

Correction to ‘TopDom: an efficient and deterministic method for identifying topological domains in genomes’

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The authors wish to acknowledge the scientific advice of Dr Hyokyeong Lee, and to add a new reference 28 to the following sentence under MATERIALS AND METHODS:

Step 2. Detect TD boundaries based on binSignal

Intuitively, local minima in the series along a chromosome represent TD boundaries. However, some local minima result from noise in the data. In order to capture the dominant local minima, we first smooth the binSignal curve. Our strategy is to approximate the binSignal curve with line segments to capture major trends, and for this purpose we adopt the linear-time algorithm of Kumar Ray et al. (15,16,28).

28. Lee, H., Moody-Davis, A., Saha, U., Suzuki, B.M., Asarnow, D., Chen, S., Arkin, M., Caffrey, C.R., Singh, R. (2012) Quantification and clustering of phenotypic screening data using time-series analysis for chemotherapy of schistosomiasis. *BMC Genomics*, 13(Suppl 1), S4. doi: 10.1186/1471-2164-13-S1-S4.

These details have been corrected only in this correction notice to preserve the published version of record.