Characterization of the Viscoelastic Behavior of **a Simplified** Collagen Micro-fibril based on Molecular Dynamics Simulations

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Abstract

Collagen fibril is a major component of connective tissues such as bone, tendon, blood vessels, and skin. The mechanical properties of this highly hierarchical structure are greatly influenced by the presence of covalent cross-links between individual collagen molecules. This study investigates the viscoelastic behavior of a collagen lysine-lysine cross-link based on creep simulations with applied forces in the range of 10 to 2000 pN using steered molecular dynamics (SMD). The viscoelastic model of the cross-link was combined with a system composed by two segments of adjacent collagen molecules hence representing a reduced viscoelastic model for a simplified micro-fibril. It was found that the collagen micro-fibril assembly had a steady-state Young's modulus ranging from 2.24 to 3.27 GPa, which is in agreement with reported experimental measurements. The propagation of longitudinal force wave along the molecule was implemented by adding a delay element to the model. The force wave speed was found to be correlated with the speed of one-dimensional elastic waves in rods. The presented reduced model with three degrees of freedom can serve as a building block for developing models of the next level of hierarchy, i.e., a collagen fibril.

Keywords: collagen micro-fibril, cross-link, viscoelastic properties, steered molecular dynamics, creep simulations, quasi-linear viscoelastic (QLV) theory

1. Introduction

Structural and connective tissues in animals, e.g., bone, tendon, cartilage and blood vessels, are generally collagen-rich materials in which a well-organized hierarchical structure can be distinguished. While the mechanical behavior of these tissues at the macroscopic scale is generally viscoelastic, the contribution of each level of hierarchy and transmission of force between them on the overall mechanical behavior is not fully understood (Silver et al., 2006). The knowledge of micromechanics of collagen molecule is essential in developing computational models that can predict the effects of changes at the molecular level, e.g., mutations, diseases, etc. on the biomechanics of collagenous tissues.

At the lowest hierarchical scale, i.e., the collagen molecule, most previous computational studies were focused on the elastic properties of the molecule (Bhowmik et al., 2009; Buehler and Ackbarow, 2007; Buehler, 2006a, 2006b; Gautieri et al., 2010, 2008). The viscoelastic properties of collagen molecule were studied in a series of papers by Gautieri and colleagues (Gautieri et al., 2013, 2012b), (Vesentini et al., 2013), and also more recently by our group (Ghodsi and Darvish, 2015). The next level of hierarchy, i.e., a micro-fibril, is the focus of this paper. Here, a micro-fibril is referred to a combination of two collagen molecules connected via a cross-link.

It is generally believed that covalent intermolecular cross-links between collagen molecules play a fundamental role in the micro-fibril mechanical behavior as cross-links transfer force from one molecule to another. The micro-mechanics of cross-links in collagen micro-fibril has been investigated using computational models by Buehler et al. (Buehler, 2008) and Uzel and Buehler (Uzel and Buehler, 2011). Buehler et al. quantified the effect of the number of cross-links (cross-link density) on the elastic and fracture properties of an arrangement of micro-fibrils. Uzel and Buehler developed a molecular model of one cross-link in a micro-fibril of type I collagen and reported the force response of the assembly to an extension with constant velocity. When a cross-link is not present in the model, Gautieri et al. investigated the shear interaction between collagen molecules in a micro-fibril (Gautieri et al., 2012b) and the intermolecular slip mechanism between two collagen molecules (Gautieri et al., 2009).

In terms of the experimental work at fibrillar level, direct mechanical measurements using atomic force microscopy (AFM) (Heim et al., 2007; van der Rijt et al., 2006) and micromechanical systems (MEMS) (Eppell et al., 2006; Shen et al., 2010, 2008) were performed to investigate the elastic modulus and strength of a fibril. Recently, a few investigations on the viscoelastic properties of collagen fibrils were reported (Shen et al., 2011; Svensson et al., 2010b; Vesentini et al., 2013). The time-scale of the rate dependent measurements in these studies are in the range of microseconds to seconds which makes a direct comparison of the viscoelastic properties between their results and molecular-based computational results impractical. However, the Young's

moduli obtained in the mentioned studies were found to be applicable to the validation of the computational model developed in this study.

