Latent Geometry for Complementarity-Driven Networks

Maksim Kitsak$^{1,2}$

$^1$Network Science Institute, Northeastern University, 177 Huntington ave, Boston, MA, 02115, USA. $^2$Delft University of Technology, Faculty of Electrical Engineering, Mathematics and Computer Science, 2628 CD, Delft, The Netherlands

Networks of interdisciplinary teams, biological interactions as well as food webs are examples of networks that are shaped by complementarity principles: connections in these networks are preferentially established between nodes with complementary properties. We propose a geometric framework for complementarity-driven networks. In doing so we first argue that traditional geometric representations, e.g., embeddings of networks into latent metric spaces, are not applicable to complementarity-driven networks due to the contradiction between the triangle inequality in latent metric spaces and the non-transitivity of complementarity. We then propose the cross-geometric representation for these complementarity-driven networks and demonstrate that this representation (i) follows naturally from the complementarity rule, (ii) is consistent with the metric property of the latent space, (iii) reproduces structural properties of real complementarity-driven networks, if the latent space is the hyperbolic disk, and (iv) allows for prediction of missing links in complementarity-driven networks with accuracy surpassing existing similarity-based methods. The proposed framework challenges social network analysis intuition and tools that are routinely applied to complementarity-driven networks and offers new avenues towards descriptive and prescriptive analysis of systems in science of science and biomedicine.

Network embeddings or mappings of networks to latent geometric spaces are standard tools in the arsenal of data analysis, and are routinely used in machine learning, visualization, network science, and graph theory. In general, a procedure of network embedding is a mapping network nodes to points in a suitable latent metric space, such that latent distances between connected node pairs are smaller than those between disconnected node pairs.

Latent-geometric distances are often interpreted as generalized measures of node similarities [1]: the closer the two nodes in the latent space the more similar they are and the more likely they are to be connected in the network of interest. It is the similarity interpretation of latent distances that lies at the origin of many applications of network embeddings, including link prediction [2][12], soft community detection and clustering [13–16], network navigation [17–20], and search [21–23].

Of our interest in this letter are networks that are based not on similarity but complementarity principles: nodes are connected in these networks if their properties are complementary. Examples of complementarity-driven networks include interdisciplinary collaboration networks, molecular interaction networks, and food webs. Indeed, individuals with complementary expertise are more likely to solve an interdisciplinary problem of interest, interactions often take place between molecular with complementary chemical properties and/or binding interfaces. While cannibalism is certainly present in food webs, in general species preferentially eat other complimentary species.

The major challenge behind the geometric representation of complementarity-driven networks is that unlike similarity, complementarity is not transitive. Indeed, imagine a toy complementarity-driven network consisting of three nodes $A$, $B$, and $C$, such that nodes $A$ and $C$ are both connected to $B$, Fig. 1a. Being both complementary to $B$, nodes $A$ and $C$ are not necessarily complementary to each other and, as a result, are not likely to be connected. If embedded to a metric space, however, nodes are likely to be mapped to points such that latent distances $d(A, B)$ and $d(B, C)$ are small. The metric property of the latent space then dictates that $d(A, C) \leq d(A, B) + d(B, C)$, suggesting that nodes $A$ and $C$ are likely to be connected, while not being complementary to each other. It is the contradiction between the metric property of the latent space and non-transitivity of complementarity that may explain the rel-

FIG. 1: (a) Embedding of a network into a metric spaces imposes constraints on distances due to the triangle inequality. (b) These constraints are consistent with the similarity interpretation of latent distances since the former is transitive: if $A$ is similar to $B$ and $B$ is similar to $C$, then $A$ is similar $C$. (c) Triangle inequality is not consistent with complementarity: if $A$ is complementary to $B$ and $B$ is complementary to $C$, $A$ is not guaranteed to be complementary to $C$. 
This contradiction is closely related to the failure of the triadic closure principle observed in protein interaction networks [24]: proteins with a large number of common interaction partners are not likely to interact with each other. Instead, the authors of this work established that proteins are likely to interact with other proteins, that are similar to their existing interaction partners and used this principle to develop a link prediction method, based on the statistics of paths of length ℓ = 3 and called L3, to predict missing protein interaction [24]. The ideas behind the L3 method were further developed and generalized for unipartite [25] and bipartite [26] networks.

