Community Structure in Time-Dependent, Multiscale, and Multiplex Networks

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Summary: During the last decade, the science of networks has grown into an enormous interdisciplinary endeavor, with methods and applications drawn from across the natural, social, and information sciences. One of the most important and prominent ideas from network science is the algorithmic detection of tightly-connected groups of nodes known as communities. Here we develop a formulation to detect communities in a very broad setting by studying general dynamical processes on networks. We create a new framework of network quality functions that allows us to study the community structure of arbitrary \textit{multislice} networks, which are combinations of individual networks coupled through additional links that connect each node in one network slice to itself in other slices. This new framework allows one for the first time to study community structure in a very general setting that encompasses networks that evolve in time, have multiple types of ties (multiplexity), and have multiple scales.
Although the study of graphs, or networks, has a long tradition in fields such as sociology and mathematics, only much more recently have networks become ubiquitous in both academic and everyday settings. Indeed, during the last decade, network science has rapidly grown into an enormous interdisciplinary endeavor, with methods and applications drawn from across the natural, social, and information sciences.\textsuperscript{1-4} One of the most important and prominent tools in network analysis is the detection of cohesive, mesoscopic structures known as communities, which are defined intuitively as groups of nodes that are more tightly connected to each other than they are to the rest of the network.\textsuperscript{5-7}

Perhaps the most popular means of quantifying the notion of communities is to use a quality function to count intra- versus inter-community edges compared to what one would expect to obtain at random. Given a specification of a network as an adjacency matrix $A$, where the component $A_{ij}$ details a direct connection between nodes $i$ and $j$, one can construct a quality function $Q$ for the partitioning of nodes into communities as\textsuperscript{8, 9}

$$Q = \sum_{ij} [A_{ij} - P_{ij}] \delta(c_i, c_j),$$

where $\delta(c_i, c_j) = 1$ if nodes $i$ and $j$ have been assigned to the same community and 0 otherwise, and $P_{ij}$ is the expected weight of the edge between $i$ and $j$ under a specified null model. The choice of null model is a crucial consideration in studying network community structure,\textsuperscript{5} ideally utilizing information about the type of network under consideration. After selecting a null model appropriate to the network and application at hand, one can use any of an increasing number of available computational heuristics (simulated annealing, greedy algorithms, spectral methods, etc.) to assign nodes to communities to optimize the quality $Q$.\textsuperscript{5, 6}

The most popular null models describe either uniformly randomized networks\textsuperscript{9} or randomized networks with specified expected degree distributions.\textsuperscript{10} They allow one to consider weighted or unweighted edges,\textsuperscript{8} unipartite (one-mode) or bipartite (two-mode) graphs,\textsuperscript{11, 12} resolution parameters to specify the spatial scale of communities,\textsuperscript{5, 6, 9} and communities with signed edges.\textsuperscript{13, 14} However, none of the available community-detection methods is directly applicable to time-dependent networks—one must instead rely on detecting communities separately at each time and then use ad hoc methods or special constraints to piece together the structures obtained at different times.\textsuperscript{15-17} Moreover, although tensor decompositions\textsuperscript{18} have recently been used to cluster data for networks with different types of con-
nections (multiplex networks), no quality-function method has ever been used for multiplex network data. Indeed, the application of quality functions for community detection in networks has thus far remained limited to networks that are specified by single, static adjacency matrices.

In the present work, we develop a method that removes these limits. We formulate a family of null models that allows us to generalize the notion of community structure beyond single-slice networks to multislice networks that are defined using many coupled adjacency matrices. The different connections encoded by the adjacency matrices that couple the individual slices are very flexible—they can represent variations across time (time-dependent networks), across different types of ties (multiplex networks), or even across different scales (multiple-resolution communities).

Important to our method is the recently-recognized equivalence between modularity-like quality functions and Laplacian dynamics of populations of random walkers, which we extend to multislice networks using several fundamental generalizations (including an additional parameter that controls the coupling between slices). We thereby derive simple null models for multislice networks that are principled and grounded in the existing quality-function methodology. Community detection in multislice networks can then proceed using the same computational heuristics that are currently employed for single-slice networks (though, as with the standard definition of modularity, such quality functions have complex energy landscapes, so care is needed in interpreting results on real networks). Our methodology for coupling adjacency matrices in terms of associated Laplacian dynamics can be used for a wide variety of graph types—including directed, bipartite, and signed network slices—providing remarkable flexibility in the study of network community structure. We demonstrate the wide applicability of our approach using examples that have multiple resolutions (Zachary Karate Club), vary over time (voting patterns in the U.S. Senate), and are multiplex (the “Tastes, Ties, and Time” cohort of university students).

