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Emergent Structure-dependent Relaxation Spectra in Viscoelastic Fiber Networks in Extension

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Abstract

Viscoelasticity plays an important role in the mechanical behavior of biological tissues undergoing dynamic loading. Exploring viscoelastic relaxation spectra of the tissue is essential for predicting its mechanical response. Most load-bearing tissues, however, are also composed of networks of intertwined fibers and filaments of, e.g., collagen, elastin. In this work, we show how non-affine deformations within fiber networks affect the relaxation behavior of the material leading to the emergence of structure-dependent time scales in the relaxation spectra. In particular, we see two different contributions to the network relaxation process: a material contribution due to the intrinsic viscoelasticity of the fibers, and a kinematic contribution due to non-affine rearrangement of the network when different fibers relax at different rates. We also present a computational model to simulate viscoelastic relaxation of networks, demonstrating the emergent time scales and a pronounced dependence of the network relaxation behavior on whether components with different relaxation times percolate the network. Finally, we observe that the simulated relaxation spectrum for Delaunay networks is comparable to that measured experimentally for reconstituted collagen gels by others.

Graphical Abstract

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Abstract

Viscoelasticity plays an important role in the mechanical behavior of biological tissues undergoing dynamic loading. Stress relaxation tests provide a convenient way to explore the viscoelastic behavior of the material, while providing an advantage of interrogating multiple time scales in a single experiment. Most load bearing tissues, however, are composed of networks of intertwined fibers and filaments. In the present study, we analyze how the network structure can affect the viscoelastic relaxation behavior of a tissue leading to the emergence of structure-based time scales in the relaxation spectra.

Keywords

fiber networks; viscoelasticity; relaxation spectra

1. Introduction

At a very basic level, a linear viscoelastic material can be modeled by combining elements with elastic and viscous mechanical characteristics, e.g., the Maxwell fluid combines a spring and a dashpot in series, and the standard linear solid has a Maxwell element and a dashpot in parallel. In such cases, under the assumption of linearity, it is straightforward to calculate a characteristic time scale over which the stress relaxes under constant strain. In general, however, a viscoelastic material can exhibit multiple relaxation time scales, and these characteristic relaxation times can depend on a variety of factors, such as magnitude of initial stress, temperature, or rate of loading, and thus more complex models are required to predict stress relaxation [1, 2, 3].

Most biological soft tissues exhibit some degree of viscoelasticity [4], and their viscoelastic mechanical properties affect their characteristic functions, especially if the tissue undergoes dynamic loading, e.g., tendons, lung. Because of its analytical and experimental convenience, the stress relaxation test (i.e., monitoring stress following a step stretch) is an attractive tool. Stress relaxation also has the advantage of interrogating multiple time scales in a single experiment. Thus, the viscoelasticity of tissues has been widely studied with stress relaxation tests, including tendons [5, 6], ligaments [7, 8], arteries [9, 10], and skin [11]. To explain these experimental findings, various models have been explored, e.g., models using combinations of the Maxwell, and Voigt materials described above [12]; models utilizing a simple exponential decay function [13, 14]. By far, however, the most popular models used to explain the viscoelastic behavior of connective tissues have been based on the quasilinear viscoelastic (QLV) model developed by Fung [15, 16, 17, 18].

While viscoelastic behavior of tissues at the macroscale has been widely observed and modeled, the origins of this viscoelasticity and how it is affected by the lower hierarchical structures within the tissue are less well studied. The microstructure of many biological materials is composed of an intertwined network of fibers and filaments of, e.g., collagen, embedded in the non-fibrillar portion of the extracellular matrix. Several studies using rheological protocols have experimentally probed the non-linear viscoelastic properties of biopolymer networks, e.g., [19, 20, 21]. These studies have observed and modeled several

interesting behaviors such as strain-stiffening [22, 23], crosslink-dependent stiffening [24], and strain-dependent relaxation rates [25]. The majority of this existing body of work has focused on shear deformations, especially, small-strain sinusoidal oscillations of gels in shear. The non-linear viscoelastic response under extension – which, for connective tissues is often a more relevant mode of deformation – has received less attention.

Furthermore, the heterogeneity within networks, i.e., the presence of fibers with different mechanical properties, and its effect on the viscoelastic behavior of the network has been less studied. The mechanical functionality of the network derives directly from the composition, organization, and mechanics of its microstructure. Obviously, a network composed of viscoelastic fibers will exhibit viscoelastic stress relaxation, and the characteristic time scales over which the network relaxes will be determined in large part by the rate of relaxation of the constituent fibers. We hypothesized, however, that the structure of the network can also influence the relaxation time spectrum, and it is this aspect of network relaxation which we explored in the current work. For instance, if the fibers in the network relax at different rates, the resulting changes in internal loads over time could lead to non-affine reorganization of the network fibers, which in turn could affect the overall stress relaxation behavior of the network.

2. Methods

We begin this section with a theoretical analysis of stress relaxation of a network, and then describe an approach to modeling the non-affine mechanics of a network and its stress relaxation behavior.

The convention used in the rest of this work, except when stated otherwise, is as follows: superscript indices denote node or fiber number, and subscript indices indicate direction, e.g., f_i^n is the force acting on node n along direction i , $i = 1, 2$, or 3 . A comma in the subscript indicates differentiation with respect to the directions denoted by indices directly following the comma. The summation convention applies both to subscript and to superscript indices. This indexing convention will give rise to some terms which can be interpreted as higher order tensors. We note that it is possible to reduce the dimensions of the tensors in subsequent equations by using indices calculated by combining the corresponding superscripts and subscripts, e.g., the matrix of nodal positions in 3-D x_i^b can also be reordered as a vector x_{3b+i-1} , and similarly the fourth order tensor G_{ik}^{bn} can be reorganized as a matrix $G_{3b+i-1\ 3n+k-1}$. While reducing the dimensions of the higher order tensors would be helpful if we want to apply tools of linear algebra to analyze equations containing such quantities, in this work, we will only investigate special cases with node motions restricted to only one axis, which will automatically restrict the maximum dimension of the tensors involved to 2. Thus, all derivations will be done using the top and bottom index notation described above which, we believe, is more concise and easier to follow. When an equation is shown in matrix notation, we use bold lower case font to denote vectors, bold uppercase font for matrices, and script letters for higher order tensors.

