BOOK OF ABSTRACTS

BENET 2020
9TH BELGIAN NETWORK RESEARCH MEETING

UNIVERSITEIT GENT

CSI
COMPLEX SYSTEMS INSTITUTE

BENET 2020
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The 9th edition of the Belgian Network Research Meeting was held online and hosted by the Complex Systems Institute at Ghent University on November 12, 2020. Webpage of the meeting: https://csi.ugent.be/events/benet/.

The purpose of this annual gathering is to foster communication among Belgian researchers employing the network paradigm on their work, regardless of the discipline. The scope of the meeting includes but is not restricted to social & organisational theory, economics & finance, social media & online activities, human communication & mobility, information diffusion & opinion dynamics, political networks & collective action, ecology, ethology, food webs, biology & bioinformatics, epidemiology, physics, mathematics & statistics, modelling and data analysis.

Previous editions were held in Hasselt (UHasselt 2019), Ghent (UGent 2017), Louvain-la-Neuve (UCLouvain 2016), Namur (UNamur 2015), Brussels (ULB 2014), Leuven (IIS/KUL 2013), Antwerp (UA 2012), and Brussels (VUB 2011). To keep updated about future events and activities of the network, subscribe to the list http://listserv.vub.ac.be/mailman/listinfo/benet.

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PROGRAMME

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13:23-13:41	Timoteo Carletti	Random walks on hypergraphs
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13:59-14:07	~~Anujan Poologaindran~~	~~Probing the Brain's Small-World Architecture with Neurosurgery~~
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15:48-15:56	Eladio Montero-Porras	Networks make us more cautious: using Drift Diffusion Model to measure the learning process in Prisoner's Dilemma on different network topologies
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LIST OF ABSTRACTS

Synergistic information in a dynamical model implemented on the human structural connectome reveals spatially distinct associations with age

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Implementing the Ising model on a 2D lattice, we showed that the joint synergistic information shared by two variables on a target one peaks before the transition to an ordered state (critical point). Here we implemented the same model on individual structural connectomes, to answer these questions:

1. Does the synergy still peak before the critical point in a nonuniform network?
2. Are the hubs of structural connectivity also hubs of synergy?
3. Is there association with age?

We found that synergy still peaks before the critical temperature and that hubs of structural connectivity are not among the nodes towards which synergy is highest. Furthermore, using robust measures of association we found both positive and negative associations of synergy.

Random walks on hypergraphs

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In the last twenty years network science has proven its strength in modelling many real-world interacting systems as generic agents, the nodes, connected by pairwise edges. Yet, in many relevant cases, interactions are not pairwise but involve larger sets of nodes, at a time. These systems are thus better described in the framework of hypergraphs, whose hyperedges effectively account for multi-body interactions. We hereby propose and study a new class of random walks defined on such higher-order structures, and grounded on a microscopic physical model where multi-body proximity is associated to highly probable exchanges among agents belonging to the same hyperedge. We provide an analytical characterisation of the process whose behaviour is ruled out by a generalised random walk Laplace operator that reduces to the standard random walk Laplacian when all the hyperedges have size 2 and are thus meant to describe pairwise couplings. We illustrate our results on synthetic models for which we have a full control of the high-order structures, and real-world networks where higher-order interactions are at play. As a first application of the method, we compare the behaviour of random walkers on hypergraphs to that of traditional random walkers on the corresponding projected networks, drawing interesting conclusions on node rankings in collaboration networks (left panel in the Figure). As a second application, we show how information derived from the random walk on hypergraphs can be successfully used for classification tasks involving objects with several features, each one represented by a hyperedge (right panel in the Figure). Taken together, our work contributes to unveiling the effect of higher order interactions on diffusive processes in higher-order networks,

