USING SPATIAL VISUALIZATIONS AND REAL-WORLD SOCIAL NETWORKS TO UNDERSTAND LANGUAGE EVOLUTION AND CHANGE

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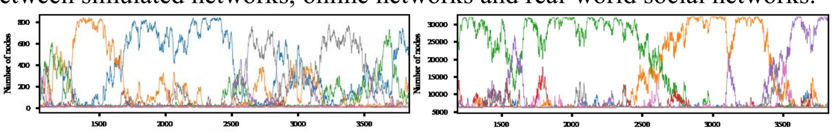
Over the last decade, computational modelling has emerged as a powerful tool for studying language evolution and change in social networks. The main aim of these studies is to explore the propagation of variants in different networks. In particular, Fagyal, Swarup, Escobar, Gasser, & Lakkaraju (2010) proposed a degree-biased voter model (DBVM) to investigate the role of hubs and loners in the community: different linguistic variants could spread in a bi-directional closed network, with higher in-degree agents (i.e., with more possible connections) having a higher probability to be chosen as interaction partners. The model revealed that while hubs promoted the spread of variants in the network and facilitated convergence, the loners (i.e., the more isolated agents) played a key role in language change: loners seem to serve as “variant-keepers” and maintain their unique variants despite the prevalence of another norm. By doing so, they seem to prevent the loss of variants and eventually reintroduce these variants to the entire community.

However, the network structure used in Fagyal et al. (2010) was based on a simulated artificial network, which does not necessarily adhere to all properties of real-world networks. Moreover, the exact role of loners was evaluated based on extreme and indirect manipulations, such as removing loners from the network altogether. In this study, we extend the model of Fagyal et al. (2010) by (a) incorporating more realistic social networks, and (b) visualizing the process of language diffusion to examine the exact role of loners.

We first replicated Fagyal et al. (2010)’s model using the same parameters, and obtained similar diffusion results (Figure 1a): over time, competing variants (represented by different colours) alternately became the norm. We then visualized the process of language diffusion spatially across multiple simulations (Figure 2). This method directly demonstrated the unique role of the loners: At first (t=0; Figure 2a), the eight possible variants were uniform and randomly distributed. After multiple interactions (t=150; Figure 2b), one variant (in green) spread throughout the network and became the norm. Nevertheless, some agents maintained less dominant variants (in blue), and the loners kept even rarer variants (in purple). Later (t=300; Figure 2c), those variants became the norm, while rarer variants were still maintained.

We then tested the model on a large-scale, real-world "who-trust-whom" online social network, which was extracted from the review website Epinions (Richardson, Agrawal & Domingos, 2003). We found the same diffusion dynamics in the real-world network and in the artificial network (Figure 1b). Finally, we scaled down the Epinions network and manipulated the numbers of edges (i.e., the number of possible connections). The results showed similar trends, i.e., alternating linguistic norms over time. Importantly, we found that increasing the number of connections led to a longer and smoother fixation of linguistic variants. This result has important implications for the process of cultural transmission and language evolution, and suggests that language change is slower in a dense network. It is also in line with claims of greater variability and less conventionalization in emerging sign languages from dense communities (Meir, Israel, Sandler, Padden & Aronoff, 2012), and is in line with the empirical work showing that norms are easier to maintain in a high-density community (Milroy, 1987). In on-going work, we are using more common communication networks (e.g., Twitter) to further reduce the gap between simulated networks, online networks and real-world social networks.



(A) Original atificial network **(B)** Real-world Epinions network

Figure 1. Changes in the prominence of linguistic variants over time in the original network (A) and in the real-world Epinions network (B)

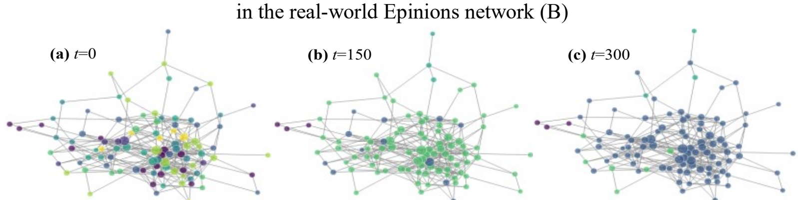


Figure 2. (a) t=0, eight linguistic variants are assigned uniformly and randomly to agents; (b) t=150, green variants are dominant in the network; (c) t=300, blue variants are dominant in the network.

Acknowledgments

We thank three anonymous reviewers and the audiences at the Symposium on Representations, Usage and Social Embedding in Language Change in Manchester in 2019 for their comments.

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