An Attract-Repel Decomposition of Undirected Networks

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Abstract

Dot product latent space embedding is a common form of representation learning in undirected graphs (e.g. social networks, co-occurrence networks). We show that such models have problems dealing with ‘intransitive’ situations where \( A \) is linked to \( B \), \( B \) is linked to \( C \) but \( A \) is not linked to \( C \). Such situations occur in social networks when opposites attract (heterophily) and in co-occurrence networks when there are substitute nodes (e.g. the presence of Pepsi or Coke, but rarely both, in otherwise similar purchase baskets). We present a simple expansion which we call the attract-repel (AR) decomposition: a set of latent attributes on which similar nodes attract and another set of latent attributes on which similar nodes repel. We demonstrate the AR decomposition in real social networks and show that it can be used to measure the amount of latent homophily and heterophily. In addition, it can be applied to co-occurrence networks to discover roles in teams and find substitutable ingredients in recipes.

1 Introduction

Network data is ubiquitous across many disciplines ranging from the natural sciences [Jeong et al., 2001; Barabasi and Oltvai, 2004] to the social sciences [Granovetter, 1983; Easley et al., 2010; Jackson, 2010]. However, networks are high dimensional objects and thus can be difficult to work with. Finding easy representations of how nodes are connected is an important topic of study. In the symmetric (or undirected) case a workhorse method are dot product models [Lovász and Vesztergombi, 1999; Ng et al., 2002; Perozzi et al., 2014; Tang et al., 2015; Grover and Leskovec, 2016; Athreya et al., 2017; Lerner et al., 2019]. In dot product models each node in a network is associated with an embedding (a.k.a latent vector) in Euclidean space and dot product between vectors reflects the strength of an edge between two nodes.

We show that the dot product model can fail in the sense that while the network has simple structure, the dot product model requires a high dimensionality to represent the network well. Such failure will occur whenever networks exhibit a lack of ‘transitivity’ \( A \) is strongly connected to \( B \) and \( B \) is strongly connected to \( C \) but \( A \) is not connected to \( C \). In such cases the dot product model struggles as representing this triangle requires us to construct vectors where \( A \) and \( B \) are close, \( B \) and \( C \) are close but \( A \) and \( C \) are far. When networks have many such combinations, representing such a network with high fidelity will require high dimensional vectors.

Such ‘forbidden triads’ [Granovetter, 1973] – or more general versions of this pattern – are ubiquitous in networks. They can occur in social networks where they can be signals of heterophily (individuals with similar attributes are less likely to be friends) or ‘enemies’ (there is clearly something going on in a citation network if two scientists cite all of the same colleagues but never cite each other). In co-occurrence networks they can indicate that nodes play similar ‘roles’ such the formation of teams or the combination of ingredients in recipes. Thus, a lossy model which has trouble describing these types of structures is likely missing something important about the network when the embedding dimension is much lower than the node count, as in most applications of network embeddings.
We show that a minimal way to expand the dot product model is to consider two sets of latent attributes: ones on which nodes attract and ones on which nodes repel. We refer to this as an attract-repel (AR) decomposition. We show how to construct AR decompositions from a combination of nuclear norm minimization and eigendecomposition. We then perform several experiments using the AR decomposition.

In experiment 1 we use it to measure latent homophily (similar types attract) and heterophily (similar types repel) in real world social networks both at the network and individual level. We show that in real social networks there is a substantial heterophilic component and so AR embeddings can more efficiently reproduce network structure than dot product models. Furthermore, we show that in a network with known community structure the relative magnitude of an individual’s repel vs. attract vectors tells us what fraction of the individual’s links are within their own community vs. outside of it. We also show that the repulsion component of an AR decomposition can be used to find individuals which fill similar roles in a team (experiment 2) or ingredients which can be substituted for one another in recipes (experiment 3).

2 Related Work

Recently Seshadhri et al. (2020) show that dot product random models cannot reproduce various macro features of real world social networks. Building on this insight (Chanpuriya et al., 2020) consider factorizing adjacency matrices with two vectors per node, a ’target’ and a ’context’ vector showing that such embeddings are able to reproduce the macro features. Ruiz et al. (2020) applies the concept of 2 embeddings per item to their dataset of a series of ’baskets’ (items purchased at a single time) to find complements and substitutes.Word2vec (Mikolov et al., 2013), a workhorse model in natural language processing, trains two embeddings per word.

The two embedding approach is overparameterized when the underlying matrix is symmetric since the symmetry imposes n equalities across dot products of the vectors $(\text{target}_i \cdot \text{context}_j = \text{target}_j \cdot \text{context}_i)$. The AR decomposition takes advantage of this symmetry to give a simpler decomposition.