Additionally, Cauchy stresses are denoted by S_{ij} or $\mathbf{S}$, and σ is used to refer to the force in a network fiber. We consider only networks of highly flexible fibers, i.e., the contour length of the fibers is much greater than its persistence length. Thus, no strain energy is stored in bending the fibers, and only axial deformations generate a resisting force within the fiber.

2.1. Theoretical analysis of network relaxation

2.1.1. Calculation of average network stress—Consider a representative volume element (RVE) containing a network with N nodes, i.e., points where fibers intersect either with each other, or with the RVE boundary. Figure 1 shows a 2-D schematic of an RVE network. Let $N = N_b + N_i$, where N_b and N_i are boundary and internal nodes, respectively. Under an imposed deformation, the average Cauchy stress in the network $\langle S_{ij} \rangle$ can be calculated from the forces on the boundary nodes using a volume averaging method described in [26, 27] and briefly shown below.

$$\begin{aligned}\langle S_{ij} \rangle &= \frac{1}{V} \int S_{ij} dV \\ \langle S_{ij} \rangle &= \frac{1}{V} \int S_{ik} \delta_{jk} dV \\ \langle S_{ij} \rangle &= \frac{1}{V} \int S_{ik} x_{j,k} dV \\ \langle S_{ij} \rangle &= \frac{1}{V} \int (x_j S_{ik})_{,k} dV - \frac{1}{V} \int x_j S_{ik,k} dV\end{aligned}$$

where V is the volume of the box enclosing the deformed network. Applying the divergence theorem to the first term and using the fact that the second term is zero by the requirement of local equilibrium, $S_{ik,k} = 0$, we write

$$\langle S_{ij} \rangle = \frac{1}{V} \oint n_k x_j S_{ik} ds.$$

The traction on the boundary $n_k S_{ik}$, however, is entirely provided by the fiber forces acting on boundary nodes. Thus, assuming that the fiber diameter is very small compared to the RVE dimension, we obtain

$$\langle S_{ij} \rangle = \frac{1}{V} \oint x_j f_i ds = \frac{1}{V} f_i^b x_j^b \quad (1)$$

where x_j^b is the coordinate along the j direction, f_i^b is the force in the i direction, acting on the boundary node b , and summation occurs over all boundary nodes, i.e., $1 \leq b \leq N_b$. In matrix form, Equation 1 may be written as

$$\left\langle \mathbf{S} \right\rangle = \frac{1}{V} \mathbf{X}_B^T \mathbf{F}_B = \frac{1}{V} \begin{bmatrix} x_1^1 & x_2^1 & x_3^1 \\ x_1^2 & x_2^2 & x_3^2 \\ \vdots & \vdots & \vdots \\ x_1^{N_b} & x_2^{N_b} & x_3^{N_b} \end{bmatrix}^T \begin{bmatrix} f_1^1 & f_2^1 & f_3^1 \\ f_1^2 & f_2^2 & f_3^2 \\ \vdots & \vdots & \vdots \\ f_1^{N_b} & f_2^{N_b} & f_3^{N_b} \end{bmatrix}. \quad (2)$$

where $\mathbf{X}_B$ is the matrix of boundary node positions, and $\mathbf{F}_B$ is the matrix of boundary node forces, with rows indicating node number, and columns denoting direction.

2.1.2. Network relaxation—For the following section, it is assumed that the network is stretched and held such that the nodes lying on the network boundary do not move, but that the internal nodes are free to reorganize as the network relaxes. Differentiating Equation 1 with respect to time and recognizing that the volume of the network domain does not change during relaxation

$$\begin{aligned} \frac{d\langle S_{ij} \rangle}{dt} &= \frac{1}{V} \left(\frac{dx_j^b}{dt} f_i^b + x_j^b \frac{df_i^b}{dt} \right), \text{ and } \frac{dx_j^b}{dt} = 0 \quad (3) \\ \therefore \frac{d\langle S_{ij} \rangle}{dt} &= \frac{1}{V} x_j^b \frac{df_i^b}{dt} \end{aligned}$$

Since the network boundaries are held fixed in a stress relaxation experiment, the force on boundary nodes f_i^b depends only on the positions of the internal nodes, i.e., $f_i^b = f_i^b(t, x_j^n)$, where $1 \leq n \leq N_b$ and $i, j = 1, 2, 3$. Thus, the derivative on the RHS of Equation 3 can be written as

$$\frac{df_i^b}{dt} = \left. \frac{\partial f_i^b}{\partial t} \right|_x + \left. \frac{\partial f_i^b}{\partial x_k^n} \right|_t \frac{dx_k^n}{dt} \quad (4)$$

Now consider a differential change in the force on an internal node m of the network

$$df_p^m = \left. \frac{\partial f_p^m}{\partial x_k^n} \right|_t dx_k^n + \left. \frac{\partial f_p^m}{\partial t} \right|_x dt \quad (5)$$

The requirement of equilibrium of the internal nodes requires that $df_p^m = 0$.

