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Title	Elasticity control of entangled chromosomes: Crosstalk between condensin complexes and nucleosomes
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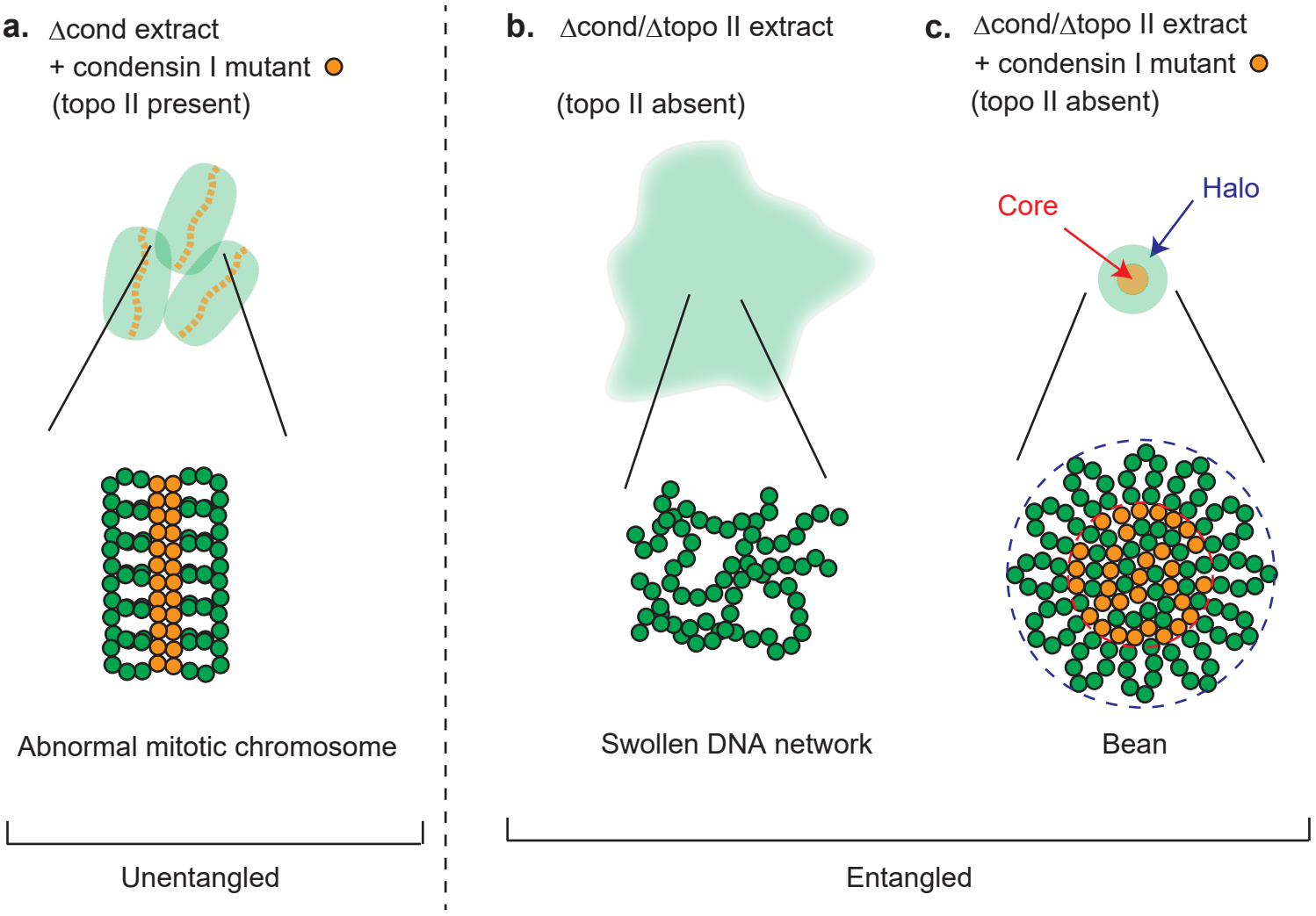


Figure 1 Polymorphism of chromatin structures observed in *Xenopus egg* extracts. Shown above are chromatin structures observed under different conditions in *Xenopus* egg extracts. Shown below are more detailed structures with mutant condensin I complexes deficient in loop extrusion (orange circles) and DNA units (green circles). **a.** Abnormal chromosome-like structures observed in a condensin-depleted extract (Δcond extract) that is supplemented with a condensin I mutant. **b.** A 'cloud' -like structure observed in a condensin/topo II-depleted extract (Δcond Δtopo II extract). **c.** A 'bean' structure observed in a condensin/topo II-depleted extract (Δcond Δtopo II extract) that is supplemented with the condensin I mutant. Under the conditions of b and c, entangled DNAs behave as a polymer network.

