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BIOINF-2013-1895.R1 - Minor Revision6 mensagens

bioinformatics.editorialoffice@oup.com <bioinformatics.editorialoffice@oup.com> 29 de maio de 2014 02:01

Para: eduardo.gusmao@rwth-aachen.de

Cc: eduardo.gusmao@rwth-aachen.de, Christoph.Dieterich@age.mpg.de, martin.zenke@rwth-aachen.de, ivan.costa@rwth-aachen.de, igcf@cin.ufpe.br

28-May-2014

Manuscript ID: BIOINF-2013-1895.R1

Title: Detection of Active Transcription Factor Binding Sites with the Combination of DNase Hypersensitivity and Histone Modifications

Dear Mr. Gusmão,

The reviews of your manuscript are now in hand. On behalf of the Bioinformatics Associate Editor, Inanc Birol, I am pleased to report that the reviewers found your manuscript acceptable for publication in Bioinformatics, subject to the suggested revisions. I am therefore returning your original manuscript for revision in line with the editorial and reviewer comments which can be found at the foot of this e-mail.

Please submit your revised version through the Author Center by clicking on the purple button 'Click here to Submit a Revision' in the Bioinformatics ScholarOne Manuscripts web site (<http://mc.manuscriptcentral.com/bioinformatics>).

Please ensure that you use either mandatory template format which can be found at:-
http://www.oxfordjournals.org/bioinformatics/for_authors/submission_online.html

We ask that revisions are submitted within one month. The system will automatically remove the revision option if a revised paper has not been submitted within this time.

To facilitate the production process we ask that you upload the following revised manuscript files at the revision stage:

EITHER: (i) A .doc or .rtf file of the revised manuscript, with all tables, figures, schemes and equations inserted in the document.

OR: (ii) All necessary LaTeX files that will be required by the typesetter (including bioinfo.cls, bib, .bst and .ps files) along with postscript and PDF versions of the complete manuscript.

Please can you mark-up the changes made after revision by using the track changes function or highlighting these in red text.

Please upload your final clean version of supplementary materials with your revised submission. This should be in pdf or Word format, not LaTeX.

I would also ask that you prepare an accompanying letter explaining exactly how each of the major points raised by the reviewers was addressed. This can be done either in a file uploaded alongside your revised manuscript as a Response to Reviewers file or through the Author Center where you can enter your responses directly in the appropriate box during the revision submission.

Please note that if you decide that you would like your figures printed in colour a charge of £350 per colour figure applies. If appropriate, you will be invoiced after your paper has been published in the print journal.

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Subject: BIOINF-2013-1895.R1 - Minor Revision

[Texto das mensagens anteriores oculto]

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30 de maio de 2014 07:36

Para: Eduardo Gade Gusmão <eduardo.gusmao@rwth-aachen.de>, Ivan Gesteira Costa Filho <ivan.costa@rwth-aachen.de>

Great Job !

We made it.

All best wishes,

Christoph

P.S.: Thanks Ivan for inviting me towards the Brazil workshop.

Dr. Christoph Dieterich

Max-Planck-Institut für Biologie des Alterns
Max Planck Institute for Biology of Ageing

Am 29.05.2014 um 02:01 schrieb bioinformatics.editorialoffice@oup.com:
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30 de maio de 2014 08:29

acho que o paper já praticamente passou. Revisores 1 e 3 estão obviamente ok, só o 2 precisa de alguma argumentação e algumas análises adicionais nos resultados. Podemos também por mais resultados para a questão de ES do revisor 3.

> reviewer 2

Este ta quereno encrecar um pouco, mas acho que nao vai ser problema, ja que os outros 2 gostaram ...

>1. The manuscript makes a fundamental assumption about active binding sites with regard to histone modification state around the binding sites. It is not clear what >fraction of TFs follow this pattern. Are there specific families where this observation is not necessarily true?

O que poderíamos fazer eh pegar a classificacao de TF do

<http://nar.oxfordjournals.org/content/41/D1/D165.long>

eh associar com o AUC individuais de cada fator. Outra coisa que podemos analisar eh a associacao do AUC com o info. content.

>2. On a related note, what is the false negative rate of the method? The training is based on manual annotation of a particular locus and therefore does not capture >the binding sites that do not follow the histone modification pattern. One way to look at this is to analyze the DNase hotspots not annotated to contain footprints by >the HMM method. Are there are specific motifs enriched in these peaks?

Isso eh valido (e possivelmente simples de fazer). De outro lado o FPR pode ser calculado na nossa metodologia de avaliacao.

>3. The results also show multiple footprints within a single peak -- do each of these footprints correspond to the binding of a different factor or is this an artifact of the way the HMM is set up? This is important information for downstream analyses such as motif discovery.

Obviamente acreditamos no cobinding, mas isto eh dificil de argumentar ja que nao existe maneira experimental de provar cobinding. Poderiamos avaliar quanto por cento dos footprints tem TP para alguns dos fatores, mas obviamente so far sentido se tivermos medido todos os possiveis TFs da celula. Talves para k562 valha a pena. Outra coisa que podemos fazer eh comparar o numero de footprints em promotor/enhancer e nos CTCFs (que deve ser sozinhos).

> Reviewer: 3

>Also, from a biological point of view, it is highly surprising that ES cells would not need separate parameterization >(but maybe the relevant parameters are in fact rolled into the preprocessing of the data...). Its chromatin >landscape is very different from differentiated cells (cf de Wit, Bouwman et al Nature 2013), and it might be worth > to add a comment in this regard.

Podemos reviver aquela análise das histonas separadas por célula.

Ufa, quase lah. Entao, qual a data mesmo da sua volta? Nao estou vendo as datas no calendario do grupo!

abs,

Ivan

2014-05-29 2:01 GMT+02:00 <bioinformatics.editorialoffice@oup.com>:

[Texto das mensagens anteriores oculto]

[Texto das mensagens anteriores oculto]

Ivan Gesteira Costa Filho <ivan.costa@rwth-aachen.de>
Para: Christoph Dieterich MPI-AGE <Christoph.Dieterich@age.mpg.de>
Cc: Eduardo Gade Gusmão <eduardo.gusmao@rwth-aachen.de>

30 de maio de 2014 08:43

Hi,

Yes, it is looking good and finger crossed for the brazilian workshop.

best,

Ivan

2014-05-30 7:36 GMT+02:00 Christoph Dieterich MPI-AGE
<Christoph.Dieterich@age.mpg.de>:

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