shading light on mechanisms at the hearth of biased information spreading in complex networked systems.
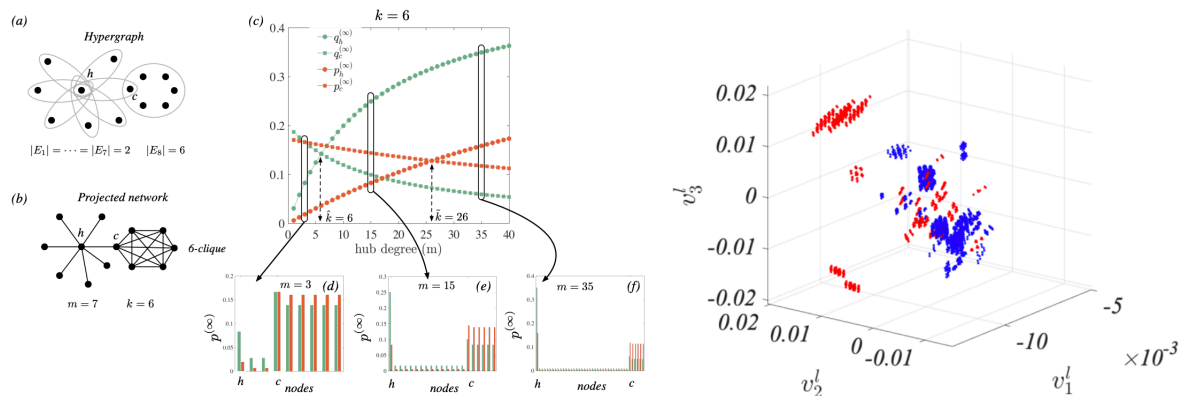
The (m, k)-star-clique network. (a): hypergraph made by m + k = 13 nodes, divided into m = 7 hyperedges of size 2 and one large hyperedge of size k = 6. The node h belongs to all 2-hyperedges, while the node c belongs to one 2-hyperedge and to the 6-hyperedge. (b): the projected network (hyperedges mapped into cliques). (c): we show the dependence on m of the asymptotic probability of finding the walker on the node h (circle) or on the node c (square), in the projected network (green symbols) and in the hypergraph (orange symbols). (d), (e) and (f): we report the asymptotic probabilities and for three values of m: , and , where and .

Classification of the mushrooms according to their features. We report a 3D embedding of the mushroom data set taken from UCI Machine Learning Depository, using the first three hypergraph Laplace eigenvectors. Each combination colour refers to a known class, red for poisonous and blue for edible.

Directed Graph Mapping: A Novel Computational Approach to Guide Ablation of Cardiac Arrhythmia
Nele Vandersickel
Ghent University, Belgium

Networks provide a powerful methodology with applications in a variety of biological, technological and social systems such as analysis of brain data, social networks, internet search engine algorithms, etc. To date, directed networks have not yet been applied to characterize the excitation of the human heart. In clinical practice, cardiac excitation is recorded by multiple discrete electrodes. During (normal) sinus rhythm or during cardiac arrhythmias, successive excitation connects neighboring electrodes, resulting in their own unique directed network. This in theory makes it a perfect fit for directed network analysis. In this talk, we will apply directed networks to the heart in order to describe and characterize cardiac arrhythmias. We will demonstrate the proof-of-principle using in-silico and clinical data. Tools used in network theory (detecting the cycles in the network) will allow determination of the mechanism and location of certain cardiac arrhythmias. We show that the robustness of this approach exceeds the existing state-of-the art methodology used in clinics. Furthermore, implementation of these techniques in daily practice can improve the accuracy and speed of cardiac arrhythmia analysis. It may also provide novel insights in arrhythmias that are still incompletely understood.