In this study, models of a micro-fibril, consisting of two collagen molecules with different lengths connected via a lysine-lysine cross-link were constructed. The viscoelastic behavior of the cross-link was characterized based on constant force input SMD simulations. The constitutive models of collagen molecules and cross-link were combined into a reduced constitutive model to describe the viscoelastic behavior of the micro-fibril. The micro-fibril reduced model was verified via SMD simulations of the whole micro-fibril.

2. Materials and methods

2.1. Collagen and cross-link molecular structure

The models of collagen molecule used in this study were similar to the ones developed in Ghodsi and Darvish (Ghodsi and Darvish, 2015) with 16X referring to the full-length molecule. The model of the cross-link was characterized in a quarter-size micro-fibril (4X-XL-4X), with XL referring to the cross-link, and it was verified in half-size and full-length micro-fibrils (8X-XL-8X and 16X-XL-16X). A (simplified) micro-fibril in this study was defined as the assembly of two collagen molecules with different lengths and a lysine-lysine cross-link. Using models of the micro-fibril with shorter lengths was advantageous as the effect of the cross-link in the creep response could be differentiated easier and also it was computationally more efficient since many simulations were needed for model characterization.

The atomic structures for 4X, 8X, and 16X were constructed as $[(\text{Gly-Pro-Hyp})_{85}]_3$, $[(\text{GPO})_{170}]_3$, and $[(\text{GPO})_{338}]_3$ respectively as described in our previous work (Ghodsi and Darvish, 2015) and identical molecules were used as N-terminal and C-terminal molecules. The cross-link was constructed similar to (Uzel and Buehler, 2011) to represent a lysine-lysine covalent bond. Three Telopeptides were attached to the C-terminal region of the triple-helix structure for the purpose of forming the cross-link. The C-telopeptides sequences of human were obtained from Genbank RegSeq to form two NM_000088.3 (SAGFDFSFL PQPPQEKAH DGGRYYRA) and one NM_00089.3 (GGGYDFGYD GDFYRA) and were attached to the two α_1 chains and the α_2 chain of the triple helix respectively, using the Molefacture plugin from the Visual Molecular Dynamics (VMD) (Humphrey et al., 1996). The two collagen molecules were positioned in a way to mimic the overlap zone of a micro-fibril with an approximate length of 0.46D with the D-spacing distance of 67 nm. Two α_1 chains telopeptides were manipulated in a hair-pin/hook shape to match the particular structure suggested in a previous study (Orgel et al., 2000) (Figure 1a and b). Since the atomic structure of collagen was simplified (GPO), the 87 residue of the N-terminal triple helix (a hydroxyproline

residue (O)) was changed to a lysine residue (K). The cross-link was formed between K17 of one of the C-terminal α_1 -telopeptides and the K87 of the N-terminal (Orgel et al., 2000; Reiser et al., 1992). To form the chemical structure of the cross-link, the amino group of the C-telopeptide K17 and all the hydrogen atoms of the amino group of N-terminal K87 were removed and a covalent bond was added between the N and C atoms of NH and Methylene (CH₂) groups (Figure 1b and c).

2.2. *In silico* creep test and modeling

In order to mimic a creep test, constant force SMD simulations were performed on the micro-fibrils. The SMD simulations were performed using NAMD 2.8 (Phillips et al., 2005), with CHARMM force field (MacKerell A. D. et al., 1998). Hydroxyproline amino acid parameters were manually added to the CHARMM force field using the procedure suggested by Anderson (Anderson, 2006). The micro-fibril was solvated in a box of TIP3P water molecules with a size that ensured that it was embedded in water during the entire simulation. Energy minimization for 50000 conjugate gradient steps was performed to achieve a local minimum in the energy landscape of the system (Phillips et al., 2005). Subsequently, the system was equilibrated for 10 ns in order to reach a relaxed state. This time was verified to be sufficient by monitoring the root mean square deviation (RMSD) of the alpha-carbons (C α -atoms) to reach a constant value with fluctuations of less than 3.0 Å. An integration time step of 1 fs that is common for this type of MD simulations was used. During the equilibrium process, the system temperature was gradually raised to 310K (body temperature) and was kept constant at this temperature during the SMD simulation. The Lowe-Andersen thermostat with a cut-off distance of 2.7 Å and collision rate of 50 ps⁻¹ was employed to control the kinematic energy of the system (Koopman and Lowe, 2006).

