under the form of a single number between 0 and 1. To test the efficiency of statistical fidelity, we apply our composite metric in the field of complex networks, by assessing topological similarity and realism of social networks and urban road networks. Pinned against other statistical methods, such as the cosine similarity, Pearson correlation, Mahalanobis distance and fractal dimension, we highlight the superior analytic power of statistical fidelity.

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1. Introduction

An increasing number of interdisciplinary fields of science are focused on network science, since the theory of complex networks can be used to reveal similar properties when modelling many real-world phenomena. The ability to emphasize similar properties works regardless of the network's origin, i.e. natural or synthetic [12,19]. State-of-the-art literature consists of network models which describe spatial proximity, distribution of friendships, neural networks, mechanisms of protein interactions, food chains in the animal kingdom, layouts of urban transportation, scientific collaborations, sexual interaction patterns between people, semantics of words in different languages, recipe-based interaction of ingredients, global market networks, political ties [1,11,14,16,19,30,38,43], etc. As such, complex networks fall into four main categories [43]: technological [19,40,44], biological [2,11,26], social [1,8,11], and semantic [38,43].

Within the network paradigm, the capacity to collect and analyse massive amounts of data has a big impact on scientific fields such as biology, economy and physics [19]. However, the emergence of data-driven computational science has been much slower, carefully directed by a few intrepid computer scientists, physicists and social scientists [4,19,27,29,45]. Regardless of the representation of nodes, edges, edge directions and edge weights, graph models of big data [12,14] are often subjected to numerical comparison, sampling and statistical analysis to extract relevant patterns. To that end, network scientists employ a wide range of comparison techniques, but there is no single computational methodology to express similarity/dissimilarity in an objective and synthetic manner.

CONTACT Alexandru Topirceanu ✉ alext@cs.upt.ro

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Tolerance-based interaction: a new model targeting opinion formation and diffusion in social networks

Alexandru Topirceanu[1], Mihai Udrescu[1], Mircea Vladutiu[1] and
Radu Marculescu[2]

[1] Department of Computer and Software Engineering, Politehnica University Timisoara,
Timisoara, Romania
[2] Department of Electrical and Computer Engineering, Carnegie Mellon University, Pittsburgh,
PA, United States

ABSTRACT

One of the main motivations behind social network analysis is the quest for understanding opinion formation and diffusion. Previous models have limitations, as they typically assume opinion interaction mechanisms based on thresholds which are either fixed or evolve according to a random process that is external to the social agent. Indeed, our empirical analysis on large real-world datasets such as Twitter, Meme Tracker, and Yelp, uncovers previously unaccounted for dynamic phenomena at population-level, namely the existence of distinct *opinion formation phases* and *social balancing*. We also reveal that a phase transition from an erratic behavior to social balancing can be triggered by network topology and by the ratio of opinion sources. Consequently, in order to build a model that properly accounts for these phenomena, we propose a new (individual-level) opinion interaction model based on tolerance. As opposed to the existing opinion interaction models, the new tolerance model assumes that individual's inner willingness to accept new opinions evolves over time according to basic human traits. Finally, by employing discrete event simulation on diverse social network topologies, we validate our opinion interaction model and show that, although the network size and opinion source ratio are important, the phase transition to social balancing is mainly fostered by the democratic structure of the small-world topology.

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Corresponding author
Mihai Udrescu,
mudrescu@cs.upt.ro,
mudrescu@gmail.com

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INTRODUCTION

Social network analysis is crucial to better understand our society, as it can help us observe and evaluate various social behaviors at population level. In particular, understanding the social opinion dynamics and personal opinion fluctuation (*Golbeck, 2013*; *Geven, Weesie & Van Tubergen, 2013*; *Valente et al., 2013*) plays a major part in fields like social psychology, philosophy, politics, marketing, finances and even warfare (*Easley & Kleinberg, 2010*; *Pastor-Satorras & Vespignani, 2001*; *Fonseca, 2011*). Indeed, the dynamics of opinion fluctuation in a community can reflect the distribution of socially influential people across that community (*Kempe, Kleinberg & Tardos, 2003*; *Hussain et al., 2013*; *Muchnik, Aral &*

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Simulated fault injection methodology for gate-level quantum circuit reliability assessment

