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Erratum

Erratum to: Stochastic Dynamics of Membrane Protrusion Mediated by the DOCK180/Rac Pathway in Migrating Cells

ERIK S. WELF and JASON M. HAUGH

Department of Chemical and Biomolecular Engineering, North Carolina State University, Box 7905, Raleigh, NC 27695, USA

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In our previously published article,[2] we described a computational model and analysis investigating the stochastic dynamics of cell protrusion during cell migration. In that work, we presented results of stochastic simulations plotted in two-dimensional parameter space. To supplement this analysis, the associated region of model bistability was identified by analysis of the deterministic model equations, and this region was plotted on the same graphs (panels a & b in each of Figs. 2–6). Since publication of our article, we became aware that certain parameter combinations thought to lie in the bistable region are, in fact, monostable. We wish to thank Dr. Michael Savageau (Biomedical Engineering, UC Davis), who studied our model during the preparation of his review article,[1] for bringing the matter to our attention. We traced the error to the use of incorrect values of certain parameters in the bistability analysis. Whereas the values reported in the paper are correct for the stochastic model results, the bistability analysis was performed using three incorrect parameter values as shown in Table C1.

Shown below as Fig. C1 are the corrected figure panels, which now show the bistability regions using the correct parameter values as used in the stochastic simulations.

One of our previous conclusions concerned the lack of a definitive relationship between phenotypic switching in the stochastic simulations and model bistability.[2] This conclusion was based, in part, on stochastic simulations for parameter sets that were supposed to lie in regions of bistability (Fig. 2e and Fig. 5e of the paper). Since the corrected results show that the parameter sets in question do not lie in the bistable regime, we have performed additional simulations to confirm that the original conclusions are valid (Figure C2). In these simulations, the analysis shown in Fig. 5 of the original paper was repeated with a larger value of the C_s parameter in order to expand the region of bistability. Comparison of stochastic runs on either side of the bistability region, as originally intended, confirms that although switching between protrusion and adhesion phenotypes is likely to occur in regions of parameter space that are close to the region of bistability, model bistability is not required for this behavior. As explained in the original article, bistable regions of parameter space usually lie between those regions that give monostable low and monostable high protrusion, and in the vicinity of the interface between the two, the stochastic model readily produces transient departures from the stable state.

TABLE C1. Summary of parameter values erroneously used to determine regions of bistability as shown in Figs. 2–6 of the article.

Parameter	Value used in stochastic simulation	Value used to determine bistability in the paper
C_s	10	100
C_n	20	100
$k_{d,x}$	10	1

Address correspondence to Jason M. Haugh, Department of Chemical and Biomolecular Engineering, North Carolina State University, Box 7905, Raleigh, NC 27695, USA. Electronic mail: jason_haugh@ncsu.edu

