


## Author Correction: PaintSHOP enables the interactive design of transcriptome- and genome-scale oligonucleotide FISH experiments

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Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-021-01187-3>, published online 5 July 2021.

In this article, the last sentence of the second paragraph read, “To our knowledge, no framework exists to solve common problems such as the freeform appending of additional necessary sequences to probe sequences such as primer pairs for PCR amplification to support a broad range of experimental designs or the batched construction of probe sets against multiple targets in parallel.” To clarify the relationship between PaintSHOP and existing tools, this has been changed as follows: “We set out to create a free-to-use framework with genome-level scalability and a web-based design interface that could accommodate a broad variety of oligo FISH technologies.” The error has been corrected in the PDF and HTML versions of the article.

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## Author Correction: Graphical assessment of tests and classifiers

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Correction to: *Nature Methods* <https://doi.org/10.1038/s41592-021-01232-1>, published online 27 July 2021.

In the version of this article initially published, an error appeared in the eleventh paragraph, in the sentence reading “But we know that when  $m^+/m$  is small, even good classifiers can have unacceptably low precision ( $TP/(TP + FN)$ ) because decision errors in the normal and larger class (FN) can greatly outnumber decision successes (TP)”. The two instances of “FN” should instead have read “FP” i.e., as “...( $TP/(TP + FP)$ ) because decision errors in the normal and larger class (FP)...”

These changes have been made to the online version of this article.

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