

CORRECTION

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Correction to: SpectralTAD: an R package for defining a hierarchy of topologically associated domains using spectral clustering

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The original article can be found online at <https://doi.org/10.1186/s12859-020-03652-w>.

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Following publication of the original article [1], the authors identified misformatted equations in the published article. The correctly formatted equations are given below.

1. Calculating the normalized symmetric Laplacian:

$$\bar{L} = D^{-\frac{1}{2}}CD^{-\frac{1}{2}}$$

2. Solve the generalized eigenvalue problem:

$$\bar{L}\bar{V} = \lambda\bar{V}$$

3. The result is a matrix of eigenvectors $\bar{V}_{w \times k}$, where w is the window size, and k is the number of eigenvectors used, and a vector of eigenvalues where each entry λ_i corresponds to the i_{th} eigenvalue of the normalized Laplacian \bar{L} .

4. Normalize rows and columns to sum to 1:

$$\widehat{V}_{i.} = \frac{\bar{V}_{i.}}{\|\bar{V}_{i.}\|}$$

5. Find the mean silhouette score over all possible numbers of clusters m and organize into a vector of means:



$$\bar{s}_m = \frac{\sum_{i=1}^m s_i}{m}$$

6. Find the value of m which maximizes \bar{s}_m

The original article has been updated.

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Reference

1. Cresswell, et al. SpectralTAD: an R package for defining a hierarchy of topologically associated domains using spectral clustering. *BMC Bioinformatics*. 2020;21:319. <https://doi.org/10.1186/s12859-020-03652-w>.