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

Carine Legrand^{1,2} and Francesca Tuorto^{1,*}

¹Division of Epigenetics, DKFZ-ZMBH Alliance, German Cancer Research Center, Im Neuenheimer Feld 580, 69120 Heidelberg, Germany and ²Independent researcher, Kreuzstr. 5, 68259 Mannheim, Germany

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):

$$\operatorname{codon} \operatorname{usage}_{c}^{\operatorname{global}} = \frac{\sum_{g} n_{c,0,g} \cdot \operatorname{codon} \operatorname{usage}_{c,g}}{\sum_{c} \sum_{g} n_{c,0,g}}$$
(2)

$$\operatorname{codon} \operatorname{usage}_{c}^{\operatorname{global}} = \frac{\sum_{g} n_{0,g} \cdot \operatorname{codon} \operatorname{usage}_{c,g}}{\sum_{c} \sum_{g} n_{c,0,g}}$$
(2)

The authors apologise for this error.

^{*}To whom correspondence should be addressed. Tel: +49 6221 423806; Fax: +49 6221 423802; Email: f.tuorto@dkfz.de

[©] The Author(s) 2022. Published by Oxford University Press on behalf of Nucleic Acids Research.

This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License

⁽http://creativecommons.org/licenses/by-nc/4.0/), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contact journals.permissions@oup.com