Mihai Udrescu *, Lucian Prodan, Mircea Vlăduţiu

University Politehnica, 2, V. Parvan Blvd., 300223 Timişoara, Romania

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A B S T R A C T

In quantum computation the importance of fault tolerance is paramount, due to the low reliability of the quantum circuit components. Therefore, several fault tolerance assessing tools and methodologies have been developed; most of them are analytic, dependent on the adopted fault model, and based on some simplifying assumptions. Simulation could have been a more realistic and accurate alternative had it not be confronted with the high complexity of simulating quantum circuits. However, a hardware description language (HDL) implementation for simulated fault injection (SFI) was proposed and tested for limited-size quantum circuits. This paper proposes a new, hybrid simulation-analytic, SFI-based methodology for quantum circuit fault tolerance assessment that is scalable to arbitrary size circuits. Each logical qubit from the quantum circuit is encoded by several physical qubits, and each logical gate can be decomposed into physical gates (acting on physical qubits). The HDL-based SFI evaluation result from the physical qubit level comes under the form of a failure rate, which is then fed to the analytical assessment process performed at the logical level. The analytical and simulation results prove the fact that, while maintaining a high accuracy of reliability assessment, this hybrid methodology can be applied to larger quantum circuits.

1. Introduction

Quantum computation (QC) has yet to become completely feasible and scalable, due to the inner nature of quantum physics, i.e. the quantum states are extremely fragile and therefore prone to frequent errors [13]. As already prescribed by ITRS in its document dedicated to the emerging research devices, in order to deal with these reliability problems, efficient fault tolerance (FT) techniques have to be refined and then applied in QC [11]. Several approaches for QC fault tolerance have already been proposed, but their effectiveness is still an open issue, due to the technological uncertainties [1,2,17,27,28].

As such, developing a technology-independent reliability assessment tool for quantum circuits becomes extremely important [22]. One possibility to evaluate the FT efficiency is to use analytical methods for computing quantum circuit's reliability [8]. This alternative is fast, inexpensive, scalable and useful at all design stages, but it is based on some simplifying assumptions which in turn affect its accuracy. The second possibility is to rely on testing real quantum devices; it is the most accurate and expensive but – at the same time – highly dependent of the actual technological implementation, therefore appropriate only for the later design stages [7]. The third possibility, consisting of SFI techniques, is a tradeoff between accuracy and cost, being already used for conventional circuit design [10,12]. However, the problem with this alternative is that it is not scalable, due to the fact that quantum circuit simulation requires exponential run-times with the circuit size [6,23,26].

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* Corresponding author.
E-mail addresses: mudrescu@cs.upt.ro (M. Udrescu), lprodan@cs.upt.ro (L. Prodan), mvlad@cs.upt.ro (M. Vlăduţiu).

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Design for Dependability in Emerging Technologies

LUCIAN PRODAN, MIHAI UDRESCU, OANA BONCALO, and
MIRCEA VLADUTIU
Politehnica University of Timisoara

As current microelectronics will reach their physical limits within the foreseeable future, emerging technologies may offer a solution for maintaining the trends to increase computing performance. Biologically-inspired and quantum computing represent two emerging technology vectors for novel computing architectures within nanoelectronics. However, potential benefits will come at the cost of increased device sensitivity to the surrounding environment. This article provides a dependability perspective over these technologies from a designer's standpoint. Maintaining or increasing the dependability of unconventional computational processes is discussed in two different contexts, a bio-inspired computing architecture (the *Embryonics* project) and a quantum computational architecture (the *QUERIST* project).

Categories and Subject Descriptors: B.8.1 [**Performance and Reliability**]: Reliability, Testing, and Fault-Tolerance; C4 [**Performance of Systems**]: Fault-tolerance, reliability, availability, and serviceability

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1. INTRODUCTION

As modern life has come to rely extensively on computers, their accurate and fast operation is expected. From the very start, a major aim of computer designers was to achieve any additional performance that was possible; they are now focusing their priority on dependable delivery of best performance.

Author's address: L. Prodan, Politehnica University of Timisoara, Timisoara, Romania; email: lprodan@cs.upt.ro.

