

Biological algorithm for data reconstruction

Robert Gilmore, Daniel Cross, & Ryan Michaluk

Department of Physics, 3141 Chestnut St, Philadelphia, PA 19104
djc49@drexel.edu

We present a simple algorithm inspired by Genome sequencing which “reconstructs” a single long trajectory of a dynamical system from many short trajectories¹. Such a procedure would be useful in situations where many data sets are available but each is insufficiently long to apply a meaningful analysis directly². We apply the algorithm to numerical data taken from the Rössler and Lorenz dynamical systems and to experimental data taken from the Belousov-Zhabotinskii chemical reaction. Topological information was reliably extracted from each system and geometrical and dynamical measures were computed.

1. C. Komalapiya, M. Thiel, M. C. Romano, N. Marwan, U. Schwarz, and J. Kurths, Phys. Rev. E 78, 066217 (2008).
2. D. J. Cross, R. Michaluk, and R. Gilmore, Phys. Rev. E, in press (2010).