The two embedding approach is inspired by word2vec (Mikolov et al., 2013), a workhorse model in natural language processing. Since word2vec predicts co-occurrences within a window, if a co-occurs with b then b co-occurs with a so it may seem that word2vec is a symmetric model and so amenable to an AR decomposition. However, in practice, the word2vec objective is optimized using negative sampling which downsamples common words and upsamples rare words which means the implied matrix is not exactly symmetric (Levy and Goldberg, 2014).

Real similarity/dissimilarity matrices (e.g. similarity between words as rated by psychology experiment participants) can often be non-metric. Laub and Müller (2004) shows in several exploratory analyses that the negative eigenspaces appear to have interpretable characteristics. Van der Maaten and Hinton (2012) focuses on visualizing such matrices using multiple embeddings similar to our AR decomposition. This work is related to ours though differs in that in dissimilarity matrices the diagonal is held fixed (all elements are 0 dissimilar to themselves) whereas a key part of our approach is that we treat self-edges as a nuisance parameter rather than one that needs to be represented by the embedding.

3 The AR Decomposition of Symmetric Networks

We begin with a set of nodes $V = \{1, 2, \ldots, n\}$. There is an edge weight between any two nodes $p_{ij}$. We let $P_{ij}$ be the $n \times n$ matrix of edge weights.

For this paper we are interested in looking at symmetric networks, so $P_{ij} = P_{ji}$. This includes, for example, undirected social networks (e.g. friendship graphs, coauthorship networks), co-occurrence graphs, or trade flows.

We begin with the following question: is there a succinct representation of the network $P$?

We first introduce the following proposition:

**Proposition 1.** Any symmetric matrix $M$ has a family of decompositions of the form

$$M = D + AA' - RR'$$
where $D$ is a diagonal matrix.

The decomposition above is overparametrized - there are many choices of $D, A, R$ that satisfy the equation above. This naturally leads to the question of which decomposition from the family is the ‘correct’ one.

Our main idea is that when we consider network analysis the self-edges of the original matrix $P$ (i.e. the elements $P_{ii}$) are typically not considered as meaningful edges. Therefore, we consider treating the diagonal above as a nuisance parameter and choosing the ‘simplest’ decomposition in terms of $A$ and $R$. In other words, we are looking for the simplest decomposition of only the off-diagonal elements.

**Definition 1.** The AR decomposition of a matrix $M$ is the solution to the optimization problem:

$$
\min_{D,A,R} \|A\|_F + \|R\|_F \\
\text{s.t.} \quad M = D + AA' - RR'
$$

(1)

The rank of the AR decomposition is defined as $\text{rank}(A) + \text{rank}(R)$.

We can further show that choosing the $D, A, R$ matrices as in the optimization problem above is equivalent to choosing a diagonal for the matrix $M$ while keeping the off diagonal terms to find the simplest possible matrix in terms of nuclear norm $\|\cdot\|_*$. Under some mild conditions on the matrix the nuclear norm is a convex envelope of the matrix’s rank (Recht et al., 2010) and so it has been suggested to use nuclear norm minimization as a way of finding low rank solutions to matrix completion problems.

**Proposition 2.** Let $A,R$ be solutions to 1. For a matrix $M$ let $M^{OD}$ refer to the off diagonal terms. Then the matrix $\hat{M} = AA' - RR'$ a the solution to

$$
\min_{\hat{M}} \|\hat{M}\|_* \\
\text{s.t.} \quad \hat{M}^{OD} = M^{OD}
$$

(2)

The equivalence between choosing a diagonal to minimize the nuclear norm and choosing the simplest AR decomposition in terms of Frobenius norm gives us a way to compute the AR decomposition using convex optimization. We refer to the solution produced by this as the decomposition of the matrix.

1. Construct the augmented matrix $\hat{P}$ whose off-diagonal (OD) is defined by the graph and solve the convex problem:

$$
\min_{\hat{P}} \|\hat{P}\|_* \quad \text{s.t.} \quad \hat{P}_{ij} = p_{ij} \forall i \neq j
$$

2. Compute the eigendecomposition of $\hat{P} = Q'DQ$. Any symmetric matrix has such a decomposition with real eigenvalues.

3. (Optional) To use a $k$ dimensional embedding, truncate the $n-k$ smallest eigenvalues to 0

4. Let $D^-$ be the negative eigenvalues and $D^+$ be the positive ones. Let $Q^-$ correspond to the eigenvectors with negative eigenvalues and $Q^+$ be the eigenvectors with positive eigenvalues.

5. Let $A = Q^+\sqrt{D^+}$ and let $R = Q^-\sqrt{-D^-}$

Note that we can modify the algorithm to construct an $A$-only decomposition, which we will show in the next section always exists, by adding a constraint to the nuclear norm minimization problem in step 1 such that $\hat{P}$ is positive semi-definite (PSD) which will guarantee that all eigenvalues are weakly positive and so the $R$ component will have rank 0.