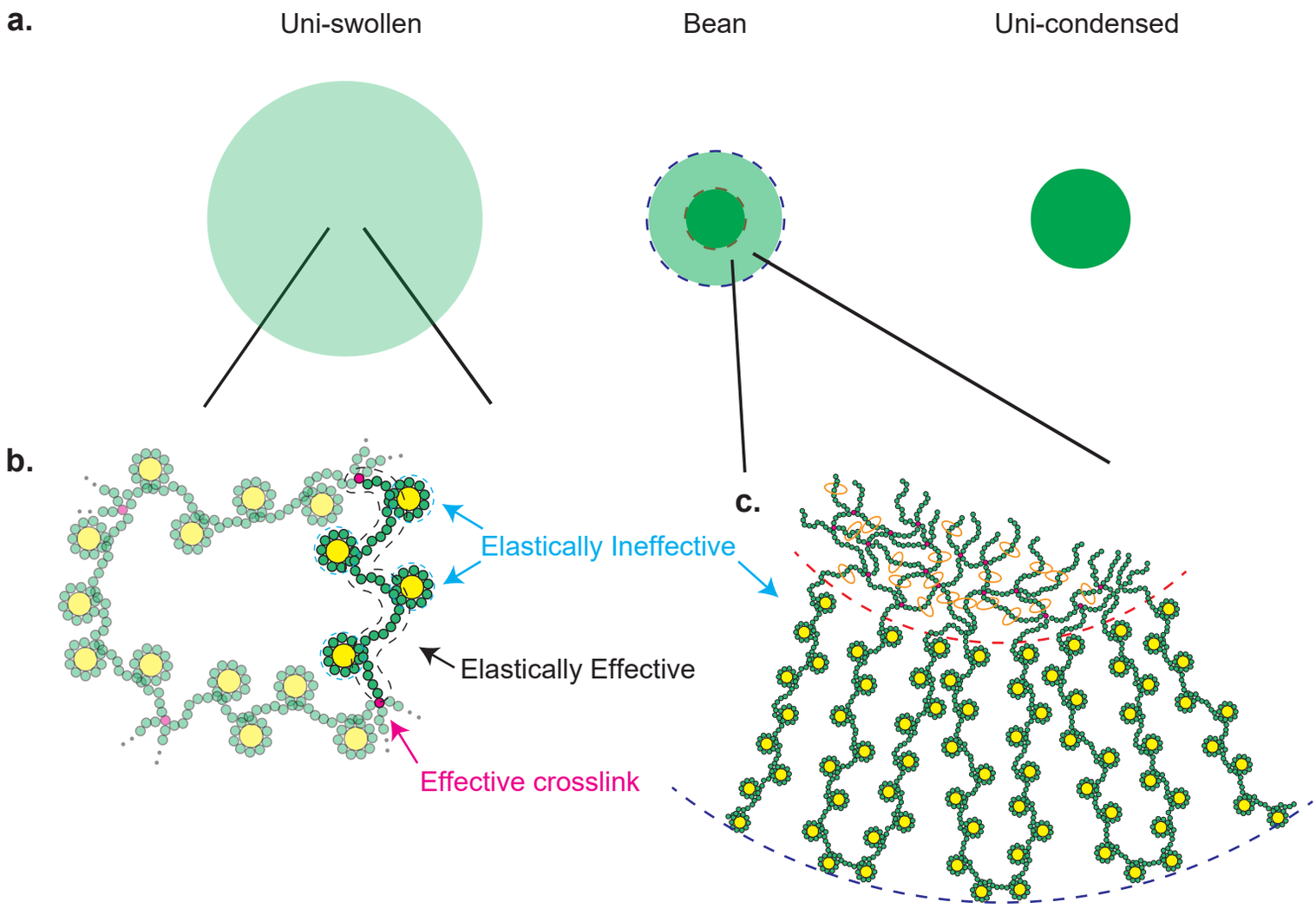


Figure 2 Elastically effective and ineffective chains in an entangled DNA network. a. Three possible structures formed by entangled DNAs: the uni-swollen state (left), the bean structure (middle), and the uni-condensed state (right). **b.** DNA chains connected to the network at two points via effective crosslinks due to DNA entanglements (magenta) respond to the deformation of the network and thus are elastically effective (indicated by the black broken lines). DNA units wrapped around histones (yellow circles) do not respond to such network deformation and thus are elastically ineffective (indicated by the cyan broken line). **c.** The DNA loops in the halo do not contribute to the elastic free energy due to the entanglement, thereby being elastically ineffective.