To enable geometric representations of complementarity-driven networks we propose a cross-geometric framework for statistical inference on complementarity-driven networks. We postulate that each node $i = 1, ..., N$ in the network is characterized by two points $x^1$ and $x^2$ in a latent metric space $\mathcal{M}$ and the connection probability between any two nodes takes the form of

$$p_{ij} = p \left[ d \left( x^1_i, x^2_j \right) \right] + p \left[ d \left( x^1_j, x^1_i \right) \right] - p \left[ d \left( x^2_i, x^1_j \right) \right] p \left[ d \left( x^2_j, x^1_i \right) \right],$$

(1)

where $p(x)$ is any decreasing integrable function with the range of $[0, 1]$, and $d(x, y)$ is the distance between points $x$ and $y$ in $\mathcal{M}$.

It is straightforward to verify that the proposed framework does not violate the transitivity constraint. Indeed, within the cross-geometric framework any node $A$ is represented by two points $x^1_A$ and $x^2_A$, and connection between any two nodes $A$ and $B$ is higher if either cross-distance $d \left( x^1_A, x^2_B \right)$ or $d \left( x^2_A, x^2_B \right)$ is small. Within the cross-geometric framework the formation of the $A$-$B$-$C$ toy wedge network, Fig. 2a, is possible in two cases: (i) points $x^1_A, x^2_B,$ and $x^2_C$ are close to each other, Fig. 2a, or (ii) point $x^1_A$ is close to point $x^2_B$, and $x^2_C$ is close to $x^2_B$, Fig. 2c. Neither case creates constraints on distances $d \left( x^1_A, x^2_C \right)$ and $d \left( x^2_C, x^2_B \right)$, relevant for the formation of the $A$-$C$ link. 2b, c.

The emerging cross-geometry of the proposed complementarity framework is easy to justify: two points corresponding to a given node characterize node’s orientation with respect to relevant node properties. Examples of such properties could be scientist’s expertise in two complementary disciplines, e.g., biology and statistics, in the case of a scientific collaboration network, or biochemical properties of a molecule. For some complementarity systems it might be necessary to include more than two points per node, and we discuss this possible generalization in Appendix C.

Cross-distances $d \left( x^1_i, x^2_j \right)$ and $d \left( x^2_i, x^1_j \right)$ in the connection probability of Eq. (1) quantify the complementarity between the two relevant node properties: the closer the two properties are, the higher is the extent of their complementarity. At first glance, it may seem unreasonable to place both node properties in the same space $\mathcal{M}$. A more intuitive setting could be a multi-space model, where node properties belong to distinct latent spaces $\mathcal{M}_1$ and $\mathcal{M}_2$, and connections are possible due to a certain mapping function $f: \mathcal{M}_1, \mathcal{M}_2 \rightarrow p \in [0, 1]$. We show in Appendix A that both single and multi-space formulations are compatible, and the former is the special case of the latter if node properties are correlated.

In this work we do not aim to learn latent spaces underlying real complementarity-driven systems, nor do we aim to learn the functional form of the probability function $p(d)$ in Eq. (1) – this will be the subject of the future research. Instead, we consider one example of the cross-geometric model that is using the hyperbolic disk as a latent space, $\mathcal{M} = \mathbb{H}^2$. We refer to this model as the Complementary-based Random Hyperbolic graph (CHRG). We demonstrate below that CHRG results in complementarity model networks with structural properties of real networks: heterogeneous distributions of node degrees and common neighbors, as well as vanishing density of short 3-loops, as captured by clustering coefficient. Further, we use the CHRG as a null-model to learn cross-geometric representations of real networks.

CHRG is based on the random hyperbolic graph [30] and uses the 2-dimensional hyperbolic disk $\mathbb{H}^2$ as a latent space. Points in $\mathbb{H}^2$ are described by polar coordinates $r \in [0, R]$ and $\theta \in [0, 2\pi]$, and distances between any two points $\{r^1, \theta^1\}$ and $\{r^2, \theta^2\}$ are calculated using the hyperbolic law of cosines:

$$\cosh d = \cosh r^1 \cosh r^2 - \sinh r^1 \sinh r^2 \cos \Delta \theta^{12},$$

(2)

where $\Delta \theta^{12} = \pi - |\pi - |\theta^1 - \theta^2||$. Similar to the RHG, we assume that angular coordinates are assigned uniformly at random, $\rho(\theta^t) = U[0, 2\pi]$, while radial coordinates are drawn from $\rho(r^t) = \frac{\sinh(\alpha r^t)}{\cosh(\alpha R) - 1}$, $r \in [0, R]$ for $t = 1, 2$. Here $\alpha > \frac{1}{\pi}$ is the parameter controlling the radial node density and affecting resulting degree distribution of the CRHG.