Probing the Brain's Small-World Architecture with Neurosurgery
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Across social, technological, and biological networks, 'small-worldness' is a ubiquitous topological property that enables regional specialisation and global information flow. The brain is also a network that exhibits quintessential small-world properties. To date, our knowledge on the small-worldness of biological neural networks has been derived through studying multiple species (C.elegans to Homo sapiens) at varying scales of resolution (microscopic to macroscopic). However, the practice of human neurosurgery that deliberately deletes large parts of a graph has not been reverse-translated to understand this basic fundamental network phenomenon. Herein, we assess the brain's small-worldness following focal cortical neurosurgery in n=17 adult patients over a one-year span. Specifically, we longitudinally constructed within-subject functional brain networks and quantified the impact of cancer, surgery, and rehabilitation on the brain's small-world architecture. We demonstrate that small-worldness is acutely affected due to surgery and its trajectory during short-term and long-term recovery. Compared to controls, brains after surgery have an altered small-worldness, suggesting that the whole physical brain is not a pre-requisite for normal information processing and cognitive functioning. For the first time, we shed light on the effect of physically deleting large swaths of a graph on small worldness in a real-world system and discuss the implications of our findings.

The cell cycle as a temporal network of protein interactions

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The cell cycle consists of a succession of protein interactions, ultimately leading to the division of the cell. The time-ordering of these interactions is crucial, and is ensured by checkpoints along the cycle. Static network representations of this system loose all temporal information about interactions. We model the cell cycle as a temporal Protein Interaction Network (PIN), where the activity of links changes over time, by integrating temporal information to a static PIN. We infer the 4 main biological phases of the cell cycle, as well as other physiological events and sub-phases, by applying hierarchical clustering to the snapshot matrices of the temporal PIN. This type of technique was introduced (Masuda & Holme, 2019) in networks with full temporal knowledge, outside of biology. Importantly, here we show that the method yields biological insights with only a low percentage of the links being temporal. We further show the robustness of the method with respect to changes in the choice of clustering method, distance metric, and temporal data used.
Temporal network modelling applied to biological networks can improve our understanding not only of the cell cycle, but also of many other biological networks, for which timing is important, but for which we lack full temporal knowledge interactions.

Investigating the Relationship Between Hierarchy and Centrality Measures in Complex Networks

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Identifying influential nodes in complex networks is essential for many crucial applications such as preventing epidemic spreading, uncovering key influencers for marketing campaigns, identifying terrorist networks. Hierarchy and centrality measures are two main ways of assessing

the importance of a node. Hierarchy measures are mainly based on flows of resources or containment ordering. Centrality measures are either: neighborhood-based, path-based, and iterative refinement-based measures. Numerous works investigating the interplay of centrality measures, however the relationship between centrality and hierarchy remains untouched. In [1] we report the results of a series of experiments aimed at assessing the relations between influential centrality and hierarchy measures. How the network topology affects this relationship is also investigated. Results show that the extent to which centrality and hierarchy measures provide similar or different information is related to the network macroscopic topological properties. Specifically, density and transitivity are decisive predictors to determine the correlation/similarity between centrality and hierarchy measures. The results can be exploited in two directions. Indeed, centrality and hierarchy measures can be substituted when they are well correlated for efficiency purposes or combined when their correlation is low for effectiveness purposes.
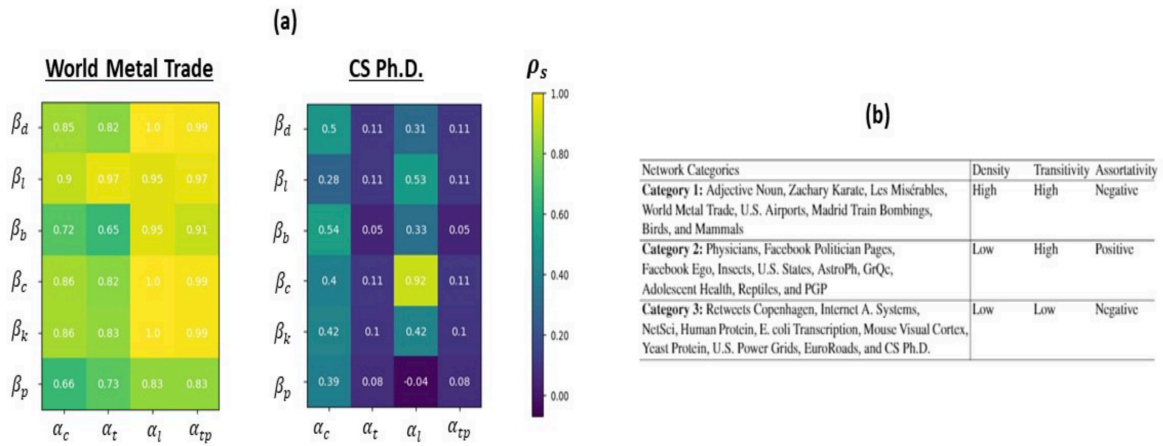
Figure 1: (a) Heatmaps of the Spearman's correlation for the various combinations of hierarchy α_i and centrality β_j measures of 6 real-world networks. The hierarchy measures are α_c= k-core, α_t= k-truss, α_l = LRC, and α_t = triangle participation. The centrality measures are β_d = Degree, β_l = Local, β_b = Betweenness, β_c = Current-flow Closeness, β_k = Katz, and β_p = PageRank. (b) Categories of networks with their aggregated topological characteristics.

