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Research paper

Equivalent mechanical properties of biological membranes from lattice homogenization

M. Assidi[1], *F. Dos Reis*, *J.-F. Ganghoffer*[*]

Laboratoire d'Énergétique et de Mécanique Théorique et Appliquée, École Nationale Supérieure d'Électricité et de Mécanique, UMR 7563, ENSEM-INPL, 2, Avenue de la Forêt de Haye, BP 160, 54054 Vandoeuvre CEDEX, France

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ABSTRACT

The goal of this manuscript is to set up a novel methodology for the calculation of the effective mechanical properties of biological membranes viewed as repetitive networks of elastic filaments, based on the discrete asymptotic homogenization method. We will show that for some lattice configurations, flexional effects due to internal structure mechanisms at the unit cell scale lead to additional flexional effects at the continuum scale, accounted for by an internal length associated to a micropolar behavior. Thereby, a systematic methodology is established, allowing the prediction of the overall mechanical properties of biological membranes for a given network topology, as closed form expressions of the geometrical and mechanical micro-parameters. The peptidoglycan and the erythrocyte have been analyzed using this methodology, and their effective moduli are calculated and recorded versus the geometrical and mechanical lattice parameters. A classification of lattices with respect to the choice of the equivalent continuum model is proposed: The Cauchy continuum and a micropolar continuum are adopted as two possible effective medium, for a given beam model. The relative ratio of the characteristic length of the micropolar continuum to the unit cell size determines the relevant choice of the equivalent medium. In most cases, the Cauchy continuum is sufficient to model membranes in most of their configurations. The peptidoglycan network may exhibit a re-entrant hexagonal lattice, for which micropolar effects become important. This is attested by the characteristic length becoming larger than the beam length for such configurations. The homogenized moduli give accurate results for both membranes, as revealed by comparison with experimental measurements or simulation results from the literature at the network scale. A first insight into the nonlinear mechanical behavior of the hexagonal and triangular networks is lastly investigated using a perturbative method.

1. Introduction

The membrane of biological cells is made of the assembly of filaments which are linked together as part of a network or are associated with the cell membrane to build a two-dimensional thin sheet. Two-dimensional biological networks may be wrapped around a cell as its wall or attached to its plasma or nuclear membrane. Structural elements

[*] *Corresponding address:* ENSEM-INPL, 2 Avenue de la Forêt de Haye, 54500 Vandoeuvre-Les-Nancy, France. Tel.: +33 3 83 59 57 24; fax: 33 3 83 59 55 51.

E-mail addresses: mohamed.assidi@gmail.com (M. Assidi), francisco.dos-reis@wanadoo.fr (F. Dos Reis), jean-francois.ganghoffer@ensem.inpl-nancy.fr (J.-F. Ganghoffer).

[1] Tel.: +33 621345616.

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of biological cells are soft and responsible for the large deformability and easy motion of the cell, contrary to most of the engineered man-made thin structural materials. The mechanics of biological membranes is clearly related to the network architecture and to the elasticity of the building entities of the network, which are known to obey entropic elasticity. The main originality advocated in this work (compared to the literature works referenced before) is the explicit derivation of the full stiffness matrix of biological membranes, viewed as planar repetitive networks of connected threads, as closed form expressions of the geometrical and mechanical micro-parameters of the underlying network. Moreover, we shall justify the use of continuum models with an enriched kinematics such as micropolar continua according to length scale considerations. As a third novel aspect, the construction of the effective mechanical response in the large strain regime using the same homogenization technique will be done. The development of predictive nanomechanical models aiming at understanding the impact of the network architecture and mechanical properties on the continuum scale is important, as the experimental determination of the mechanical properties of biological membranes is delicate, and the membrane anisotropy and large deformability have to be accounted for, Boey et al. (1998), Discher et al. (1998). As stated in Lim et al. (2006), mechanical models for cells are derived using either the micro/nanostructural approach or the continuum one. Although providing less insight into detailed molecular mechanical events and biochemical couplings, the continuum approach is easier and more straightforward to use in computing the mechanical properties of the cell and its response under biomechanical loading. Moreover, the established continuum mechanical model can provide details on the distribution of stress and strains induced in the cell and can be integrated in finite element simulations at the scale of the whole cell. However, the identification of the continuum behavior of a membrane is challenging, as it may be highly anisotropic due to unequal chain length and properties of the threads within the molecular network may vary; furthermore, biological membranes are prone to large distensions and one should ideally consider nonlinear effects. Hence, micromechanical approaches are needed in order to bridge the scales and to provide a constitutive law at a continuum scale, whereby the equivalent continuum properties are related to both the geometrical and mechanical nanostructural parameters of the network. The derivation of the equivalent mechanical properties of cellular biological structures is also interesting in order to understand the somewhat peculiar observed behavior (anisotropy, negative Poisson's ratio, (Boal et al., 1993)) and to possibly evaluate the load bearing capacity of the membrane architecture. Especially, closed form expressions of those effective properties would allow relating the mesoscopic to the maroscopic level, to understand the nanoscale origin of the mechanical behavior of the membrane wall, and to assess the effect of the membrane topology (comparison of different membrane architectures will be possible).

