Supplemental Materials

Molecular Biology of the Cell

Gros et al.

Legends for supplemental figures and videos

Supplemental Figure 1. All time points represent the time in phase III. (A) Traces of the distance between the centrosome and the synapse as a function of time in a model without any dynein molecules. Colors indicate different simulations. (B) Traces of the radial distance from the centrosome to the central axis of the cell as a function of time in a model without any dynein. Colors indicate different simulations. (C) Traces of the distance between the centrosome and the synapse as a function of time in a model without actin confining dynein to the synapse. In this model, dynein is attached to the surface of the MT-bounding volume and thus it is not in a separate space from the MTs.

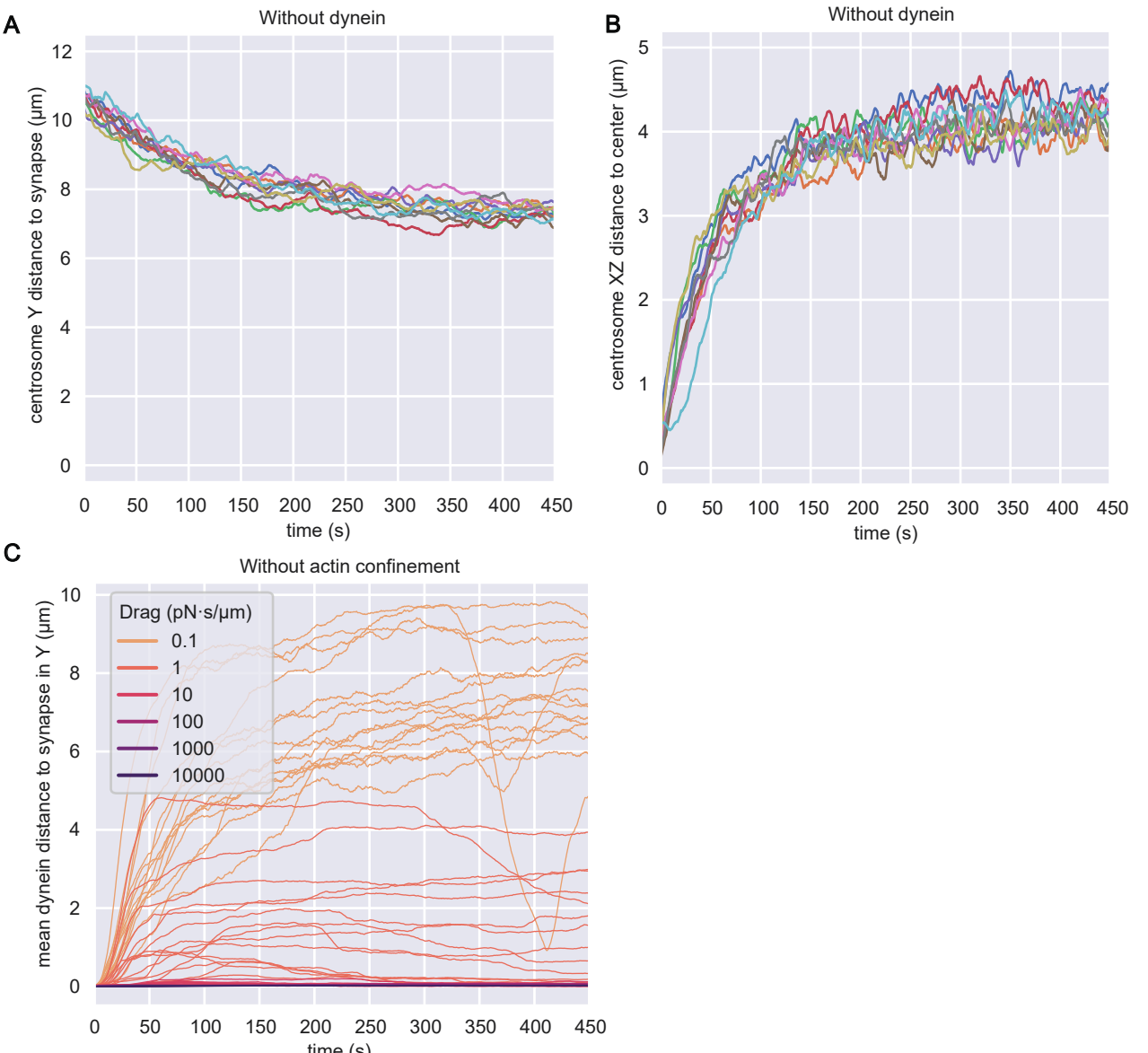
Supplemental Figure 2. Force in Y on dynein in phase III. The positions of dynein molecules at all time points in phase III are shown and the force magnitude in Y on dynein is encoded by the color gradient. A positive force is directed towards the centrosome, a negative force points into the membrane. The boundary of the 14 µm-diameter synapse is represented by a red circle and the boundary of the 8 µm diameter area of initialization by a red dashed line. This initialization area is roughly comparable to the edge of the MT binding region. Two example simulations per drag coefficient are shown in the two rows.