Different from the RHG, CRHG dictates that each node is characterized by two points in $\mathbb{H}^2$, and connections between nodes are established with the probability in Eq. (1), where $p(d)$ is parameterized as

$$p(d) = \frac{1}{1 + e^{-\frac{d}{\alpha}}},$$

(3)
Here $T \in (0,1)$ is the temperature parameter controlling the relevance of long-distance connections, and $R > 0$ is the radius of the hyperbolic disk, controlling the expected average degree of synthetic networks.

Following the hidden variable formalism [27], it is straightforward to express the structural properties of the CRHG in terms of those in the RHG model. Indeed, the expected degree of a node characterized by the coordinates \( \{r_1, \theta_1, r_2, \theta_2\} \), to the leading order, is
\[
\mathbf{\overline{k}}(r_1, \theta_1, r_2, \theta_2) = \mathbf{\overline{k}}^{\text{RH}}(r_1) + \mathbf{\overline{k}}^{\text{RH}}(r_2),
\]
where $\mathbf{\overline{k}}^{\text{RH}}(r)$ is the expected degree of a node with radial coordinate $r$ in the RHG:
\[
\mathbf{\overline{k}}^{\text{RH}}(r) = \frac{4N\alpha}{2\alpha - 1} \frac{T}{\sin \pi T} e^{-r/2},
\]
where $\alpha = 2\alpha + 1$.

Similarly, the expected number of common neighbors between nodes $i$ and $j$ can be expressed, to the leading order, as
\[
\mathbf{\overline{m}}_{ij} = \mathbf{\overline{m}}^{\text{RH}}(r_1, \theta_1; r_j, \theta_j) + \mathbf{\overline{m}}^{\text{RH}}(r_2, \theta_2; r_j, \theta_j),
\]
where $\mathbf{\overline{m}}^{\text{RH}}(r_1, \theta_1; r_j, \theta_j)$ is the expected number of common neighbors in RHG between nodes $\{r_1, \theta_1\}$ and $\{r_j, \theta_j\}$. Then, the probability $P(m)$ of $m$ common neighbors is the convolution of those in the RHG model
\[
P(m) = \sum_{m'=0}^{m} P^{\text{RH}}(m-m') \mathbf{\overline{m}}^{\text{RH}}(m') \sim m^{-\gamma},
\]
where $\gamma = 2\alpha + 1$.

[FIG. 3: Link prediction with cross-geometric hyperbolic framework. Link prediction results obtained with the Complementarity HyperLink (CHL) compared to HyperLink (HL) and other representative methods in (a) human protein-protein interaction network, (b) C. cerevisiae protein-protein interaction network, (c) Messel food web, and (d) Hamster social network. All experiments correspond to the $1 - q = 0.5$ fraction of removed links. Considered link prediction methods are the (CHL) Complementarity HyperLink (our method), the L3 method [27], the Structural Perturbation Method (SPM) [28], Katz index [29] with parameter $\beta = 0.1$ (Katz01) and $\beta = 0.9$ (Katz09), Preferential Attachment (PA) [30], Hyperlink (HL) [14], Cannistraci Resource Allocation (CRA) [31], Resource Allocation (RA) [32], Adamic Adar (AA) [33], Jaccard Index (JACC) [34], and the number of common neighbors (CN) [35].]
since $P^H(m) \sim m^{-\tau}$, where exponent $\tau = \tau(\gamma, T) > 2$, as documented both in empirical \cite{38,39} and theoretical \cite{40} studies.

The expression for clustering coefficient in the CHRG is more involved and is omitted here for brevity, what is important is that clustering coefficient vanishes in the large $N$ limit, as

$$\bar{c}(N) \sim N^{-1},$$  

consistent with the non-transitivity of complementarity.

To highlight the practical utility of the developed complementarity framework we next obtain cross-geometric hyperbolic representations of four real-world networks: the network of protein interactions in yeast \cite{41} and human \cite{42,43} cells, the Messel shell food web \cite{44}, and the social network of the website hamsterster.com \cite{45}, and use the obtained representations to predict missing links in these networks.

To this end, we remove a fraction of $1 - q$ links uniformly at random in the network of interest. In doing so, we go over every existing link in the network and remove it with probability $1 - q$. We then obtain cross-geometric representation of the resulting truncated network, see Appendix \cite{B} and rank unconnected node pairs in the truncated network by the sum of the cross-distances between the corresponding points:

$$\text{rank}_{ij} = d(x_i^1, x_j^2) + d(x_i^2, x_j^1),$$  

the smaller the rank the higher is the chance of a missing link.

