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Supplemental Information

Diffusion on Membrane Domes, Tubes, and Pearling Structures

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Supporting Information: Diffusion on membrane domes, tubes and pearling structures

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1 Complementary results and simulations

1.1 Conservation of the total protein density

We consider a diffusive process where the boundary conditions are such that there is no flux of proteins at the boundaries of the spatial domain. This means that there are not proteins entering or leaving the membrane. Under these conditions, the total amount of proteins $m_{\text{tot}} = \int \sigma da$, must be constant in time. In our simulations, we have set as $m_{\text{tot}} = 0.24$ at $\bar{t} = 0$. In Fig. 1 we show m_{tot} as function of time, where, as predicted, m_{tot} is constant over time on the bud. Exactly the same plot is obtained on all the other shapes considered, and for the sake of brevity we do not show all of them.

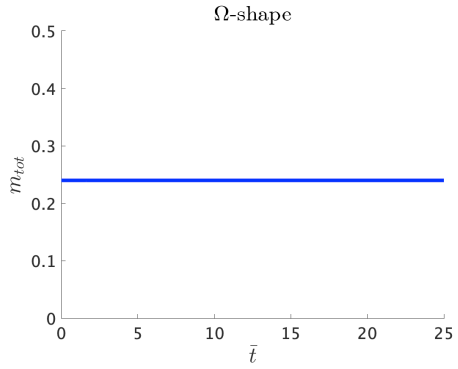
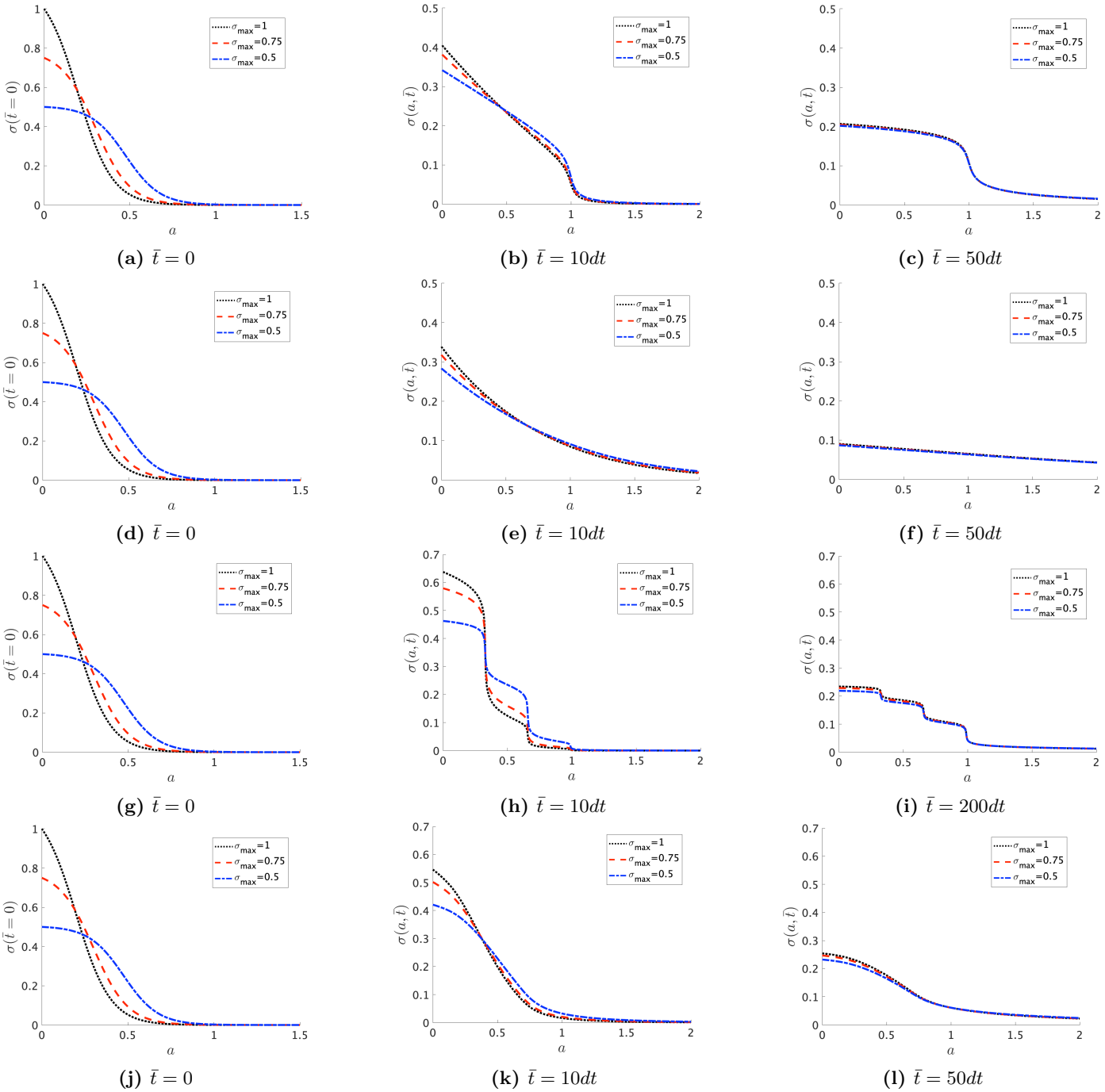