To implement the boundary conditions, the three C α -atoms of the top molecule N-terminal were fixed and six constant force levels of $F = 50, 100, 250, 500, 1000$, and 2000 pN were directly applied to the center point of the three C α -atoms of the bottom collagen C-terminal. These forces were selected based on previous studies (Gautieri et al., 2012b; Ghodsi and Darvish, 2015) and based on the fact that higher forces caused excessive deformation in the cross-link.

The measures of strain are depicted in Figure 1d and e. For the entire micro-fibril, an overall tensile-type strain was considered.

$$\varepsilon_{mf} = \Delta L_1 / L$$

1

in which ΔL_1 and L are the change in length and the initial length of the micro-fibril respectively. For the cross-link, however, due to the nature of its deformation, a shear-type strain was defined.

$$\varepsilon_{cl} = \Delta L_2 / h$$

2

in which ΔL_2 is the change in length of the cross-link, parallel to the molecule direction, and h is the length of the cross-link that is perpendicular to the direction of the molecule.

A quasi-linear viscoelastic (QLV) behavior was assumed for the cross-link and the micro-fibril mechanical response as described in (Ghodsi and Darvish, 2015). According to this theory, the strain time history was assumed to consist of two separable functions, a steady-state strain which was only a function of force $\varepsilon_\infty(F)$ and a reduced creep function of time $J(t)$.

$$\varepsilon(t, F) = J(t)\varepsilon_\infty(F)$$

3

The form of these functions was determined based on the simulation results and are explained in the Results section.

3. Results

3.1. Creep responses of micro-fibril and cross-link

A comparison of micro-fibril responses for different sizes is given in **Figure 2**. For simplicity, three force levels of 100, 500, and 1000 pN were selected for this comparison. It can be seen that the steady-state strain increased for higher input forces and it was less for larger molecule sizes. The difference in the asymptotic strain at one force level was due to the cross-link. The deformation in the cross-link region was the same at each force level, while the deformation in each collagen molecule segment was proportional to the length. Thus, the effect of the linear displacement in the cross-link region was more pronounced in the shorter micro-fibril segments and resulted in a higher overall strain. The creep responses of only the cross-link region for the six input force levels are shown in **Figure 3a**. These curves were obtained from the quarter-size micro-fibril.

3.2. Creep behavior of Cross-link region

Based on the curves in **Figure 3a**, the steady-state strain versus force was plotted (**Figure 3b**) and a bilinear function, in the form of **equation 4**, was fitted to the results with 500 pN force considered to be the cut-off force.

$$\varepsilon_{cl}^\infty(F) = \begin{cases} A_1 F & F \leq 500 \text{ pN} \\ A_2 F + A_3 & F > 500 \text{ pN} \end{cases}$$

4

in which the coefficients were determined as: $A_1 = (3.383 \pm 0.188) \times 10^{-3} \text{ pN}^{-1}$ for the first slope, $A_2 = (7.741 \pm 9.019) \times 10^{-4} \text{ pN}^{-1}$ for the second slope, and $A_3 = 1.325 \pm 1.194$ with $R^2 = 0.997$ and 0.992 , respectively. To explain the nature of the bilinear **equation 4**, snapshots of the cross-link region at the steady-state strain under the application of different forces were studied

(Figure 3c). It was evident that for force levels lower than 500 pN, the cross-link region was still in the unwinding process while beyond this force, the telopeptide and Lys-Lys cross-link formed a chain that deformed mainly at the level of the covalent bonds of the backbone. This would result in a higher stiffness, which can explain the change in the slope after 500 pN.

The strain-time curves were normalized based on their maximum value (Figure 4a) and they showed that after about 0.7 ns the steady-state strain was reached. It was found that the growth of the creep response started after some delay, which was more pronounced at lower forces. This delay could be partly attributed to the time that was required for the force wave to propagate from one end of the molecule (C-terminal) to the other end (N-terminal). Another contributing factor to the delay could be the curved structure of the molecule that partially unwound due to the applied force. In order to isolate the creep response from the wave propagation effect, the delay times were determined and removed to align the reduced creep functions for different force levels (Figure 4b). A single reduced creep function was assumed, in the following form

$$J(t) = 1 - \exp(-\beta t) \quad 5$$

and the growth rate β was determined based on least square minimization using Microsoft Excel Solver. Equation 5 was found to be a good representative of the creep behavior ($R^2 = 0.994$), and the obtained value for β was $6.286 \pm 0.695 \text{ ns}^{-1}$.