### 4 Motivating Examples

We have shown that every matrix has an AR decomposition where the diagonal is treated as a nuisance parameter. In social network analysis a commonly used model is the dot product random graph which models the probability of a node $i$ being connected to node $j$ as proportional to $g(v_i \cdot v_j)$ where $g$ is a link function (Young and Scheinerman, 2007; Sussman et al., 2012). We can now show
that the $R$ matrix is in some sense not needed at all - the dot product random graph can perfectly represent the off-diagonal elements given enough dimensions.

**Proposition 3.** Any symmetric matrix $M$ has a family of decompositions of the form

$$M = D + AA'$$

where $D$ is a diagonal matrix.

However, we will now show that these representations can be unsatisfying in the sense that very simple networks can require very high dimensional embeddings to faithfully represent them.

![Figure 1: This graph has simple structure but requires high dimensionality to be represented faithfully by a dot product model.](image)

Consider the graph in Figure 1. There is a simple structure to the graph: purple nodes connect to green nodes. We say that a dot product model represents the graph if $v_i \cdot v_j = 1$ for all linked nodes and 0 for all unlinked nodes. Consider the general version of this graph where there are $n_{\text{per}}$ nodes of each type. We can show the following result:

**Proposition 4.** Any vectors $\{v_1, \ldots, v_k\}$ which represent the generalized version of the graph in Figure 1 must have dimension $\geq 2n_{\text{per}} - 1$.

We relegate the full proof to the Appendix, however, we can give the intuition quite simply: the dot product model in low dimensions is ‘transitive’ in that if $A$ is close to $B$ and $B$ is close to $C$, $A$ must also be close to $C$. In order to express such unclosed triangles the dot product model needs additional free parameters or, in other words, extra dimensions.

By contrast for any $n_{\text{per}}$ there is a simple AR representation of the following form: let $a_i = \frac{1}{\sqrt{2}}$ for all nodes $i$. Let $r_i = \frac{1}{\sqrt{2}}$ for green nodes and $r_i = -\frac{1}{\sqrt{2}}$ for purple nodes.

The figure above shows that dot product models have a problem representing heterophily a.k.a. the fact that sometimes ‘opposites attract.’ In the Appendix, we expand this analysis to a popular class of network generating models: stochastic block models (Holland et al., 1983).

Such issues are not relegated to social networks. A similar problem for the dot product model appears in another canonical setting: matrix factorization based recommender systems (Koren et al., 2009). In such systems we have as set of users and a set of items. In the simplest case we have a set of entries $e_{ij}$ which are 1 if user $i$ purchased product $j$ and 0 otherwise. We want to approximate $e_{ij}$ as a low dimensional vector $u_i$ for the user and $m_j$ for the item.

Consider a purchase dataset constructed from a hypothetical sandwich shop. The shop has $M$ breads and $M$ lunch meats. Individuals come into the shop and order their favorite meat on their favorite bread. Bread and meat preferences are uniform in the population and there is no correlation between an individual’s meat preference and their bread preference. This gives us a bread-meat co-purchase dataset where each row is a $2M$ dimensional vector with a single 1 in the first $M$ columns and a single 1 in the second $M$ columns. Let $D$ be the co-purchase dataset which includes 1 of each legal combination.

**Proposition 5.** Any vectors $\{u_1, \ldots, u_N\}, \{m_1, \ldots, m_M\}$ which represent the sandwich dataset $D$ must have dimension $\geq 2M - 1$.

A major use of recommender systems is to construct recommendations of the form “users who purchased $X$ also purchased $Y$”. This is a statement about the co-purchase matrix, not necessarily the full data matrix. Looking at the co-purchase graph between items shows the connection between the issue in the social network case and the sandwich case. Here all breads are co-purchased with all meats but never with each other, yielding the same graph as in Figure 1. Thus, the same 2-d representation of items suffices to consider all interesting interactions (i.e. excluding the ‘item with itself’ interaction).
5 Experiments

5.1 Heterophily in Real Social Networks

The AR decomposition lets us decompose a social network into its heterophilic and homophilic parts. In particular, we can compare the variance in $A$ to the variance in $R$ to look at the amount of latent homophily vs. latent heterophily present in the network.

We first consider the anonymized ego-networks (an ego network takes a focal ego, takes all of their friends, and maps the friendships between them) of 627 users of a music social network\(^1\). We consider users with at least 50 friends (mean ego network size = 81.6).

