

ERRATUM

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Erratum to: A survey of best practices for RNA-seq data analysis

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Erratum

During editing of the article by Conesa *et al.* [1], an error was introduced to some of the citations, such that incorrect references were provided for some articles the second time they were cited. The following sentences are affected:

Algorithms that quantify expression from transcriptome mappings include RSEM (RNA-Seq by Expectation Maximization) [40], eXpress [41], Sailfish [35] and kallisto [42] among others. These methods allocate multi-mapping reads among transcript and output within-sample normalized values corrected for sequencing biases [35, 41, 43].

The citation for Sailfish should be [34] (Patro *et al.*, *Nat Biotechnol.* 2014;32:463–4) in both sentences.

Additional factors that interfere with intra-sample comparisons include changes in transcript length across samples or conditions [50], positional biases in coverage along the transcript (which are accounted for in Cufflinks), average fragment size [43], and the GC contents of genes (corrected in the EDaseq package [21]).

The citation for EDaseq should be [20] (Risso *et al.* *BMC Bioinformatics.* 2011;12:480)

The NOISeq R package [20] contains a wide variety of diagnostic plots to identify sources of biases in RNA-seq data and to apply appropriate normalization procedures in each case.

The citation for NOISeq should be [19] (Tarazona *et al.* *Nucleic Acids Res.* 2015;43:e140)

These effects can be minimized by appropriate experimental design [51] or, alternatively, removed by batch-correction methods such as COMBAT [52] or ARSYN [20, 53].

The citations for ARSYN should be [19, 53] (Tarazona *et al.* *Nucleic Acids Res.* 2015;43:e140, Nueda *et al.* *Biostatistics.* 2012;13:553–66).

All these approaches are generally hampered by the intrinsic limitations of short-read sequencing for accurate identification at the isoform level, as discussed in the RNA-seq Genome Annotation Assessment Project paper [30].

The citation for the RGASP article should be [29] (Engström *et al.* *Nat Methods.* 2013;10:1185–91).

We refer the reader to [30] for a comprehensive comparison of RNA-seq mappers.

This citation should be [29] (Engström *et al.* *Nat Methods.* 2013;10:1185–91).

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Received: 17 August 2016 Accepted: 17 August 2016

Published online: 26 August 2016

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References

1. Conesa A, Madrigal P, Tarazona S, Gomez-Cabrero D, Cervera A, McPherson A, et al. *Genome Biol.* 2016;17:13.

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