

Correction to ‘RiboVIEW: a computational framework for visualization, quality control and statistical analysis of ribosome profiling data’

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In Equation (2) on page 3, the count of footprints in the A-site in the numerator, should be $n_{0,g}$ to denote coverage, independently of the codon identity in the A-site (and not $n_{c,0,g}$, which would denote specific codons). This is shown correctly in the supplementary code and in the supplementary information.

The formulas below show the former incorrect (first) and the corrected (second) Equation (2):

$$\text{codon usage}_c^{\text{global}} = \frac{\sum_g n_{c,0,g} \cdot \text{codon usage}_{c,g}}{\sum_c \sum_g n_{c,0,g}} \quad (2)$$

$$\text{codon usage}_c^{\text{global}} = \frac{\sum_g n_{0,g} \cdot \text{codon usage}_{c,g}}{\sum_c \sum_g n_{c,0,g}} \quad (2)$$

The authors apologise for this error.

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