Recently, Lambiotte et al.19 rederived modularity from the continuous-time normalized Laplacian dynamics

\[ \dot{p}_i = \sum_j \frac{1}{k_j} A_{ij} p_j - p_i \]

on a unipartite, undirected network defined by the adjacency matrix components \( A_{ij} \) with node strengths \( k_i = \sum_j A_{ij} \). They introduced a notion of stability of communities under such dynamics by directly comparing the joint probability at stationarity of independent appearances at nodes \( i \) and \( j \) with the linear (in time) ap-
proximate map from node $j$ to node $i$. In so doing, they derived a quality function that is equivalent to Newman-Girvan (NG) modularity\textsuperscript{10} at unit time and were also able to recover the standard Potts generalization of NG modularity\textsuperscript{9} that includes a resolution parameter (interpreted as an inverse time).

Here we extend this formalism to multislice networks with three important generalizations [see the Supplementary Information (SI) for mathematical details]. First, we restrict the independent joint probability contribution in Lambiotte \textit{et al.}\textsuperscript{19} to one that is conditional on the type of connection necessary to step between two nodes. Using bipartite networks as an example, this yields a generalization of Barber’s null model\textsuperscript{24} with a resolution parameter. Second, we generalize the Laplacian dynamics to include motion along multiple types of connections. Using directed networks as an example, this yields a generalization of the standard null model for directed networks\textsuperscript{25, 26} that again incorporates a resolution parameter. This generalization of the Laplacian dynamics also recovers, via a similar derivation, a recently-developed null model for signed networks.\textsuperscript{13} Third, we interpret the Laplacian dynamics flexibly to permit different spreading weights on the different types of links. This allows us to introduce multiple resolution parameters similar to another recently-proposed null model for signed networks.\textsuperscript{14}

\section*{Multislice Networks}

Having shown (see the SI) that our generalizations recover the appropriate null models for other categories of networks (bipartite, directed, and signed), we now apply our methodology to the far more general framework of multislice networks. We suppose that each slice $s$ of a network is represented by adjacencies $A_{ijs}$ between nodes $i$ and $j$ and specify inter-slice couplings $C_{jrs}$ that connect node $j$ in slice $r$ to itself in slice $s$ (see Fig. [1]). For simplicity, we restrict our attention to undirected network slices ($A_{ijs} = A_{jis}$) and undirected couplings ($C_{jrs} = C_{jsr}$), but we can incorporate additional structure in the slices and couplings in the same manner as demonstrated in the SI for single-slice examples. For convenience, we notate the strengths of each node individually in each slice, so that $k_{js} = \sum_i A_{ijs}$, $c_{js} = \sum_r C_{jrs}$, and we define the \textit{multislice strength} $\kappa_{js} = k_{js} + c_{js}$. We study a continuous-time Laplacian process analogous to those above (and in the SI) that respects the intra-slice nature of $A_{ijs}$ and the inter-
slice couplings of $C_{jsr}$, specified by $\dot{p}_{is} = \sum_{jr} (A_{ijs} \delta_{sr} + \delta_{ij} C_{jsr}) p_{jr} / \kappa_{jr} - p_{is}$, which has steady state probability distribution $p_{is}^* = \kappa_{jr} / (2\mu)$, where $2\mu = \sum_{jr} \kappa_{jr}$. We then specify the associated multislice null model using the probability $p_{is|jr}$ of sampling node-slice $is$ conditional on whether the multislice structure allows one to step from node-slice $jr$ to node-slice $is$ (considering intra- and inter-slice steps separately):

$$p_{is|jr} p_{jr}^* = \left[ \frac{k_{is} k_{jr}}{2m_s \kappa_{jr}} + \frac{C_{jsr} c_{jr}}{\kappa_{jr} \kappa_{jr}} \right] \frac{\kappa_{jr}}{2\mu} .$$

The second term in brackets, which describes the conditional probability of motion between two slices, leverages the known definition of the $C_{jsr}$ coupling. That is, the conditional probability of stepping from node-slice $jr$ to node-slice $is$ along an inter-slice coupling is non-zero if and only if $i = j$, and it is proportional to the probability $C_{jsr}/\kappa_{jr}$ of selecting the precise inter-slice link that connects to slice $s$ from all edges connected to $jr$. The inter-slice strengths $c_{jr}$ cancel naturally as part of this calculation. Subtracting this conditional joint probability from the linear (in time) approximation of the exponential describing the Laplacian dynamics on the multislice networks, we obtain a multislice generalization of modularity (see SI for details):

$$Q_{\text{multislice}} = \frac{1}{2\mu} \sum_{ijsr} \left\{ \left( A_{ijs} - \gamma_s \frac{k_{is} k_{js}}{2m_s} \delta_{sr} \right) + \delta_{ij} C_{jsr} \right\} \delta(c_{is}, c_{jr}) ,$$

where we have utilized reweighting of the conditional probabilities, which allows one to have a different resolution $\gamma_s$ in each slice. We have absorbed the corresponding resolution parameter for the inter-slice couplings into the (as yet unspecified) magnitude of the elements of $C_{jsr}$, which we now suppose for simplicity take binary values $\{0, \omega\}$ indicating absence/presence of inter-slice links.