We shall employ the so-called discrete asymptotic homogenization technique as in Caillerie et al. (2006), which is perfectly suited to the discrete architecture of the membrane at the nano-level. Two types of equivalent continuum shall be considered, a classical Cauchy continuum and a micropolar medium, according to the value of a characteristic micropolar length. This last aspect constitutes the main and novel thrust of this contribution, especially when considering biological membranes.

2. Impact of microstructural irregularity

Homogenization techniques for discrete media have been extensively used in the last decade, but they have a significant limitation in that they do not account for natural variations in the lattice topology, which are observed for most biological materials. Most models of 2D cellular structures are based on idealized unit cells intended to describe the micro-structural features of an average cell supposed to be representative of the real underlying structure. Those approaches do however not account for the complex and rather diverse mechanisms leading to membrane rearrangements usually referred to as remodeling; those mechanisms involving a complex machinery of proteins can be broadly classified as fusion or fission, including exocytosis and endocytosis, budding and fusion of transport carriers, relaxation of the elastic energy, as listed in the recent review paper (Kozlov et al., 2010).

The network topology may also vary as abnormal RBC skeletons have been reported, Hansen et al. (1997). Those variations lead to irregular cells and to non-periodic arrangement of the cell walls. Therefore, a quantitative study to investigate how the micro-structural variability can affect the macroscopic effective mechanical properties has been performed as a preliminary step. Statistical variations in the underlying models have been accounted for (Silva et al., 1995; Silva and Gibson, 1997; Zhu et al., 2001; Alkhader and Vural, 2008). Several methods described in Kraynik et al. (1991) account for a variability in the arrangement of cell walls of hexagonal honeycombs by modifying the initial two-dimensional unit cell analysis, Warren and Kraynik (1987). Those authors develop structure-property relationships for arrays of hexagonal cells endowed with varying sizes and shapes, but they conserve an angle of 120° between the three struts common to each node. The results of those authors lead to the conclusion that the specific spatial arrangement and size distribution of the unit cells hardly affect their elastic response.

In order to generate a microstructural irregularity (or non-periodicity), a spatial perturbation has been applied to the vertices of a regular triangular truss network in random directions (Der Burg et al., 1997; Chen et al., 1999; Chen and Fleck, 2002; Alkhader and Vural, 2008), expressed by the following equations:

$$\chi_i' = \chi_i + \lambda r \cos(\theta) \qquad \gamma_i' = \gamma_i + \lambda r \sin(\theta) \tag{1}$$

where θ is a uniformly distributed random variable, r is a random variable and χ_i' and γ_i' are the perturbed coordinates, with the non primed component being the original coordinates. λ is the perturbation parameter which specifies the degree of irregularity; note that it has been chosen in a manner that cell convexity is preserved. Fig. 1 shows different cellular structures generated for different values of λ. Each topology is 9×9