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### Erratum

**Citation for published version:**

Waddington, D, Springbett, AJ, Burt, JS & Burt, D 2000, 'Erratum: A chromosome-based model for estimating the number of conserved segments between pairs of species from comparative genetic maps' *Genetics*, vol 155, no. 2, pp. 993.

**Link:**

[Link to publication record in Edinburgh Research Explorer](#)

**Document Version:**

Author final version (often known as postprint)

**Published In:**

Genetics

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### CORRIGENDUM

In the article by David Waddington, Anthea J. Springbett and David W. Burt (*Genetics* **154**: 323–332) entitled “A Chromosome-Based Model for Estimating the Number of Conserved Segments Between Pairs of Species From Comparative Genetic Maps,” the following equations should be modified:

page 324, column 2, line 51, to

$$[n | y]_1 = \frac{(Dy)^n \exp(-Dy)}{n!(1 - P_{0k})};$$

page 325, column 1, line 11, to

$$[n | y]_2 = \frac{(Dy)^n \exp(-Dy)}{n!(1 - P_{0k} - P_{1k})};$$

page 325, column 2, lines 32 and 33, to

$$S_{\text{obs}} = \sum_k (1 - P_{0k}) S_k;$$

where

$$P_{nk} = \int_0^{nk} \frac{(Dy)^n \exp(-Dy)}{n!} [y]_k dy,$$

and  $S_{\text{obs}}$  is the predicted number of observed segments. This corrects the treatment of truncated Poisson distributions for integration. Estimated numbers of conserved segments are increased by 18–96%, on average by 45%. The random genome model is supported for all cases except the chicken-mouse comparison using range data.