A Compartmental Model for Zika with human to human and vertical vector transmission

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The main objective of the study of Zika transmission is to determine the best approach to reduce human mortality and morbidity caused by the disease. Therefore, it is essential to identify the relative importance of the different factors that contribute to the transmission and prevalence of the disease. Although many mathematical models have been formulated to study zika transmission dynamics in the presence of vertical transmission [1] and human to human transmission [2], they did not take into account the combination of both types of transmission. The question raised is does the combination of both transmission types results in a higher number of infection cases? To answer this question, a deterministic model of Zika with vertical transmission in vector population and human-to human transmission are developed (figure 1). It includes the immature phase of mosquitoes (eggs), adult mosquitoes (susceptible, exposed and infectious) and human hosts (susceptible, exposed, infectious and recovered). Using the homogeneous mean-field approach the dynamics of the epidemic spreading is analysed. Results show that neglecting the vertical transmission in the vector population leads to an underestimation of the proportion of the infected

population. Furthermore, it reduces the speed of the disease spreading. The same effect is observed if one does not consider the sexual transmission. A sensitivity analysis of the reproductive number $R0$ is performed in order to gain a better understanding on the main parameters driving the dynamics of the disease. It appears that the most sensitive parameters by decreasing order are: the adult mosquito mortality rate (μv), the mosquito bite rate (a), the transmission probability mosquito to human (βvh) and the transmission probability human to mosquito (βhv). Furthermore, the proportion at equilibrium of infected humans is very sensitive to the rate of transition from the immature vector stage to the adult stage (ϕ), the human to human transmission rate (βhh) and the human recovery rate (γh). These results confirm that Zika control policies that target the vector population and the recovery rate of individuals are quite effective solutions for Zika control.
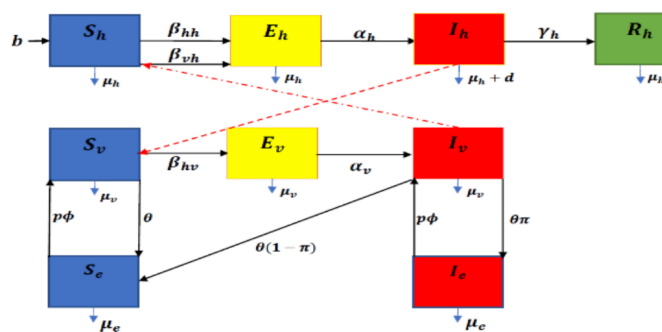