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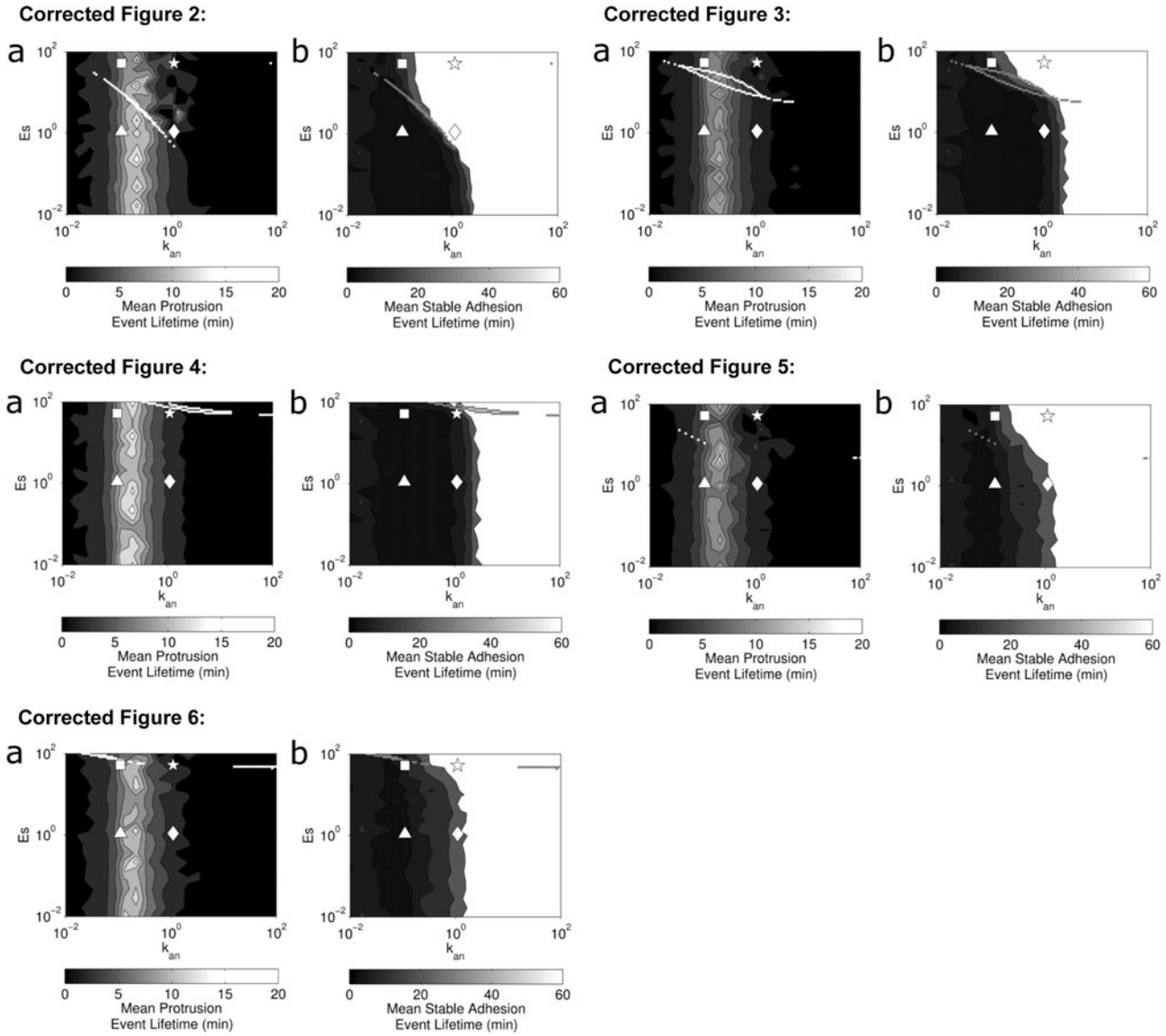

FIGURE C1. Corrected versions of panels *a* & *b* in Figs. 2–6 of the original paper.

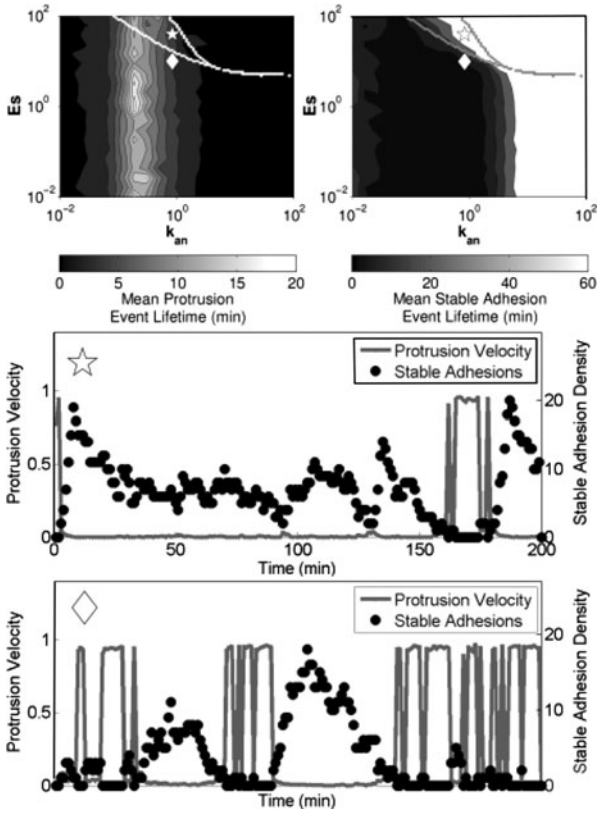

FIGURE C2. Stochastic simulation of protrusion/adhesion dynamics. The analysis is analogous to Fig. 5 of the original paper (I_n = 10, I_s = 1), except that the value of C_s is increased from 10 to 100 in order to expand the region of bistability.

REFERENCES

[1]Savageau, M. A. Biomedical engineering strategies in system design space. *Ann. Biomed. Eng.* 39:1278–1295, 2011.

[2]Welf, E. S., and J. M. Haugh. Stochastic dynamics of membrane protrusion mediated by the DOCK180/Rac pathway in migrating cells. *Cell. Mol. Bioeng.* 3:30–39, 2010.