We introduce here a numerical taxonomy procedure for clustering pattern sets using their approximated Minkowski functionals. We demonstrate that this procedure is robust in distinguishing different spatial processes, even when the number of points in the patterns are small, vary wildly from pattern to pattern, or when the patterns are drawn from very similar processes. We then place this routine in a quantitative biology context by analyzing two point pattern sets of fluorescently labeled inter-cellular proteins, LAT and TAC, that have been acquired from experiments with immune cells. Overall, we find that this routine is a robust method for distinguishing point pattern sets, and provides meaningful insight regarding the homogeneity of a spatial process.

Simple Stochastic Models for Cell Division
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The experimental measurements show that probability density function for cell generation times in mitosis is non-exponential and goes through the maximum meaning that the rate of cell division depends on the age of cells (the time since their birth). The standard Gillespie approach based on the assumption of time independent rate constants is not applicable to model the cell division process. We are aimed to construct the simple model which considers the cell division as a stochastic process. The probability per unit time that a cell undergoes mitosis is time-dependent function that accounts for the typical generation time distributions.

The simulations give results analogous to the solution of the von Foerster equation. In addition, we consider the loss of the cells due to their death which is taken as an age-independent process. The simulations enable to establish the relationship between the average generation time and the growth curves for the cell populations and the ones defined by probability density functions. We find how the average net growth rate for the cell populations scales with the different death rates.

We characterize the exponential growth of cell populations by the deviations from the average by the respective dispersions $\sigma^2$ which are found also to grow exponentially with time. However, the relative standard deviation, i.e., the ratio of $\sigma$ to the average size of population converges quickly to a constant value that depends on the spread of generation time distribution. The more narrow spread of generation times for the same average generation times yields the smaller variations in sizes for the growing cell populations. The model is generalized for the case that involves the transformation of one type of cells to another in addition to cell reproduction of both types.

An Improved Non-Affine Arruda-Boyce Type Constitutive Model for Bio-polymer Networks
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This work investigates, by means of computational modeling, the mechanical properties of soft collagen tissues on the basis of elasticity theory. Bio-polymer networks are structurally disordered and thus compelled to deform non-affine. To capture that in our computational modeling, we supplement the well-known affine Arruda-Boyce model with positional disorder and compute the resultant changes in mechanical response.

We characterize this mechanical behavior as a response to various homogeneous deformations in 3D networks, assuming different constitutive behavior for the individual fibers (in the small deformations linear regime, hookean springs under the entropic elasticity assumption, and in the nonlinear regime freely-jointed and worm-like chains), as well as different coordination numbers (4, 6 or 8 chains connecting at each cross linking point) of the resulting fiber networks. Furthermore we compare the moduli of the simulated network structures with their affine deformed counterparts.

Previous work has clearly demonstrated that non-affine deformation modes in elastic (bio)polymer networks greatly affect their mechanics. As the original Arruda-Boyce model can be represented with a particular form of strain-energy function that is micro-mechanically motivated, incorporation of the non-affinity yields amended predictions of the macroscopic mechanical behavior of soft fibrous networks, based on an improved representation of microscopic network structure and deformations. We show that shear and bulk moduli in the Arruda-Boyce model can be as off as 30% when compared with the shear and bulk moduli in the non-affine model.

This entire evaluation of the ways non-affinity enhances the well known Arruda-Boyce model sets the groundwork for developing accurate constitutive relations for fibrous biological materials, for use in finite element analysis of soft tissues.