Fig 1. The flow chart represents the interactions and transfer of a vector-borne disease in both human and vector populations. The host population is split into states: Susceptible S_h, Exposed E_h, Infectious I_h, and recovered R_h. The vector population is split into 3 states: Susceptible S_v, Exposed E_v and Infectious I_v. The eggs population is split into 2 states: Susceptible S_e, Exposed and Infectious I_e. Relevant parameters are transmission probability human to mosquito (β_{hv}), the transmission probability human to mosquito (β_{hv}), the human to human transmission rate (β_{hh}), the immature vector stage to the adult stage (ϕ), the mosquito bite rate (a), the adult mosquito mortality rate (μ_v), the human recovery rate (γ_h), Number of Aedes eggs laid per day (θ), Vertical transmission rate(π), Daily human recruitment rate(b), incubation rate of an vector(α_v).
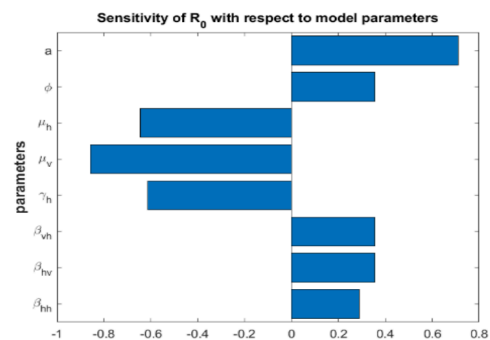

Fig2 Sensitivity Analysis of the reproductive number

$$R_0 = \frac{R_h + \sqrt{R_h^2 + 4R_v}}{2}$$

$$R_h = \frac{b\alpha_h\beta_{hh}}{\mu_h(\alpha_h + \mu_h)(\mu_h + \gamma_h + d)}$$

$$R_v = \frac{pb\alpha_h\alpha_v\phi(\phi + \mu_e)\beta_{vh}\beta_{hv}}{\mu_v\mu_h(\alpha_h + \mu_h)(\gamma_h + d + \mu_h)(\alpha_v + \mu_v)(\mu_v(\phi + \mu_e) - \phi\pi\theta)}$$

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Designing a Multi-stakeholder Relationship Framework of the Internet Governance Ecosystem

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In June, the UN Secretary General published the Roadmap for Digital Cooperation, which provides an overview of the current status of Internet Governance. The report emphasises to take a "multi-stakeholder "systems" approach for cooperation and regulation that is adaptive, agile, inclusive and fit for purpose for the fast-changing digital age." For my research, I seek to design an interactive map which conveys the relationships between stakeholders in the internet governance ecosystem based on three types of relationships: legal, financial and working. During my presentation, I want to present different systems thinking methodologies that could design my research and explore these models to create the interactive map. I would also want to identify the particular models that are best served for my project.

Dynamical and Complex Systems Theory for the Space Debris Environment
Jerome Daquin
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Six decades of space activities have led to a congested near-Earth environment, analogous to the 7-th continent of plastic waste in Earth's ocean. The space debris, uncontrolled remnants and hazards linked to human space activities, have dramatically increased in number over the years. To date, more than 8000 satellites have been launched, about 250 exploded in orbit and current models and technologies estimate the number of the most dangerous defuncts to be more than 20000. In this talk, I will review some aspects of the long-term dynamics of terrestrial orbits, especially in the range of medium altitude. I will then present the objectives of my research within the framework of my F.R.S.-FNRS postdoctoral fellowship. In particular, I will highlight how network theory could be beneficial for current space environmental approaches aiming to make the near-Earth environment a sustainable resource in the long-term.

Self-organizing dynamics in complex systems on non-normal networks
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The study of dynamical systems on complex networks has gained an increasing interest in the past 20 years, due to rich collective behavior induced by the interaction topology. Recently, it has been found that the connection matrix of most of real-world networks such as biological, ecological, or social ones, is characterized by a high level of non-normality [1]. Inspired by this fact, in this work we focused on the self-organizing dynamics on non-normal networks. The main property of the non-normal dynamics in the linear regime is a strong transient growth of the perturbations of a stable state [2]. In our studies [1,3], we have shown that this dynamical signature can translate in the nonlinear regime into an instability mechanism. Through the formalism of the Master Stability Function (MSF) [4], i.e., a numerical tool allowing us to compute the maximum Lyapunov exponent as a function of the coupling, we show that a system of coupled oscillators in the synchronized state, may lose its stability due to the non-normality of the coupling network. The same mechanism can be also interpreted as responsible for the pattern formation in spatially extended systems by inducing the instability of a stationary homogeneous state [3].