In the absence of such a reweighting, $\gamma_s = \gamma$ for all $s$, so that the corresponding prefactor of $C_{jsr}$ is $(1 - \gamma)$. The choice $\gamma = 1$ then recovers the usual interpretation of modularity as a count of the total weight of intra-slice edges minus the weight expected at random, and (as expected) the specified deterministic $C_{jsr}$ contribution drops out entirely. In contrast, by leveraging the notion of stability under Laplacian dynamics, we have derived a principled generalization of modularity to multislice networks that introduces the single parameter $\omega$ to control the extent of inter-slice correspondence of communities. When $\omega = 0$, there is no benefit from extending communities across slices, and the optimal partition is obtained from independent optimization of the corresponding quality function.
Figure 1: Schematic of a multislice network, considering a network sampled four different ways. The four slices $s = \{1, 2, 3, 4\}$ are represented by the adjacencies $A_{ij}$, encoding the intra-slice ties and shown as solid black lines. The inter-slice ties, shown as dashed red curves, are encoded by $C_{jrs}$, specifying the strength of coupling for node $j$ between slices $r$ and $s$. For clarity, we show the inter-slice couplings for two nodes only, depicting two different types of couplings: (1) coupling between neighboring slices, appropriate for ordered slices that one encounters for data across time or using multiple resolution parameters; and (2) coupling from all slices to all slices, appropriate for categorical slices that occur in multiplex networks.

In each slice. At the other extreme, when $\omega$ becomes sufficiently large, the quality-optimizing partitions force the community assignment of a node to remain the same across all slices in which that node appears, and the multislice quality reduces to that of an adjacency matrix summed over the contributions from the individual slices with a null model that respects the degree distributions of the individual contributions. The generality of this framework also allows one to include different weights across the $C_{jrs}$ couplings. Additionally, note that the linearity of (3) with respect to the $\{\gamma_s, \omega\}$ parameters necessitates that the modularity-optimizing domain of a single partition is convex in this parameter space (see SI for the proof and a brief discussion of consequences).
Applications

For our first demonstration of multislice community detection, we perform simultaneous community detection across multiple resolutions (scales) in the well-known Zachary Karate Club benchmark network, which encodes the friendships between 34 members of a karate club at a U.S. university in the 1970s. Keeping the same 34-node unweighted adjacency matrix across slices ($A_{ijs} = A_{ij}$ for all $s$), the resolution associated with each slice is dictated by a value from a specified sequence of $\gamma_s$ parameters, which we choose to be the 16 values $\gamma_s = \{0.25, 0.5, 0.75, \ldots, 4\}$. In Fig. 2, we depict the community assignments that we obtained when the individual nodes are coupled with strengths $\omega = \{0, 0.1, 1\}$ between each neighboring pair of the 16 ordered slices. For each $\omega$, we took the higher quality partition from that given by a spectral method plus Kernighan-Lin (KL) node-swapping steps and a generalization of the Louvain algorithm plus KL steps. We note that, despite this approach, the depicted $\omega = 1$ partition can be clearly improved by leveraging the definition of the inter-slice coupling; future algorithmic improvements could explicitly merge and break communities across slices where appropriate. When $\omega = 0$, the optimal partition corresponds to the union of the independent partitions of the individual resolution parameters. As $\omega$ increases, the coupling between neighboring slices encourages the partition of the $34 \times 16 = 544$ nodes in the complete multislice network to include communities that straddle multiple slices in the hierarchy of scales. Increasing $\omega$ further eventually forces the communities to span the full range of the considered resolutions (not shown), with a partition corresponding to the average $\gamma_s$ value (with $\langle \gamma_s \rangle = 2.125$ here). Even at the smallest value of the resolution parameter that we used ($\gamma = 0.25$), we already observe a split into two communities when $\omega > 0$ (recalling that the actual club fractured into two groups). We simultaneously obtain all of the other network scales, such as the partitioning of the Karate Club into four communities at the default resolution of NG modularity. We can additionally identify nodes that have an especially strong tendency to break off from larger communities (e.g., nodes 24–29 in Fig. 2). Multislice community detection thereby allows us to systematically track the development of multiple network scales simultaneously.

