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binding pocket that would require a conformational change to accommodate ubiquitin (Fig. 4A). Because the β sheet of the Ubp8 fingers region is in an open conformation even in the absence of ubiquitin (Fig. 4A), it is possible that interactions between Ubp8 and the other DUBm subunits help to maintain a conformation that favors ubiquitin binding. Interactions of the upper portion of the fingers domain with Sgf73 helix $\alpha 2$ and with Sus1 (Figs. 1A and 4C) form extensive contacts that may favor the open conformation of Ubp8. Sgf73 may also play a general role in stabilizing the conformation of the Usp domain. Ubp8 forms the most extensive interface with Sgf73, with a total area of 3075 Å², as compared with the other pairwise domain interactions in the DUBm. Note that Sgf73 is the “mortar” that holds together the two lobes of the DUBm complex (Fig. 4C); it promotes interactions between the two lobes and aligns Sgf11 and Sus1, which also contact the Usp domain at the interface between the two lobes. Although the structure of the Ubp8 Usp domain on its own is not known, it is possible that these extensive interactions with Sgf73 may also help to stabilize the overall USP fold or to affect protein dynamics in a way that favors the catalytically competent structure.

The structure of the SAGA DUBm suggests how this module interacts with its natural, *in vivo* substrate, monoubiquitinated histone H2B within a nucleosome. The electrostatic surface potential of the DUBm (Fig. 4D) reveals a basic region that could favor interactions with the negatively charged DNA when the nucleosome is positioned with ubiquitinated K123 of H2B in the active site of Ubp8. This region of the DUBm is positively charged because of the zinc finger module of Sgf11, which contains four basic residues (R78, R84, R91, and R95) (fig. S11) that are conserved in ATXN7L3, the human homolog of Sgf11. Two additional C-terminal arginine residues, R98 and R99, which are disordered in

the structure but are also conserved in the human homolog, would further contribute to the strong positive charge in this region. Figure S12 shows a model for how a yeast nucleosome (3I) monoubiquitinated at K123 of H2B can dock on the DUBm, with ubiquitin in the active site as seen in the Ubal-bound structure (Fig. 1D). This arrangement brings the basic patch on the DUBm in close approach with the DNA, which favors interactions with the sugar-phosphate backbone. The interdependent structural and functional roles of the four SAGA DUBm proteins in mediating biochemical activity, substrate binding, and incorporation into the larger SAGA complex is likely an example of how other subcomplexes of SAGA, and other coactivator and corepressor complexes, cooperate to regulate transcription.

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32. We thank A. DiBello for helping with the ubiquitin aldehyde synthesis, E. Hurt for providing the Sus1 clone, S. Corcoran at the General Medicine and Cancer Institutes Collaborative Access Team (GM/CA-CAT) beamline at the Advanced Photon Source for assistance with data collection and processing, and M. Bianchet for advice and discussions. C.E.B. is supported by a Ruth Kirchstein Fellowship from the National Institute of General Medical Science, NIH (F32GM089037), and T.Y. is a Special Fellow of the Leukemia and Lymphoma Society. GM/CA-CAT has been funded in whole or in part with federal funds from the National Cancer Institute (Y1-CO-1020) and the National Institute of General Medical Science (Y1-GM-1104), NIH. Use of the Advanced Photon Source was supported by the U.S. Department of Energy, Basic Energy Sciences, Office of Science, under contract no. DE-AC02-06CH11357. Coordinates and structure factors have been deposited in the Protein Data Bank with accession codes 3MH5 (DUBm bound to Ubal) and 3MHH (apo DUBm).

Supporting Online Material

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Network Diversity and Economic Development

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Social networks form the backbone of social and economic life. Until recently, however, data have not been available to study the social impact of a national network structure. To that end, we combined the most complete record of a national communication network with national census data on the socioeconomic well-being of communities. These data make possible a population-level investigation of the relation between the structure of social networks and access to socioeconomic opportunity. We find that the diversity of individuals' relationships is strongly correlated with the economic development of communities.

