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Discrete and continuous models of protein sorting in the Golgi

HAIJUN GONG, Department of Physics, Carnegie Mellon University, RUSSELL SCHWARTZ, Department of Biological Sciences, Carnegie Mellon University — The Golgi apparatus plays an important role in processing and sorting proteins and lipids. Golgi compartments constantly exchange material with each other and with other cellular components, allowing them to maintain and reform distinct identities despite dramatic changes in structure and size during cell division, development and osmotic stress. We have developed two minimal models of membrane and protein exchange in the Golgi — a discrete, stochastic model [1] and a continuous ordinary differential equation (ODE) model — both based on two fundamental mechanisms: vesicle-coat-mediated selective concentration of soluble N-ethylmaleimide-sensitive factor attachment protein receptor (SNARE) proteins during vesicle formation and SNARE-mediated selective fusion of vesicles. Both show similar ability to establish and maintain distinct identities over broad parameter ranges, but they diverge in extreme conditions where Golgi collapse and reassembly may be observed. By exploring where the models differ, we hope to better identify those features essential to minimal models of various Golgi behaviors. [1] H. Gong, D. Sengupta, A. D. Linstedt, R. Schwartz. *Biophys J.* 95: 1674-1688, 2008.

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