

Example #1: Two-dimensional model | linear | I-BAR only | $\mu = +1.00$ | endpoint | see Fig. 2C

```

% geometry parameters
shape = 'flat';
shape_parameters = [];
m.L = 1240;
m.dL = 40;
m.width = m.dL;

% biological parameters
m.dh = 1;
m.D = 3;
m.stretch_modulus = 0;
m.rigidity = 50;
lbar.rigidity = 35;
Nbar.rigidity = 0;
m.c0 = 0;
lbar.c0 = -1/20;
Nbar.c0 = 1/20;
lbar.k1 = 0.11;
Nbar.k1 = 0.11;
lbar.k2 = 36;
Nbar.k2 = 36;
lbar.standard_state_concentration = 1;
Nbar.standard_state_concentration = 1;
lbar.mu0 = 0;
Nbar.mu0 = 0;
lbar.mu = 1.0;
Nbar.mu = -4.0;
% lbar.conc = 10;
% Nbar.conc = 10;
lbar.area = 50;
Nbar.area = 50;
actin.k_on = 0;
actin.k_off = 0;
actin.conc = 0.2412;
actin.dh = 2.7;
actin.start_position = -500;
lbar_start_saturation = 0;
Nbar_start_saturation = 0;

% numerical parameters
tend = 5000;
plot_on = true;
save_on = false;
plot_everyt = 5000;
plt.ylim = [-100 600];
plt.save_plt = true;
save_everyt = 2;

```

% Note: 240 nm are used to hold the membrane

% Note: rigidity 0 eliminates contribution of the N-BAR

% Note: -4.0 eliminates contribution of the N-BAR

% Note: eliminates contribution of actin

% Note: eliminates contribution of actin

% Note: membrane fluctuations will not interact with actin

% Note: decides the length of the simulation

% Note: plot intervals (here only endpoint)

% Note: if [] scale will auto-adjust

% Note: set to true for saving pictures

Example #2: Two-dimensional | circular | $\mu = +1.00$ | endpoint | see Fig. 2H

```

% biological parameters
m.R = 1000;           % Note: Radius (not diameter) of circle
m.dR = 40;
m.width = m.dR;
m.dh = 1;
m.D = 3;
m.stretch_modulus = 0;
m.rigidity = 50;
lbar.rigidity = 35;
Nbar.rigidity = 35;
m.c0 = 0;
lbar.c0 = -1/20;
Nbar.c0 = 1/20;
lbar.k1 = 0.11;
Nbar.k1 = 0.11;
lbar.k2 = 36;
Nbar.k2 = 36;
% lbar.conc = 10;
% Nbar.conc = 10;
lbar.standard_state_concentration = 1;
Nbar.standard_state_concentration = 1;
lbar.mu0 = 0;
Nbar.mu0 = 0;
lbar.area = 50;
Nbar.area = 50;
lbar.mu = 1.0;        % Note: concentration of I-BAR (=μ)
Nbar.mu = 1.0;        % Note: concentration of N-BAR (=μ)
actin.k_on = 0;       % Note: eliminates contribution of actin
actin.k_off = 0;      % Note: eliminates contribution of actin
actin.conc = 0.2412;
actin.dh = 2.7;
actin.start_position = -500;
lbar_start_saturation = 0;
Nbar_start_saturation = 0;

%% numerical parameters
tend = 300;
plot_on = true;
save_on = false;
plot_everyt = 300;
save_everyt = 2;
plt.save_plt = false;

```

Example #3: Two-dimensional | linear | with actin | $\mu = +2.50$ | endpoint | see Fig. 4B

```

% geometry parameters
shape = 'flat';
shape_parameters = [];
m.L = 2240; % % Note: 240 nm are used to hold the membrane
m.dL = 40; % initial submission = 15
m.width = m.dL;

% biological parameters
m.dh = 1;
m.D = 3;
m.stretch_modulus = 0;
m.rigidity = 50;
lbar.rigidity = 35;
Nbar.rigidity = 35;
m.c0 = 0;
lbar.c0 = -1/20;
Nbar.c0 = 1/20;
lbar.k1 = 0.11;
Nbar.k1 = 0.11;
lbar.k2 = 36;
Nbar.k2 = 36;
lbar.standard_state_concentration = 1;
Nbar.standard_state_concentration = 1;
lbar.mu0 = 0;
Nbar.mu0 = 0;
lbar.mu = 2.5; % Note: concentration of I-BAR (=μ)
Nbar.mu = 2.5; % Note: concentration of N-BAR (=μ)
% lbar.conc = 10;
% Nbar.conc = 10;
lbar.area = 50;
Nbar.area = 50;
actin.k_on = 11.6; % Note. Association rate of actin
actin.k_off = 1.4; % Note. Dissociation rate of actin
actin.conc = 0.2412; % Note. Concentration of actin
actin.dh = 2.7; % Note. Size of actin/2
actin.start_position = -0; % Note: Distance cytoskeleton to membrane
lbar_start_saturation = 0;
Nbar_start_saturation = 0;

% numerical parameters
tend = 300; % Note: Duration of simulation
plot_on = true;
save_on = false;
plot_everyt = 300;
plt.ylim = [-35 105]; % Note: Field of view (leave [] for auto-adjustment)
plt.save_plt = true; % Note: true = save pictures
save_everyt = 2; % Note: interval of saving

```