$$\therefore \frac{dx_k^n}{dt} = - \left(\frac{\partial f_p^m}{\partial x_k^n} \right)^{-1} \frac{\partial f_p^m}{\partial t} \quad (6)$$

From Equations 6 and 4,

$$\frac{df_i^b}{dt} = \left. \frac{\partial f_i^b}{\partial t} \right|_x - \left(\frac{\partial f_i^b}{\partial x_k^n} \right) \left(\frac{\partial f_p^m}{\partial x_k^n} \right)^{-1} \frac{\partial f_p^m}{\partial t} \bigg|_x \quad (7)$$

Let $G_{ik}^{bn} = \left. \frac{\partial f_i^b}{\partial x_k^n} \right|_t$ be the Jacobian matrix relating internal node motion to boundary forces,

and $J_{pk}^{mn} = \left. \frac{\partial f_p^m}{\partial x_k^n} \right|_t$ be the Jacobian matrix for the internal nodal forces. Then Equation 7

becomes

$$\frac{df_i^b}{dt} = \left. \frac{\partial f_i^b}{\partial t} \right|_x - G_{ik}^{bn} (J_{pk}^{mn})^{-1} \frac{\partial f_p^m}{\partial t} \bigg|_x, \quad (8)$$

and Equation 3,

$$\frac{d\langle S_{ij} \rangle}{dt} = \underbrace{\frac{1}{V} x_j^b \frac{\partial f_i^b}{\partial t} \bigg|_x}_{\text{Material}} - \underbrace{\frac{1}{V} x_j^b G_{ik}^{bn} (J_{pk}^{mn})^{-1} \frac{\partial f_p^m}{\partial t} \bigg|_x}_{\text{Kinematic}}. \quad (9)$$

The first term on the RHS of Equation 9 arises due to the relaxation of the fibers connected to the boundary nodes, and it can be viewed as the *material* contribution to the network relaxation as its rate of change depends solely on the material, i.e., the constitutive equation, of the fibers. The second term arises from the reorganization of the internal nodes occurring within the network as its fibers relax, and thus, represents the *kinematic* part of the relaxation which depends on the structure of the network. The product $\mathcal{G}^{-1}$ works as a transformation matrix relating the changes in internal nodal forces to the resultant changes in boundary forces.

The force balance at every network node at each time step introduces additional algebraic constraints that relate nodal forces to forces in the network fibers. Thus, we can write $f_i^b = C_i^{br} \sigma^r$, and $f_p^m = C_p^{mr} \sigma^r$ for boundary and internal nodes, respectively, where σ^r is the force in fiber r . Equation 9 then becomes

$$\frac{d\langle S_{ij} \rangle}{dt} = \frac{1}{V} x_j^b \left(\left. \frac{\partial (C_r^{br} \sigma^r)}{\partial t} \right|_x - G_{ik}^{bn} (J_{pk}^{mn})^{-1} \left. \frac{\partial (C_p^{mr} \sigma^r)}{\partial t} \right|_x \right), \quad (10)$$

or, in matrix notation

$$\frac{d\langle \mathbf{S} \rangle}{dt} = \frac{1}{V} (\mathbf{X}_B)^T \left(\left. \frac{\partial \mathcal{E}_B \boldsymbol{\sigma}}{\partial t} \right|_x - \mathcal{E}_F^{-1} \left. \frac{\partial \mathcal{E}_I \boldsymbol{\sigma}}{\partial t} \right|_x \right). \quad (11)$$

where $\boldsymbol{\sigma}$ is the vector of fiber forces, and $\mathcal{E}_B$ and $\mathcal{E}_I$ are tensors relating fiber forces to forces on boundary and internal nodes, respectively.

2.2. Network modeling

Stress relaxation of networks was simulated by representing networks as trusses composed of viscoelastic cylindrical members (fibers) connected by means of pin-joints (nodes) allowing free rotation.

2.2.1. Single fiber mechanics—Individual fibers within a network were modeled as one-dimensional viscoelastic elements following the Maxwell constitutive law (Figure 2(a))

$$\frac{\dot{\sigma}}{E} + \frac{\sigma}{\eta} = \dot{\lambda}, \quad (12)$$

where σ is the force generated in the fiber, E is the modulus of the linear spring element, η is the viscosity of the dashpot element, λ is the fiber stretch, and a dot over the symbol indicates a derivative with respect to time. When a fiber is stretched and held,

$$\dot{\sigma} = -\frac{E}{\eta} \sigma = -\frac{1}{\tau} \sigma, \quad (13)$$

where the ratio $\tau = \frac{\eta}{E}$ is the characteristic time over which the force in the fiber decays and approaches a steady state value of zero.

2.2.2. Network mechanics—Networks formed by connecting Maxwell fibers at nodes were stretched uniaxially by imposing a displacement on all nodes lying on one face of the network while keeping the opposite face fixed in space. Nodes lying on the faces perpendicular to the other two coordinate directions were forced to lie in a plane, and these faces were displaced such that the total volume of the box containing the network remained constant. Thus, network domain incompressibility was imposed by moving the network faces in an affine manner.

Network nodes were identified as either boundary nodes, which included all nodes lying on a network face and constrained to move with the network face, or internal nodes, which were free to move and equilibrate. Fiber stretching due to the motion of the network boundary generated forces on all network nodes, boundary as well as internal. At every time step, however, the equilibrium solution of the network force problem had no net force on any internal node. The nodal positions corresponding to this equilibrium solution were

calculated using Newton's method by computing the Jacobian matrix J such that $J_{ij} = \frac{\partial f_i}{\partial x_j}$,

where f is total force on a node, and x is its position. We used backward-Euler integration for the time dependent terms in the fiber constitutive equations. Newton iteration was applied at every time step until the net force on all internal nodes was less than a specified tolerance. The volume-averaged Cauchy stress in the network was then calculated using Equation 1. All computations were carried out through scripts written in MATLAB [28]. The network mechanics model described above has been used previously to model the pre-failure mechanics of soft tissues, and to capture the non-affine deformations occurring within the network during deformation [29].