Figure 2: In the ego network dataset we see that much of the variance can be explained via a low rank reconstruction (panel a) and that the AR decomposition is much more efficient at reconstructing the network. Panel b shows this more starkly, it can take $30\% - 70\%$ more dimensionality to reach the same level of reconstruction fidelity using the $A$ over the $AR$ decomposition.

Denote by $\hat{P}^k$ the $k$ dimensional approximation to $\hat{P}$. We look at the rank $k$ error as $e(k) = \sum_{i\neq j}(\hat{p}_{ij} - \hat{p}_{ij}^k)^2$. The normalized reconstruction error is $\frac{e(k)}{\sum_{i\neq j}(p_{ij})^2}$ and the reconstruction fidelity is $1 -$ the reconstruction error.

Another choice of diagonal has $d_i = \sum_{j\neq i}A_{ij}$. This is the unsigned graph Laplacian. We look at the off diagonal reconstruction error of this diagonal choice as well referring to it as the Unsigned Spectral Decomposition (USpectral).

We compute the $A$ and $AR$ decompositions using the nuclear norm based procedure described earlier. To compute the approximate nuclear norm minimizing diagonal we use singular value thresholding (SVT\cite{Cai2010}) from the $R$ package filling\cite{You2020}.

We also use the generalized Gabriel bi-cross-validation (BCV) procedure proposed in\cite{Owen2009} to construct an estimate of each network’s optimal approximation rank. In BCV the row and column indices are split into folds, one fold of the matrix, is held out while the rest of the matrix is used to fit a low-rank approximation. The rank chosen is the one which minimizes average held out loss. We use a split of 10 folds. The average BCV chosen normalized rank is approximately $9\%$ of the full rank indicated by a gray line on the plot.

\(^1\)These networks were collected via a the network’s public API\cite{Rozemberczki2020} and are available on the Stanford Network Analysis Project\cite{https://snap.stanford.edu/data/deezer_ego_nets}.
Figure 3: The fraction of an individual’s variance explained by negative eigenvalue vectors (||r_i||), a.k.a. the individual level latent heterophily, is strongly correlated with a observed measure of heterophily, fraction of e-mail communications outside one’s own department.

Figure 2 panel a shows the reconstruction error averaged over the 627 networks by the normalized rank (\(k\), \(\text{nrank}(P)\)) of the approximation. The AR decomposition attains a much lower error than the A only decomposition. The USpectral decomposition does quite poorly at reconstruction of the non-self edges of the graph compared to the AR or even the nuclear norm minimizing A decomposition. However, we note that the Laplacian embeddings have other properties and are not intended simply for optimal representation of the network.

Panel b shows the A vs AR comparison in a different way. We plot how large of an embedding we need to recover a fixed fidelity decomposition on average across the 627 networks. We see that the A decomposition requires a \(\sim 50\%\) higher dimensionality to recover the network with the same fidelity as the BCV chosen AR decomposition.

So far we have focused on the variance explained by the negative eigenvalues as a measure of heterophily in the whole network. This concept can also be applied at the individual level - \(\frac{||r_i||}{||r_i|| + ||a_i||}\) is a proxy for what fraction of the variance in node i’s adjacency matrix is explained by the repel-component.

We consider the EU e-mail network dataset (Leskovec et al., 2007; Yin et al., 2017). This network consists of 1005 individuals at a European research institution. We use a symmetric version of the network where an edge exists between two individuals if they have ever emailed each other. Each individual also belongs to one of 42 different research departments. We construct the AR decomposition as above with BCV selecting a 57 dimensional representation.

Figure 3 shows that there is a strong relationship between \(\frac{||r_i||}{||r_i|| + ||a_i||}\) and the fraction of an individual’s edges that are outside of their own research department.

5.2 Structural Roles in Networks

There are two notions of ‘similarity’ in the graph embedding literature. First order similarity refers to whether two nodes are connected. Second order similarity refers to whether nodes have similar neighborhoods (i.e. are linked to similar nodes). Sometimes second order similarity is referred to as ‘structural equivalence’ (Lorrain and White, 1971).2 These two similarities can reflect different information about the graph and some popular embedding approaches (e.g. LINE (Tang et al., 2015)) actually produce two separate embeddings one which reflect first-order and one which reflects second-order similarity and then concatenate them together to use them as node embeddings. A simple way to capture both types of similarity is to train two embeddings per node, a ‘target’ and a ‘context’, to learn \(p_{ij} = t_i \cdot c_j\). One way to construct such embeddings is via an SVD (or logistic SVD) of the
The AR decomposition makes it easy to find both first and second order similarities. This can be defined as $1\text{Sim}_{ij} = a_i a_j - r_i r_j$. First order similarity is just the implied strength of an edge between two nodes. Second order similarity can also be defined as $2\text{Sim}_{ij} = a_i a_j + r_i r_j$. Note that nodes that have a high $2\text{Sim}$ score are precisely those which have similar patterns of connections to other nodes.