In our second example, we consider roll call voting in the United States Senate across time. The Senate is one of the two chambers of the legislative branch (collectively called the Congress) of the U.S. federal government. It
Figure 2: Multislice community detection of the Zachary Karate Club\textsuperscript{21} across multiple resolutions. Colors depict community assignments of each of the 34 nodes (numbered vertically, after renumbering nodes to graphically group similarly-assigned nodes) in each of the 16 slices (numbered horizontally, with resolution parameters $\gamma_s = \{0.25, 0.5, 0.75, \ldots, 4\}$). Each node-slice point is uniquely assigned to a community. For comparison, dashed lines indicate the partition obtained with NG modularity. The inter-slice couplings are $\omega = 0$ (top), $\omega = 0.1$ (middle), and $\omega = 1$ (bottom).
currently consists of 100 Senators (two from each state) who serve staggered six-year terms such that approximately
one-third of the Senate is elected every two years. The data we study is from the 1st–110th Congresses, covering
the years 1789–2008 and including 1884 individual Senators.\textsuperscript{1} We define weighted connections between each pair
of Senators in terms of a similarity between their voting dynamics, which are obtained independently for each two-
year Congress.\textsuperscript{22} One can gain additional understanding of this network, and the underlying political processes, by
applying multislice community detection to the collection of these 110 network slices taken as a whole. In this
multislice network, we couple each individual Senator to him/herself when appearing in consecutive Congresses. If a
Senator from Congress $s$ does not serve in Congress $s + 1$, then we do not introduce inter-slice coupling between slices
$s$ and $s + 1$ for this individual. That is, both link strengths and nodes (Senators) change from one slice to another.

Multislice community detection uncovers interesting details about the continuity of individual and group voting
dynamics over time that are simply not captured by the union of the 110 independent partitions of the individual
Congresses. Again using a generalization of the Louvain algorithm plus KL steps, we depict a partition in Fig. 5
into 9 communities obtained using inter-slice coupling $\omega = 0.5$ for the 1884 unique U.S. Senators in each Congress
in which they voted. The community structure highlights a number of historical turning points in U.S. politics. For
instance, the Congresses in which three communities appear simultaneously are each historically significant: The 4th
and 5th Congresses were the first with political parties; the 10th and 11th Congresses occurred during the political
drama of former Vice President Aaron Burr’s indictment for treason; the 14th and 15th Congresses witnessed the
beginning of changing group structures in the Democratic-Republican party\textsuperscript{22} amidst the dying Federalist party; the
31st Congress included the Compromise of 1850; the 37th Congress occurred during the beginning of the American
Civil War; the 73rd and 74th Congresses followed the landslide 1932 election amidst the Great Depression; and the
85th–88th Congresses brought the major American civil rights acts, including the Congressional fights over the Civil
Rights Acts of 1957, 1960, and 1964 (observe that all 44 Democratic Senators in the community colored green during

\textsuperscript{1}At least five Senators in the data (available at voteview.com\textsuperscript{29}) are each assigned two different identification
numbers, corresponding to different periods of their careers. We take the data as provided, counting such Senators
twice, and merely remark that politically-minded studies should include such considerations.
this time period came from Southern states). A more complete political study using multislice community detection, systematically changing $\omega$, would enable one to examine similar results in extensive detail.

Finally, we apply multislice community detection to a multiplex network of 1640 college students at an anonymous, northeastern American university.\textsuperscript{23} We include the following symmetrized ties from the first wave of this data (covering the first year of university attendance): (1) Facebook friendships; (2) picture friendships, in which a student has posted and tagged a photograph of another online; (3) roommates, in which two students share a first-year dormitory room, creating clusters of 1–6 students; and (4) “housing group” preferences identified by the students. Because the different tie types are categorical, the natural inter-slice couplings connect an individual corresponding to one type of connection to him/herself in each of the other 3 types of networks. This type of inter-slice coupling thus has a different nature from the inter-slice couplings above that connected only neighboring ordered network slices.

In Table 1 we provide a summary of the basic results that we obtained by varying the inter-slice coupling strength $\omega$. We tabulate the total number of communities and the numbers of individuals assigned to 1, 2, 3, or 4 communities in the multislice network across the four types of connections. Again, $\omega = 0$ yields separate communities for each slice, with each individual placed into four separate communities. Communities merge across slices as $\omega$ increases, most predominantly when the patterns of connection are relatively similar between two slices. This reduces the total number of communities and results in the grouping of individuals who appear across slices. For $\omega \in [0.2, 0.5]$, a significant majority of the individuals appear in only 1 or 2 communities, indicating that their social networks maintain group-level similarities across the four types of connections. Another significant set of students is grouped into 3 different communities, and a small minority maintain 4 separate assignments, suggesting stark differences in their positions in the 4 single-category network slices. Finally, for $\omega = 1$, the inter-slice coupling is sufficiently strong that it forces the 4 multislice nodes corresponding to an individual student to be assigned to the same community. Further investigation of such different community assignments across slices can be used to more clearly compare and contrast the roles of individuals in each network slice and in the complete multislice network. Additionally, a multislice approach might provide a novel mechanism for dealing with the problem of overlapping
Figure 3: Multislice community detection of U.S. Senate roll call vote similarities at $\omega = 0.5$, where each of the 110 slices across time (covering the years 1789–2008) corresponds to a single two-year Congress. Colors indicate the assignments to the 9 communities of the 1884 unique Senators (sorted vertically and connected across Congresses by dashed black lines) in each Congress they appear (horizontal). The same assignments are also shown according to state affiliations. The dark blue and red communities correspond closely to the modern Democratic and Republican parties, respectively. The historical period of each community is indicated by colored horizontal bars, with accompanying text enumerating the nominal party affiliations of the Senator-Congress nodes: Pro-Administration (PA), Anti-Administration (AA), Federalist (F), Democratic-Republican (DR), Whig (W), Anti-Jackson (AJ), Adams (A), Jackson (J), Democratic (D), and Republican (R). Vertical gray bars indicate Congresses in which three communities appeared simultaneously, highlighting interesting periods of U.S. history (see the main text).
community assignments, as the hard partitioning of each node-slice in the multislice network allows an individual to be placed in different communities across slices. Indeed, multiplexity is itself a strong motivation for developing methods that allow communities to overlap\textsuperscript{5,6,30}