2.2.3. Network stress relaxation—Network relaxation was simulated by stretching the network uniaxially in the X direction in the first time step, and subsequently holding the network in the deformed configuration to obtain the evolution of network stress with time. At every time step, an instantaneous relaxation time was calculated as

$$\tau_{inst} = - \left\langle S_{11} \right\rangle \left(\frac{d\langle S_{11} \rangle}{dt} \right)^{-1}. \quad (14)$$

Additionally, a relaxation spectrum was computed for the network by fitting the stress-time curve to a Prony series (or a Generalized Maxwell model, Figure 2(b)) using a discrete spectral fitting algorithm developed by Babaei et al. [30]. Briefly, using a non-negative least squares regression method, the algorithm computed values for E_n corresponding to an interval of time constants $\tau_n = \frac{E_n}{\eta_n}$ selected *a priori*, and spaced equidistantly on a logarithmic

scale. The algorithm was tested against various simulated datasets, and was robust in handling noisy data. For our network relaxation data, the chosen interval of the time constants was discretized into 1000 parts, i.e., the data was fit to a Prony series with 1000 Maxwell branches; the range of the time constant interval was selected such that its lower bound was at least a decade lower than the characteristic relaxation time of the fastest fiber in the network, and similarly, the upper bound was a decade larger than the slowest fiber relaxation time in the network.

2.3. Case studies

First, we applied the theoretical and modeling approaches described above to a simplified end-to-end chain of fibers. We used the simplified case to compare the theoretical prediction and the model, and to better understand the kinematic contribution to network relaxation. We

then simulated stress relaxation of 3-D Delaunay networks, and used the 3-D networks to study the effect of network composition on its effective relaxation behavior.

2.3.1. A three-fiber four-node 1-D arrangement (3F-4N)—We used the simple arrangement of fibers shown in Figure 3 to confirm a match between the relaxation behavior predicted by Equation 10 and that obtained from the network model. Restricting the nodal motions to 1-D removes any non-linearities arising from fiber rotation, i.e., $\mathcal{E}_{\mathbf{B}}$, and $\mathcal{E}_{\mathbf{I}}$ are constant over time as the network reorganizes, which makes it easy to calculate a predicted time constant from Equation 10.

2.3.2. 3-D networks—We next used the network model to obtain relaxation spectra for 3-D networks comprising of fibers with two different characteristic relaxation times, and we compared our results to the spectrum obtained experimentally for re-constituted collagen gels by Pryse et al. [31]. Briefly, Pryse et al. strained collagen gel specimens to a strain of 2% in under 20 ms using a specially designed loading apparatus. The stretched gels were then held isometrically while force was recorded for 30 minutes at a sampling frequency of 5 Hz. The experimental data were subsequently fit to a Prony series with three Maxwell branches, which Pryse et al. identified as the optimal number of branches they needed to obtain a good fit to their data. We also compared our simulated viscoelastic spectra to that reported by Babaei et al. [30] for the same collagen gel data. Babaei et al. used their discrete spectral fitting algorithm, described briefly above, to reanalyze the data of Pryse et al.

Network generation.: We generated networks using a Delaunay [32] tessellation wherein connections were formed between randomly generated points such that the circumsphere of any tetrahedron formed by a set of four connected nodes did not contain any other network node (Figure 4(a)). Networks were generated using the MATLAB function *delaunay* [28]. Delaunay networks have been used in previous studies modeling fibrous tissues [33].

Networks generated were isotropic and were trimmed to fit within a unit cube in the computational domain. The physical space represented by this unit volume of computation domain (Figure 1) was calculated from the equation [27]

$$X = \sqrt{\frac{\pi r^2 l_{total}}{\phi}} \quad (15)$$

where X is the conversion factor relating the physical and computational domains, r is the fiber radius, l_{total} is the unitless total fiber length in the network in the computational domain, and ϕ is the fiber volume fraction. All fibers in the network had the same radius of $r = 100$ nm [34], and the number of nodes and fibers was selected such that the unit cube containing the network represented a physical domain of side $X \approx 10\mu\text{m}$. Prior to simulating stress relaxation, the network was also confirmed to be sufficiently resolved, i.e., there was no change in the elastic network stress-stretch response with a further increase in the number of nodes and fibers.

Network relaxation spectra and comparison with reconstituted collagen.: The fibers in the network were divided into two types: fast relaxers and slow relaxers (Figure 4(a)). The characteristic relaxation time of the fast relaxers was less than that of the slow ones, i.e., $\tau_{fast} < \tau_{slow}$. Values for the characteristic times were selected to match the fastest and slowest relaxation times identified by Pryse et al. for reconstituted collagen gels with $\tau_{fast} = 4.73$ seconds, and $\tau_{slow} = 775.35$ seconds.

Next, we simulated stress relaxation of the network for different compositions of the two types of fibers. Starting with a network composed of all fast relaxing fibers, we increased the composition of the slow relaxers by changing 2% of the fibers at a time. Fibers to be changed to slow relaxers in each step were selected at random. This process of simulating stress relaxation of the network at different compositions was repeated for 5 networks. The relaxation protocol simulated was similar to that used by Pryse et al., where the network was stretched by 2% in 20 ms and held.