Our link prediction results are summarized in Fig. 3. We observe that all similarity-based methods (lower half of each panel in Fig. 3) predict missing links in the four considered networks with accuracy lower than that of the methods that are not similarity-based (upper half of each panel in Fig. 3). This result is expected, since real networks of interest are driven by the complementarity rule, and similar nodes are not expected to be connected. Our second observation is that the cross-geometric representation, which we label as CHL in Fig. 3 is substantially more accurate in missing link prediction that any similarity based method, including the original HyperLink. Further, CHL performs comparable with the most accurate non-similarity based methods, validating the cross-geometric framework \cite{D}.

In summary, we would like to emphasize that the proposed cross-geometric framework is not specific to hyperbolic spaces: any metric space of arbitrary dimensionality may serve as a latent space in this framework. Here we presented the minimal version of the cross-geometric framework, where each network node corresponds to two points in the latent space. Higher order generalizations of the framework are straightforward and discussed in Appendix \cite{C}.

It also important to note that the proposed cross-geometric framework can not be mapped to a higher-dimensional version of the conventional latent-geometric framework, where each node is mapped to a single point. In the latter, the higher is the pairwise match between node coordinates, the smaller is the distance and the higher is the connection probability. In the former, on the other hand, the match of all node coordinates is not required: connections are established with high probability if at least one cross-distance is small. At the same time, the proposed cross-geometric framework is closely related to bipartite networks, which can be regarded as the special class of complementarity-driven networks, see Appendix \cite{B}.

The cross-geometric framework not only opens new avenues for the analysis of complementarity-driven systems such as biological networks, interdisciplinary collaboration, and food webs, it also challenges traditional ap-
for social networks and are routinely applied to other networks classes.

One example is the notion of the shortest path, which is often envisioned as a certain discrete trajectory in the network space, Fig. 4a. Such trajectory is possible in the cross-geometric framework: a chain of connections may form due to a spatial alignment of complementary points into a geometric trajectory, Fig. 4b. While such an alignment is definitely sufficient for the formation of a network chain, it is by no means necessary: another possibility is a collection of pairwise, yet disjoint, proximities between corresponding points in the latent space, as seen in Fig. 4c.

Network community, in its classical formulation, is a group of nodes densely connected within and sparsely connected outside the group. Based on this definition, network communities in social sciences are often envisioned as collections of node-points localized in certain network space, Fig. 5. While the cross-geometric framework admits this interpretation as well, Fig. 5b, communities that are partially localized in the latent space are also possible, Fig. 5c.

Shortest paths and communities have been adopted from similarity-based networks and are routinely used in the analysis of complementarity-driven networks. Network communities are routinely used to quantify disease and functional modules in biological networks [46–48], and scientific communities in collaboration networks [49, 50]. Shortest paths, on the other hand, are often used to quantify network-based separations between network modules of interest [51, 52]. While we do not question the use of paths and communities in complementarity-driven networks, we call for careful interpretation of the obtained results that should be consistent with the cross-geometric framework.

Acknowledgements

We thank R. Aldecoa, C. V. Cannistraci, D. Zinoviev, D. Korkin, P. van der Hoorn, D. Krioukov, I. Voitalov, H. Hartle, L. Torres, and B. Klein for useful discussions and suggestions. This work was supported by ARO Grant No. W911NF-17-1-0491 and NSF Grant No. IIS-1741355.

---

FIG. 5: Communities in complementarity-driven networks. Shown in (a) is the toy network consisting of a 5 node clique as well as (b)-(c) two configuration of points in the space that might lead to it. (b) In this configuration the clique network arises due to the complete clustering of all points. (c) This configuration demonstrates how the clique network in (a) may arise from partially clustered points in the latent space. In contrast, the complete clustering of all points in the latent space is the only possibility for the clique similarity-driven network.
A latent space mapping for link prediction, Adv. Neural Inf. Process. Syst. (2018), arXiv:1802.04868.

[10] A. Brew, A latent space mapping for link prediction, Neur. Inf. Process. , 1 (1998).

[11] M. Kitsak, I. Voitalov, and D. Krioukov, Link prediction with hyperbolic geometry, (2019) arXiv:1903.08810.

[12] G. García-Pérez, R. Alikarbaharisi, A. Ghasemi, and M. A. Serrano, Predictability of missing links in complex networks, (2019), arXiv:1902.00035.

[13] M. E. J. Newman and T. P. Peixoto, Generalized communities in networks, Phys. Rev. Lett. 115, 088701 (2015).

[14] K. Zuev, M. Boguná, G. Bianconi, and D. Krioukov, Emergence of soft communities from geometric preferential attachment, Sci. Rep. 5, 9421 (2015).