Probabilistic Modeling of Tolerance-based Social Network Interaction

Mihai Udrescu and Alexandru Topirceanu*
Department of Computers and Information Technology, Politehnica University Timisoara, Romania

***Abstract*— Social network analysis focuses on understanding opinion formation and diffusion, but often relies on models which have limitations, as they typically assume opinion interaction mechanisms based on thresholds which are either fixed or evolve according to an external random process. However, a new opinion interaction model was developed which relies on so-called node *tolerance*. This new tolerance model assumes that individual's inner willingness to accept new opinions evolves over time according to basic human traits. This model discusses the existence of a stable opinion equilibrium (*social balance*) or a convergence towards intolerance (lack of opinion fluctuation), by employing computer simulation. This paper provides a probabilistic evaluation of the tolerance-based social network interaction model. As such, a Markov chain model is used in order to assess the asymptotic behavior of a social agent. In other words, the main result of this evaluation is the probability of tolerant behavior as the time approaches infinity. We obtain a clear numerical differentiation between topologies with local or preferential links, and topologies with random or long-range links in terms of the tolerance balance their are able to maintain in time.**

Keywords: opinion dynamics, agent interaction model, tolerance, Markov chains, computer simulation.

I. INTRODUCTION

The ability to monitor and quantify social opinion dynamics and fluctuation [1], [2], [3] at both micro- and macroscopic levels of society plays an important part in fields like social psychology, philosophy, politics, marketing, finances and even warfare [4], [5], [6]. The dynamics of opinion in a community can reflect the distribution of socially influential people across that community [7], [8], [9]; this is because social influence is the ability of agents (individuals) to alter others' opinion in either one-on-one or group settings [10], [11], [12]. Without social influence, the society would have an erratic behavior which would be hard to predict.

Existing studies on opinion formation and evolution [13], [14], [15], [3], [16], [17] revolve around the contagion principle of opinion propagation. However, such studies offer limited predictability and realism because they are generally based on opinion interaction models which use either fixed thresholds [18], [19], or thresholds evolving according to simple probabilistic processes that are not driven by the internal state of the social agents [20], [21]. To mitigate these limitations, the dynamical features of opinion spreading have to be targeted by a mathematical model. Many recurring real-world observations can be explained using the tolerance model introduced as a new social interaction model which takes into account the evolution of individual's inner state [22]. The model was validated using empirical data from Yelp, Twitter and MemeTracker, and by using our opinion dynamics simulation framework - SocialSim, which includes multiple complex topological models, as well as customizable opinion interaction and influence models.

The work started in [22] proposes that we assume a social network where continuous opinion is exchanged between agents through a single diffusion interaction mechanism [16].

Given a social network $G = \{V, E\}$, we define the neighborhood of agent $i \in V$ as $N_i = \{j \mid (i, j) \in E\}$. The disjoint set of stubborn agents $V_0, V_1 \in V$ (opinion sources) never change their opinion, while all other (regular) agents $V \setminus \{V_0 \cup V_1\}$ update their opinion based on the opinion of one or all of their direct neighbors. We use $o_i(t)$ to represent the opinion of agent i at time t. Normal (regular) agents can start with a predefined random opinion value $o_i(0) \in [0, 1]$. The process of changing the opinion of regular agents is triggered according to a Poisson distribution and consists of either adopting the opinion of a randomly chosen direct neighbor, or an averaged opinion of all direct neighbors.

We represent with $s_i(t)$ the state of an agent i at moment t having continuous opinion $o_i(t)$. In case of the discrete opinion representation $o_i(t) = s_i(t)$; in case of the continuous opinion representation $s_i(t)$ is given by equation 1.

$$s_i(t) = \begin{cases} 0 & if\ \ 0 \le o_i(t) < 0.5 \\ none & if\ \ o_i(t) = 0.5 \\ 1 & if\ \ 0.5 < o_i(t) \le 1 \end{cases} \tag{1}$$

In our proposed interaction model, the social agent a updates his/her current opinion $o_a(t)$, upon interaction with a randomly chosen neighbor n (having opinion $o_n(t)$), at the next time step $t + 1$. In the assumed social network, agents a and n are neighbor nodes if there is a link (or edge) that directly connects them. Some agents do not have an opinion, so interacting with these agents will generate no opinion update. If agent a interacts with an agent n that has an opinion, the updated opinion of node a at time $t + 1$ is given by:

$$o_a(t + 1) = \theta_a o_n(t) + (1 - \theta_a)\, o_a(t). \tag{2}$$

In equation 2 it is assumed that the tolerance θ_a (of node a) towards other agents' opinions is fixed. However, reference [22] argues that tolerance is variable and evolves according

