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Homophily patterns in a large-scale sample of ego networks from the United States

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Homophily, that is, the tendency of individuals with a relationship to be similar, is a pervasive pattern of social networks. While the general homophily patterns of the US across standard demographics and attributes are well described in the literature, most of the literature on ego networks has used relatively small samples. This implies that some aspects, such as how different demographics interact to generate homophily, how homophily changes for different subgroups, or how segregation varies geographically in the US, remain unexplored. In this work we leverage a sample of more than 15,000 ego networks from a large-scale online survey, the Covid States Project, with viable samples for most US states. As part of this non-probability survey, we asked respondents to provide information on their three closest alters, including their gender, race, age, partisanship, and how far they live. We have longitudinal data for a subset of these respondents, and, for a larger sample of about 25,000 respondents, if each of their alters is vaccinated against COVID-19. This dataset allows examining how the probability of a strong tie increases when individuals have multiple attributes in common, using case-control logistic regressions. We take a close look at homophily levels for attributes such as race for different SES and age subgroups. In addition, we explore how segregation levels for close ties vary across 40 different US states. By doing so, we are able to detect particularly segregated population segments or areas. We also explore if close ties at shorter distances are more or less homophilous than ties at longer distances. Finally, we describe homophily levels by vaccination status, and, using our longitudinal data, point at potential tie dissolution mechanisms due to discordant vaccination decisions.

Keywords

ego networks, homophily, online survey, core ties, geography

Topics

- Egonetworks and applications

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