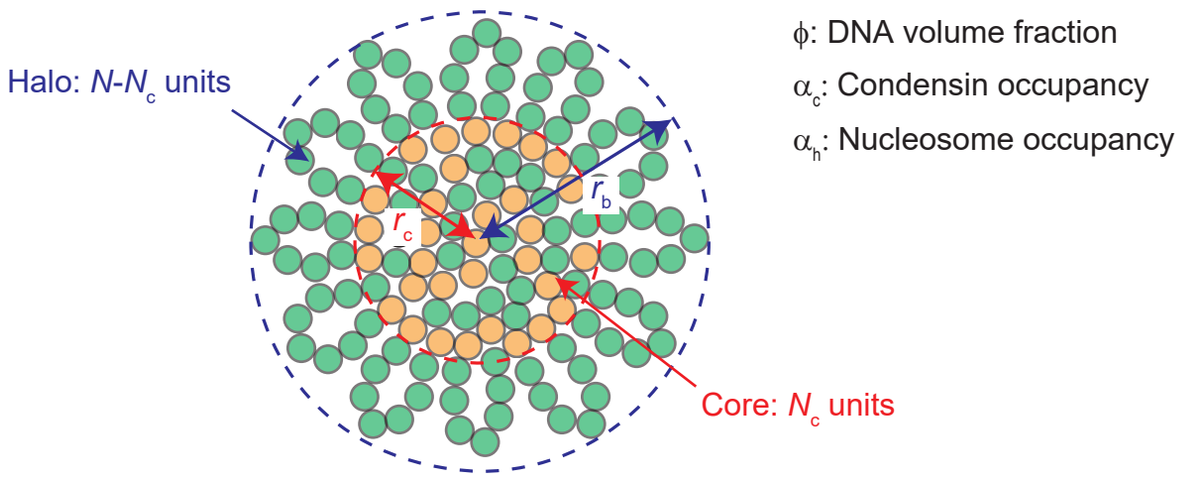


Figure 3 Model of the bean structure. The bean is composed of the core and the halo. The core and the halo are modeled as an entangled DNA network and a brush of DNA loops. Each DNA segment can form nucleosomes, can be occupied by mutant condensins or can be bare. A fraction N_c/N of DNA units is distributed in the core and the other DNA units are distributed in the halo. The bean is characterized by the DNA volume fraction ϕ, the occupancies, α_c and α_h, of DNA by the mutant condensin complexes and nucleosomes.

