Corrigendum

Linnorm: improved statistical analysis for single cell **RNA-seq expression data**

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The authors wish to make the following correction to their article:

Under MATERIALS AND METHODS, Linnorm algorithm, Calculating the data transformation parameter, λ , on page 3, the text below equation (3)

Here, we use $S(\lambda)$ to represent the homoscedasticity and $S(\lambda)$ to represent the skewness of the dataset. $V(\lambda)$ and $S(\lambda)$ are combined using the Euclidian distance, where the square root is omitted because it is a monotonic function.

Should be replaced by

Here, we use $V(\lambda)$ to represent the homoscedasticity and $S(\lambda)$ to represent the skewness of the dataset. $V(\lambda)$ and $S(\lambda)$ are combined using the Euclidian distance, where the square root is omitted because it is a monotonic function.

The correction has also been made in the published article, in addition to a number of spelling corrections.

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