

Corrections

CHEMISTRY, BIOPHYSICS AND COMPUTATIONAL BIOLOGY

Correction for “Nonequilibrium candidate Monte Carlo is an efficient tool for equilibrium simulation,” by Jerome P. Nilmeier, Gavin E. Crooks, David D. L. Minh, and John D. Chodera, which appeared in issue 45, November 8, 2011, of *Proc Natl Acad Sci USA* (108:E1009–E1018; first published October 24, 2011; 10.1073/pnas.1106094108).

The authors note that Reference 62 appeared incorrectly. The corrected reference appears below.

Additionally, the authors note that Equations 39, 41, and 42 appeared incorrectly. The corrected equations appear below.

$$x_t = x_t^* + \frac{\Delta t}{\gamma m} F_t(x_t^*) + \sqrt{2} \left(\frac{\Delta t}{\gamma m} \right)^{1/2} \xi_t, \quad [39]$$

$$x_t = x_t^* + \frac{\Delta t}{\gamma m} F_t(x_t^*) + \sqrt{2} \left(\frac{\Delta t}{\gamma m} \right)^{1/2} \xi_t \quad [41]$$

$$x_t^* = x_t + \frac{\Delta t}{\gamma m} F_t(x_t) + \sqrt{2} \left(\frac{\Delta t}{\gamma m} \right)^{1/2} \tilde{\xi}_t,$$

$$\tilde{\xi}_t = -\frac{1}{\sqrt{2}} \left(\frac{\Delta t}{\gamma m} \right)^{1/2} [F_t(x_t) + F_t(x_t^*)] - \xi_t. \quad [42]$$

62. Athènes M, Marinica M-C (2010) Free energy reconstruction from steered dynamics without post-processing. *J Comput Phys* 229:7129–7146.

www.pnas.org/cgi/doi/10.1073/pnas.1207617109

BIOPHYSICS AND COMPUTATIONAL BIOLOGY

Correction for “Successful prediction of the intra- and extracellular loops of four G-protein-coupled receptors,” by Dahlia A. Goldfeld, Kai Zhu, Thijs Beuming, and Richard A. Friesner, which appeared in issue 20, May 17, 2011, of *Proc Natl Acad Sci USA* (108:8275–8280; first published May 2, 2011; 10.1073/pnas.1016951108).

The authors note that their conflict of interest statement was omitted during publication. The authors declare that R.A.F. is a founder of Schrodinger, Inc.

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