*Erratum***A Quantitative Measure of Error Minimization in the Genetic Code****David Haig,¹ Laurence D. Hurst²**¹ Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA² Department of Biology and Biochemistry, University of Bath, Claverton Down BA2 7AY, UK

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Re: J Mol Evol (1991) 33: 412–417. The results of a programming error were incompletely corrected in this paper. The data for the two measures of hydrophobicity (“polar requirement” and “hydropathy”) which were the principal focus of the paper are correct. The data for “molecular volume” and “isoelectric point” are correct in Table 2 but wrong in Tables 3 and 4. Corrected values are printed below. The sample size in Table 4 has been increased from 10,000 to 100,000 randomly generated codes. Thanks are due to Christina Burch for finding this error. The major change in interpretation is that the natural code is average (rather than nonconservative) for changes in isoelectric point. An additional error occurs in Fig. 1, where First Base and Second Base are transposed in the axis labels.

Table 3. MS₁, MS₂, MS₃, and MS₀ for the natural code

	MS ₁	MS ₂	MS ₃	MS ₀
Polar requirement	4.88	10.56	0.14	5.19
Hydropathy	5.18	21.78	1.17	9.39
Molecular volume	2521	3350	931	2266
Isoelectric point	6.133	5.832	2.235	4.728

Table 4. The proportion, *P*, of randomly generated codes (from a sample of 100,000) in which single-base substitutions have a smaller average effect than in the natural code

	<i>P</i> ₁	<i>P</i> ₂	<i>P</i> ₃	<i>P</i> ₀
Polar requirement	0.0031	0.2209	0.0001	0.0001
Hydropathy	0.0005	0.9035	0.0139	0.0083
Molecular volume	0.0949	0.3256	0.4257	0.1101
Isoelectric point	0.5826	0.4374	0.7399	0.5636