The stress-time curves obtained from the simulated relaxation of each of the different compositions of the networks were compared to the relaxation data of Pryse et al. to find the composition that best matched the experimental data and the simulated curves. Since we used Maxwell fibers in our model, the network stress always dropped to zero over time, in contrast to the experimental data, for which the gels exhibited a non-zero steady state stress. Thus, to compare the experimental and simulated stress-time curves, we subtracted the steady state stress from the data of Pryse et al., and normalized both datasets to the peak stress, i.e., the stress at 2% stretch. Mean squared error (MSE) was used as the measure of goodness of fit between the experimental data and simulated curves.

Fiber percolation.: As the composition of the slow relaxers was gradually increased, we also probed the network for percolating slowly-relaxing paths, i.e., continuous paths of only slow fibers connecting the two loaded faces of the network (Figure 4(b)). Fiber percolation was evaluated by calculating the shortest path between all pairs of nodes lying on the two opposite faces using a Floyd-Warshall algorithm [35]. Paths of only slow fibers were identified by appropriately modifying the adjacency matrix A of the network such that for every pair of nodes in the network

$$A^{ij} = \begin{cases} 1 & \text{if node } i \text{ is connected to node } j \text{ by a slow fiber} \\ 0 & \text{otherwise} \end{cases}$$

3. Statistical Methods

All analyses of simulation results were done in R [36]. Error bars shown in the following section represent standard error of the mean.

4. Results and Discussion

4.1. Three-fiber four-node arrangement (3F-4N) relaxation

4.1.1. Theoretical prediction of relaxation behavior—For the node and fiber numbering as shown in Figure 3, nodes 1 and 4 are boundary nodes, while nodes 2 and 3 are

interior. A linear arrangement such as this provides two benefits. Firstly, since the nodes are restricted to move along a line, the dimensions of the quantities involved in Equation 10 reduce. For instance, $f_i^b = f_1^b = \mathbf{f}_B = [f_1^1 f_1^4]$, and

$$G_{ij}^{bn} = G_{11}^{bn} = \frac{\partial f_i^b}{\partial x_j^n}, \text{ or } \mathbf{G} = \begin{bmatrix} \frac{\partial f_1^1}{\partial x_1^2} & \frac{\partial f_1^1}{\partial x_1^3} \\ \frac{\partial f_1^4}{\partial x_1^2} & \frac{\partial f_1^4}{\partial x_1^3} \end{bmatrix}.$$

Similarly,

$$J_{ij}^{mn} = J_{11}^{mn} = \frac{\partial f_i^m}{\partial x_j^n}, \text{ or } \mathbf{J} = \begin{bmatrix} \frac{\partial f_1^2}{\partial x_1^2} & \frac{\partial f_1^2}{\partial x_1^3} \\ \frac{\partial f_1^3}{\partial x_1^2} & \frac{\partial f_1^3}{\partial x_1^3} \end{bmatrix}.$$

Another benefit of the linear arrangement is that the forces in all the fibers are equal since there can be no net force on the internal nodes at equilibrium. Also, the magnitude of the boundary node forces are equal to the fiber forces, and they point in opposite directions, i.e., $|f_1^1| = |f_1^4| = \sigma$, and $f_1^1 = -f_1^4$. From Equation 1 then,

$$\langle S_{11} \rangle = \frac{1}{V} \sigma (x_1^1 - x_1^4).$$

The volume of the network box for this linear arrangement is, however, simply the end-to-end length of the arrangement, i.e., $V = (x_1^1 - x_1^4)$. Thus,

$$\langle S_{11} \rangle = \sigma. \quad (16)$$

For the 3F-4N arrangement from Figure 3,

$$\mathbf{G} = \begin{bmatrix} E_1 & 0 \\ 0 & E_3 \end{bmatrix}, \text{ and } \mathbf{J} = \begin{bmatrix} -(E_1 + E_2) & E_2 \\ E_2 & -(E_2 + E_3) \end{bmatrix}.$$

and the constraint matrices relating nodal forces to fiber forces are

$$\mathbf{C}_B = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 0 & -1 \end{bmatrix}, \text{ and } \mathbf{C}_I = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \end{bmatrix}.$$

Substituting in Equation 11, we get

$$\begin{aligned} \frac{d\langle \mathbf{S} \rangle}{dt} &= \frac{1}{V} \mathbf{X}_B^T \begin{bmatrix} 1 & 0 & 0 \\ 0 & 0 & -1 \end{bmatrix} \\ &\quad - \begin{bmatrix} E_1 & 0 \\ 0 & E_3 \end{bmatrix} \begin{bmatrix} -(E_1 + E_2) & E_2 \\ E_2 & -(E_2 + E_3) \end{bmatrix}^{-1} \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \end{bmatrix} \left. \frac{\partial \boldsymbol{\sigma}}{\partial t} \right|_x \end{aligned} \quad (17)$$

where $\boldsymbol{\sigma} = [\sigma^1, \sigma^2, \sigma^3]^T = \sigma[1, 1, 1]^T$, and from Equation 13, for Maxwell fibers,

$$\left. \frac{\partial \boldsymbol{\sigma}}{\partial t} \right|_x = \mathbf{T}^{-1} \dot{\boldsymbol{\sigma}} = -\sigma \begin{bmatrix} \tau_1 & 0 & 0 \\ 0 & \tau_2 & 0 \\ 0 & 0 & \tau_3 \end{bmatrix}^{-1} \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix}$$

Following some algebraic manipulation, and using Equation 16, Equation 17 becomes,

$$\frac{d\langle S_{11} \rangle}{dt} = \frac{1}{V} \mathbf{X}_B^T \left(\frac{E_1 E_2 E_3}{E_1 E_2 + E_2 E_3 + E_1 E_3} \begin{bmatrix} \frac{1}{E_1 \tau_1} & \frac{1}{E_2 \tau_2} & \frac{1}{E_3 \tau_3} \\ -1 & -1 & -1 \\ \frac{1}{E_1 \tau_1} & \frac{1}{E_2 \tau_2} & \frac{1}{E_3 \tau_3} \end{bmatrix} \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix} \left(S_{11} \right) \right) \quad (18)$$

