

Instructions for using the MSD-Bayes package

1. Create a matrix containing the values in the MSD curves for which you wish to obtain a model probability. Each MSD curve must be a column of the matrix. (Typically at least 4-5 curves are needed to obtain a non-singular estimate of the covariance matrix, and 10 curves is preferred. Please see Monnier et al, *Biophysical Journal* 2012 for more information on the method.)
2. Create a vector (with length equal to the number of rows in the MSD curves matrix) containing the values of the time lags (e.g. in seconds) corresponding to the above MSD values.
3. Set parameters for the Bayesian inference procedure, or use default values. Typically a user would only specify the set of motion models to be tested, which can include the following: 'D' = pure diffusion model; 'DA' = anomalous diffusion model; 'DR' = confined diffusion model; 'V' = pure flow (directed motion) model; 'DV' = diffusion plus flow; 'DAV' = anomalous diffusion plus flow; 'DRV' = confined diffusion plus flow; 'N' = null or stationary-particle model (constant model). If your MSD curves contain significant localization error, an 'E' can also be added to the end of any of the above models (except the null model) to include an additional constant term in the fit model (e.g. 'DE' = pure diffusion plus constant term model). The set of motion models should be specified as a cell array of strings, contained in a field called 'models' of the parameter structure array. For example, set the models as follows:

```
msd_params.models = {'N', 'D', 'DA', 'DR', 'V', 'DV', 'DAV', 'DRV'};
```

4. Run Bayesian inference by calling the function 'msd_curves_bayes' as follows:

```
results = msd_curves_bayes(timelags, MSD_curves, msd_params);
```

5. The results structure contains the model probabilities and parameter estimates in the following fields:

<code>results.mean_curve.D.PrM;</code>	This is the probability of the D model. Simply replace the D with any of the other model abbreviations above to get their probabilities.
<code>results.mean_curve.DA.D;</code> <code>results.mean_curve.DA.A;</code>	These are the fit parameter values for the DA model, D for the diffusion coefficient and A for the anomalous exponent. Other fit parameters can be found similarly, by using the appropriate model abbreviation and parameter abbreviations (V for velocity, R for confinement radius, E for localization error, and C for the constant term in the null model).