We can look at how these similarities together tell us things that they cannot individually. An interesting case is nodes which have low $1\text{Sim}$, in other words they are only weakly directly connected but have high $2\text{Sim}$. In co-occurrence networks these are nodes which occur in the same context but rarely together - in other words, they have similar roles or, in economic parlance, they are substitutable (Ruiz et al., 2020).

A simple way to discover substitutes for a node $i$ is to compute $2\text{Sim}_{ij} - 1\text{Sim}_{ij}$. However, plugging in the definitions shows us that finding substitutes given an AR decomposition is as simple as finding nearest $R$ neighbors.

### 5.3 Similar Team Roles

We begin by looking at data from the online game DotA2. In this game individuals are placed in a team of 5, each individual chooses one of $\sim 120$ ‘heroes’, and the team competes against another team of 5.

Heroes in DotA are different and specialized. To be a successful team, a group needs to have a balanced set of heroes. Each hero can fill one or more of 9 possible roles. These roles are Carry, Disabler, Durable, Escape, Initiator, Jungler, Nuker, Pusher, and Support. See [https://dota2.fandom.com/wiki/Role](https://dota2.fandom.com/wiki/Role) for more details. Heroes usually can fill more than one role, though role types are correlated (for example, most Nuker heroes are usually not Durable).

![DotA2 Roles](image)

Figure 4: In our DotA data we see that similarity in $A$ vectors does not predict similarity in roles very well but similarity in $R$ vectors (produced without knowing roles) does.

We use a publicly available Kaggle dataset[^1] of $\sim 39,000$ DotA matches. From this data we construct a co-occurrence matrix for the heroes. Letting $c_{ij}$ be the co-occurrence between $i$ and $j$. Because the co-occurrences are extremely right skewed, we consider the matrix of $\log(c_{ij} + 1)$ though qualitatively all our results go through using the raw co-occurrence counts as well.

We take the $AR$ decomposition of this co-occurrence matrix. We again use the BCV procedure to select the dimensionality of the embedding. The BCV procedure selects a 10 dimensional representation and we find that 5 of these dimensions are associated with negative eigenvalues and 5 are associated with positive ones.

[^1]: Available here: [https://www.kaggle.com/c/mlcourse-dota2-win-prediction/overview](https://www.kaggle.com/c/mlcourse-dota2-win-prediction/overview)
We take what are (as of the time of this paper) the roles the DotA-wiki states that each hero can play and construct a 9 dimensional vector with a 1 if the hero can play that role and a 0 otherwise. We then compute the cosine similarity between the role vectors of any two heroes. Let $\theta_{ij}$ denote this cosine similarity. A higher cosine similarity means that heroes occupy more similar roles.

Given that a well balanced team should cover many roles, we expect that heroes with similar role vectors should be less likely to co-occur. Figure 4 shows that there is a strong correlation between the $\theta_{ij}$ and $v_i \cdot v_j$ but not so much between $\theta_{ij}$ and $u_i \cdot u_j$.

5.4 Substitutable Ingredients

We now investigate a different task. We use a dataset of 180,000+ recipes available on Kaggle. We construct the log co-occurrence matrix of the 1000 most common ingredients in these recipes. We compute the AR decomposition of this matrix using the same methodology as the experiment above. We use the rank chosen by BCV ($k = 125$).

We then look at some commonly substituted cooking ingredients. We did not use all examples on the site for two reasons. First, some of them were not in the top 1000 most commonly used ingredients. Second, some substitutions explicitly require a mixture of multiple (3 or more) other ingredients, which is not achievable in the current version of our model.

In Table 1 we take some focal ingredients and show their 3 nearest $R$ neighbors using the cosine similarity. We see that using $R$-similarity as a substitutability metric seems to yield qualitatively good results in this dataset.

We see that some ingredients have good substitutes while others do not. For example, nearest neighbors of many items have $R$ similarities between .7 and .9 and seem sensible (canola oil for vegetable oil or greek yogurt for yogurt or baking cocoa for unsweetened chocolate). However, beer’s closest $R$ neighbors are the less sensible apple juice and corn oil with much lower similarity scores (around .3 – .4).