From Equation 18, it is clear that the stress in the system of fibers relaxes with a constant effective relaxation time of

$$\tau_{inst} = \left(\frac{1}{E_1} + \frac{1}{E_2} + \frac{1}{E_3} \right) \left(\frac{1}{\frac{1}{E_1 \tau_1} + \frac{1}{E_2 \tau_2} + \frac{1}{E_3 \tau_3}} \right) \quad (19)$$

which can be viewed as a scaled harmonic mean of the relaxation times of the individual fibers, weighted by their respective stiffness moduli. The effective relaxation time is not necessarily equal to the relaxation time of any individual fiber τ_1 , τ_2 , or τ_3 . If the fibers are identical, then the network relaxes at the same rate as the fibers. The above result can also be generalized to any number of fibers arranged end-to-end. For such an arrangement with N_f fibers, the relaxation time of the system will be given by

$$\tau_{inst} = \sum_{i=1}^{N_f} \frac{1}{E_i} \left(\frac{1}{\sum_{i=1}^{N_f} \frac{1}{E_i \tau_i}} \right).$$

4.1.2. Simulation of relaxation behavior—Stress relaxation of the 3F-4N arrangement with various spatial combinations of fast and slow relaxation times was simulated to obtain the instantaneous relaxation time, and stress-time curves like the ones

shown in Figure 5(a) and (b) for the case where the relaxation time of the middle fiber ($\tau_2 = 1$ s) was longer than that of the two outer ones ($\tau = \tau_3 = 0.1$ s). The value of the effective relaxation time predicted by Equation 19 always matched that calculated from the simulations. Note that the effective relaxation time of the system is constant and does not change over time as the nodes are constrained to move on a line, and $\mathcal{E}_B$, and $\mathcal{E}_I$ are constant.

4.2. 3-D Delaunay network relaxation

4.2.1. Effect of network composition on relaxation

Instantaneous relaxation time.: Figure 6(a) shows plots of the evolution of the instantaneous relaxation times of a network for different compositions. The two dashed lines show the effective relaxation time of the network when all fibers have the same relaxation time, i.e., $\tau_{fiber} = \tau_{slow} = 775.35$, or $\tau_{fiber} = \tau_{fast} = 4.73$ seconds. As expected, if all the fibers relax at the same rate, the forces on internal nodes are always balanced, reducing the kinematic contribution to zero. The solid lines in Figure 6(a) show the instantaneous relaxation time for the same network at different intermediate compositions of slow and fast relaxers – ratios of 70-30, 50-50, and 30-70% slow and fast relaxers, respectively – with the arrow indicating the direction of increasing fast relaxer composition. In these cases, the instantaneous relaxation times for the 3-D network vary over time as the constraint tensors $\mathcal{E}_B$ and $\mathcal{E}_I$ evolve with the equilibration of forces on internal nodes. The instantaneous relaxation time of the network immediately following the stretch lies between τ_{fast} and τ_{slow} , but at long times, the contribution of the fast relaxing fibers to the overall network behavior drops significantly, and the instantaneous behavior of the network is dominated by the slow relaxers. Figure 6(b) shows the normalized stress-time curve for the network at the three compositions mentioned above, again, with the arrow pointing in the direction of increasing composition of rapidly-relaxing fibers.

The variation of the instantaneous relaxation time right after the stretch, and as the system approaches steady-state, with change in network composition is shown in Figure 7. As the percentage of slowly-relaxing fibers in the networks increases, the initial effective relaxation time (dots) increases slowly. The near-steady-state relaxation time (triangles), however, increases rapidly and approaches that of the slow relaxers in the network. Since the fast relaxers decay out more quickly over time, the instantaneous relaxation time is always greater near steady-state than during the initial relaxation. The effect of fiber percolation can also be seen in Figure 7. The dashed vertical line on the left shows the network composition for which slow fiber percolation was first detected, while the dashed vertical line on the right indicates the network composition at which the fast relaxing fibers stop percolating. Before the slow relaxers percolate, the steady-state network relaxation time does not reach the slow rate. Once a percolating path of slow relaxers has formed, however, the steady-state relaxation behavior of the network is governed by the slow relaxers. Žagar et al. [23] have shown a similar effect of fiber percolation on the non-linear strain-stiffening trend observed in biopolymer networks.

Relaxation spectra. Evolution of the relaxation spectrum with changing network composition can be viewed in the series of snapshots shown in Figure 8. At the two extreme cases, when the network is made up of only one type of fiber, the spectrum shows a solitary peak. As the network composition changes, however, we see evolution of the spectral landscape with multiple peaks arising, shifting, and disappearing. For instance, for the case of the network composed of an equal number of slow and fast relaxers (Figure 8(c)), the spectrum shows four distinct peaks. The two extreme peaks at 4.9 s, and 722.5 s are close to the relaxation times of the two fiber types. The intermediate peaks at 10.6 s, and 64.2 s, different from the characteristic times of the two fiber types, arise due to the contribution of the kinematic term.

4.2.2. The relaxation spectrum of reconstituted collagen gels—Since all five network architectures tested showed similar relaxation trends, for the next part, we picked one network at random. The relaxation response of that network when it was composed of 43.7% slow relaxers was identified as being the best fit to the experimental stress relaxation data based on the mean squared error (Figure 9(a)). The relaxation spectrum of the network with this composition is shown in Figure 9(b) along with the three time constants calculated by Pryse et al. for collagen gels. The intermediate structure-dependent time constants in the simulated spectrum were on the same order of magnitude as the middle time constant identified by Pryse et al.

