Random Vibrational Networks and Renormalization Group

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We consider the properties of vibrational dynamics on random networks, with random masses and spring constants. The localization properties of the eigenstates contrast greatly with the Laplacian case on these networks. We introduce several real-space renormalization techniques which can be used to describe this dynamics on general networks, drawing on strong disorder techniques developed for regular lattices. The renormalization group is capable of elucidating the localization properties, and provides, even for specific network instances, a fast approximation technique for determining the spectra which compares well with exact results.

The study of linear equations with random coefficients has a long history, dating back to the study of random matrices [1], systems with no spatial structure at all. Later work incorporated spatial structure, focusing on the case of regular lattices, starting with Anderson’s work studying electron localization via the Schroedinger equation [2]. The Bethe lattice was also introduced as a work studying electron localization via the Schroedinger equation [2]. The Bethe lattice was also introduced as a soluble case [3], illustrating the localization transition in these systems.

Recently, the study of dynamics on more general networks has become of interest [4]. The systems above can be included in the case of networks, as can additional systems, such as sparse random matrices, or small world networks [5]. Networks contrast with regular lattices, as the concept of locality on networks may not be well defined. This concept of locality is essential to physics, where so many subjects rely on introducing slowly varying “hydrodynamic” fields to describe the long wavelength dynamics. Small world networks illustrate the problem: there is always a route between any two nodes in the network which involves traversing sites which are near each other in physical distance, but there may be a much shorter route which involves using some long jumps.

In this work, we consider the specific problem of a random network of masses connected by springs. This problem is chosen for several reasons. It includes, but is richer than, the related problem of a Laplacian on a network [6]. It also has physical applications to vibrational modes in amorphous and granular media [7]. Finally, this problem is a good problem for studying the application of real-space renormalization group techniques, originally developed for regular lattices, to arbitrary networks, including random graphs and small-world networks. Real-space techniques were originally developed for application to statistical mechanics systems without randomness. Since then, they have been applied to a number of disordered systems, in some cases yielding exact results [8]. The advantage of these techniques is that, without assuming any specific structure of the system as required for momentum space techniques, they are able to reveal the geometry of the network [9]. We will see that not only are these techniques able to provide very accurate approximations, but also to find the correct notion of locality for the given network.

Random Networks, Random Masses— We consider a random network of masses connected by springs. This generalizes the problem studied by Dyson [10] in one-dimension. The equation of motion for a particle $i$ of mass $m_i$ connected by springs with spring constants $k_{ij}$ to other particles $j$ is

$$\partial_t^2 x_i = -\sum_j O_{ij} x_j,$$

(1)

where the matrix $O$ has elements $O_{ij} = -k_{ij}/m_i$ for $i \neq j$ and $O_{ii} = \sum_j k_{ij}/m_i$ (we define $O$ with these signs so its eigenvalues will be positive). By a rescaling of coordinates, $x_i \to m_i^{1/2} x_i$, we can study instead the matrix $L$ defined by $L_{ij} = m_i^{1/2} O_{ij} m_j^{-1/2}$. Then, $L$ has the same eigenvalues as $O$, but is a symmetric matrix.

It is possible to relate this problem to a random hopping problem, studied in quantum mechanics. Introduce a matrix $H_{(jk),i}$, where the index $i$ labels a site and the index $(jk)$ labels a link between sites (by definition, the links $(jk)$ and $(kj)$ are the same). Then, take $H_{(ij),i} = H_{(ij),i} = \sqrt{k_{ij}}/m_i$ and $H_{(ij),j} = H_{(ij),j} = -\sqrt{k_{ij}}/m_j$. The matrix $H$ connects sites to links and vice-versa. The matrix $H^2$ is block-diagonal: it connects sites to sites and links to links. Restricting to just the block of $H^2$ which connects sites to sites, we find that $L = H^2$.

