

CORRECTION

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Correction: MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts

Andrea Hita^{1,2}, Gilles Brocart¹, Ana Fernandez^{1,2}, Marc Rehmsmeier², Anna Alemany^{3†} and Sol Schwartzman^{1*†} 

The original article can be found online at <https://doi.org/10.1186/s12859-021-04544-3>.

[†]Anna Alemany and Sol Schwartzman contributed equally to this work

*Correspondence: sol.schwartzman@diagenode.com

¹ Epigenetics Unit, Diagenode s.a., Liège, Belgium
Full list of author information is available at the end of the article

Correction to: BMC Bioinformatics (2022) 23:39

<https://doi.org/10.1186/s12859-021-04544-3>

Following the publication of the original article [1], the authors identified an error in Fig. 2 and caption 2c. The correct figure is given below, and the caption has been updated from “Reads r_i ($i = 1, 10$)” to “Reads r_i ($i = 1, 11$).”

The original article [1] has been corrected.



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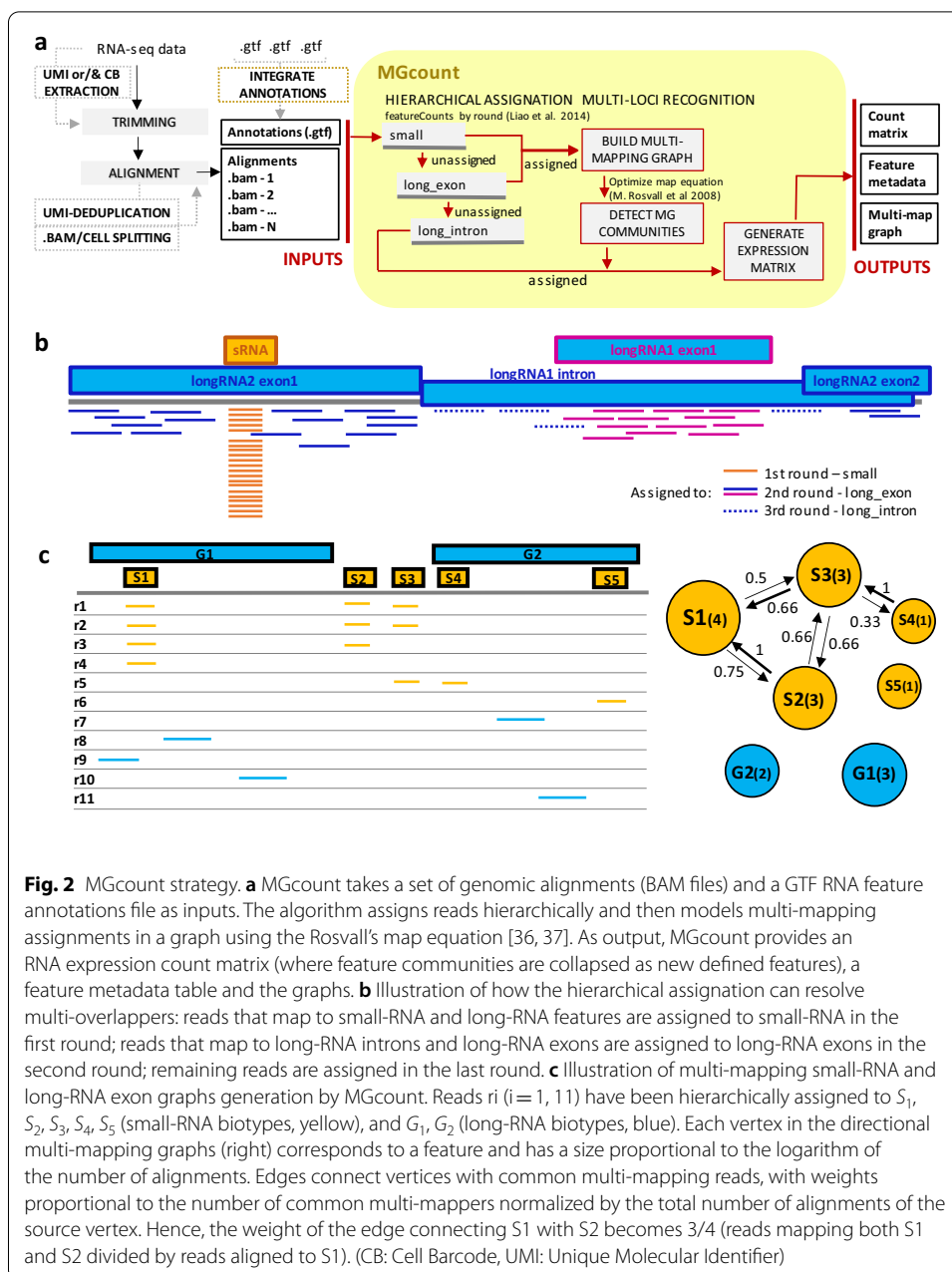


Fig. 2 MGcount strategy. **a** MGcount takes a set of genomic alignments (BAM files) and a GTF RNA feature annotations file as inputs. The algorithm assigns reads hierarchically and then models multi-mapping assignments in a graph using the Rosvall’s map equation [36, 37]. As output, MGcount provides an RNA expression count matrix (where feature communities are collapsed as new defined features), a feature metadata table and the graphs. **b** Illustration of how the hierarchical assignation can resolve multi-overlappers: reads that map to small-RNA and long-RNA features are assigned to small-RNA in the first round; reads that map to long-RNA introns and long-RNA exons are assigned to long-RNA exons in the second round; remaining reads are assigned in the last round. **c** Illustration of multi-mapping small-RNA and long-RNA exon graphs generation by MGcount. Reads r_i ($i = 1, 11$) have been hierarchically assigned to S_1, S_2, S_3, S_4, S_5 (small-RNA biotypes, yellow), and G_1, G_2 (long-RNA biotypes, blue). Each vertex in the directional multi-mapping graphs (right) corresponds to a feature and has a size proportional to the logarithm of the number of alignments. Edges connect vertices with common multi-mapping reads, with weights proportional to the number of common multi-mappers normalized by the total number of alignments of the source vertex. Hence, the weight of the edge connecting S_1 with S_2 becomes $3/4$ (reads mapping both S_1 and S_2 divided by reads aligned to S_1). (CB: Cell Barcode, UMI: Unique Molecular Identifier)

Author details

¹Epigenetics Unit, Diagenode s.a., Liège, Belgium. ²Department of Biology, Humboldt-Universität Zu Berlin, Berlin, Germany. ³Department of Anatomy and Embryology, Leiden University Medical Centre, Leiden, The Netherlands.

Published online: 01 June 2022

Reference

- Hita, et al. MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts. BMC Bioinformatics. 2022;23:39. <https://doi.org/10.1186/s12859-021-04544-3>.

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