The simulated relaxation spectrum is also consistent with the findings of Babaei et al. (Figure 10). Falling roughly within the interval of time constants defined by our fast and slow relaxers, they identified four peaks at 2.6 s, 16.1 s, 72.7 s, and 1520 s. They also found two additional time constants that were less than the characteristic time we used for our fast relaxers, and thus were not seen in our simulations.

We did not aim to describe accurately the viscoelastic relaxation of reconstituted collagen gels with our model. Neither was it our goal to explore the source of viscoelasticity in individual fibers via an analysis of overall network behavior, e.g., as done by Gardel et al. [37] to study single F-actin filament mechanics. Rather, our goal was to investigate how structure-based effects of interactions between multiple viscoelastic elements manifest in the relaxation spectrum of a network. Similar to the theory developed by Storm et al. [38] exploring the in-built strain-stiffening effect of crosslinked networks, we show that a system of interconnected viscoelastic fibers can exhibit certain relaxation time scales that are inherently related to their network structure. The similarity between the experimental and simulated spectra seen above suggests that the viscoelastic response of collagen is at least in part influenced by its network structure, and that some of the time constants identified by Babaei et al. possibly arise as a result of the reorganization of fibers within the network.

4.2.3. Model limitations—During uniaxial deformation the volume of the network domain in our model was assumed to remain constant. In biological networks, however, water expulsion during deformation can lead to a reduction in volume [39]. While this change in network volume will affect the initial stress generated in the network immediately after deformation, the model described here assumed that it would not significantly affect the relaxation behavior of the material in a stress relaxation test.

Secondly, the choice of representing network fibers as Maxwell elements severely limits the applicability of this model to simulating mechanics of collagen networks. Given our goal of exploring the structure-related relaxation times arising from the network, however, this choice of fiber was justified as it allowed us to accurately capture the relaxation behavior of the network as it approached steady state. We also simulated networks with fibers represented as standard linear solids (SLS); the relaxation spectra of these SLS networks were very similar to those obtained for the Maxwell fiber networks, however, we were not able to capture accurately the longterm relaxation times due to the network stress approaching a non-zero steady state value, i.e., $\tau_{network} \rightarrow \infty$.

Furthermore, the non-affine reorganization of internal nodes discussed above is by no means the sole mechanism behind the broad relaxation spectrum of biopolymer gels. Certainly, other factors also contribute to the overall relaxation behavior, e.g., Broedersz et al. [24] showed the presence of multiple relaxation times arising out of crosslink binding and unbinding within the gel. The model presented here assumes that the viscoelasticity of the network stems from the viscoelastic behavior of individual collagen fibers. While studies have shown a viscoelastic trend in the behavior of isolated collagen fibrils [40, 41], network viscoelasticity could also arise from several other contributions, e.g., fiber motion through the embedding material, fiber sliding through physical crosslinks, or bond breaking and remodeling. There could also be a range of individual fiber relaxation times within a gel, and the distinction between those characteristic times likely is not as clear-cut as assumed in our model. While we consider this a suitable first approximation, further research will need to address the effects of these factors on the relaxation behavior of networks.

5. Conclusion

In this paper, we expanded on the previously developed theoretical framework of calculating a volume averaged stress in a deformed network [26] to analyze stress relaxation of viscoelastic fiber networks. We showed the presence of evolving time scales in the relaxation spectrum of the network that arise from its heterogeneous structure and the non-affine deformations occurring within it. We also presented a model to simulate viscoelastic mechanics of networks, and we used this model to study the effect of changing network composition on its relaxation time spectrum. For a 3-D network composed of only fibers with two different characteristic relaxation times, the instantaneous relaxation time of the system evolves over time and shows a highly non-linear behavior. The relaxation spectrum for such a network shows multiple peaks, and it is very similar to that obtained for reconstituted collagen gels, suggesting that some of the relaxation time scales observed in the viscoelastic spectra of collagenous tissues might be purely structure-based, arising from their inherent network arrangement.

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Appendix A: Comments on the kinematic relaxation term

A thorough mathematical analysis of the kinematic relaxation term, and the factors influencing the origin of network structure-dependent timescales arising in the relaxation equation was out of the scope of this work. We focused our attention instead on simulating network relaxation, and on investigating the manifestation of the kinematic effect in the relaxation spectrum obtained for the network simulation. In this brief section, however, we point out a few preliminary observations that can be made about the kinematic term, and how it could be used to predict the effect of network architecture on its viscoelastic relaxation.

The kinematic term in matrix form reduces to $\mathbf{K} = -\mathbf{G}\mathbf{J}^{-1}\mathbf{C}_I$. The matrix $\mathbf{K}$ can be viewed as a transformation relating the rate of change of fiber forces in the network to the rate of change of forces on the boundary nodes. For example, for a network with $N_b < N_f$ the singular value decomposition of $\mathbf{K}$ can be written as

$$\mathbf{K} = -\mathbf{G}\mathbf{J}^{-1}\mathbf{C}_I = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^T = \quad (20)$$

$$\begin{bmatrix} \mathbf{u}_1 & \mathbf{u}_2 & \dots & \mathbf{u}_{N_b} \end{bmatrix} \begin{bmatrix} \lambda_1 & 0 & \dots & 0 \\ 0 & \lambda_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & \dots & \lambda_{N_b} & \dots \\ \vdots & \vdots & \vdots & \vdots \\ 0 & \dots & \dots & 0 \end{bmatrix} \begin{bmatrix} \mathbf{v}_1 & \mathbf{v}_2 & \dots & \mathbf{v}_{N_f} \end{bmatrix}^T$$

