Read_Me file for plotting Velocity-Velocity Correlation Functions

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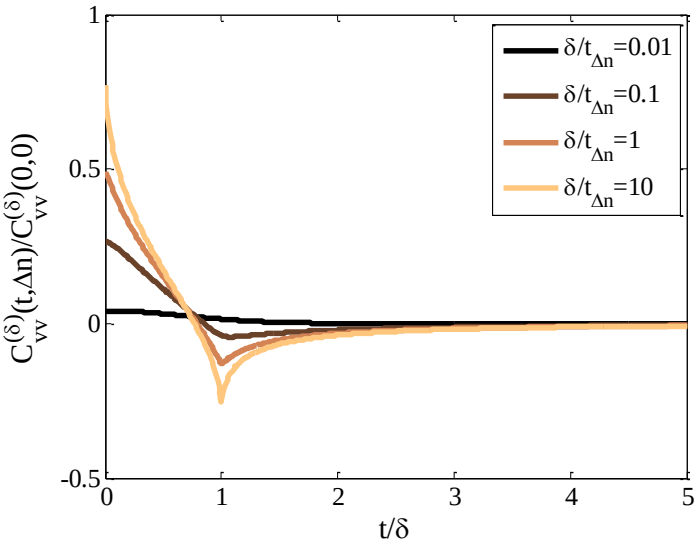
This package contains the scripts plot_vel_corr.mat, calc_vel_corr.mat, and a folder containing the numerical tables of calculated correlation values. The numerical tables are calculated as described in [1] and represent the theoretical prediction for the velocity correlations between polymer segments before the chain end effects manifest (ie, for times much less than the whole polymer relaxation timescale). The specific model chosen is a Rouse polymer in a viscoelastic medium, which describes the motion of chromosome loci in live cells [1,2].

The script calc_vel_corr.mat calculates the normalized velocity-velocity correlation function curves for the given parameters using interpolation on the numerical tables. The user only needs to access the plot_vel_corr.mat script, where they can change three sets of parameters: “alpha”, “delta_range”, and “plot_range”. “alpha” should be a number between 0.25 and 1. “alpha” is the power law exponent associated with the mean square displacement of a particle in a viscoelastic medium. “delta_range” is the set of delta/t_(delta n) values that you wish to examine. “delta_range” should be a vector whose values lie between 10^-3 and 10^3. “plot_range” is the x-axis range of the plot for t/delta. This should be a 2 element vector whose minimum is greater than or equal to 0 and whose maximum is less than or equal to 5. If no value is defined when calling calc_vel_corr, the default value is [0 5].

Below is an example plot using the default values entered in the plot_vel_corr.mat script:



1. T.J. Lampo, A.S Kennard, and A.J. Spakowitz “Physical modeling of dynamic coupling between chromosome loci”. Biophys. J., accepted. (2015).
2. S.C. Weber, A.J. Spakowitz, and J.A. Theriot “Bacterial chromosomal loci move subdiffusively through a viscoelastic cytoplasm” Phys. Rev. Lett. 104:238012 (2010).