

CORRECTION

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Correction to: Detect tissue heterogeneity in gene expression data with BioQC

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Correction

After the publication of this work [1], a mistake was noticed in the Eq. 1. Given an $m \times n$ expression matrix with m genes and samples of n tissues, the correct definition of the *Gini index* for gene i is:

$$G_i = \frac{1}{n} \left(n + 1 - 2 \left(\frac{\sum_{j=1}^n (n+1-j)x'_{ij}}{\sum_{j=1}^n x'_{ij}} \right) \right), \quad (1)$$

where x'_{ij} is the j th value in the non-descending ordered vector of x_i ($i = 1, \dots, m, j = 1, \dots, n$). In the original version of the manuscript, the variable j in the parentheses of the nominator was erroneously written as i .

The authors apologize for the mistake and thank Mr. Tao Fang for pointing out this mistake.

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1. Zhang JD, et al. Detect tissue heterogeneity in gene expression data with BioQC. *BMC Genomics*. 2017;18:277. <https://doi.org/10.1186/s12864-017-3661-2>.

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