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## GENERAL INFORMATION

1. Title of Dataset: **“The role of the Arp2/3 complex in shaping the dynamics and structures of branched actomyosin networks”**

2. Author Information

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3. We thank Garyk Papoian and his group for sharing the MEDYAN code with us. The assistance of James Komianos and Aravind Chandrasekaran in implementing Arp2/3 branchers into the code is greatly appreciated. This work was supported by the National Science Foundation Grants CHE 1743392, PHY 1522550, and the Center for Theoretical Biological Physics PHY 1427654. The authors acknowledged the use of the uHPC OAC 1531814 and Sabine clusters managed by the Core facility for Advanced Computing and Data Science at the University of Houston. Additional support was also provided by the D.R. Bullard-

Welch Chair at Rice University, Grant C-0016 and an endowment from the William Wheless III Professorship at UT Health Science Center at Houston.

## DATA & FILE OVERVIEW

### 1. File List:

#### a. CBS\_MX\_LY\_RepZ folders

CBS\_MX\_LY\_RepZ folders contain all simulation data including simulation inputs and trajectories. X signifies the number of motors in the simulation. Y signifies the number of linkers in the simulation. Z signifies the repetition ID. For example, CBS\_M16\_L3000\_Rep5 indicates that the folder contains a simulation with 16 ensemble motors and 3000 linkers. Also, this simulation is the fifth repetition of its kind.

#### b. systeminput.txt, chemistryinput.txt, and restartoutput.txt

systeminput.txt, chemistryinput.txt, and restartoutput.txt files contain the input files for each individual trajectory. restartoutput.txt is only necessary for restart trajectories. For the syntax of these files, please refer to <http://medyan.org/docs/UsageGuide.pdf>.

#### c. birthtimes.traj, chemistry.traj, forces.traj snapshot.traj, and tensions.traj

These files contain the output for each individual trajectory. For the syntax of these files, please refer to <http://medyan.org/docs/UsageGuide.pdf>.

#### d. ClusterSizeDistribution.traj

This file contains the cluster size distribution output, including number of clusters connected by only actin filament and distribution of clusters connected only by actin filament, for each individual trajectory. The syntax of the file is as follows:

```
Frame      time      N_clusters      N_n      N_w      Biggest_cluster
N_clusters_only      N_clusters_f-b-l      N_clusters_f-b-m
N_clusters_f-b      Number_of_brancher_connection
Number_of_linker_connection      Number_of_motor_connection
MotorConnectivityChange      Cluster_distribution
ClusterDistribution_only      ClusterDistribution_f-b-l
ClusterDistribution_f-b-m      ClusterDistribution_f-b
```

#### e. snapshot\_complete.traj and chemistry\_complete.traj

snapshot\_complete.traj and chemistry\_complete.traj are concatenated trajectory files of snapshot.traj and chemistry.traj of a simulation, respectively.