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Networks make us more cautious: using Drift Diffusion Model to measure the learning process in Prisoner's Dilemma on different network topologies
Eladio Montero-Porras
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Different types of people learn how to make decisions differently, especially when making complex choices informed by social network interactions. The details about these differences are still largely unknown. In this work, we investigate how differences in cooperativeness are linked with our deliberation process in different social contexts. We study how long it takes for subjects to learn to play the game and how this depends on the network structure. The Drift Diffusion Model (DDM) gives us a unique perspective and ability to quantify the subject's cautiousness by observing response times. We found that subjects playing Prisoner's Dilemma in a network act more cautious with respect to a pairwise setting. Moreover, subjects start to learn the game within 10-30 rounds, and from this moment on, they do not change much how they play the game. We then categorise subjects in those who cooperate/defect most of the time regardless of what others do, and those who adapt their actions to what the other players do in the previous round. Our DDM analysis predicatively shows that those who react to others' actions perceive a difference in their cautiousness between playing in a fixed-neighbors setting versus a shuffled-neighbors network setting.

Distance-aware version of the Axelrod model of cultural influence

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We propose a variation of the popular Axelrod model for cultural influence in which the interaction probability between two agents, rather than on the number of shared cultural features, depends upon the Manhattan distance between their cultural states. The advantage of this model, which we call the Distance-aware Modified Axelrod (DAMA), is that agents have a "finer" view of each other opinions. As in the original Axelrod model, here the state of an agent is defined by a F-vector, where each component (feature), can take q values; the normalization of the new model is such that it coincides with the original one for $q = 2$, for any F. We study the DAMA model numerically in a square regular lattice, in 1D and 2D, and on a fully connected one. We find that the proposed modification has indeed major qualitative consequences: in particular, in the DAMA model cultural variability (i.e., higher values of q) turns out to favour agreement, rather than acting as a disorder factor, as it does in the original model. This effect can be understood in terms of the fraction of active bonds in a random system, which, as $q \to \infty$, increases and tends to one in the DAMA model, while it vanishes in the original model. To attain fragmented final states in the DAMA model for higher values of q, a mechanism contrasting ordering is needed, as for example an interaction cut-off distance. In our presentation we will discuss the results obtained when such a balance is present.

Obtaining knowledge on network data: a visualization perspective using DyNetVis

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Visualization is an important resource to understand complex systems, which are often modeled into complex and/or temporal networks. Even more, visualization is especially useful to gain knowledge, generate insights, find patterns, trends, and anomalies in the data that are usually not

expected. However, visualizing these networks is a challenging problem due to the complexity of the data. In this sense, we present Dynamic Network Visualization (DyNetVis), an interactive, freely available, and open-source software that provides several state-of-the-art visualization techniques for temporal networks. Such techniques allow finding different topological and temporal behaviors in the data, such as community formation and network evolution, while preserving the user's mental map. The software also provides visual scalable solutions (regarding the network size) and visualization of dynamic processes, such as epidemics and random walks. The usefulness of DyNetVis has been validated through several case studies involving real-world networks from various disciplines. It allows the user to gain insights and ideas that lead to new discoveries, thus resulting in faster and reliable decision making.