In addition, we note that the notion of substitution discovered here does not always mean a substitution which preserves the same character of the dish. For example, pancakes can be made with milk or with buttermilk, and indeed we see that milk is a substitute for buttermilk. However, milk

| target         | substitute   | $R$ score |
|----------------|--------------|-----------|
| baking mix     | bisquick     | 0.78      |
| baking mix     | biscuit mix  | 0.73      |
| baking mix     | quick mix    | 0.70      |
| baking powder  | baking soda  | 0.85      |
| baking powder  | whole wheat flour | 0.51 |
| baking powder  | all-purpose flour | 0.42 |
| beer           | apple juice  | 0.40      |
| beer           | mango        | 0.39      |
| beer           | corn oil     | 0.39      |
| brown sugar    | sugar        | 0.74      |
| brown sugar    | honey        | 0.69      |
| brown sugar    | light brown sugar | 0.68 |
| buttermilk     | skim milk    | 0.52      |
| buttermilk     | soymilk      | 0.48      |
| buttermilk     | chckpea      | 0.39      |
| chicken broth  | chicken stock| 0.85      |
| chicken broth  | vegetable broth | 0.63 |
| chicken broth  | vegetable stock | 0.61 |
| lemon          | lemon juice  | 0.71      |
| lemon          | lemon juice  | 0.66      |
| onion          | red onion    | 0.71      |
| onion          | scallion     | 0.71      |
| onion          | yellow onion | 0.68      |
| orange juice   | honey        | 0.61      |
| orange juice   | orange       | 0.50      |
| orange juice   | lemon        | 0.47      |
| parmesan cheese| mozzarella   | 0.64      |
| parmesan cheese| cheddar      | 0.62      |
| parmesan cheese| olive oil    | 0.53      |
| parsley        | fresh parsley| 0.93      |
| parsley        | flat leaf parsley | 0.65 |
| parsley        | dried parsley| 0.59      |
| pecan          | walnut       | 0.85      |
| pecan          | nut          | 0.75      |
| pecan          | sliced almond| 0.65      |
| red wine       | dry red wine | 0.79      |
| red wine       | dry white wine| 0.68     |
| red wine       | white wine   | 0.61      |
| unsalted butter| butter       | 0.74      |
| unsalted butter| margarine    | 0.67      |
| unsalted butter| heavy cream  | 0.48      |
| unsweet chocolate| unsweet choc | 0.83   |
| unsweet chocolate| cacao       | 0.74      |
| unsweet chocolate| unsweet cacao| 0.71      |
| vegetable oil  | olive oil    | 0.96      |
| vegetable oil  | canola oil   | 0.88      |
| vegetable oil  | olive oil    | 0.67      |
| vinegar        | cider vinegar| 0.89      |
| vinegar        | white vinegar| 0.87      |
| vinegar        | apple cider vinegar | 0.82 |
| yogurt         | plain yogurt | 0.73      |
| yogurt         | greek yogurt | 0.70      |
| yogurt         | vanilla yogurt | 0.53    |

Table 1: Substitutes for various focal ingredients found by looking at cosine similarity neighbors in the $R$ component.
pancakes will taste very different from buttermilk pancakes as buttermilk is acidic while regular milk is not.

Nevertheless, we see that R similarity, which is high when 2Sim is high but 1Sim is low, seems to be a good way to detect substitutable nodes in co-occurrence networks.

6 Conclusion

We have shown that the workhorse dot product (or A-only) model of networks has trouble modeling a lack of triadic closure or heterophily in networks. We have shown that the AR decomposition is an extension which allows us to model these issues in a parsimonious way.

We have shown that real world ego networks have substantial heterophilic components. In addition, we have shown that nodes that are not linked to each other yet are linked to similar nodes can be interpreted as having a special relationship (e.g. they are ‘substitutes’ when the network is a co-occurrence graph).

The implied generative model behind the AR decomposition when applied to social networks is, as with standard latent position random graph models, one where edge formation is independent conditional on the latent positions of the nodes. This is a reasonable assumption for some cases but not others. Thus, expanding beyond this assumption is an interesting avenue for future work.

In addition, scaling the AR decomposition is a problem in itself. Our proposed construction of the AR decomposition requires the solution to a nuclear norm optimization. Though nuclear norm minimization is a convex problem, it scales poorly when graphs grow to thousands or millions of nodes (Recht et al., 2010). For this reason, studying whether AR decompositions can be easily computed via stochastic gradient descent or other scalable optimization methods is an important next step.
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7 Appendix to “An Attract-Repel Decomposition of Undirected Networks”

7.1 Stochastic Block Models

We now look at the relationship of the AR decomposition to a popular model in the literature: the stochastic block model (SBM) [Holland et al., 1983]. These models are used in network analysis in fields as different as looking at human social networks to modeling protein interactions [Airoldi et al., 2006, Abbe, 2017]. The SBM works as follows: there are \( d \) blocks. Each node belongs to one block. For blocks \( i, j \) there is a probability \( b_{ij} \) that a node from \( i \) is connected to a node from \( j \). Let \( B \) be the matrix of node connection probabilities. We assume \( B \) has rank \( d \). Let \( P_B \) be the implied matrix of probability of connections in a population of \( n \) nodes. Again, ignore the diagonal.