3.3. Propagation of Force Wave in Collagen Molecule

To investigate the factors contributing to the delay observed in the cross-link response, a series of SMD simulations on collagen segments with different lengths ($[(\text{GPO})_{21}]_3$, $[(\text{GPO})_{42}]_3$, $[(\text{GPO})_{85}]_3$, $[(\text{GPO})_{150}]_3$, and $[(\text{GPO})_{338}]_3$) were performed to characterize the speed of the force wave. In these simulations, a constant force of 10, 50, 100, 250, 500, or 1000 pN was applied at one end (three C α -atoms at the C-terminal) and the other end (the N-terminal) was free. The delay (time of travel) was found by subtracting the times when displacement started at the two terminals. To measure displacement the center of masses of the C α -atoms was used and to remove the noise, a moving average scheme with ten bins was employed. Figure 5a depicts snapshots of the SMD simulation on segment $[(\text{GPO})_{85}]_3$ under the application of 50 pN force which shows that after 0.2 ns the displacement at the free end is clearly visible. The displacement time histories at the two ends were plotted to find the exact delay (in figures similar to Figure 5b). This figure shows that for $[(\text{GPO})_{85}]_3$ the delay was about 0.07 ns. Based on the delays measured in different segment lengths, the velocity of force wave propagation v_m was calculated for each case (assuming constant velocity).

In order to be able to predict v_m for a given molecule size, a relationship between this velocity and the theoretical wave velocity was determined. It was shown in an earlier work (Young et al., 2013), that the velocity of propagation of longitudinal

waves in proteins could be estimated by the Newton-Laplace equation $v_t = \sqrt{E/\rho}$, in which E is the Young's modulus and ρ is the density of the molecule. This equation results from the solution of one-dimensional wave propagation in rods. For the ideal segments used in this study, $\rho = 1.00204 \times 10^{-3} \text{ Kg/m}^3$ and the Young's modulus was taken from the steady state creep responses reported in (Ghodsi and Darvish, 2015). The values of v_m versus v_t are depicted in Figure 6 and show a linear relationship between these quantities, which can be written as:

$$v_m = (0.803 \pm 0.073)v_t - (1080.1 \pm 305.2) \quad 6$$

Equation 6, together with Equations 4 and 5 fully characterize the mechanical behavior of the cross-link in a micro-fibril with different overall lengths.

3.4. Verification of the micro-fibril model

Models of the micro-fibrils with different lengths were formed by combining the models of two collagen segments from (Ghodsi and Darvish, 2015) and the model of the cross-link developed in this study. The properties (lengths and growth rates) used for the C-terminal and N-terminal segments are summarized in Table 1. The results of these (reduced) models were compared with the full MD simulation results of the corresponding micro-fibrils that are summarized in Figure 7, which show a good agreement across different sizes and forces with $R^2 > 0.988$. We considered this agreement as verification of the proposed reduced model of a micro-fibril as no further tuning of model parameters were implemented at this stage.

4. Discussion

A reduced viscoelastic model of a simplified collagen micro-fibril was developed that to the best of our knowledge has not been reported previously. This model was based on a combination of the viscoelastic models of molecule segments that were reported previously and a viscoelastic model of the cross-link that was developed in this study. The combined model revealed that the propagation of force (force wave) was significant in the overall creep response of the micro-fibril. This wave could be modeled with several discrete masses along the length of the molecule, which would result in a large number of degrees of freedom (DOF). Instead, for simplicity, the effect of the force wave was lumped into a delay parameter for each molecule. A discrete model representation of the micro-fibril reduced model (Figure 8) consists of 3 DOF. The N-terminal molecule is connected in series (share the same force) with the cross-link region and the C-terminal molecule. The delay (δ), due to the force wave propagation in the N-terminal molecule, is added in series to the cross-link region and the C-terminal molecule responses. The collagen molecule segment is represented approximately by a generalized Voigt model as discussed in (Ghodsi and Darvish,

2015). As the length of the segment is increased, the effective viscosity is increased, which is represented by additional parallel dashpots. The cross-link region is also represented by a Voigt model.