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*Department of Computer and Information Technology, Politehnica University Timisoara (UPT), Timisoara, Romania `alext@cs.upt.ro`

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Bio-Inspired Redistribution of Urban Traffic Flow Using a Social Network Approach

Cristian Cosariu, Alexandru Iovanovici, Lucian Prodan, Mihai Udrescu and Mircea Vladutiu

***Abstract*—In present days, the road network in any major city faces the constant pressure of accommodating an ever increasing number of vehicles while conserving a congestion-free status. However, identifying key intersections that will soon become congested is a difficult task, performed by tedious, thorough simulations; even more difficult is to adapt the road network so as to increase its efficiency and avoid congestion. We argue upon the social component of road traffic and propose an alternative way to detect hotspots leading to congestion by using techniques borrowed from complex network analysis. We will use the betweenness centrality and argue upon its power-law distribution, which we set out to redistribute and equalize. The paper introduces a genetic algorithm that redistributes the betweenness values at a community level in a city by changing street directions and number of available lanes in order to reduce (and possibly even eliminate) congestion hotspots. Experimental results in terms of reducing traffic loads from hotspots and transferring to neighboring streets yield an improvement with a factor of up to 90% times without adding significant costs or modifying the existing infrastructure.**

***Index Terms*—road networks; complex networks; genetic optimization; betweenness centrality; complex network analysis; intelligent transportation system;**

I. INTRODUCTION

ONE increasingly demanding and unsolved problem of modern days is coping with the traffic conditions in large cities around the world. It is a well known fact that traffic and time spent by drivers in their cars may have a significant impact on personal life, career and safety. It is also a cause of stress and frustration to most inhabitants of large cities, as well as a cause of environmental pollution.

Apart from economical challenges, extending the road network is affected mainly by geographical limitations. Outside urban areas, the constraints imposed by geography can usually be overcomed.

A much more complex situation concerns large cities, in which geography is much more conservative, allowing very few opportunities for building new roads. Therefore adapting the road network to keep it congestion-free is based on optimizing its topology (number of lanes and their associated directions) and an efficient control of traffic flow (traffic lights).

To address these issues, we take a step back from the current optimization techniques [1], [2] of traffic congestion and reassess the underlying road topology. In this paper we propose a local optimization at the topological level of street neighborhoods, or communities, in any city by using concepts from complex and social networks analysis.

Anywhere in our society, daily traffic is made of people commuting in order to fulfill professional obligations or seeking personal entertainment, shaping the traffic to match social requirements. Therefore, applying principles related to complex and social network analysis in order to analyze and optimize road networks is motivated by direct implication of human relations into the traffic aspects. Also, it is augmented by the specific measurements such as shortest path betweenness centrality , which copes well with large amount of data and it was proposed to work with traffic assignment model [3]. Moreover, a social perspective also provides innovative means of analyzing the structure of entities with a social-like structure [4]. Thus, we can detect most influential nodes (i.e. intersections) and areas with respect to traffic flow, identify patterns of communication and also study the dynamics inside the network. This strongly relates to road networks in cities [5], [1], as it is important to determine, or even predict when possible, which areas are critical for the traffic throughput and which nodes are most influential defining possible hotspots for congestion. The results can help alleviate congestion or control their severity and also to forecast the impact of increased traffic flow.

A range of scientific issues can be represented and empirically studied using networks, with biological and social patterns, the World Wide Web, metabolic networks, food webs, neural networks and pathology networks being relevant examples. They can be mathematically represented and topologically studied to reveal some unexpected structural features [6], [7]. Most of these networks possess a certain community structure that has substantial importance in building an understanding regarding the dynamics of the network [8], [9].

Our approach revolves around finding congestion hotspots in a given road network, pointed by their relatively high betweenness centrality and adapting the number of lanes and their associated directions so as to level the distribution of betweenness values. We will show that this will in turn help adjacent intersections redistribute traffic flow, leading to a more balanced traffic. Since this is difficult to perform at global scale, covering the city road network as a whole, our approach will apply at local scale, to sub-graphs of the city road network (called communities, not dissimilar to neighborhoods); having optimized communities will in turn lead to a more balanced, and therefore fluent, traffic at a global scale.

