General histogram function: hist (FileName, InitialTime, FinalTime)

Description: This function enables users to obtain a histogram during a certain time period.

Parameters:

* FileName

Acceptable value: String (Must provide)

Description: It is the path to the file (.dat), which is usually named as ‘histogram\_complexes\_time.dat’, representing the histogram data to be analyzed.

Sample: FileName = /Users/UserName/Documents/histogram\_complexes\_time.dat

* InitialTime

Acceptable value: Float (Must provide)

Unit: s

Description: It is the initial time that users desire to examine and plot on the histogram. The acceptable range should not smaller than the starting time or exceed the ending time of simulation.

Sample: InitialTime = 0.5

Note: If the InitialTime and FinalTime both input as -1, the entire time range indicated in the reading(.dat) file will be taken as input.

* FinalTime

Acceptable value: Float (Must provide)

Unit: s

Description: It is the final time that users desire to examine and plot on the histogram. The acceptable range should not smaller than the value of InitialTime or exceed the ending time of simulation.

Sample: FinalTime = 1.0

Note: If the InitialTime and FinalTime both input as -1, the entire time range indicated in the reading(.dat) file will be taken as input.

Histogram function for maximum number of monomers: hist\_max (FileName, InitialTime, FinalTime)

Description: This function enables users to obtain a histogram (# of molecules vs. time) of maximum number of monomers in single molecule during a certain time period.

Parameters:

* FileName

Acceptable value: String (Must provide)

Description: It is the path to the file (.dat), which is usually named as ‘histogram\_complexes\_time.dat’, representing the histogram data to be analyzed.

Sample: FileName = /Users/UserName/Documents/histogram\_complexes\_time.dat

* InitialTime

Acceptable value: Float (Must provide)

Unit: s

Description: It is the initial time that users desire to examine and plot on the histogram. The acceptable range should not smaller than the starting time or exceed the ending time of simulation.

Sample: InitialTime = 0.5

Note: If the InitialTime and FinalTime both input as -1, the entire time range indicated in the reading(.dat) file will be taken as input.

* FinalTime

Acceptable value: Float (Must provide)

Unit: s

Description: It is the final time that users desire to examine and plot on the histogram. The acceptable range should not smaller than the value of InitialTime or exceed the ending time of simulation.

Sample: FinalTime = 1.0

Note: If the InitialTime and FinalTime both input as -1, the entire time range indicated in the reading(.dat) file will be taken as input.

Histogram function for average number of monomers: hist\_mean (FileName, InitialTime, FinalTime, ExcludeMono)

Description: This function enables users to obtain a histogram (# of molecules vs. time) of mean number of monomers in single molecule during a certain time period.

Parameters:

* FileName

Acceptable value: String (Must provide)

Description: It is the path to the file (.dat), which is usually named as ‘histogram\_complexes\_time.dat’, representing the histogram data to be analyzed.

Sample: FileName = /Users/UserName/Documents/histogram\_complexes\_time.dat

* InitialTime

Acceptable value: Float (Must provide)

Unit: s

Description: It is the initial time that users desire to examine and plot on the histogram. The acceptable range should not smaller than the starting time or exceed the ending time of simulation.

Sample: InitialTime = 0.5

Note: If the InitialTime and FinalTime both input as -1, the entire time range indicated in the reading(.dat) file will be taken as input.

* FinalTime

Acceptable value: Float (Must provide)

Unit: s

Description: It is the final time that users desire to examine and plot on the histogram. The acceptable range should not smaller than the value of InitialTime or exceed the ending time of simulation.

Sample: FinalTime = 1.0

Note: If the InitialTime and FinalTime both input as -1, the entire time range indicated in the reading(.dat) file will be taken as input.

* ExcludeMono

Acceptable value: True or False (Optional)

Default: False

Description: Is monomers excluded from the counting when plotting the mean number of molecules.

Sample: ExcludeMono = True