[15] L. Yang, X. Cao, D. Jin, X. Wang, and D. Meng, A Unified Semi-Supervised Community Detection Framework Using Latent Space Graph Regularization, IEEE Trans. Cybern. (2015), 10.1109/TNCYB.2014.2377154.

[16] D. K. Sewell and Y. Chen, Latent Space Approaches to Community Detection in Dynamic Networks, Bayesian Anal. 12, 351 (2017).

[17] M. Boguná, F. Papadopoulos, and D. Krioukov, Sustaining the Internet with hyperbolic mapping, Nat. Commun. 1, 62 (2010).

[18] A. Gulyás, J. J. Bíró, A. Krösi, G. Rétvári, and D. Krioukov, Navigable networks as Nash equilibria of navigation games, Nat. Commun. 6, 7651 (2015).

[19] I. Voitalov, R. Aldecoa, L. Wang, and D. Krioukov, Geohyperbolic Routing and Addressing Schemes, ACM SIGCOMM Comput. Commun. Rev. 47, 11 (2017).

[20] G. García-Pérez, M. Boguná, and M. A. Serrano, Multiscale unfolding of real networks by geometric renormalization, Nat. Phys., 1 (2018).

[21] J. Kleinberg, in Proc. Int. Congr. Math. Madrid, August 2220, 2006 (European Mathematical Society Publishing House, Zuerich, Switzerland, 2006) pp. 1019–1044.

[22] S. Ratnasamy, P. Francis, M. Handley, R. Karp, and S. Shenker, A scalable content-addressable network, ACM SIGCOMM Comput. Commun. Rev. 31, 161 (2001).

[23] J. Risson and T. Moors, Survey of research towards robust peer-to-peer networks: Search methods, Comput. Networks 50, 3485 (2006).

[24] I. A. Kovács, K. Luck, K. Spirohin, Y. Wang, C. Pollis, S. Schlabach, W. Bian, D.-K. Kim, N. Kishore, T. Hao, M. A. Calderwood, M. Vidal, and A.-L. Barabási, Network-based prediction of protein interactions, Nat. Commun. 10, 1240 (2019).

[25] A. Muscoloni, I. Abdelhamid, and C. V. Cannistraci, Local-community network automata modelling based on length-three-paths for prediction of complex network structures in protein interactomes, food webs and more, bioRxiv , 346916 (2018).

[26] S. Daminelli, J. M. Thomas, C. Durán, and C. Vittorio Cannistraci, Common neighbours and the local-community-paradigm for topological link prediction in bipartite networks, New J. Phys. 17 (2015), 10.1088/1367-2630/17/11/113037.

[27] I. A. Kovács, K. Luck, K. Spirohin, Y. Wang, C. Pollis, S. Schlabach, W. Biao, D.-K. Kim, N. Kishore, T. Hao, M. A. Calderwood, M. Vidal, and A.-L. Barabási, Network-based prediction of protein interactions, bioRxiv , 275529 (2018) arXiv:275529.

[28] L. Li, L. Pan, T. Zhou, Y.-C. Zhang, and H. E. Stanley, Toward link predictability of complex networks, Proc. Natl. Acad. Sci. 112, 2325 (2015).

[29] L. Katz, A new status index derived from sociometric analysis, Psychometrika 18, 39 (1953).

[30] A.-L. Barabási and R. Albert, Emergence of scaling in random networks, Science 286, 509 (1999).

[31] C. V. Cannistraci, G. Alanis-Lobato, and T. Ravasi, From link-prediction in brain connectomes and protein interactomes to the local-community-paradigm in complex networks, Sci. Rep. 3, 1613 (2013).

[32] T. Zhou, L. Li, and Y. C. Zhang, Predicting missing links via local information, Eur. Phys. J. B 71, 623 (2009).

[33] L. A. Adamic and E. Adar, Friends and neighbors on the Web, Soc. Networks 25, 211 (2003).

[34] P. Jaccard, Etude comparative de la distribution florale dans une portion des Alpes et des Jura, Bull. del la Société Vaudoise des Sci. Nat. 37, 547 (1901).

[35] D. Liben-Nowell and J. Kleinberg, The Link Prediction Problem for Social Networks, Proc. Twelfth Annu. ACM Int. Conf. Inf. Knowl. Manag., 566 (2003).

[36] A. Iamnitchi, M. Ripeanu, and I. Foster, in INFOCOM 2004, Twenty-third Annu. Jt. Conf. IEEE Comput. Commun. Soc., Vol. 2 (IEEE, 2004) pp. 952–963.

[37] E. Burgos, H. Ceva, L. Hernández, R. P. J. Perazzo, and M. Boguñá, Hyperbolic geometry of complex networks, Phys. Rev. E 82, 036106 (2010).