While the reduced model could be verified based on creep SMD simulations of micro-fibrils with different lengths, it could not be completely validated due to lack of comparable experimental data. The elastic response was validated by comparing the steady-state Young's modulus of the micro-fibril model with the available experimental data (Sasaki and Odajima, 1996a; Shen et al., 2008; Svensson et al., 2010a, 2010b). Since the viscoelastic model in this study was nonlinear (QLV), the steady-state Young's modulus increased with the applied force and was in the range of 2.24 – 3.27 GPa. The creep response time constant (inverse of the growth rate) was compared with available experimental results. The available experimental values are summarized in [Table 2](#). It is important to note that this validation can be at most qualitative because the model of micro-fibril simulated in this study consisted of only two idealized collagen segments and a cross-link while in the experimental studies, longer fibrils were extracted from real tissues. It is evident that the test method has a significant effect on the reported values of the Young's modulus with the X-ray diffraction and MEMS testing resulting in values that were one order of magnitude lower than the ones obtained using AFM testing. The values determined from AFM testing were closer to the values found in this study. A difference of several orders of magnitudes was observed between the creep time constant of the present work and the time constant of Shen et al. work. This discrepancy can be attributed to the simplified damping mechanism in the model and the fact that in the experiments, the input force is applied gradually (in the order of milliseconds to seconds) while the force in SMD simulations is applied instantaneously. The obtained range Young's modulus and the time constant of the micro-fibril were in good agreement with other computational studies on collagen molecule and fibril. Gautieri et al. estimated the time constant and Young's modulus of collagen fibril to be approximately 0.5×10^{-9} s and 6.0 GPa respectively (Gautieri et al., 2013).

The molecule force wave propagation speed given in [Equation 6](#) showed that v_m was about 0.3 to 0.7 times v_t depending on the force level ([Figure 6](#)). The fact that v_m was always less than the corresponding v_t can be partly explained by the three-dimensional geometry of the molecule and its interaction with the surrounding water molecules. A one-dimensional bar model for wave propagation is idealized and does not include the three-dimensional intertwined triple helix of collagen. It has been shown that different structures in proteins may provide different pathways for the force wave to propagate, resulting in different wave speeds (Young et al., 2013). As collagen molecule elongates, formation and rupture of hydrogen bonds may occur between the surrounding water molecules and collagen chains and also within the collagen chains (Ghodsi and Darvish, 2015). It has been shown that hydrogen bonds can play a significant dissipating role in the energy transfer in proteins (Ghodsi and Kazemi, 2011; Xu and Buehler, 2010). It can therefore be concluded that the three-dimensional molecule would be a dispersive system

and it is expected that the group velocity of wave propagation (the velocity at which the wave packets are transferred) would be smaller than the phase velocity (the velocity at which the wave peaks and troughs are moving) (Whitham, 1974). In the 1D elastic model, both of these velocities are the same (v_t) while the measured velocity v_m from SMD simulations is the group velocity. The other factor contributing to the observed delay could be the unwinding of the triple-helix structure. The test, performed in Section 3.3 to study the delay times in a simple collagen molecule can be modified to assess the contribution of the unwinding of the triple-helix and its curved structure on the delay times. For example, the collagen molecule can first be stretched until it is completely unwound and straightened, and then this molecule can be used to estimate the delay that is only due to wave propagation.

A limitation of this study is that only one type of cross-link was modeled. In addition to the type of cross-link (e.g., lysyl-based and hydroxylysyl-based), its maturity level (e.g., divalent and trivalent) would also affect the mechanical behavior of the collagen fibril (Eyre et al., 2008). Nevertheless, it is expected that different types of cross-link would have qualitatively similar mechanical behavior as the one studied in this study. To study the effect of maturity, the micro-fibril model should generally be expanded to a fibril model with more than two collagen molecules. Another limitation is that the collagen molecules used in this study were idealized. However, the same methodology can be applied to collagen molecules with the real amino acid sequence to obtain the corresponding reduced models.

Finally, it should be noted that this study is a preliminary step toward modeling of a complete collagen micro-fibril structure. A complete micro-fibril consists of five collagen molecules packed together in a staggered form. In such structure, water molecules may get trapped between the collagen molecules. These trapped water molecules, as well as the lateral interaction of the five collagen molecules, generate additional viscosity that was not considered in the present study (Gautieri et al., 2012a).