**Conclusions**

In conclusion, we have developed a novel “multislice” community detection method that makes it possible to study community structure in a much broader class of networks than was previously possible. Instead of detecting communities in one static network at a time and then attempting to patch together the results across different network data, our method allows one for the first time to study network community structure in terms of quality functions using multiple times, multiple resolution parameter values, and multiple types of links simultaneously. Using this method, we have demonstrated interesting insights in real-world networks that would have been difficult or impossible to obtain without the simultaneous consideration of multiple network slices. Although we used multiple slices across only one kind of variation at a time, our framework applies equally well to networks that have multiple such features (e.g., time-dependent multiplex networks), and we expect multislice community detection to be a powerful tool for studying such systems. Our methodology can also be used in conjunction with any random graph ensemble for which one can write Laplacian dynamics, providing unprecedented flexibility in the study of network community structure.

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Community detection results for the first wave of the multiplex “Tastes, Ties, and Time” network.\textsuperscript{23}

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Table 1: We use the default spatial resolution ($\gamma = 1$) in each of the four slices of data (Facebook friendships, picture friendships, roommates, and housing groups) and vary the inter-slice coupling strength $\omega$ of individuals to themselves across connection types. This changes the aggregate number of multislice communities as well as the number of individuals assigned on a per slice basis to 1, 2, 3, or 4 communities.
Supplementary Information

We here provide additional details for several of the results that we discussed in the main text. We begin by reviewing salient results from Ref. 19 concerning the connection between normalized Laplacian dynamics on networks and the modularity quality function for network community structure. We then generalize this methodology to reproduce the null models for bipartite, directed, and signed networks, culminating in the specification of the corresponding quality function for multislice networks. We additionally consider a similar analysis for standard (unnormalized) Laplacian dynamics in multislice networks. Finally, we prove that the domains of optimization of each network partition are convex in the space of parameters for quality functions that are linear in those parameters and comment on possible consequences of this result.

The normalized Laplacian dynamics on a network, \( \dot{p}_i = \sum_j \frac{1}{k_j} A_{ij} p_j - p_i \), have a steady state given by \( p^*_j = \frac{k_j}{2m} \), where \( 2m = \sum_i k_i = \sum_{ij} A_{ij} \) describes the total strength (i.e., edge weight) in the network. In Ref. 19, Lambiotte et al. quantified a measure of the stability \( R(t) \) of a specified partition of the network into communities using the probability that a random walker remains within the same community after time \( t \), in statistically steady conditions, relative to that expected under independence. Using the operator \( L_{ij} = A_{ij}/k_j - \delta_{ij} \) of the dynamics, where \( \delta_{ij} \) is the Kronecker delta, they specified this stability as

\[
R(t) = \sum_{ij} \left[ (e^{tL})_{ij} p^*_j - p^*_i p^*_j \right] \delta(c_i, c_j),
\]

where the contribution from an independence assumption appears in the second term in brackets. Expanding the matrix exponential in (4) to first-order in \( t \), \( (e^{tL})_{ij} \approx \delta_{ij} + tL_{ij} \), Lambiotte et al. demonstrated that \( R(t) \) directly yields the quality function

\[
Q(t) = \frac{1}{2m} \sum_{ij} \left[ tA_{ij} - \frac{k_i k_j}{2m} \right] \delta(c_i, c_j)
\]

up to \( \delta_{ij} \) factors that always contribute to the sum and are thus immaterial in identifying partitions that optimize \( Q(t) \).

The resulting quality function reduces to NG modularity for \( t = 1 \). Moreover, dividing by \( t \) (which has no effect on the optima for specified \( t \)) provides a direct interpretation of the resolution parameter \( \gamma = 1/t \) when the quality is written in the usual form: \( Q = \frac{1}{2m} \sum_{ij} \left[ A_{ij} - \gamma \frac{k_i k_j}{2m} \right] \delta(c_i, c_j) \). Hence, the stability of the community partition relative to
that expected under independence provides a natural definition for the null model employed in the quality function.