[38] M. Boguná and R. Pastor-Satorras, Class of correlated random networks with hidden variables, Phys. Rev. E 68, 036112 (2003).

[39] A. Iamnitchi, M. Ripeanu, and I. Foster, in INFOCOM 2004, Twenty-third Annu. Jt. Conf. IEEE Comput. Commun. Soc., Vol. 2 (IEEE, 2004) pp. 952–963.

[40] M. Kitsak, F. Papadopoulos, and D. Krioukov, Latent geometry of bipartite networks, Phys. Rev. E 95, 032309 (2017).

[41] H. Yu, P. Braun, M. A. Yildirim, I. Lemmens, K. Venkatesan, J. Sahalie, T. Hirozane-Kishikawa, F. Gebreas, N. Li, N. Simonis, T. Hao, J.-F. Rual, A. Dricot, A. Vazquez, R. R. Murray, C. Simon, L. Tardivo, S. Tam, N. Syrzlakap, C. Fan, A.-S. de Smet, A. Motyl, M. E. Hudson, J. Park, X. Xin, M. E. Cusick, T. Moore, C. Boone, M. Snyder, F. P. Roth, A.-L. Barabási, J. Tavernier, E. D. Hill, M. Vidal, and M. Yldrm, High-quality binary protein interaction map of the yeast interactome, Nature 428, 409 (2004).

[42] J. Das and H. Yu, HINT: High-quality protein interactomes and their applications in understanding human disease, BMC Syst. Biol. 6, 92 (2012).
Appendix A: Cross-Geometry in Collaboration Networks

In the cross-geometric framework, proposed in the main text each network node corresponds to two points in the latent space, and connection probabilities, governed by Eq. (1), depend on distances between the opposing points $d(x_i, x_j)$ and $d(x_i, y_j)$. We interpret different points $x_i$ and $y_j$ corresponding to node $i$ as different node properties relevant for link formation, and distances $d(x_i, x_j)$ and $d(x_i, y_j)$ as measures of complementarity between the corresponding properties. To support this interpretation we consider a minimal model of a collaboration network where we derive the cross-geometric framework analytically.

The model includes a collection of $T$ interdisciplinary tasks, and the execution of each task $k$ requires two complementary skills $x_k$ and $y_k$, that are modeled as points in different latent spaces $\mathcal{M}_1$ and $\mathcal{M}_2$, respectively. Within the model, skills for each task are drawn uniformly at random from joint pdf $p_T(x,y)$. Tasks can be executed collaboratively by agents from two cohorts that possess either a skill of type 1 or a skill of type 2. To be precise, we postulate that every agent $i = 1, \ldots, N_1$ from cohort 1 has skill $x_i$, while every agent $j = 1, \ldots, N_2$ from cohort 2 has skill $y_j$. Similar to tasks, skills of the agents are points, respectively, in spaces $\mathcal{M}_1$ and $\mathcal{M}_2$. Intuitively, the probability that agent $i (j)$ can carry out her/his portion of the task $k$ is prescribed by probability function $r_1[d(x_i, x_k)] (r_2[d(y_j, y_k)])$, such that the smaller distance $d(x_i, x_k)$ ($d(y_j, y_k)$) is the higher is the probability to execute the corresponding part of task $k$.

The probability for two agents to co-execute task $k$ is

\[
p(i,j|k) = r_1[d(x_i, x_k)] r_2[d(y_j, y_k)] ,
\]

and the expected number of tasks co-executed by two agents is given by the sum of the $p(i,j|k)$ over all available tasks:

\[
m_{ij} = T \int dx dy p_T(x,y) r_1[d(x_i, x)] r_2[d(y, y_j)] .
\]
The choice of uncorrelated task coordinates, $\rho_T(x,y) = \rho_1(x)\rho_2(y)$, results in the degenerate collaboration model, where the co-productivity of any two agents $i$ and $j$ is proportional to the product of their corresponding productivities, $k_i$ and $k_j$, $m_{ij} \propto k_i k_j$.

