



Eduardo Gade Gusmão <eggduzao@gmail.com>

Fwd: Decision on Nature Methods submission NMETH-BC24264B-Z1 mensagem

Ivan Gesteira Costa Filho <ivan.costa@rwth-aachen.de>

22 de janeiro de 2016 15:45

Para: Eduardo Gade Gusmão <eggduzao@gmail.com>, Martin Zenke <martin.zenke@rwth-aachen.de>, Manuel Allhoff <allhoff@ices.rwth-aachen.de>

Dear all,

Revisions are in and this is this is the long list of things to be done.

"Through-out the manuscript the authors use the term "experimental bias" ... The authors need to change this term, because it is misleading and incorrect. I suggest they use "footprint normalization" or "experimental normalization"

We are in! Congrats everyone!

Ivan

----- Forwarded message -----

From: <n.rusk@us.nature.com>

Date: 2016-01-22 15:32 GMT+01:00

Subject: Decision on Nature Methods submission NMETH-BC24264B-Z

To: ivan.costa@rwth-aachen.deCc: methods@us.nature.com

19th Jan 2016

Dear Dr Costa Filho,

Your revised Analysis, "Analysis of computational footprinting methods for DNase sequencing experiments", has now been seen again by our referees. In light of their advice, I am happy to inform you that if you revise your manuscript appropriately in response to the referees' comments and our editorial requirements detailed below, in the attached files, and in files from our copy editor which I will send next week, we can in principle offer to publish the paper in Nature Methods.

Please do NOT start the revision before you have received the files from our copy editor.

We ask that you limit the revised manuscript to no more than 3000 words, excluding abstract, methods, acknowledgments, author contributions, references and figure legends, which should be shortened as much as possible.

I am attaching a file with my edits, since this is quite a technical topic I ask you to pay special attention to avoiding jargon and clearly defining the methods you used. I have added some queries to the text in the attached file. Please respond to those and leave the Track change function in Word turned on, so I can see what you changed.

In addition, please address the following issues:

1) We are trying to improve the quality and transparency of statistics and methods reporting in our papers. When revising your manuscript, please fill out the checklist at http://www.nature.com/nmeth/pdf/sm_checklist.pdf to confirm that all relevant elements have been included in the manuscript. (If you have already filled out this checklist for a previous version of the manuscript, please only fill in the information relevant to any new experiments.) Submit this checklist, and any previous version of the checklist, with your revised manuscript.

2) Include accession numbers for all sequence, structure or microarray data required for publication. See below for details. We urge you to arrange for data to be released within one month from now so it will be available at publication.

3) In the interest of our colorblind readers we ask that you use a color combination other than red and green for contrast. Replacing red with magenta or green with turquoise are two possible color-safe alternatives.

To further increase transparency, we encourage you to provide, in tabular form, the raw data underlying the graphical representations used in your figures. This is in addition to our well-established data-deposition policy for specific types of experiments and large datasets. For readers, the source data will be made accessible directly from the figure legend. Spreadsheets can be submitted in .xls, .xlsx or .csv formats. Only one (1) file per figure is permitted: thus if there is a multi-paneled figure the source data for each panel should be clearly labeled in the csv/Excel file; alternately the data for a figure can be included in multiple, clearly labeled sheets in an Excel file. As with Supplementary Information, files sizes of up to 30 MB would be permitted; however it is anticipated that the vast majority of source data files will be much smaller than this. When submitting source data files with your manuscript please select the Source Data file type and use the Title field in the File Description tab to indicate which figure the source data pertains to.

In general, when preparing the final version, please keep in mind that Nature Methods will be read by people from a wide range of disciplines. The paper should therefore be written in a way that will be accessible to non-specialists, avoiding jargon as far as possible and explaining points that may not be obvious to those outside the field.

Before sending us your revised manuscript, care should be taken to adjust the format to fit the style of Nature Methods so as to avoid delays in publication. Complete guidelines are available in the attached checklist, which must be signed and returned, and on our web site at <http://www.nature.com/nmeth/authors/submit/index.html>

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Biological materials should be deposited in established public repositories when an appropriate one exists and accession numbers provided. All sequence read, structure and microarray data must be freely available in public repositories and accession numbers provided. For plasmids and other engineered sequences the sequence may be reported in the manuscript but the biological material should be deposited with AddGene.

We may need to make further editorial changes before sending the manuscript to production, but we can return to these once we have received your revision.

Please upload the text (in Microsoft Word format, version 2010 or earlier) and figures as TIFF or EPS files using the link provided below.

<http://mts-nmeth.nature.com/cgi-bin/main.plex?el=A1M1DNJ4A6BBkb1J1A9ftdmky5AR7irnFTZYDlk3gUtgZ>

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We hope to receive your revised manuscript in ten days. Please let us know if circumstances will delay submission beyond this time. [If we receive your revised manuscript by XXX, it may be possible to include your paper in the group that will be published in the XXX issue.]

If you have any further questions or concerns, please feel free to contact me.

Best regards,

Nicole

Nicole Rusk, Ph.D.
Senior Editor
Nature Methods

Reviewers' Comments:

Reviewer #2:

Remarks to the Author:

I am happy that the authors decided to not only consider my suggestions, but actually thought how to make them work best in their context. This has involved a lot of work since the first submission, but I hope the authors agree that it was a worthwhile effort. As it stands now, this is a much-needed contribution that quantifies a number of disparate arguments.

Reviewer #3:

Remarks to the Author:

Overall, this manuscript is acceptable once terminology in the manuscript is changed to clarify some key points.

Through-out the manuscript the authors use the term "experimental bias" to mean difference between Dnase-seq experiments due to local chromatin conformation, sequence specificity, and fragmentation. The fact that the authors call chromatin conformation a bias is truly troubling to this reviewer, since the assay's goal to measure chromatin accessibility. The authors need to change this term, because it is misleading and incorrect. I suggest they use "footprint normalization" or "experimental normalization" to describe their approach. Normalization is exactly what they are trying to perform by correcting for the different experimental conditions (one-hit vs two-hit, DNaseI concentrations) and for DNaseI sequence specificity.

Attached:

- format checklist
- SI titles file
- ISI template
- figure corrections

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