Figure 1: The total amount of proteins m_{tot} on the bud as a function of time. Consistent with the zero flux boundary condition imposed to solve the diffusion equation on the different shapes, m_{tot} is conserved over time.

1.2 Sensitivity to different initial density profiles

As mentioned in the main section, we have chosen a initial density profile of the form $\sigma(a(s), \bar{t} = 0) = c(1 - \tanh(5(a(s) - a_0)))$, where c is adjusted in such a way that the value of $\sigma(a = 0, \bar{t} = 0) = 0.5$ and a_0 is adjusted to give a total amount of proteins $m_{\text{tot}} = 0.24$. However, different values of $\sigma_{\max} \equiv \sigma(a = 0, \bar{t} = 0)$ yield different values of a_0, so we can consider various initial density profiles that gives the same m_{tot}. In Fig. 2 we show different initial density profiles, $\sigma(a(s), \bar{t} = 0) \sim 1 - \tanh(5(a(s) - a_0))$ and the density profiles obtained with each of these initial conditions at later time steps on the Ω-shape (Figs. 2b and 2c), the dome (Figs. 2e and 2f), the pearled structure with $n = 3$ buds (Figs. 2h and 2i) and the tube (Figs. 2k and 2l) showing that as time proceeds the effect of having different initial condition vanishes, as the density profiles tend to become equal regardless of the chosen initial profile. In the case of the pearled structure, a longer time is needed for the profiles to become equal.

Different initial conditions lead to different density profiles during the first time steps of the simulations, as shown in Fig. 2, but the initial conditions have no effect on the amount of proteins in the budded region m_{bud} as time evolves, as shown in Fig. 3, indicating that the diffusion of proteins away from the budded region does not depend on the initial condition.



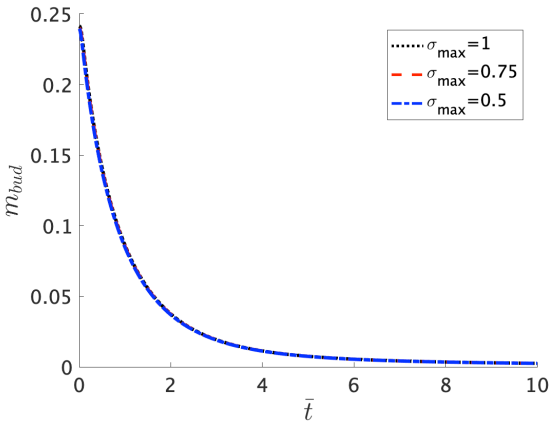
(a) $\bar{t} = 0$ **(b)** $\bar{t} = 10dt$ **(c)** $\bar{t} = 50dt$