Variance and covariance of distributions on graphs

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In recent work, we introduced a way to calculate the variance and covariance of distributions which are defined on the nodes of a network. These new measures fill an important methodological gap in the analysis of networks and associated data. I will introduce the proposed measures and illustrate the potential of our methodology for the analysis of data on networks based on a `network of knowledge' parsed from Wikipedia and a collection of scientific papers. Furthermore, by calculating the distribution with the maximum variance we find a new core-periphery measure for the nodes of a network, giving rise to a new k-core decomposition. Further details can be found in our preprint: https://arxiv.org/abs/2008.09155

Exploring the mesoscopic structure of the world air transportation network

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Air transportation networks have been extensively studied in the network science literature. Researchers focus on airlines networks, national, regional, continental and worldwide networks using monoplex or multiplex approaches. Inspired by recent results on community-aware centrality measures [1], in this work, an extensive analysis of the macroscopic, mesoscopic and microscopic topological properties of the world air transportation network is performed. Based on the community structure uncovered by the Louvain algorithm, the original network is split into local components and global components. The local components are made of the communities by removing the intercommunity links. The global components are formed by removing all the intracommunity links and subsequent isolated nodes. Results reported in figure 1 shows that the main local components are geographically distributed over seven areas (North America, Europe, East & Southeast Asia, Africa-West and South Asia Oceania, South America, Russia). The main global component is distributed among all these areas (figure 2). A comparative analysis of the macroscopic, mesoscopic and microscopic properties of these various main networks reveal some consistencies. Indeed, density of all the components is low. However local components are all denser than the overall network. Transitivity is low and more particularly for the global component. All the networks are disassortative. Except for the Russia component, the hub dominance is relatively small. The study also reveals some dissimilarities. For example, the diameter of the local components ranges from 4 to 9 as compared to a value of 12 for the original network. The highest k-core subnetworks (k=31 and k=29) of the original network are mainly

localized in the European component, and in the North America components. The maximum k-truss subnetwork (k=24) of the original network is in the North America component. It is followed by the European component (k=22). The remaining components exhibit low values of max k-truss. Comparative evaluation of degree and betweenness centrality measures allows to clearly identify the reasons behind the anomalies reported in several studies [2,3]. One of the main advantages of this approach is to get a better understanding of the similarity and differences of the various regional air transportation systems. Results indicate that it is more informative than considering the world air transportation network as a single entity. Indeed, if one considers the centrality measures, it allows to clearly distinguish airports having a regional influence from those with an international influence.
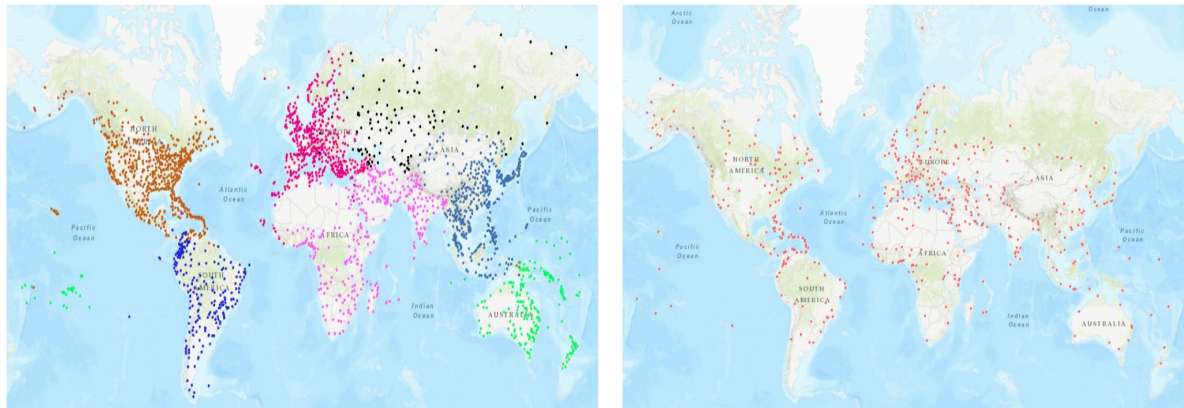

Figure 1 The 7 main local components. Each color represents a component

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