**Generalized Laplacian Dynamics** We extend the formalism of Lambiotte et al.\textsuperscript{19} to multislice networks by considering three crucial generalizations.

First, we restrict the expected independent contribution given by the probability of a random walker remaining within the same community after time $t$ in the statistically steady state to one that is conditional on the type of connection necessary to step between two nodes. That is, we replace the $p^*_i p^*_j$ independent contribution in (4) with a conditional independent contribution $\rho_{i|j} p^*_j$, where $\rho_{i|j}$ is the conditional probability at stationarity of jumping to node $i$ from node $j$ along a specific edge type that is allowed by the specified category of networks, giving $\hat{R}(t) = \sum_{ij} \left[ (\delta_{ij} + tL_{ij}) p^*_j - \rho_{i|j} p^*_j \right] \delta(c_i, c_j)$. For instance, consider undirected bipartite networks. Such networks have two types of nodes (e.g., a person might belong to an organization), and every edge must connect a node of one type to a node of the other. The adjacency matrix in the operator $L_{ij} = A_{ij}/k_j - \delta_{ij}$ takes a bipartite form (i.e., it consists of off-diagonal blocks), and one ostensibly obtains the same $p^*_j = k_j/(2m)$ steady state. However, $\rho_{i|j} = b_{ij} k_i/m$, where $b_{ij}$ is a bipartite indicator that is equal to 1 if nodes $i$ and $j$ are of different types and 0 otherwise. The denominator in $\rho_{i|j}$ is $m$ (as opposed to $2m$) because the probability of stepping to node $i$ conditional on the additional information that the jump is along an edge going towards a node of $i$’s type doubles the probability. Again neglecting $\delta_{ij}$ contributions, dividing by $t$ and setting $\gamma = 1/t$ yields

$$Q_{\text{bipartite}} = \frac{1}{2m} \sum_{ij} \left[ A_{ij} - \gamma b_{ij} \frac{k_i k_j}{m} \right] \delta(c_i, c_j),$$

which extends the $\gamma = 1$ Barber bipartite null model\textsuperscript{24} by incorporating the resolution parameter $\gamma$.

Second, we generalize the Laplacian dynamics to include motion along multiple types of connections. For example, consider a directed network (so that $A_{ij}$ is no longer symmetric) with $k^\text{in}_i = \sum_j A_{ij}$ and $k^\text{out}_j = \sum_i A_{ij}$. We define the normalized Laplacian dynamics to include motion equally along both incoming and outgoing edges, subject to the normalization $k_j = k^\text{in}_j + k^\text{out}_j$. This yields $\dot{p}_i = \sum_j L_{ij} p_j = \sum_j \frac{1}{k_j} (A_{ij} + A_{ji}) p_j - p_i$. This has the steady state $p^*_j = k_j/(2m)$, where $2m = \sum_j k_j = 2 \sum_{ij} A_{ij}$. The change induced by the consideration of the
A directed network occurs in the conditional probability $\rho_{ij}$, which must respect the type of edge (incoming versus outgoing) that is used to arrive at node $i$ as well as the fraction of such edges available in the departure from node $j$. This yields

$$\rho_{ij}p_j^* = \left( \frac{k_{ij}^\text{in} k_{ij}^\text{out}}{m k_j} + \frac{k_{ij}^\text{out} k_{ij}^\text{in}}{m k_j} \right) \frac{k_j}{2m} = \frac{k_{ij}^\text{in} k_{ij}^\text{out} + k_{ij}^\text{out} k_{ij}^\text{in}}{2m^2},$$

(7)

where each additive term combines the probability of picking a particular type of edge when departing node $j$ with the probability of arriving at node $i$ given that the motion is on that type of edge. Because of the symmetry in summing over $\{i,j\}$ pairs, the resulting partition quality can be rewritten as

$$Q_{\text{directed}} = \frac{1}{m} \sum_{ij} \left[ A_{ij} - \gamma \frac{k_{ij}^\text{in} k_{ij}^\text{out}}{m} \right] \delta(c_i, c_j),$$

(8)

which (as with bipartite networks) yields the natural extension of the corresponding standard ($\gamma = 1$) null model for directed networks\textsuperscript{25,26} by incorporating the resolution parameter $\gamma$. This approach contrasts with that of Lambiotte \textit{et al.}, which restricts consideration to motion following the link directions\textsuperscript{19,31}

