

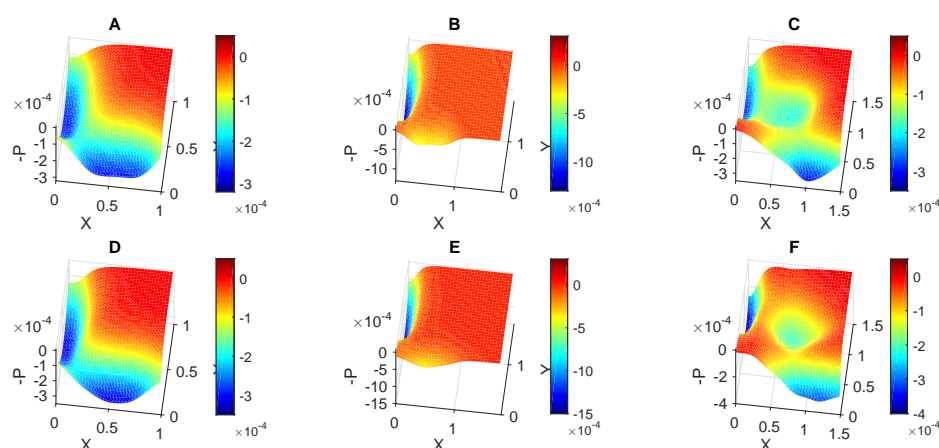
## Supporting information for: Landscape of gene networks for random parameter perturbation

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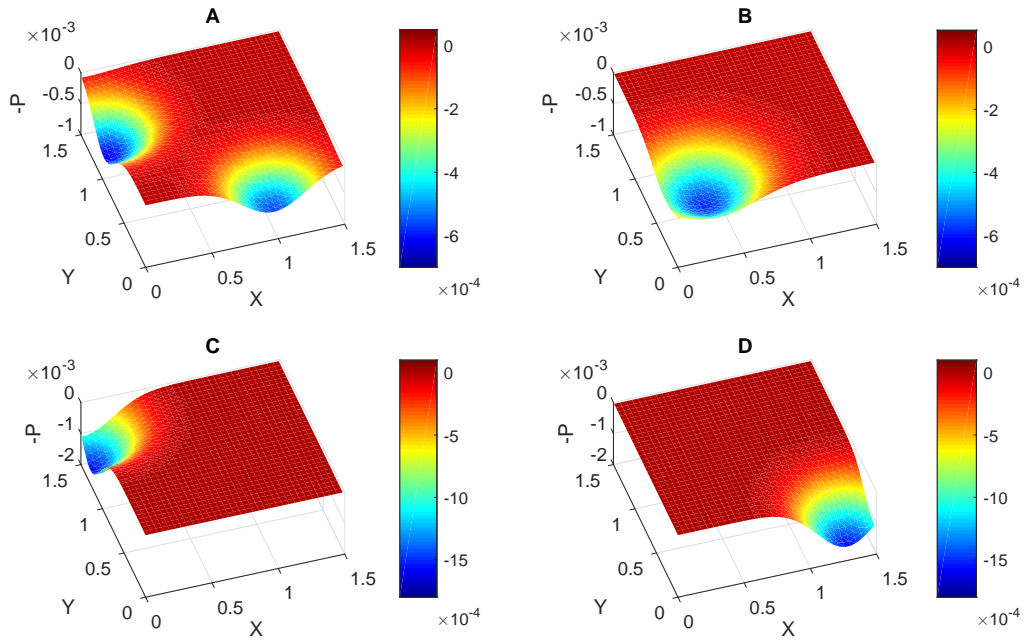
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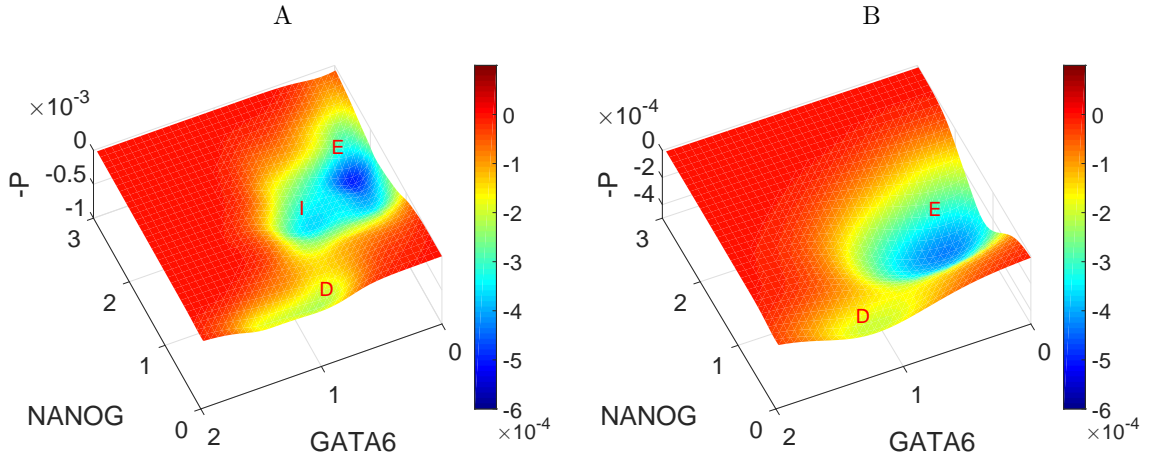
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**Figure S1.** Landscapes from different angles for the MR model (A, D), MRSA1 model (B, E), and MRSA2 model (C, F). The landscape is robust against different types of distributions (Uniform distribution for A, B, C, and Gaussian distribution for D, E, F) used to sample the parameters.



**Figure S2.** Landscapes for the mutual repression with two self-activations (MRSA2) model at certain specific parameter choices. (A)  $a=0.5$ ,  $b=0.5$ ,  $S=0.5$ ,  $k=1$ ,  $n=4$ . (B)  $a=0.3$ ,  $b=0.3$ ,  $S=0.5$ ,  $k=1$ ,  $n=4$ . (C)  $a_1=0.1$ ,  $a_2=0.8$ ,  $b=0.5$ ,  $S=0.5$ ,  $k=1$ ,  $n=4$ . (D)  $a_1=0.8$ ,  $a_2=0.1$ ,  $b=0.5$ ,  $S=0.5$ ,  $k=1$ ,  $n=4$ . It can be seen that with different specific parameter values the landscape exhibits different properties, e.g., monostable state, bistable state.



**Figure S3.** Landscapes from different angles for the ES cell developmental network at different noise level. The parameter range is set as  $a : 0.01 - 0.5$ ,  $b : 0.5 - 1$ . (A) is for diffusion coefficient  $D=0.01$ , and (B) is for  $D=0.05$ .