Theoretical work suggests that the structure of social relations between individuals may affect a community's economic development. More precisely, economic opportunities are

more likely to come from contacts outside a tightly knit local friendship group. Hence, highly clustered, or insular, social ties are predicted to limit access to social and economic prospects

from outside the social group, whereas heterogeneous social ties may generate these opportunities from a range of diverse contacts (1, 2). To date, however, the correspondence between network diversity and a population's economic well-being has not been quantified, largely because of the inability to obtain data that includes measures of network structure and economic development at the population level (3, 4). These data limitations have constrained related research to quantifying the effects of individual network-

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tie formation. Previous studies have found that individuals benefit from having social ties that bridge between communities. These benefits include access to jobs and promotions (5–13), greater job mobility (14, 15), higher salaries (9, 16, 17), opportunities for entrepreneurship (18, 19), and increased power in negotiations (20, 21). Although these studies suggest the possibility that the individual-level benefits of having a diverse social network may scale to the population level, the relation between network structure and community economic development has never been directly tested (22).

As policy-makers struggle to revive ailing economies, understanding this relation between network structure and economic development may provide insights into social alternatives to traditional stimulus policies. To that end, we analyzed the most complete record of a national communication network studied to date and coupled this social network data with detailed socioeconomic indicators to measure this relation directly, at the population level. The communication network data were collected during the month of August 2005 in the UK. The data contain more than 90% of the mobile phones and greater than 99% of the residential and business landlines in the country. The resulting network has 65×10^6 nodes, 368×10^6 reciprocated social ties, a mean geodesic distance (minimum number of direct or indirect edges connecting two nodes) of 9.4, an average degree of 10.1 network neighbors, and a giant component (the largest connected subgraph) containing 99.5% of all nodes (23).

Although the nature of this communication data limits causal inference, we were able to test the hypothesized correspondence between social network structure and economic development using the 2004 UK government's Index of Multiple Deprivation (IMD), a composite measure of relative prosperity of 32,482 communities encompassing the entire country (24), based on income, employment, education, health, crime, housing, and the environmental quality of each region (25). Each residential landline number was associated with the IMD rank of the exchange in which it was located, as shown in Fig. 1. Obtaining the socioeconomic profile for a given telephone exchange area involves aggregating over the census regions within the exchange area. First we uniquely mapped each census region to the exchange area with which it has the greatest spatial overlap. We subsequently aggregated, for each exchange area, the population-weighted average of the IMD for the census regions assigned to each exchange:

$$\mu_{\text{weighted}} = \sum_{i=1}^n w_i x_i \quad (1)$$

and

$$\sigma_{\text{weighted}}^2 = \sum_{i=1}^n w_i (x_i - \mu_{\text{weighted}})^2 \quad (2)$$

where x_i is the census rank for the i th census region that makes up the exchange area and w_i is the population weight of the i th census region given by the fraction of the total population of the exchange area residing in the i th census region.