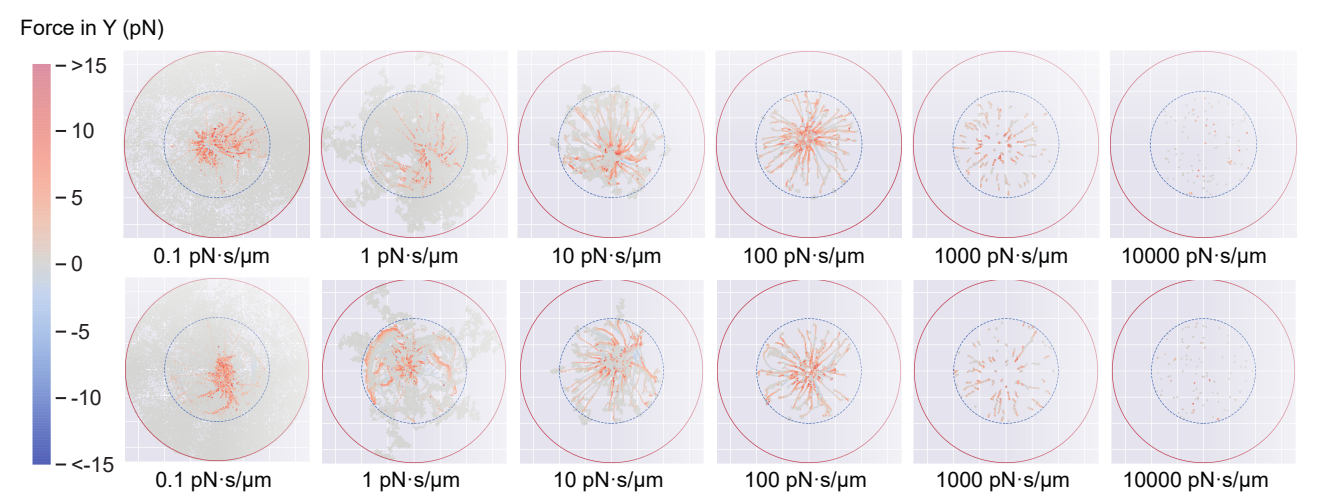
Supplemental Figure 3. All time points represent the time in phase III. (A) Traces of the position of the centrosome as a function of time in the in the XZ plane to the central axis for MT-capture-shrinkage dynein and in (B) for MT-sliding dynein. Different colors indicate different values of the unbinding rate k_{detach}. (C) The number of dynein molecules in the biggest cluster of dyneins as a function of time, for the runs with MT-sliding dynein. The colors encode different runs of our simulations. To reduce the noise, we average the trajectories over a window of 1.6 seconds and show the 95% confidence interval as the shaded area. For each panel we changed the numerical value of the unbinding rate as given on the top.