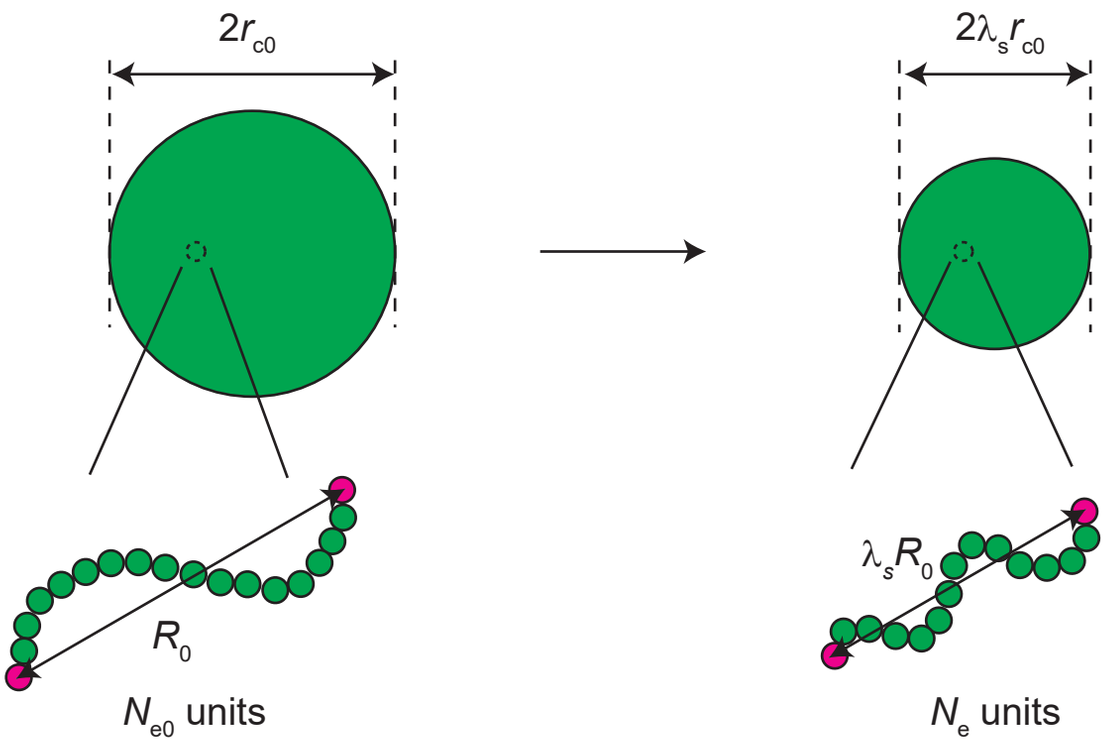


Figure 4 Affine deformation. In the relaxed (reference) state, the radius of the core is r_{c0} and the average distance between the two effective crosslinks that connect a DNA chain composed of N_{e0} is R_0. If the core is swollen or deswollen to the radius r_c (= $\lambda_s r_{c0}$), the average distance between the effective crosslinks changes to $\lambda_s R_0$ (affine deformation). If the halo is assembled, the number of DNA units in the chain between the effective crosslinks becomes N_e.

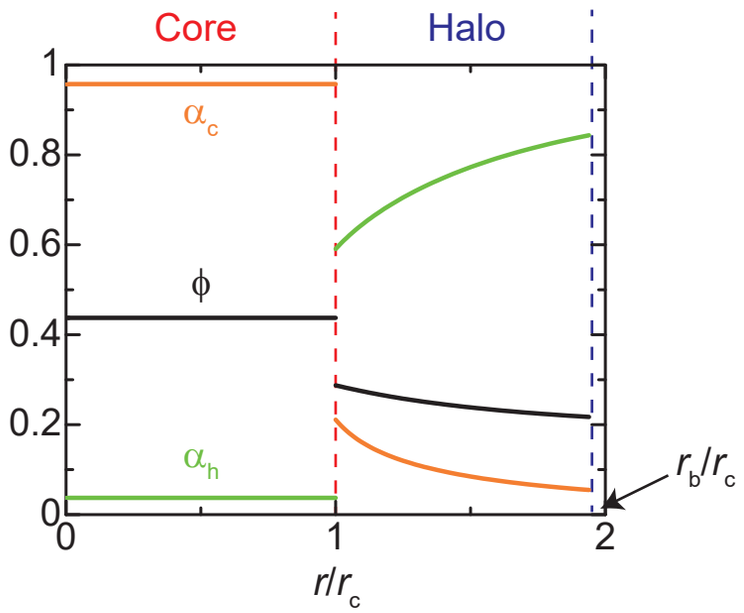


Figure 5 Profiles of DNA volume fraction and occupancies of DNA by the mutant condensin complexes and nucleosomes. The DNA volume fraction (black) and the occupancies, α_c and α_h, of DNA by the mutant condensin complexes (orange) and nucleosomes (light green). The values of parameters used for the calculation are summarized in Table 1. We used μ_c-ε_c= -1.3 for the chemical potential of the mutant complexes.

