

Correction

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Correction: Splice site identification using probabilistic parameters and SVM classification

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Published: 5 July 2007

Received: 5 July 2007

BMC Bioinformatics 2007, 8:241 doi:10.1186/1471-2105-8-241

Accepted: 5 July 2007

This article is available from: <http://www.biomedcentral.com/1471-2105/8/241>

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We proposed a method for the identification of splice sites [1] and it was tested against two data sets – DGSplicer (402695 acceptor and 285451 donor sites) and NN269 (6876 acceptor and 6316 donor sites).

The better performance on the bigger data set (DGSplicer) supports our claim about the validity of the proposed method. However, after the publication of this work it was brought to our attention that the results associated with the smaller dataset (NN269) in our paper were incorrectly

scaled in the x-axis. The correct result generated by our proposed method (MM1-SVM) for this dataset is given in Figure 1 and Figure 2 below. This affects the results of Figures 2, 3, 4 and 5 of our original paper and Figures 1 and 2 in the additional file of the paper.

We regret any inconvenience caused by this incident and we would like to thank Dr. Gunnar Rättsch and Dr. Soeren Sonnenburg from Max Planck Society for bringing this error to our attention.

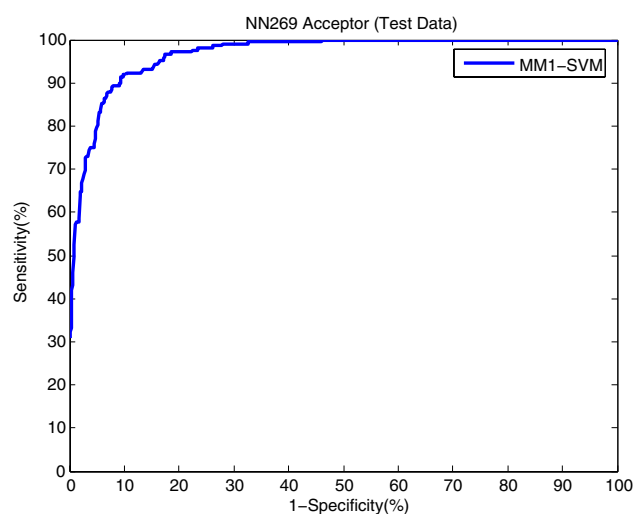


Figure 1
ROC showing the performance of MM1-SVM on NN269 acceptor splice site test data.

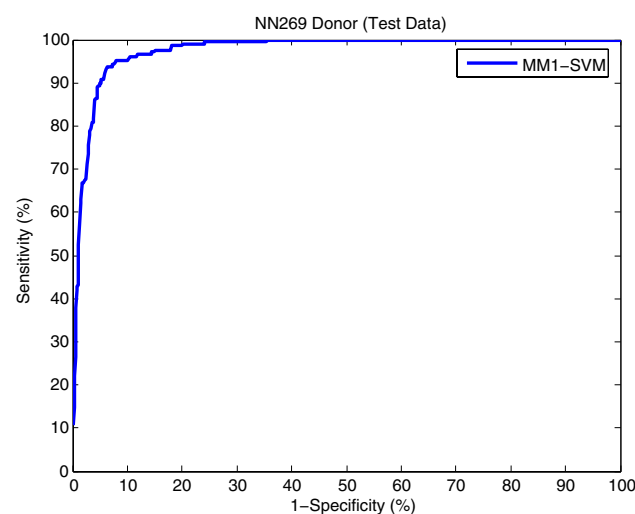


Figure 2
ROC showing the performance of MM1-SVM on NN269 donor splice site test data.

References

1. Baten AKMA, Chang BCH, Halgamuge SK, Li J: **Splice site identification using probabilistic parameters and SVM classification.** *BMC Bioinformatics* 2006, **7**:

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