Automatically, $O$ has a zero mode associated with a uniform motion of all the masses. This will be essential to the renormalization procedure defined below, as we will study the behavior of $O$ for small eigenvalues. In the case that all $m_i = 1$, $L$ is a Laplacian on the network with different couplings $k_{ij}$ between nodes. If instead $m_i = 1/n_i$, with $n_i$ the number of nodes connected to $i$, and $k_{ij} = 0, 1$ depending on whether nodes $i, j$ are connected, then we obtain another definition of the network Laplacian [11]. We will find that including random masses leads to, in many cases, greatly different localization properties than without; further, we will see that the renormalization procedures naturally lead to variations in the mass.
Renormalization—Inspired by real-space techniques applied to strong disorder systems in one dimension, we consider a variety of renormalization procedures. The previous work [8] was based on a matrix such as $H$. Although it is not essential to the discussion below, we recall that the technique for operator $H$ goes as follows: pick the largest term in $H$. Let this term have magnitude $\Lambda$. This term connects a site $j$ and a link $(jk)$. Let site $j$ also be connected to link $(ij)$, while link $(jk)$ is also connected to site $k$. The approximation behind the renormalization procedure consists in assuming that $\Lambda$ is much larger than all other terms in $H$. Then, $H$ has two eigenvalues $\approx \pm \Lambda$. We then remove site $j$ and link $(jk)$ from the system and use second order perturbation theory to connect the link $(ij)$ to $k$. We find that that the resulting term in the renormalized $H$ is $H_{(ij),k} = H_{(ij),j}H_{(jk),k_i}/H_{j,(jk)}$.

Since $H^2 = L$, the renormalization of $H$ will enable us to renormalize $L$. Based on this fact, and the above procedure, we propose the following technique that can be applied directly to $L$: (1) choose the site $i$ with the largest $L_{ii}$. (2) Make the approximation that this $L_{ii}$ is much larger than $|L_{ij}|$ for any other $j$, and thus declare that $L$ has an eigenvalue equal to $L_{ii}$ with eigenvector concentrated on site $i$. (3) Remove the site $i$ from the network and define a new matrix $\tilde{L}$ connecting the remaining sites with $L_{jk} = L_{jk} + L_{ii}L_{ik}/L_{ii}$. We find that if $i$ has only the two neighbors, $j$ and $k$, then the masses of sites $j,k$ are unchanged by this procedure, while the sites are connected by a spring constant $k_{jk} = k_{ji}k_{ik}/(k_{ji} + k_{ik})$.

This procedure works if $L_{ii}$ is indeed much larger in than $|L_{ij}|$. In one dimension, this requires that the mass of site $i$ be much smaller than that of either of its neighbors. If the elements of $H$ are chosen randomly from a distribution with finite width, this leads to a random distribution of mass ratios of nearest neighbors in the original lattice. Then, since $m_k/m_j$ and $m_j/m_i$ are in this case uncorrelated, the distribution of the mass ratio $m_k/m_i$ is broader. Thus, the distribution of mass ratios broadens under renormalization, justifying the procedure.

We, however, consider a system in which the masses themselves, not the mass ratios, are chosen from a given distribution so that the mass ratios remain narrow under the renormalization and thus this procedure does not work for a one dimensional system. However, if the connectivity $n_i$ of site $i$ is large, then $L_{ii}/|L_{ij}| \approx n_i >> 1$. Thus for networks, this procedure can work. A one dimensional lattice remains a one dimensional lattice under this procedure, while any other lattice or network changes its topology [12].

Define the Green’s function $G_L(E) = 1/(E - L)$. Then, for $E = 0$, $G_L = G_L$ for the sites that remain in the network, so this procedure is exact for $E = 0$. For other $E$, it is possible to follow a renormalization procedure with $\tilde{L}_{jk} = L_{jk} + L_{ii}L_{ik}/(L_{ii} - E)$ [13].

A more powerful renormalization technique is to consider pairs of sites. This two-site technique is more accurate at each renormalization step. It also tends to increase the connectivity of the sites and randomize the masses, thus leading to a situation in which each renormalization step is more accurate than the previous. We proceed as follows: (1) choose the site $i$ with the largest $L_{ii}$, and then find its neighbor $j$ with the largest $|L_{ij}|$. (2) Consider the two-by-two submatrix of $L$ which involves only sites $i,j$. This has eigenvalues $E^\pm = (L_{ii} + L_{jj})/2 \pm \sqrt{(L_{ii} - L_{jj})/2 + L_{ij}^2}$ with $E^+ > E^- > 0$, and has eigenvectors $v^\pm$. Change basis from $i,j$ to the basis of these eigenvectors $v^+, v^-$. (3) Remove $v^+$ from the network and define a new matrix $\tilde{L}$ connecting the remaining sites with $L_{kk} = L_{kk} + L_{kk}v^+/L_{ii}$.