A more interesting case, as empirical studies seem to suggest \cite{33,55}, is the case of a strong correlation between $x$ and $y$. The simplest choice for $\rho_T(x,y)$, to this end, is dictated by deterministic relationship between skills $x$ and $y$:

$$\rho_T(x,y) = \rho_1(x)\delta(y - f(x)).$$

(A3)

where $f : \mathcal{M}_1 \rightarrow \mathcal{M}_2$ can be any injective function and $\delta(x)$ is a multi-dimensional Dirac delta function. In this case the skill of agent $i$ in $\mathcal{M}_1$ is effectively mapped onto $\mathcal{M}_2$ or vice-versa. Further, in case $\mathcal{M}_1 = \mathcal{M}_2 = \mathcal{M}$, it is convenient to think of both skill types corresponding to the same space, resulting in

$$m(x_i, y_j) = T \int dx \rho_1(x) r_1 [d(x_i, x)] r_2 [d(f(x), y_j)].$$

(A4)

Since connection probabilities $r_1(x)$ and $r_2(x)$ are decreasing functions of $x$, it follows from Eq. (A4) that the co-productivity of agents $i$ and $j$ is peaked in cases when the distances $d(f(x_i), y_j)$ are small.

In particular, if function $f : \mathcal{M}_1 \rightarrow \mathcal{M}_2$ is distance preserving, $d(x_i, x_j) = d(f(x_i), f(x_j))$, the model is reduced to the model of bipartite networks with latent geometry \cite{10}, where agents and tasks correspond two different domains. The co-productivity of two agents in this case is the link weight between $i$ and $j$ in the unipartite projection onto the agent domain:

$$m(x_i, y_j) = m(x_i, x_j)$$

$$= T \int dx \rho_1(x) r_1 [d(x_i, x)] r_2 [d(x, x_j)].$$

(A5)

where $x_j = f^{-1}(y_j)$.

We analyzed unipartite projections of latent-geometric bipartite networks in Refs. \cite{10,56}. There we demonstrated that $m(x_i, x_j)$ is maximized when $d(x_i, x_j) = 0$, regardless of the form of the connection probability function, and is small for nodes pairs separated by large distances $d(x_i, x_j)$.

One simple example of a model where agent co-productivity is a function of latent distance, is the case of 1-dimensional space $\mathcal{M} = [-K, K]$, $f(x) = x$, where $K \gg 1$, and $r_{\{1,2\}}(x) = e^{-x^2}$. Under these circumstances

$$m(x_i, y_j) = m[d(x_i, y_j)] \propto \exp^{-d(x_i, y_j)^2}.\quad (A6)$$

Since resulting network is sparse \cite{30}, the probability that agents co-execute at least one task is also a function of $d(x_i, x_j)$:

$$p_{ij} \approx 1 - e^{-m(d(x_i, y_j))} = p[d(x_i, y_j)].\quad (A7)$$

supporting the use of cross-distances in the proposed complementarity framework.

A more general version of the collaboration network is the case, where each agent $i$ has both skills 1 and 2, which are quantified by points $x_i$ and $y_i$ in spaces $\mathcal{M}_1$ and $\mathcal{M}_2$, respectively. Then, the probability of two agents $i$ and $j$ to co-execute task $k$ is either due to agent $i$ using skill 1 and agent $j$ using skill 2 or vice versa:

$$p(i, j | k) = p_{12}(i, j | k) + p_{21}(i, j | k)$$

$$- p_{12}(i, j | k)p_{21}(i, j | k),$$

(A8)

$$p_{12}(i, j | k) = r_{11}[d(x_i, x_k)] r_{22}[d(y_k, y_j)],$$

$$p_{21}(i, j | k) = r_{11}[d(x_j, x_k)] r_{22}[d(y_k, y_i)].$$

By repeating the same steps as above we obtain, to the leading order, the co-productivity for two agents

$$m_{ij} = m_{12}(i, j) + m_{21}(i, j),$$

(A9)

which in the case of the strong correlation between $x$ and $y$ in the distribution of tasks $p_T(x,y)$ leads to the cross-geometric framework in Eq. (I).

Appendix B: Complementarity and Bipartite Networks

Several parallels can be drawn between the complementarity-driven networks and bipartite (multi-partite) networks.

In a bipartite network, nodes are split into two classes or domains and connections are possible only between the nodes of different classes. Thus, a bipartite network can be regarded as a special case of a complementarity-driven networks. Here two node domains are complementary to each other, and connections are only possible between the complementary node types. Connections between similar nodes (that belong to the same domain) are strictly forbidden.

As discussed in Appendix A, agents in a complementarity-driven network may be viewed as one domain of a bipartite collaboration network, where the second, possibly hidden, domain is the domain of tasks or functions. Then the observable complementarity-driven network is nothing else but a one-mode projection of the bipartite network onto the first domain.

Appendix C: Higher order generalizations

The cross-geometric framework, proposed in the main text assumes that each network node is mapped to two
points in the latent space. Here we sketch a possible generalization of the framework to the case of an arbitrary number of features per node.