Studying the Laplacian dynamics with the operator $L_{ij} = (A_{ij}^+ + A_{ij}^-)/k_j - \delta_{ij}$ (with $k_j = k_j^+ + k_j^-$) yields a similar derivation of a null model for (undirected) signed networks, in which link weights can be either positive or negative. Edges can be separated into ones that contribute positively (for which $A_{ij}^+ \geq 0$) and those that contribute negatively (for which $A_{ij}^- \geq 0$). As before, this process has a steady state given by $p_j^* = k_j/(2m)$, where now $m = m^+ + m^-$. Because of the penalizing contribution desired from the $A_{ij}^- \geq 0$ links, we choose to weight the $A^-$ and $k^-$ contributions negatively when they appear in the partition stability formula (4). Aside from this sign convention, we calculate the conditional probability at stationarity using the same procedure as in the directed case, keeping track of whether the movement from node $j$ to node $i$ is along a positive or negative edge. This gives

$$\rho_{ij}p_j^* = \left( \frac{k_j^+ k_j^-}{2m^+ k_j^-} - \frac{k_j^- k_j^+}{2m^- k_j^+} \right) \frac{k_j}{2m} = \frac{1}{2m} \left( \frac{k_j^+ k_j^+}{2m^+} - \frac{k_j^- k_j^-}{2m^-} \right),$$

(9)

which yields

$$Q = \frac{1}{2m} \sum_{ij} \left[ A_{ij}^+ - A_{ij}^- - \gamma \left( \frac{k_j^+ k_j^+}{2m^+} - \frac{k_j^- k_j^-}{2m^-} \right) \right] \delta(c_i, c_j).$$

This quality function reduces at $\gamma = 1$ to one proposed signed null model\textsuperscript{13} and is a special case of a more general signed null model\textsuperscript{14} that includes separate resolution parameters ($\gamma^+$ and $\gamma^-$) for the positive and negative contributions. We can reconstruct the latter null model by using our third generalization, which we present next.
Our third generalization is to flexibly interpret the Laplacian dynamics in order to permit different spreading weights on the different types of links. This was not an issue in our consideration of directed networks unless one wants to weight incoming and outgoing edges differently. On the other hand, it might be desirable for signed networks to consider reweighted conditional probabilities at stationarity using some factor other than the relative strengths of the different edges at node \( j \) (even though we only consider a single specification of the underlying Laplacian dynamics). This gives

\[
Q_{\text{signed}} = \frac{1}{2m} \sum_{ij} \left[ A_{ij}^+ - A_{ij}^- - \left( \gamma^+ \frac{k_i^+ k_j^+}{2m^+} - \gamma^- \frac{k_i^- k_j^-}{2m^-} \right) \right] \delta(c_i, c_j),
\]

where we now have two resolution parameters (\( \gamma^+ \) and \( \gamma^- \)), allowing us to obtain the aforementioned more general null model for signed networks.\(^{14}\)

We employ the third generalization in the present Article so that we can consider a different resolution \( \gamma_s \) in each slice \( s \) of a multislice network. We consider inter-slice couplings that can take the values 0 or \( \omega \), where the latter can be varied to examine inter-slice ties of different strengths. When \( \omega = 0 \), all of the slices are independent, yielding an ensemble of single-slice networks to be examined individually with any existing method that one desires. On the other hand, in the limit of infinitely large \( \omega \), one is averaging over single-slice contributions using a null model that respects the degree distributions of individual slices.

**Standard Multislice Laplacian Dynamics** As discussed by Lambiotte et al.,\(^{19}\) a similar analysis of the stability of communities under standard (i.e., unnormalized) Laplacian dynamics can be used to yield a quality function with a null model corresponding to a uniform random graph.\(^9\) Here we generalize their result to the multislice setting through a natural definition of the relevant independent probabilities subject to conditions imposed by the network structure specific to our multislice setting (similar to our derivation for normalized Laplacian dynamics).

We specify the standard Laplacian dynamics on a multislice network defined by intra-slice adjacencies \( A_{ijs} \) and inter-slice couplings \( C_{jsr} \) by

\[
\dot{p}_{is} = \sum_{jr} \left( A_{ijs} \delta_{sr} + \delta_{ij} C_{jsr} \right) p_{jr} / \langle \kappa \rangle - p_{is} \kappa_{is} / \langle \kappa \rangle,
\]

where angled brackets denote an average over the entire multislice network and we recall that \( \kappa_{js} = k_{js} + c_{js} \) is the multislice strength. The steady-
state probability distribution under these dynamics is constant. Hence, \( p^*_{jr} = \frac{1}{N} \), where \( N \) is the total number of nodes in the multislice network. We then scale the conditional probability \( \rho_{is|jr} \) of stepping from node-slice \( jr \) to node-slice \( is \) appropriate to the selected standard dynamics, where the rate of leaving node-slice \( jr \) is proportional to \( \kappa_{jr} \) (cf. the constant rate of leaving \( jr \) in the normalized Laplacian dynamics in the rest of this Article). Given that we will repeat the procedure of allowing different resolution parameters (inverse times) both within and across slices, it is sufficient to consider the conditional independent probability to be of the form

\[
\rho_{is|jr} p^*_{jr} = \left[ \delta_{sr} + C_{jsr} \delta_{ij} \right] \frac{1}{N}.
\] (11)

