Corrigendum

A Bayesian model for single cell transcript expression analysis on MERFISH data

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The authors of the above paper wish to inform the reader that an affiliation for Johannes Köster was not noted in the original publication and also that the ‘Availability and Implementation’ section of the abstract should have appeared as below:

‘The presented model is implemented on top of Rust-Bio (Köster, 2016) and available open-source as MERFISHtools (https://merfish tools.github.io). It can be easily installed via Bioconda (Grüning et al., 2018). The entire analysis performed in this paper is provided as a fully reproducible Snakemake (Köster and Rahmann, 2012) workflow via Zenodo (https://doi.org/10.5281/zenodo.752340).’

The paper has been corrected online.