This procedure is the same as that above, but with a change of basis from $i,j$ to $v^+, v^-$. We will see below that this makes the procedure much more accurate. In addition to the increased accuracy at each step, the procedure tends to increase the connectivity: applying this procedure to a one dimensional lattice produces second-neighbor connections. The procedure also leads to variation in the masses: the mass of the new site $v$ is not equal to either $m_i$ or $m_j$. Thus, the procedure drives itself to a regime in which it become more accurate, due to higher connectivity and a broader distribution of masses. This procedure shows the correct idea of locality for the network: we know that, as far as the low-energy dynamics are concerned, $i,j$ are close by in the original network.

Localization Properties—We have performed numerical simulations to study localization. The specific network considered is a random graph of $N$ sites: for a given probability $p$, two sites are connected with that probability. Then, the spring constant connecting those sites is assigned from a uniform distribution between 0 and 1 (taking instead all $k_{ij} = 0, 1$ leads to little change in the results). The average connectivity of a site is equal to $p(N - 1)$. We consider three different mass distributions: (1) $m_i = 1$ for all $i$; (2) $1/\sqrt{m_i}$ is chosen uniformly between 1 and 2, giving a smooth, bounded distribution of masses; (3) $1/\sqrt{m_i}$ is chosen uniformly between 0 and 1, so that the distribution of masses is unbounded.

The energy scales with the connectivity of the the system. After removing this scaling, we find that for a system with extensive connectivity and a bounded mass distribution, the spectrum has a single zero mode and then a gap to the next eigenvalue $E$. For a system with intensive connectivity or with unbounded masses, the gap is filled in by Griffiths effects.
To determine the localization properties of a normalized eigenfunction $\psi_{i,l}$ associated with an eigenvalue $E_l$, we consider the inverse participation ratio, $\sum_i |\psi_{i,l}|^4$. In the delocalized phase, this quantity scales with $1/N$. For constant mass [14] and large connectivity, in the center of the band the states are delocalized, while they are localized near the band edge.

We have found a very different result in the case of random masses. With large connectivity and random masses, we find that all the states, with the exception of the zero mode, become localized as shown in Fig. 1. We plot the inverse participation ratio against eigenvalue, for systems with bounded, random mass. The solid line is $N = 1000, p = 1$ averaged over 100 samples while the dashed is $N = 500, p = 1$ averaged over 1000 samples. In the inset, we have divided the eigenvalue by $N$, showing a perfect collapse of the two curves, indicating that the states are localized.

![Inverse participation ratio as a function of eigenvalue.](image)

**FIG. 1.** Inverse participation ratio as a function of eigenvalue. Solid line is $N = 1000, p = 1$ with random, bounded mass. Dashed line is same except $N = 500$. Inset: eigenvalue has been scaled by system size.

For extensive connectivity, localization holds even for very weak variation in the masses. This can be understood analytically via the renormalization. Let us divide $L$ by $N$; then the $L_{ii}$ are all fluctuating variables of order unity, with fluctuations, due to the random mass, which are also of order unity. The $L_{ij}$ are of order $1/N$. Using the RG to remove sites from the system at eigenvalue $E \neq 0$, removing a single site $j$ leads to corrections of order $L_{ij}^2/(L_{jj} - E)$. The numerator is of order $1/N^2$, while due to the random mass the denominator does not vanish. Thus, the dynamics of a single site is only weakly affected by other sites, and the states are localized.

For low connectivity, we have considered systems with 100, 200, 400, 800, and 1600 sites, averaging over 1000 realizations for systems with up to 800 sites, and over 100 realizations for the largest systems, considering the three different mass distributions, with average connectivities of 1, 2, and 4. One expects that for low connectivity, greater than 1, the network approximates an infinite dimensional system, or Bethe lattice. Then, at zero eigenvalue there is an extended state, and for low eigenvalues the variations in masses and spring constants only weakly scatter the vibrational waves. Thus, one expects [15] a delocalized phase for small eigenvalues for average connectivity greater than 1.