It is known that if \( B \) is positive semi-definite and rank \( k \) then there exists an \( A \) decomposition of rank \( k \) which represents the SBM.

We can generalize this result to the AR decomposition as well as generalize our example in Figure 1.

**Proposition 6.** If \( B \) has rank \( d \) then \( P_B \) has the following properties:

1. \( P_B \) has AR decomposition of rank \( d \)
2. If \( B \) is positive semi-definite then an \( A \) decomposition of \( P_B \) can have rank \( d \)
3. If \( B \) has negative eigenvalues then any \( A \) decomposition of \( P_B \) has rank \( > d \).

**Proof of Theorem:** We first prove that \( P_B \) has an AR decomposition of rank \( k \). To do this, we will explicitly construct the decomposition. Since \( B \) is symmetric and real it has an AR decomposition of \( B = XX' - YY' \). We give each node the embedding corresponding to the embedding of it’s block. This is an AR decomposition of \( P_B \).

From this the second point follows directly.

The third point follows by contradiction. Suppose that \( P_B \) has an \( A \) decomposition of rank \( d \) (or less). Let this be \( X \). By construction it must be that all nodes with the same block \( k \) have the same embedding, call it \( x_k \). But then \( B = XX' \). But this implies that \( B \) is positive semi-definite, which we know it is not.

**Lemma 1.** The following SBMs will not be positive semi-definite:

1. **Any SBM with heterophily across blocks:** There exist some blocks \( i, j \) where nodes in \( i \) are more likely to connect to \( j \) than to \( i \) and nodes in \( j \) are more likely to connect to \( i \) than \( j \).
2. **Any SBM with a triangle:** There are 3 blocks \( i, j, k \) with the properties that
   \[ b_{ii}(b_{jj}b_{kk} - b_{jk}^2) - b_{ij}(b_{ij}b_{kk} - b_{jk}b_{ki}) + b_{ik}(b_{ij}b_{jk} - b_{jj}b_{ik}) < 0. \]

**Proof of Lemma:** By Sylvester’s Criterion for a full rank matrix to be positive semi-definite, any principal minor (submatrix of the same indexed rows and columns) must have non-negative determinant. A \( 2 \times 2 \) submatrix of \( i, j \) has the determinant
   \[ b_{ij}b_{jj} - b_{ij}^2 \]
   where the square is there due to symmetry of \( b_{ij} = b_{ji} \). If \( b_{ij} > b_{ii}, b_{jj} \) this determinant is negative meaning that \( B \) cannot be positive semi-definite and thus must have negative eigenvalues.

The proof for the second statement in the Lemma is the same, since the equation in the Lemma is in the fact that determinant of a \( 3 \times 3 \) principal minor.

The three-wise case is particularly interesting as we will see later that unclosed triangles play a special role in co-occurrence networks (note the condition in the Lemma is satisfied with a basic triangle where \( i, j \) connect to \( k \) but not to each other \( b_{ii} = b_{jj} = b_{jk} = 1 \) and \( b_{ij} = 1, b_{jk} = 1 \) but \( b_{ij} = 0 \)).

It is possible to construct higher order interaction conditions that guarantee that \( B \) is not easily \( A \) decomposable but these conditions become harder to interpret.

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The extension to a mixed membership model [Airoldi et al., 2008] is straightforward and would not change our main result.
7.2 Proofs of Main Text Results

Proof of Proposition 1. Any symmetric matrix $M$ has a decomposition of the form $A'A - R'R$. To construct this:

1. Compute the eigendecomposition of $\hat{P} = Q'DQ$. Any symmetric matrix has such a decomposition with real eigenvalues.

2. Let $D^-$ be the negative eigenvalues and $D^+$ be the positive ones. Let $Q^-$ correspond to the eigenvectors with negative eigenvalues and $Q^+$ be the eigenvectors with positive eigenvalues.

3. Let $A = Q^+\sqrt{D^+}$ and let $R = Q^-\sqrt{-D^-}$.

Since given any diagonal matrix $D$ the matrix $M + D$ is still symmetric, the decomposition continues to exist. The family of AR decompositions is thus equivalent to any choice of diagonal for $M$.

Proof of Proposition 2. By Lemma 6 of Mazumder et al. (2010) we know that for a matrix $X$ we can write

$$||X||_* = \min_{U\hat{V} = X} \frac{1}{2}(||U||_F^2 + ||V||_F^2).$$

With the minimum being attained at the factor decomposition $X = UV$.

By construction of our matrix $\tilde{M}$ it has the factor decomposition $U = [A, R]$ and $V = [A, -R]$ where $[\cdot]$ denotes column-wise concatenation.