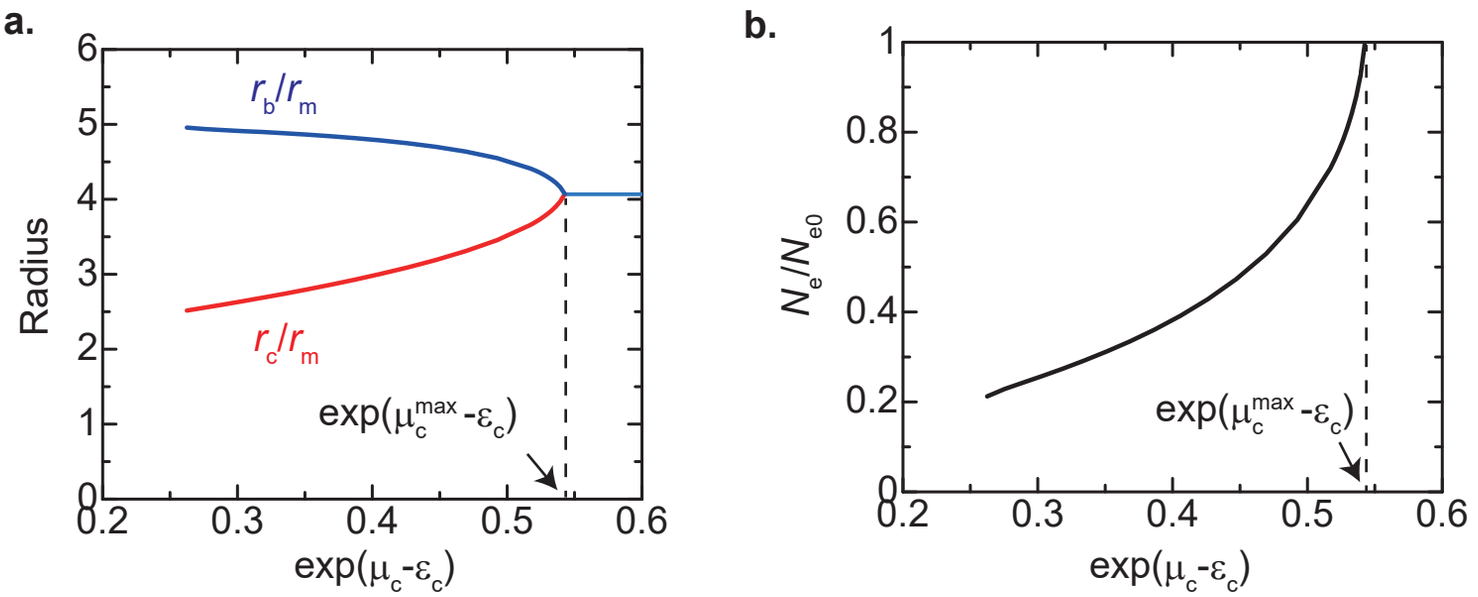


Figure 6 DNA is reeled into core as the concentration of the mutant condensin complexes increases. The radii of the core r_c (red) and the bean r_b (blue) (a) as well as the fraction of DNA units in the core (b) are shown as functions of the exponential $\exp(\mu_c-\varepsilon_c)$, which is proportional to the concentration of the mutant condensins in the exterior solution. The parameters used for the calculation are summarized in Table 1.

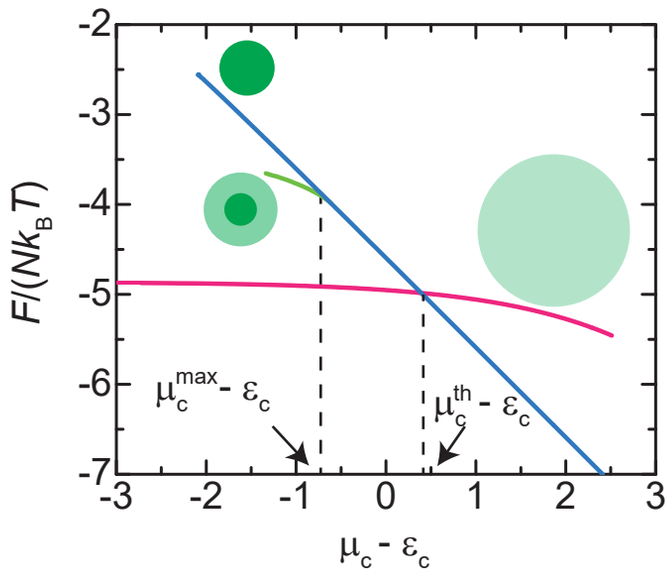


Figure 7 Free energy vs chemical potential of the mutant condensin complexes. The free energy of the system is shown as a function of the chemical potential of the mutant condensin complexes for the bean state (green), the uni-condensed state (cyan), and the uni-swollen state (magenta). The parameters used for the calculation are summarized in Table 1.