Numerically, the results for low connectivity are less clear. For average connectivity equal to 1, the inverse participation ratio is found to be independent of $N$, and thus the system appears localized. For average connectivity greater than 1, the inverse participation ratio decreases with increasing $N$; however, we do not observe a clear $1/N$ scaling of the inverse participation ratio for an average connectivity of 2. For average connectivity 4, we do see approximate $1/N$ scaling for low $E$, indicating delocalized states.

**Comparison of Eigenspectra**— We have then tested the renormalization procedure against exact results by applying the procedure to single realizations of the system. We have found that in the correct regimes, the procedures are highly accurate even for the details of specific realizations. The procedure work best for high connectivity, and for wide distributions of the masses, with the advantage of the two-site technique being that it drives the system to the regime in which it works accurately.

In Fig. 2a, we show the results of the single-site technique for a system with 100 sites, $p = 1$, and the unbounded distribution of masses. The sorted eigenvalues are plotted, with the $n$-th eigenvalue $E_n$ plotted at position $(n, E_n)$. The dashed line gives the results of the renormalization procedure, while the solid line is the exact result. For low eigenvalues, the two are indistinguishable. In Fig. 2b, we show the same for a system with 1000 sites; the two lines cannot be distinguished on the figure.

At lower connectivity, with less randomness in the mass, the two-site procedure becomes necessary. In Fig. 3a, we show a system with $N = 100, p = .01$, and the bounded, random distribution of masses. The solid line...
is the exact result, the upper dashed line is the two-site result, and the lower is the single-site result.

As one measure of the accuracy of the procedure, we sort the eigenvalues from highest to lowest, and divide the root-mean-squared error in the n-th eigenvalue by the root-mean-squared value of that eigenvalue. The result is quite accurate, with the relative error averaging, for example, $\lesssim 1\%$ for $N = 100, p = 1$ and bounded, random mass, becoming even more accurate for larger systems. As a more stringent test of the accuracy, if we instead divide the root-mean-square error by the root-mean-square sample-to-sample fluctuations in that eigenvalue, the relative error averaged over all $n$ is $\sim 15\%$ for the same system. For lower connectivity, the relative error (compared to sample-to-sample fluctuations) is worse, $\sim 28\%$ for $N = 100, p = .01$. However, for the smaller eigenvalues, the accuracy increases: for $N = 100, p = .01$, the error relative to fluctuations in the 80 lowest eigenvalues averages $\sim 11\%$.

![Graph](image)

FIG. 3. a): $N = 100, p = .01$. Exact result (solid) versus two-site renormalization (upper dashed) and single-site renormalization (lower dashed). b): 100 site periodic chain. Exact (solid), random choice of sites for renormalization (dashed), poor choice (long-dashed). Inset: a small-world network. Exact (solid), renormalization (dashed).

Finally, we test the renormalization on a periodic one dimensional chain with constant masses and springs constants, combining both low connectivity and no randomness. If, in the two-site procedure, when faced with a choice between different sites with the same $L_{ii}$, we choose randomly, the low energy properties are reasonable, while if we deliberately make poor choices, keeping the connectivity low, the results are much worse, as shown in Fig. 3b. Using a network improves on the results obtained [16] on a one dimensional chain with a similar renormalization procedure, which preserves the one dimensional structure. In the inset to Fig. 3b we consider a small-world network. We take a periodic, one dimensional chain with 500 sites and constant mass, and with probability $p = 0.0002$ we connect pairs of sites which are not already connected by the chain.

Conclusion—In conclusion, we have introduced a real-space renormalization procedure for studying certain linear operators on networks. The procedure is exact at low energy, and in many cases leads to very good results for the spectra even at much higher energy. This procedure can be used to obtain analytic results on the localization properties. It can also be used to obtain results for dynamics on a specific graph more rapidly than would be possible with matrix diagonalization routines. While for a fully connected graph it still requires $O(N^3)$ time, the prefactor is much smaller than that required for matrix diagonalization. For less connected networks, the procedure runs much more rapidly. This difference will be important when studying large social networks which may have billions of nodes.

We have also found that the introduction of random masses leads to many more localized states than constant masses. For amorphous systems, the random mass case is the relevant case.

The procedure naturally helps simplify the network by finding a simpler network with a similar spectrum. Although we have considered only linear problems, we hope that this kind of real-space procedure will be an important tool in studying nonlinear problems in future work, such as spin-glass or optimization problems.

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