Substituting the definition of the factors gets

$$||\tilde{M}||_* = \frac{1}{2}(2\sum_{ij} a_{ij}^2 + 2\sum_{ij} r_{ij}^2)$$

which simplifies to

$$||\tilde{M}||_* = ||A||_F^2 + ||R||_F^2.$$ 

Recall the construction of $\tilde{M}$ is by finding the smallest $A, R$ in terms of $||A||_F^2 + ||R||_F^2$ to fit all the off diagonal elements. Thus, these $A, R$ also solve the constrained nuclear norm minimization problem.

Proof of Proposition 3. We know that any symmetric matrix $C$ that is positive semi-definite has a decomposition of the form $C = A'A$. Thus it is sufficient to show there exists a choice of diagonal $D$ such that $M - D$ is positive semi-definite. Let $\Delta$ be the eigenvalues of $M$. If all $\Delta$ are weakly positive we are done since then $M$ is positive semi-definite. Let $\delta$ be the largest negative eigenvalue otherwise. Construct the diagonal $D_\delta$ as the constant $-\delta$.

Given a matrix $M$ the eigenvalues of $M + D$ are simply the eigenvalues of $M$ shifted up by $D$. Therefore, by construction $M - D_\delta$ has non-negative eigenvalues. But then it is positive semi-definite. Let $A_\delta$ be the decomposition of $M - D_\delta$. Then $M = D_\delta + A'_\delta A_\delta$ as required.

Proof of Proposition 4. In essence, we want to determine the rank, that is, determine the dimension of the nullspace of a matrix

$$M = \begin{pmatrix} A & R \\ R & B \end{pmatrix}$$

where $A$ is an $n \times n$ diagonal matrix with coefficients $a_1 \ldots a_n > 0$, $B$ is an $n \times n$ diagonal matrix with coefficients $b_2 \ldots b_n > 0$, and $R$ is an $n \times n$ matrix of all 1. Let’s solve!

$$M \times \begin{pmatrix} u \\ v \end{pmatrix} = 0 \iff \forall i \left\{ a_i u_i + \sum_j v_j = 0,b_i v_i + \sum_j u_j = 0 \right\}$$
Since \( a_i > 0 \) and \( b_i > 0 \), this implies
\[
\forall i \quad u_i = -\frac{1}{a_i} \sum_j v_j \quad v_i = -\frac{1}{b_i} \sum_j u_j
\]
(3)

If we were free to set \( \sum_j v_j \) and \( \sum_j u_j \) as we please, the two equations (3) would describe a 2-dimensional space. Therefore the nullspace of \( M \) has dimension at most 2. However we can also use the first of these equations to write
\[
\sum_i u_i = -\sum_i \frac{1}{a_i} \sum_j v_j
\]
(4)

Therefore our nullspace has dimension at most 1. But we can continue and use the second equations from (3) to replace \( v_j \) above:
\[
\sum_i u_i = -\left( \sum_i \frac{1}{a_i} \right) \left( \sum_j v_j \right) = \left( \sum_i \frac{1}{a_i} \right) \left( \sum_j \frac{1}{b_j} \right) \sum_k u_k
\]

Therefore, if \( r = \left( \sum_i \frac{1}{a_i} \right) \left( \sum_j \frac{1}{b_j} \right) \neq 1 \), then we must have \( \sum_i u_i = \sum_j v_j = 0 \) which means that \( u_i = v_j = 0 \); the matrix is nonsingular. On the other hand, if \( r = 1 \), then I can choose \( \sum_j v_j \) equal to any non zero value, deduce \( \sum_j u_i \) using (4), compute \( u_i \) and \( v_i \) using (3), and verify that we have described a one-dimensional nullspace.

In conclusion: if \( r = \left( \sum_i \frac{1}{a_i} \right) \left( \sum_j \frac{1}{b_j} \right) \neq 1 \), the matrix has full rank. If \( r = 1 \) the matrix has rank \( 2n - 1 \). This is the case, for instance, when \( a_i = b_j = n \).

\[ \square \]

**Proof of Proposition 5** Let \( D \) be the data matrix for all legal combinations of the sandwich problem. Consider the matrix \( C = D'D \) which is the \( 2M \times 2M \) co-occurrence matrix of all items that are purchased. We know that \( \text{rank}(C) \leq \text{rank}(D) \).

It is easy to check that if \( i \) be a meat and \( j \) be a bread (or vice versa) then \( c_{ij} = 1 \). If \( i, j \) are the same item type, then \( c_{ij} = 0 \). For any \( c_{ii} = M \). This is precisely the matrix described in the proof of Proposition 4. This matrix has rank \( 2M - 1 \). Therefore the matrix \( D \) also has rank at least \( 2M - 1 \).

\[ \square \]