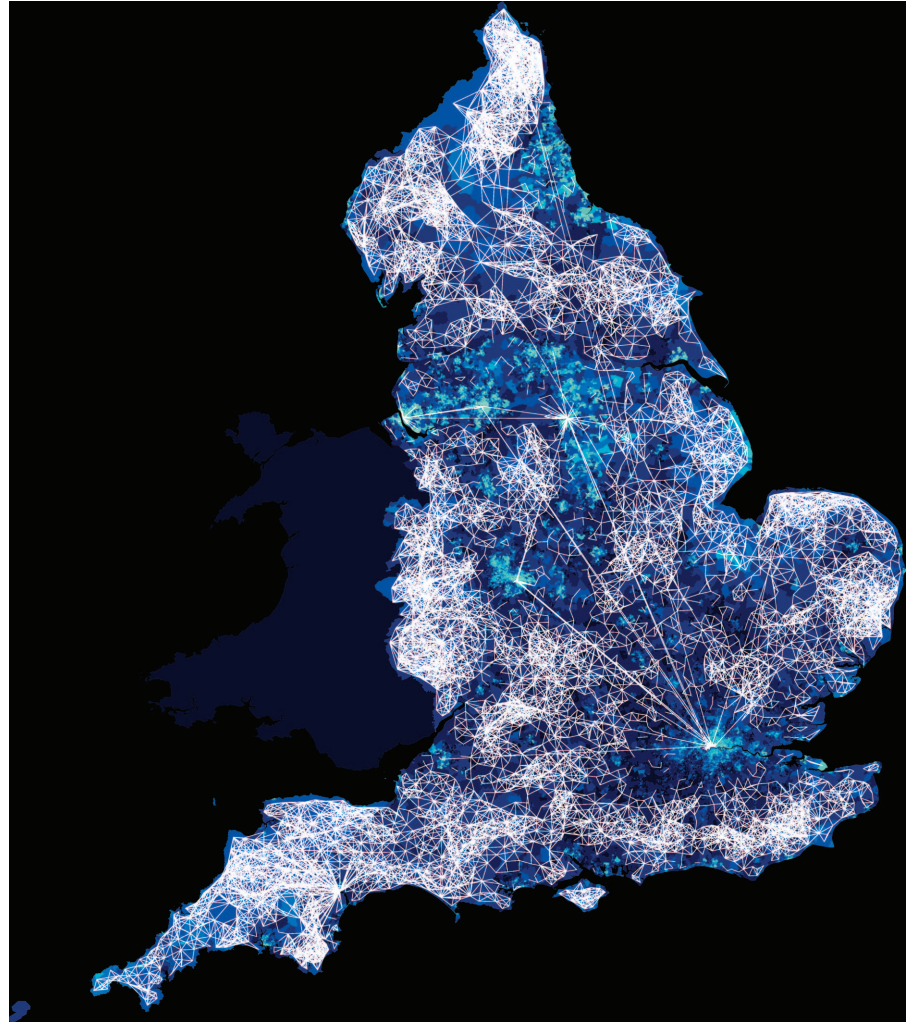


Fig. 1. An image of regional communication diversity and socioeconomic ranking for the UK. We find that communities with diverse communication patterns tend to rank higher (represented from light blue to dark blue) than the regions with more insular communication. This result implies that communication diversity is a key indicator of an economically healthy community. [(29) Crown copyright material is reproduced with the permission of the Controller of Her Majesty's Stationery Office]

We then compared the IMD rank of each community with diversity metrics associated with each member's social network. Mobile numbers were included (along with landlines) in the calculation of the nonspatial diversity measures; however, they were not used to identify members of a community (because of insufficient data on spatial location). We developed two new metrics to capture the social and spatial diversity of communication ties within an individual's social network. We quantify topological diversity as a function of the Shannon entropy,

$$H(i) = - \sum_{j=1}^k p_{ij} \log(p_{ij}) \quad (3)$$

where k is the number of i 's contacts and p_{ij} is the proportion of i 's total call volume that involves j , or

$$p_{ij} = \frac{V_{ij}}{\sum_{j=1}^k V_{ij}} \quad (4)$$

where V_{ij} is the volume between node i and j . We then define social diversity, $D_{\text{social}}(i)$, as the Shannon

entropy associated with individual i 's communication behavior, normalized by k :

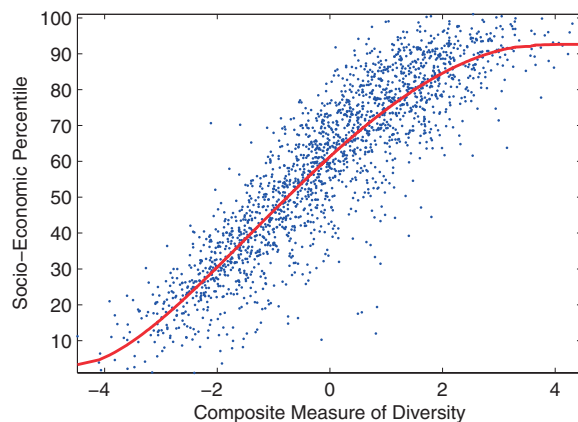
$$D_{\text{social}}(i) = \frac{- \sum_{j=1}^k p_{ij} \log(p_{ij})}{\log(k)} \quad (5)$$

The above measure of topological diversity does not take into account the geographic diversity in the calling patterns within a community. We define a similar measure for spatial diversity, $D_{\text{spatial}}(i)$, by replacing call volume with the geographic distance spanned by an individual's ties to the 1992 telephone exchange areas in the UK,

$$D_{\text{spatial}}(i) = \frac{- \sum_{a=1}^A p_{ia} \log(p_{ia})}{\log(A)} \quad (6)$$

in which p_{ia} is the proportion of time i spends communicating with a th of A total exchange areas. High diversity scores imply that an individual splits her time more evenly among social ties and between different regions.

