

Globally Coupled Chaos Violates the Law of Large Numbers but Not the Central-Limit Theorem
[Phys. Rev. Lett. 65, 1391 (1990)]

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The definition of $\mu_{i,j}$ should include $p_{i,j}(x,y)$ in front of the logarithm, and consequently Eq. (4) should read as follows:

$$\mu = -\frac{2}{N(N-1)} \int \int \sum_{i>j} p_{i,j}(x,y) \ln p_{i,j}(x,y) dx dy + \frac{2}{N} \int \sum_i P_i(x) \ln P_i(x) dx. \quad (4)$$

All calculations, of course, are carried out with the correct expression.

Although all numerical results are correct, recent simulations show a slight violation of the central-limit theorem. We have measured $q \equiv \langle (\delta h)^4 \rangle / \langle (\delta h)^2 \rangle^2$, which should equal 3 for a Gaussian distribution. Indeed, this is true within our accuracy for $a=1.95$. For $a=1.99$, however, $q \approx 3$ up to a crossover size (≈ 400), and approaches 2.52 ± 0.05 for larger N . For $a=2.0$, q approaches 2.92 ± 0.05 beyond the crossover size ≈ 4800 . Thus we conclude that the central-limit theorem is broken in general with a small and parameter-dependent discrepancy. Our main conclusions (breakdown of the law of large numbers, emergence of subtle order, and anomalous recovery of the law by noise), of course, remain invariant.

Random Energy Model for the Kinetics of RNA Folding
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A paper by Shakhnovich and Gutin,¹ which was instrumental in my understanding of the kinetics of relaxation of quenched disordered systems, was not referenced in the Letter. My paper discusses RNA structure relaxation in the light of a random energy model (REM) which has been implemented already in the context of the physics of condensed matter, specifically, in theoretical spin-glass models. The REM has been pioneered by Derrida and co-workers and the kinetics were derived by Shakhnovich and Gutin,¹ making use of analytical methods. Their main result is that the highly degenerate ground state is explored by visiting states whose energy decreases logarithmically in time. The logarithmic law is actually reproduced in my simulations for the structure relaxation of an RNA chain (Fig. 1 of the Letter) whose primary sequence is disordered. Thus, the kinetic model which Shakhnovich and Gutin built on the REM finds a concrete realization *mutatis mutandis* in the folding of an uncorrelated chain. Reference 1 is therefore inspirational and instrumental for the interpretation of the results expounded in my Letter.

¹E. Shakhnovich and A. Gutin, Europhys. Lett. **9**, 569 (1989).