5. Conclusions

The creep response of a simple micro-fibril model was studied by performing SMD simulations. From the strain growth curves, the time-dependent behavior of the cross-link region was modeled using a QLV model. The optimized viscoelastic parameters were added to our previously developed model for collagen molecule, to describe the viscoelastic behavior of the micro-fibril. The micro-fibril steady-state Young's modulus was found to be in the range of 2.24 to 3.27 GPa which is in agreement with previous experimental studies. It was shown that quantifying the propagation of force wave in the molecule is essential to expand the reduced model of the molecule to the micro-fibril level. The speed of this wave was determined to be

correlated with the theoretical value based on the theory of wave propagation in rods. The effect of wave propagation was added as a delay parameter in the reduced model of the micro-fibril which allowed this model to have only three degrees of freedom.

The reduced model reported here would open up several possibilities for future work, particularly at the fibrillar scale. The proposed model can be expanded to the fibril geometry at the length scale of a few micrometers, at which, several experimental studies are available for model validation. Additionally, there are other types of cross-links reported in collagen fibrils and the same methodology used in this study may be applied to investigate their role in the structural integrity of collagen fibrils.

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Tables:

Table 1. Micro-fibril models parameters. L represents the length of each segment and β is the creep growth rate.

Name	C-terminal segment			N-terminal segment		
	Structure	$L(\text{\AA})$	$\beta(\text{ns}^{-1})$	Structure	$L(\text{\AA})$	$\beta(\text{ns}^{-1})$
4X-XL-4X	$[(\text{GPO})_{85}]_3$	734	12.95	$[(\text{GPO})_{56}]_3$	483	22.09
8X-XL-8X	$[(\text{GPO})_{170}]_3$	1467	5.327	$[(\text{GPO})_{141}]_3$	1217	6.77
16X-XL-16X	$[(\text{GPO})_{338}]_3$	2917	2.208	$[(\text{GPO})_{309}]_3$	2667	2.478

Table 2: Comparison of the results of this study with the available experimental studies

Approach	Length (m)	Young's modulus (GPa)	Time constant τ (s)
X-ray diffraction (Sasaki and Odajima, 1996b)	$\approx 4.0 \times 10^{-2}$	0.43	not reported
MEMS testing (Shen et al., 2008)	$\approx 1.0 \times 10^{-4}$	0.86 ± 0.45	5.0 – 6.0
AFM testing (Svensson et al., 2010a)	1.93×10^{-4}	2.89 ± 0.23	not reported
AFM testing (Svensson et al., 2010b)	$\approx 2.0 \times 10^{-4}$	1.87 – 1.94	not reported
Present work (Steady-State)	5.58×10^{-6}	2.24 – 3.27	0.45×10^{-9}

Figures:

Figure 1: **(a)** Cross-link assembly representations. **(b)** The cross-linking atomic structure. **(c)** Atomistic presentation of the cross-link used in this study. **(d)** Definition of tensile strain in micro-fibril [(GPO)₈₅]. **(e)** A shearing strain was used for the measurement of strain in the cross-link region.

Figure 2: Creep response of micro-fibrils 4X-XL-4X, 8X-XL-8X, and 16X-XL-16X

Figure 3: **(a)** Creep response of the cross-link region for Case I. **(b)** Steady-state creep response of the cross-link. A bilinear function was found to be sufficient to capture the creep response. **(c)** Snapshots of the cross-link region at the steady-state strain under the application of different forces. It can be seen that for force levels lower than 500 pN, the cross-link region is still in the unwinding process while as the force goes higher the telopeptide and Lys-Lys cross-link form a chain that responds mainly with the covalent bonds of the backbone.

Figure 4: Normalized creep response (4X-XL-4X) **(a)** The delay time prior to the main response is visible for lower force levels **(b)** The creep response after removing the delay. Reduced creep functions were fitted on the results.

Figure 5: **(a)** Snapshots of the collagen segment $[(\text{GPO})_{85}]_3$ while being stretched by 50 pN force. In this case, it took about 0.1 ns for the force wave to travel through the molecule and reach the free end. **(b)** The displacements at the two ends of the collagen segment. The blue and green dots are the observed displacement at the 3 rightmost and leftmost $\text{C}\alpha$ -atoms, respectively. Solid lines represent the moving average of the respective displacement

Figure 6: Comparison between force propagation velocities obtained from the theory (v_t) and direct MD simulations (v_m) for different applied forces.

Figure 7: Strains calculated from the micro-fibril model (red lines), verified by comparing with the strains obtained from the SMD simulations on the actual micro-fibrils.

Figure 8: Schematic discrete representation of the micro-fibril model. δ represents the delay due to propagation of force wave (from right to left) along the molecule.