The paper has the following structure: in Section II we describe the related work and the theoretical concepts behind

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All the authors are with the Department of Computers, POLITEHNICA University, Timisoara, Romania. Their emails, correspondingly are:cristiancosariu@cs.upt.ro, lprodan@cs.upt.ro, iovanalex@cs.upt.ro, mudrescu@cs.upt.ro, mvlad@cs.upt.ro.

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FMNet: Physical Trait Patterns in the Fashion World

Alexandru Topirceanu* and Mihai Udrescu
Department of Computer and Software Engineering, Politehnica University Timisoara, Romania

***Abstract*—In light of a constantly growing interest and real-world applicability shown in social collaboration networks, we have gathered data from Fashion Model Directory, the largest fashion model database. As such, we model and analyze the network formed by female fashion models all around the world, which we call FMNet. Inspired by similar approaches in the actors and music industry, we compare our empirical results with Facebook, Twitter, and Google Plus online friendship networks. As a first study of its kind in the fashion world, we create a network based on physical similarities, and by using centrality measures and network motifs, we prove that FMNet has all the properties of a social collaboration network. We discover and explain role of the most influential nodes (in terms of betweenness centrality) and communities (in terms of eigenvector centrality) in FMNet. The physical patterns found in this study offer a better understanding over the evolving trends in the fashion world.**

***Index Terms*—social media analysis, fashion world, collaboration networks, physical similarity.**

I. INTRODUCTION

COLLABORATION networks cover an active area of scientific research inspired largely by the empirical study of real-world networks such as communication networks, economical networks and social networks [1], [2], [3], [4], [5], [6], [7]. Part of the *New Network Science* [8], [7], they occur in all four major types of complex network, based on the context in which they occur: biological networks (e.g., metabolic networks, transcription regulatory networks, protein-protein interaction networks, protein structure networks, neural networks, ecological networks, natural food chains) [9], [10], [11], social networks (e.g. friendship networks, citation networks, voter networks, world markets, political structures) [12], [10], [13], technological networks (e.g., computer networks, electrical circuits, road networks) [9], and semantic networks (e.g. wordnet, recipe networks) [14], [15].

One of the main drives for developing the domain of collaboration networks is the usage is social media. Online platforms, like Facebook, Twitter, Amazon, Wikipedia, offer invaluable data to researchers in the domain of Social Networks Analysis (SNA). Collaboration patterns have been found in many social activities that humans share - like education, sports, business, music [16].

Without exception, all these networks can be represented as graphs, which include a wide variety of subgraphs. A fundamental property of networks are the so called network motifs, which were introduced by Milo et. al. [17]. They represent recurrent and statistically significant subgraphs or patterns in these complex networks. The fact that motifs repeat themselves in specific networks, or even among various networks, is highly correlated with the concepts of evolutionary theory. They have recently gathered much attention as a useful concept to uncover structural design principles of complex networks [18]. Although network motifs may provide a deep insight into the functional abilities of a network, their detection is computationally challenging even by current standards.

On a first literature overview, network motifs only serve as analytical tools in the areas of Systems Biology and Genetics, where they are associated with functional roles of transcription regulation networks which control the expression of genes [19]. Experimental studies show how motifs serve as basic building blocks of transcription networks. Another example is the understanding of how some cellular components are conserved across species but others evolve rapidly [20]. However, recent studies have brought the concept of motifs to technological and social networks in order to assess functional properties of the transportation infrastructure [21], respectively collaboration patterns in online social networks [22].

The field of collaboration networks has gathered momentum back in the early 1950's, when the science of social network analysis (SNA) emerged from its theoretical roots, transforming it into a key technique used in a wide variety of fields today, related to mapping, measuring and understanding different types of relationships between people, belonging to distinct social groups or entities. Practical applications include studies over topics like disorders and diseases [23], interaction between recipes [15], measuring political preferences of Twitter users [24], or even the universe of characters from Marvel [25]. With the growing popularity of social media, an exponential increase in available data and studies can be seen in the past few years.