The columns of $\mathbf{U}$ and $\mathbf{V}$ yield orthonormal bases spanning the vector spaces of boundary node forces, and fiber forces, respectively. Thus, the columns of $\mathbf{V}$ contain information about the primary fiber paths within the network contributing to the perceived rate of change of network stress. The singular value λ_f indicates the relative importance of the contribution of fiber path $\mathbf{V}_f$. Reducing the rank of $\mathbf{K}$ by removing fiber paths with relatively insignificant contribution to the overall behavior will produce a modified network that exhibits similar viscoelastic behavior, but that is structurally different from the original network. For example, we can identify the k most important paths which contribute to 85% of the

viscoelastic behavior using $\frac{\sum_1^k \lambda_f}{\sum_1^{N_f} \lambda_f} > 0.85$. The number of non-zero values of $\mathbf{\Sigma}$ could also

potentially inform us of the maximum number of possible peaks that could show up in the relaxation spectrum.

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Figure 1:

A schematic drawing of an RVE network showing boundary and internal nodes. Volume averaged Cauchy stress is calculated from the forces acting on all boundary nodes.

Figure 2:

(a) A spring and dashpot model of the Maxwell fluid, (b) A Prony series with multiple branches of Maxwell elements in parallel with an elastic spring element.

Figure 3:

Simplified arrangement of three Maxwell fibers connected end-to-end. Numbers in circles indicate node numbers with nodes 1 and 4 held fixed during relaxation, while nodes 2 and 3 are free to move as the forces equilibrate.

Figure 4:

(a) A Delaunay network composed of fibers with two distinct relaxation times, τ_{slow} (pink), and τ_{fast} (black), (b) Similar network, but with two percolating connections of slow relaxers (shown in red).

Figure 5:

(a) Instantaneous relaxation time versus time for the simulated end-to-end arrangement of three Maxwell fibers of equal stiffness (i.e., $E_1 = E_2 = E_3$). The characteristic relaxation times of the two outer fibers was 0.1 s (lower dashed line), and that of the middle fiber was 1 s (upper dashed line). The effective relaxation time of the arrangement was 0.143 s (solid line) – different from that of any individual fiber. (b) The normalized stress in the fibers as a function of time (solid line - left Y axis), and the displacement (in the computational domain) of an internal node as the fiber stresses relax over time (dashed line - right Y axis).

Figure 6:

(a) Instantaneous relaxation times for a network with different compositions of slow and fast relaxers. The instantaneous relaxation time for a network comprising of 70-30, 50-50, and 30-70% slow and fast relaxers, respectively, (solid lines) varies over time within the interval bounded by the instantaneous relaxation times for the network with all fast relaxers (lower dashed line), and all slow relaxers (upper dashed line). The arrow indicates the direction of increasing percentage of fast relaxing fibers within the network. (b) Stress in the network over time for the three intermediate compositions shown in (a). $\tau_{slow} = 775.35$ seconds, and $\tau_{fast} = 4.73$ seconds.

Figure 7:

Change in the instantaneous relaxation time of the network immediately following the stretch (dots), and near steady-state (triangles) for different compositions of the networks ($n = 5$, error bars represent standard error of the mean). Note how the initial relaxation time increases gradually as the percentage of slow relaxers in the network rises. The steady-state time, however, rapidly approaches that of the slow relaxers. The left vertical dashed line indicates the average network composition at which slow relaxers percolate, while the right vertical line marks the average composition at which fast relaxers stop percolating within the network. $\tau_{slow} = 775.35$ seconds, and $T_{fast} = 4.73$ seconds.

Figure 8:

Relaxation spectra for a network as its composition changes from all fast relaxers (a) to all slow relaxers (e). The intermediate compositions (b,c, and d) shown are 30-70, 50-50, and 70-30 % slow and fast relaxers, respectively. $\tau_{slow} = 775.35$ seconds, and $\tau_{fast} = 4.73$ seconds.

Figure 9:

Comparison of the simulated relaxation spectrum to that of reconstituted collagen gels. (a) A network composed of 43.7 % slow relaxers best matched the experimental data of Pryse et al. [31](MSE = 0.0019). (b) Relaxation spectrum of the simulated network showing peaks at 5.1 s, 14 s, 75.8 s, and 712.6 s. Red lines mark the relaxation times computed by Pryse et al. $\tau_{slow} = 775.35$ seconds, and $\tau_{fast} = 4.73$ seconds.

Figure 10:

Comparison of the simulated relaxation spectrum to that computed by Babaei et al. [30] for the collagen gel relaxation data of Pryse et al. [31]. Red lines mark the relaxation times computed by Babaei et al. near the interval bound by the slow and fast characteristic relaxation times of the fibers used in the simulation.

Nomenclature

superscript index	node/fiber number
subscript index	direction
N_b	number of nodes on network boundary
N_i	number of internal nodes
N_f	number of fibers in the network
f_i^b	force on node b along direction i
x_i^b	position of node b along direction i
δ_{jk}	Kronecker delta function
V	volume of network domain
S_{ij}	Cauchy stress
n_k	surface normal vector
$\oint(\cdot)ds$	surface integral over surface s
G_{ij}^{bn}	Jacobian matrix relating motion of internal node n to force on boundary node b
J_{ij}^{mn}	Jacobain matrix relating motion of internal node n to force on internal node m
σ^f	force generated in network fiber f
C_i^{bf}	component of force in fiber f along direction i acting on node b
E	modulus of linear elastic element
η	viscosity of dashpot element
τ	characteristic relaxation time