Fig. 2. The relation between social network diversity and socioeconomic rank. Diversity was constructed as a composite of Shannon entropy and Burt's measure of structural holes, by using principal component analysis. A fractional polynomial was fit to the data.



Although both social and spatial network diversity scores were strongly correlated with IMD rank ($r = 0.73$ and $r = 0.58$, respectively), we found a weaker positive correlation present using number of contacts ($r = 0.44$) and a negative correlation for communication volume ($r = -0.33$). For example, whereas inhabitants of Stoke-on-Trent, one of the least prosperous regions in the UK, averaged a higher monthly call volume than the national average, they have one of the lowest diversity scores in the country. Similarly prosperous Stratford-upon-Avon has inhabitants with extremely diverse networks, despite no more communication than the national average.

The strong association between diversity and IMD rank persists using other network diversity metrics, including Burt's measure of "structural holes" (9). A structural hole is a missing relation between any two of a node's neighbors, creating an open triad. Burt's seminal work showed that remuneration within an organization increases with the number of structural holes that surround a node. Our results show that this relation scales to the level of communities, whose socioeconomic opportunities increase with the number of structural holes in the ego networks of the members ($r = 0.72$). Moreover, a composite measure constructed via principal component analysis was an even better predictor of economic development than either component alone, as illustrated in Fig. 2 ($r = 0.78$).

By coupling the most complete population-level social network studied to date with community-level economic outcomes, we were able to validate a central assumption that is widely accepted in network science but was untested at the population level: Do more diverse ties provide greater access to social and economic opportunities? Although the causal direction of this relation—whether network diversity promotes opportunity or economic development leads to more diversified contacts—cannot be established, social network diversity seems to be at the very least a strong structural signature for the economic development of a community. On a population level, the surprisingly strong correspondence we discovered between the structure of social contacts and the economic well-being of populations highlights the potential benefit of socially targeted policies for economic development. However, additional research will be required to derive reliable

policy implications. In particular, establishing the causal mechanisms underlying the observed correspondence between network diversity and economic development may require additional longitudinal social network and economic data (26–28).

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22. Previous studies have used longitudinal designs to test the hypothesized one-way causal direction between network position and individual economic benefits. These results suggest a similar causal direction at the population level, but our national data do not allow us to test for causal direction, and we cannot rule out the possibility that economic advantages may also lead to changes in network structure.
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25. The 2004 IMD was constructed before the 2005 telephone call logs were recorded. We assume that the 2004 IMD rankings are relatively constant and, therefore, make no causal inference from the temporal order. Additionally, exchange areas can also be scored with specific IMD components, such as education. Higher education may promote more diverse network ties and lead to jobs with higher income, which might account for part of the correspondence between IMD and network diversity.
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References

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Coadministration of a Tumor-Penetrating Peptide Enhances the Efficacy of Cancer Drugs

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Poor penetration of anticancer drugs into tumors can be an important factor limiting their efficacy. We studied mouse tumor models to show that a previously characterized tumor-penetrating peptide, iRGD, increased vascular and tissue permeability in a tumor-specific and neuropilin-1–dependent manner, allowing coadministered drugs to penetrate into extravascular tumor tissue. Importantly, this effect did not require the drugs to be chemically conjugated to the peptide. Systemic injection with iRGD improved the therapeutic index of drugs of various compositions, including a small molecule (doxorubicin), nanoparticles (nab-paclitaxel and doxorubicin liposomes), and a monoclonal antibody (trastuzumab). Thus, coadministration of iRGD may be a valuable way to enhance the efficacy of anticancer drugs while reducing their side effects, a primary goal of cancer therapy research.

The therapeutic efficacy of many anticancer drugs is limited by their poor penetration into tumor tissue and by their adverse ef-

fects on healthy cells, which limits the dose of drug that can be safely administered to cancer patients. In solid tumors, many anticancer drugs