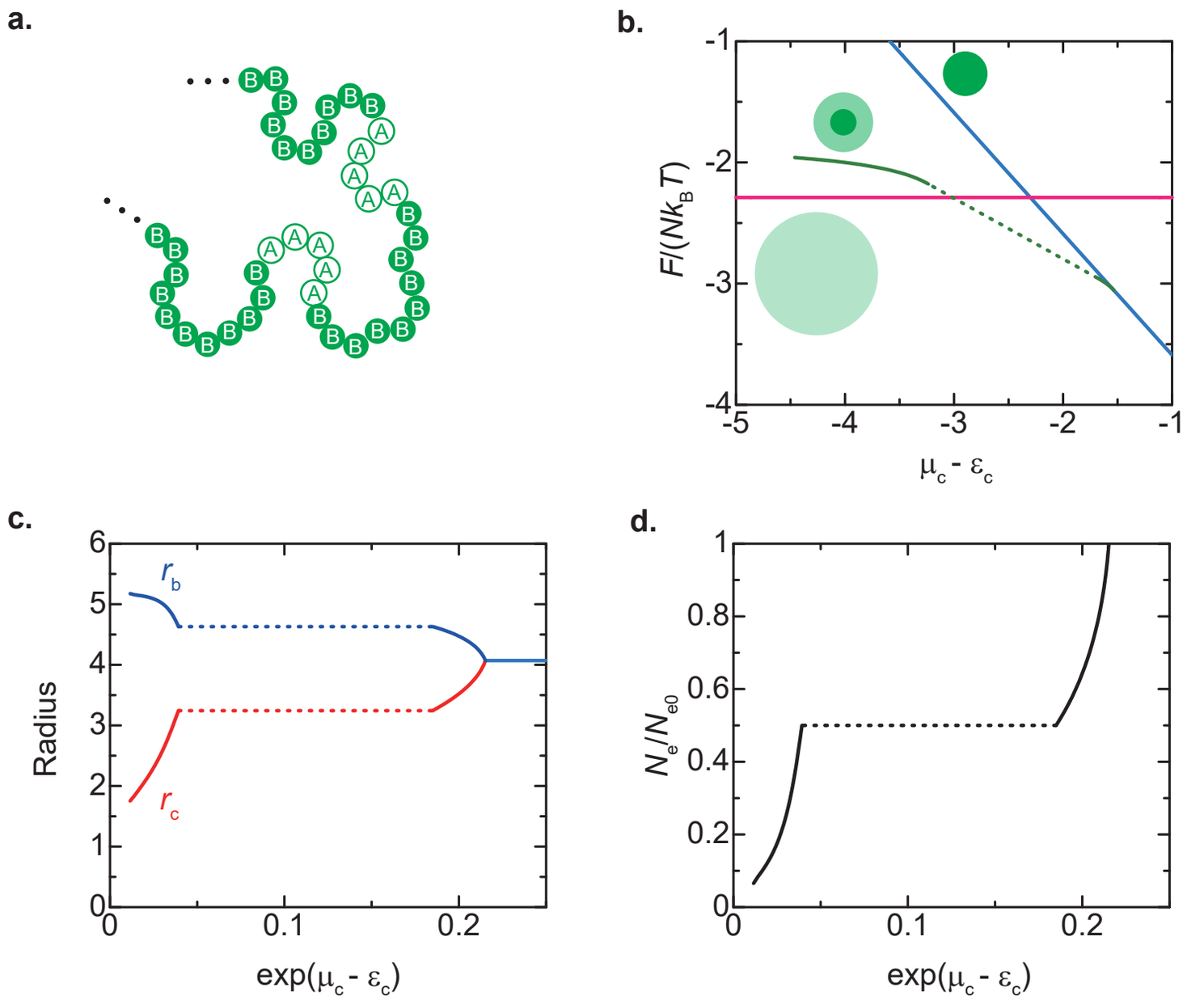


Figure 8 Multi-block copolymer model. a. DNAs are modeled as multi-block AB copolymers, which are composed of A and B blocks. The fraction of DNA units in A blocks is N_A/N and the fraction of DNA units in B blocks is 1-N_A/N. The free energy ε_{hA} to assemble nucleosomes at A blocks is larger than the free energy ε_{hB} to assemble nucleosomes at B blocks. The values of the other parameters of A and B blocks are equal and are shown in Table 1. **b**, **c**, and **d** are numerical calculations on multi-block DNAs with N_A/N=0.5, ε_{hA}= 1.0, ε_{hB}=-2.0. b. The free energy of the entangled multi-block DNAs is shown as a function of the chemical potential μ_c of mutant condensin for the bean state (green), the uni-condensed state (cyan), and the uni-swollen state (magenta). **c.** The radii of the bean (red) and the core (blue), r_b and r_c, are shown as a function of the exponential, $\exp(\mu_c-\varepsilon_c)$, which is proportional to the concentration of mutant condensins. **d.** The fraction N_e/N_{e0} of DNA units in the core is shown as a function of the exponential $\exp(\mu_c-\varepsilon_c)$. The fraction N_e/N_{e0} does not change at a window of mutant condensin concentrations, shown by the dotted lines.