Another set of studies for collaborations in the world of art, using network analysis, show that Kevin Bacon in the center of the social universe of Hollywood [26], [27]. This is based both on the "six degrees of separation" concept and on the small world phenomenon, resting on the assumption that any individual involved in the (Hollywood) film industry can be linked through his or her film roles to Kevin Bacon within no more than six steps. Other studies in the world of art include the ones on the network of musicians [16], which explains how the music world is economically biased because of the clustering of record houses. The paper discusses the concepts of meritocracy and topocracy [28], and finds that the topology strongly affects the popularity of music genres and musicians in general. Another study from the field of music sets out the explain the emergent collaboration patterns of Jazz musicians [29], [30].

Other similar and original applications of SNA can be found

Corresponding author (Alexandru Topirceanu) at Faculty of Automation and Computers, Politehnica University Timisoara, Bd. Vasile Parvan 2, 300223, Timisoara, Romania. Tel.: +40 256 403278, email: alext@cs.upt.ro

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Network Fidelity: A Metric to Quantify the Similarity and Realism of Complex Networks

Alexandru Topirceanu, Mihai Udrescu and Mircea Vladutiu
Department of Computers and Information Technology,
University “Politehnica” of Timisoara,
Bd. Vasile Parvan 2, 300223, Timisoara, Romania
{alex.topirceanu; mudrescu; mvlad}@cs.upt.ro

Abstract—**The analysis of complex networks revolves around the common fundamental properties found in most natural and synthetic networks that surround us. Each such network is commonly described through a standard set of graph metrics, yet there is no unified and efficient method of quantitatively compare networks to each other. This paper introduces the network fidelity metric delta (δ) which is aimed at offering the possibility to compare networks to each other based on individual metric measurements. Depending on the nature of the comparison, it can offer insight on network model similarity or synthetic model realism compared to a real world network. We apply the metric in a social network modeling scenario and also compare it to another metric – the fractal dimension – highlighting the superior analytic power of our metric.**

Keywords: complex networks; network comparison; realism.

I. INTRODUCTION

Social network analysis is receiving an increased interest from many fields of science since many empirical observations of our surrounding world show the same properties, regardless of whether they are of natural or artificial origin. There are topological models which describe geographical proximity, friendship distribution, neural networks in the brain, protein interaction mechanisms, natural food chains, the distribution of means of transportation, citation networks, sexual interaction patterns, the world wide web, power distribution networks, relationship of words in a language, interaction between ingredients in a recipe, the world markets [1][2][3] *etc*.

The major goal of social science is to analyze, understand and model real social networks. It can focus on the topological level of a network, i.e. how the nodes interconnect, or on the behavioral level, i.e. how the nodes interact. Both of these problems are approached through empirical studies (direct and indirect measurements, surveys, statistical analysis etc.) which lead to the proposal of a model for the observed real social network. Each model can be characterized through a set of metrics, which differ from one case to another, although only within an interval, as social networks have been shown to have the common properties mentioned above. The problem that arises is that, for a given network, like e.g. road systems, there are numerous existing models and new ones being proposed. There is a set of road-system models being accepted by the scientific community [4] but there is no method to numerically compare which model is better, or closer to the real network.

This paper presents a solution to the problem of quantifying the comparison between any complex networks which can be described using a set of metrics. Additionally, by comparison to a reference model, we can order all other models by the degree of similarity to the reference model. For this we propose a network fidelity metric δ (delta). Measuring the δ of any two networks represented with the same metrics it can be concluded which model offers the greatest realism compared to an empirical data set. By proposing the fidelity metric we set out to answer the following three questions:

1. Are two real networks similar ?
Real world social networks are diverse and hard to compare. Are some of them related ? Are, for example, neural networks similar to airline networks, or are they more similar to road systems ? The benefit of facilitating this comparison is that, once similarities are found, solutions to the problems of one model can be applied to the other model.

2. Does a proposed model accurately replicate an empirical network ?
Using the real (empirical) model as a reference, any synthetic model may be compared to it. Moreover, the fidelity metric expresses the *distance* between any models and the reference, thus they can be ordered by the degree of realism. A smaller δ means a higher realism.

3. Which proposed model is more accurate ?
There are always multiple possible models to be used to recreate a specific social scenario. The question that arises is which one to choose. Graphical comparison, or single metric comparison may easily fail in finding the best solution. Measuring the δ of all candidate solutions, one can order them by the degree of accuracy.

The focus is maintained on human social networks due to the complexity of the underlying human interaction, and due to the interest shown in them. To present the fidelity metric we have selected a number of representative models which are widely accepted to be realistic in terms of generating human society models. Thus, we use the small-

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