(d) $\bar{t} = 0$ **(e)** $\bar{t} = 10dt$ **(f)** $\bar{t} = 50dt$

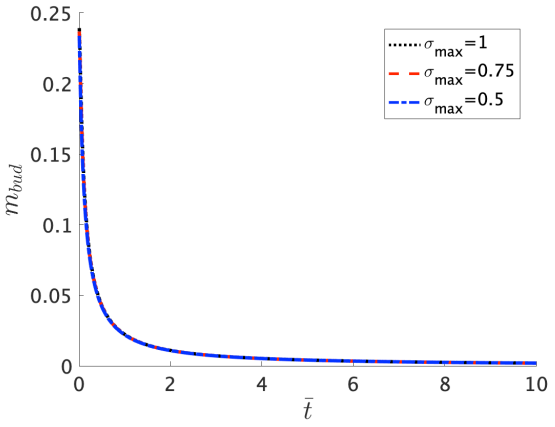
(g) $\bar{t} = 0$ **(h)** $\bar{t} = 10dt$ **(i)** $\bar{t} = 200dt$

(j) $\bar{t} = 0$ **(k)** $\bar{t} = 10dt$ **(l)** $\bar{t} = 50dt$

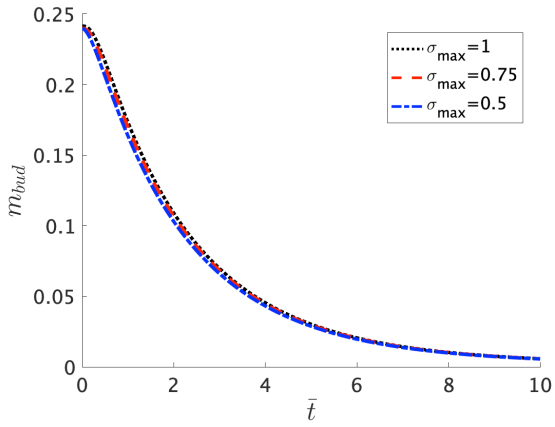
Figure 2: Three different initial protein profiles, $\sigma(a, \bar{t} = 0)$ profiles with $\sigma_{\max} = 0.5, 0.75, 1.0$, that yield the same total amount of proteins $m_{\text{tot}} = 0.24$, for different shapes: $((a) - (c))\Omega$-shape, ((d)-(f)) dome, ((g)-(i)) pearl with $n = 3$ buds and ((j)-(l)) a tube. At later times ($\bar{t} = 50dt$) the density profiles in the Ω-shape, the dome and the tube tend to become equal, regardless of the chosen initial condition, but in the case of the pearl structure, a longer time ($\bar{t} = 200dt$) is needed for the profiles to become equal.



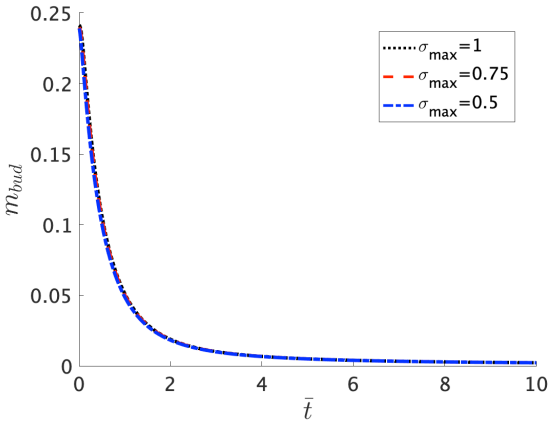
(a) Ω-shape.



(b) Dome.



(c) Pearl, $n = 3$.



(d) Tube

Figure 3: The total amount of proteins in the budded region m_{bud} as a function of time, for the initial conditions shown in Fig. 2a and for different shapes: (a) Ω-shape, (b) dome, (c) pearl with $n = 3$ and (d) a tube. These initial conditions have no effect on the time evolution of the protein density on the budded region, as the different curves are overlapping.