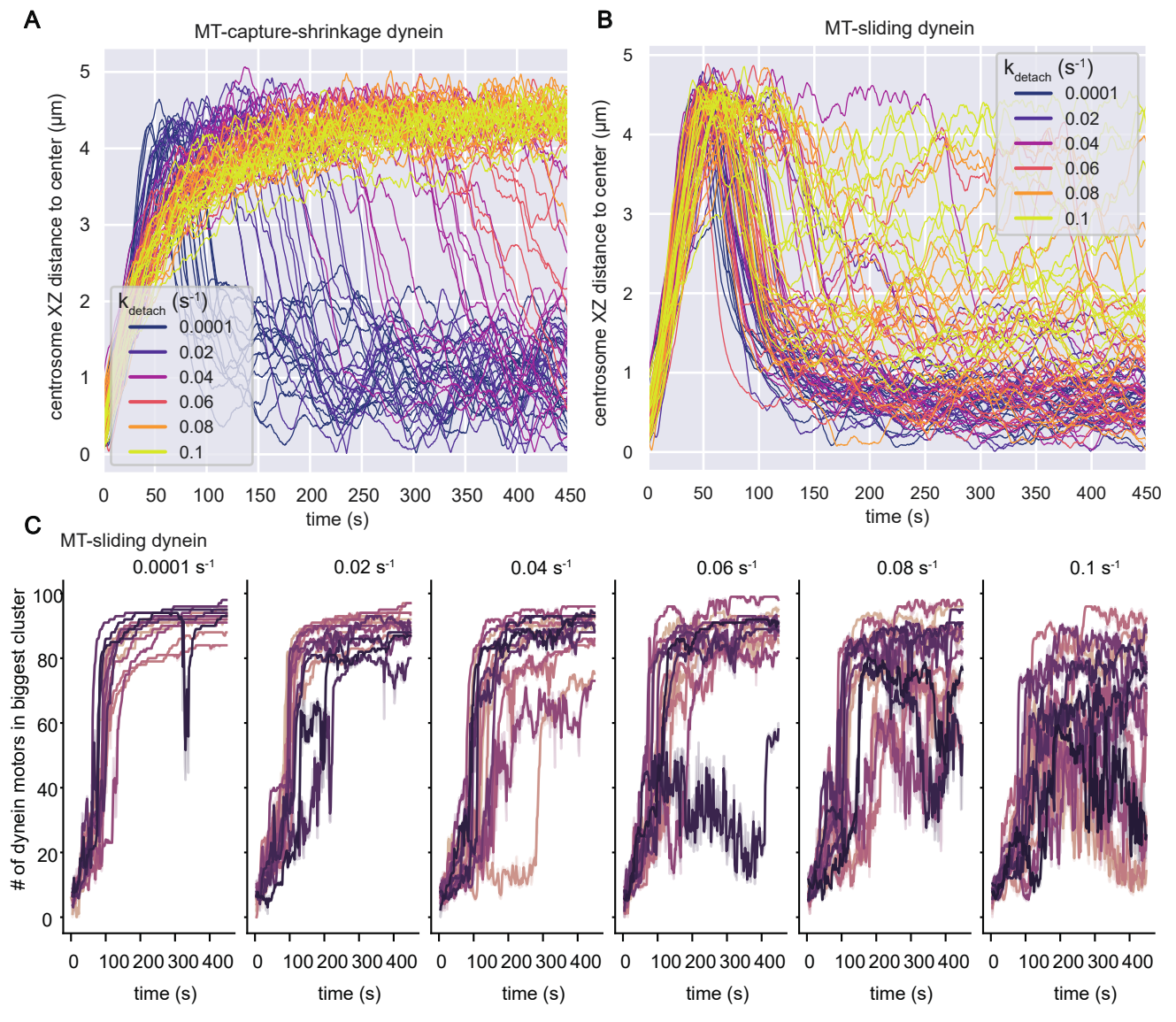
Supplemental Video V1 A side view of a full simulation run with 1 pN·s/µm drag on dynein, snapshots are shown in Figure 1E.

Supplemental Video V2 Views of phase III for all drag conditions, shown from under the synapse. The dynein movement of these runs is shown in the top row in Figure 3B.

Supplemental Video V3 Video showing the 3D volume of the TREx T cell data.


A
Without dynein
centrosome Y distance to synapse (µm)
time (s)
B
Without dynein
centrosome XZ distance to center (µm)
time (s)
C
Without actin confinement
mean dynein distance to synapse in Y (µm)
time (s)
Drag (pN·s/µm)
0.1
1
10
100
1000
10000


Force in Y (pN)
>15
10
5
0
-5
-10
<-15
0.1 pN·s/μm
1 pN·s/μm
10 pN·s/μm
100 pN·s/μm
1000 pN·s/μm
10000 pN·s/μm
0.1 pN·s/μm
1 pN·s/μm
10 pN·s/μm
100 pN·s/μm
1000 pN·s/μm
10000 pN·s/μm


A
MT-capture-shrinkage dynein
centrosome XZ distance to center (μm)
time (s)
k_detach (s^-1)
0.0001
0.02
0.04
0.06
0.08
0.1
B
MT-sliding dynein
centrosome XZ distance to center (μm)
time (s)
k_detach (s^-1)
0.0001
0.02
0.04
0.06
0.08
0.1
C
MT-sliding dynein
0.0001 s^-1
0.02 s^-1
0.04 s^-1
0.06 s^-1
0.08 s^-1
0.1 s^-1
# of dynein motors in biggest cluster
time (s)