Ignoring \( \delta_{ij} \delta_{sr} \) contributions to quality, which have no effect on identifying the optimal partition, we thus obtain

\[
Q = \sum_{ijsr} \left\{ \left( A_{ijs} - \gamma_s \delta_{sr} \right) + \delta_{ij} C_{jsr} \right\} \delta(c_{is}, c_{jr})
\] (12)

as the multislice generalization of the uniform random null model. Note that we have once again absorbed the inter-slice coupling strength directly into the binary values of \( C_{jsr} = \{0, \omega\} \). As with the multislice null model that we obtained from normalized Laplacian dynamics, the limiting behaviors of this quality function are towards independent partitioning of each slice as \( \omega \to 0 \) and towards averaging over slices for \( \omega \gg 1 \).

**Convex Domains of Optimization.** As mentioned in the main text, the linearity of \( Q \) with respect to the \( \{\gamma_s, \omega\} \) parameters necessitates that the modularity-optimizing domain of a single partition be convex in this parameter space. This result holds more generally for any community-detection quality function that is linear in its parameters. That is, if an identified partition of the network is the highest-quality partition at two points in parameter space, then it necessarily gives the best partition along the entire line segment connecting those two points.

The proof of this convexity result follows from the consideration of a line in parameter space that contains two distinct optima at different points. For the purposes of this proof, we notate the parameters (e.g., resolution parameters and/or inter-slice coupling strengths) by the vector array \( \lambda \) and the modularity-like quality function [recall (1)] as

\[
Q = \sum_{ij} B_{ij} \delta(c_i, c_j) = \sum_{ijp} \left[ A_{ij} - \lambda_p P_{ijp} \right] \delta(c_i, c_j),
\] (13)
where the notation $i$ and $j$ for the node indices naturally generalizes over the complete multislice network. That is, $Q = B : \chi = (A - \lambda \cdot P) : \chi$, where $\chi$ is the common-community indicator with elements $\delta(c_i, c_j)$ specific to the selected partition. The meaning of the double contractions (e.g., $B : \chi$) over indices and dot products over parameters $(\lambda \cdot P)$ is clear from (13).

Now assume that the partition specified by $\chi_1$ is the unique optimum for parameters $\lambda_1$. Defining $A_1 = A : \chi_1$ and $P_1 = P : \chi_1$ yields $Q_1 = A_1 - \lambda_1 \cdot P_1$. If the distinct partition specified by $\chi_2$ is strictly optimal to $\chi_1$ for parameters $\lambda_2$ (with analogous definitions for $Q_2 = A_2 - \lambda_2 \cdot P_2$), then it must follow that

$$Q_1 = A_1 - \lambda_1 \cdot P_1 > A_2 - \lambda_1 \cdot P_2 \quad \text{and} \quad Q_2 = A_2 - \lambda_2 \cdot P_2 > A_1 - \lambda_2 \cdot P_1.$$  \hspace{1cm} (14)

Combining these inequalities yields $(\lambda_2 - \lambda_1) \cdot P_1 > (\lambda_2 - \lambda_1) \cdot P_2$. If we then consider a vector array $\lambda_3$ that is collinear with $\lambda_2$ and $\lambda_1$, so that $\lambda_3 = \lambda_2 + f(\lambda_2 - \lambda_1)$ with $f > 0$, then the quality of the $\chi_1$ and $\chi_2$ partitions at $\lambda_3$ must satisfy

$$A_2 - \lambda_3 \cdot P_2 = A_2 - \lambda_2 \cdot P_2 - f(\lambda_2 - \lambda_1) \cdot P_2 > A_1 - \lambda_2 \cdot P_1 - f(\lambda_2 - \lambda_1) \cdot P_1 = A_1 - \lambda_3 \cdot P_1.$$  \hspace{1cm} (15)

That is, the partition $\chi_2$ is necessarily of higher quality than $\chi_1$ at $\lambda_3$ (though neither of them needs to be the optimum there). Therefore, non-convex domains of optimization are forbidden in the parameter space of quality functions of the form (13).

This requirement of convex domains of quality optimization might be useful for comparing results across different resolution and coupling parameters not only in the present multislice setting but for any of the other (many) network-partitioning quality functions that are linear in resolution parameters. Although other quality functions might of course be considered, we note that each quality function discussed in the present manuscript is of the general form (13). Computational results that do not conform to convex domains of optimization typically indicate regions in which further computation should uncover better optima. Indeed, for a particular application, it might be important to consider many different parameter choices in our generalized quality function. We do not worry about such details here, as our goal has been to present a new framework that allows one for the first time to study the community.
structure of multislice networks, but it is nevertheless important to mention it for further consideration. Optimizing the standard modularity quality function is known to be an NP-complete problem, and the cautions regarding modularity optimization naturally also apply in our more general framework.