We formulate such a generalization using the terminology of a collaboration network. We assume a collection of nodes, \(i = 1, \ldots, N\), each of which is characterized by \(M\) different skills, \(\{x^m_i\}\), \(m = 1, \ldots, M\). Any two nodes \(i\) and \(j\) are connected in the complementarity network if they jointly engage into at least one task \(k\), \(k = 1, \ldots, K\). Depending on the context, tasks can be explicit, e.g., scientific publications or problems in a collaboration network of implicit (unobserved), e.g., biological functions in molecular interaction networks. Thus, we introduce a collection of tasks, each of which is characterized by feature \(\{y_k\}\). The basic building block is the probability \(p^m(x^m_i, y_k)\) that node \(i\) engages in task \(k\) using its skill \(x^m_i\). The probability for node \(i\) to engage into task \(k\) through any of its tasks independently is

\[
q_{ik} = 1 - \prod_{m=1}^{M} \left[1 - p^m(x^m_i, y_k)\right],
\]

and the probability for any two nodes \(i\) and \(j\) to interact is the probability that any two nodes co-engage in at least one task:

\[
p_{ij} = 1 - \prod_{k=1}^{K} (1 - q_{ik} q_{jk}).
\]

In case \(q_{ik} \ll 1\), the connection probability in Eq. (C2) can approximated to the leading order as

\[
p_{ij} = \sum_{m=1}^{M} \sum_{n=1}^{M} g^{mn}(x^m_i, x^n_j),
\]

\[
g^{mn}(x^m_i, x^n_j) = \sum_{k=1}^{K} p^m(x^m_i, y_k)p^n(x^n_j, y_k)
\]

As seen from Eq. (C4), the general framework contains both similarity and complementarity components. In case \(M = 1\), each network node has only one feature and the connection probability \(p_{ij}\) depends on the mutual match between features \(x^1_i\) and \(x^1_j\). The case of \(M = 2\) contains both similarity, \(g^{11}\) and \(g^{22}\), and complementarity, \(g^{12}\) and \(g^{21}\), components.

We note that functions \(g^{mn}(x, y)\) comprising the cross-geometric framework in Eqs. (C3) and (C4) are not necessarily geometric, and their functional form should be learned from the network of interest.

It is established that ordinary geometric networks, including random geometric graphs and random hyperbolic graphs, are characterized by strong clustering coefficient due to the constraints imposed by the triangle inequality. Recent results in Ref. [27] imply that strong clustering should be a sufficient condition for network geometricity. What are the network geometricity conditions for complementarity-driven networks remains an open question.

Appendix D: Embedding complementarity-driven networks

Cross-geometric representations can be obtained by repurposing any existing MLE-based geometric embedding methods, e.g., Refs. [11, 17, 58, 59]. MLE-based embedders aim to find node coordinates maximizing the likelihood \(L\) that the network of interest was generated as the latent space model. Therefore, to repurpose one of the existing MLE-based embedders it is sufficient to swap the original connection probability \(p_{ij}\) in the likelihood function \(L\) with that of Eq. (1). In our work repurpose the HyperLink Embedder (HL) [11] and refer to the resulting complementarity-based embedder as the Complementarity-based HyperLink (CHL) embedder, see Appendix D.

In more precise terms, to facilitate the embedding of a trimmed network, where a fraction of \(1 - q\) links is removed uniformly at random, we are looking for node coordinate assignment \(\{x^t_i\}\) and \(\{x^2_i\}\) for every node \(i\) in the network, \(i = 1, \ldots, N\), maximizing the posterior probability

\[
L(\{x^t_i, x^2_i\}|a_{ij}, \mathcal{P}) = \frac{L(a_{ij}|\{x^t_i, x^2_i\}, \mathcal{P})P(\{x^t_i\})P(\{x^2_i\})}{L(a_{ij}|\mathcal{P})},
\]

where \(\mathcal{P}\) are the model properties, including the fraction of present links \(q \in [0, 1]\), and

\[
L(a_{ij}|\{x^t_i, x^2_i\}, \mathcal{P}) = \prod_{i<j} [q_{ij}]^{a_{ij}} [1 - q_{ij}]^{1-a_{ij}}
\]

is the likelihood for the network to be generated with complementarity framework, given that \(1 - q\) fraction of links is missing uniformly at random. Here, \(a_{ij}\) is the network adjacency matrix, and \(p_{ij}\) is the connection probability, as prescribed in Eq. (1). \(P(\{x^t_i\})\) and \(P(\{x^2_i\})\) are the prior probabilities of latent coordinates given by the model.

\[
P(\{x^t_i\}) = \prod_{i=1}^{N} \rho(x^t_i),
\]

for \(t = \{1, 2\}\). We will release the embedding code upon the publication of the article.