

Re: Pipeline, next steps

Subject: Re: Pipeline, next steps

From: Luis Serrano Pubul <luis.serrano@crg.eu>

Date: 22/09/16 19:33

To: Katerina Kirsanova <catherine.kirsanova@crg.eu>

CC: Maria Lluch Senar <maria.lluch@crg.eu>, Juan Laorden <Juan.Laorden@crg.eu>, Julia Ponomarenko <julia.ponomarenko@crg.eu>

Dear Katerina

I don't think your attitude is very constructive. María is your direct boss as she is in charge of the mico project. Please go upstairs meet with María and see how you could work with her knowing that she is the person in charge of you. I believe that you are more than qualified to do many things in this project, but this requires talking in an open and constructive way with María and Samuel. It is extremely difficult to understand you, and to make sense of what you do. So please talk to María, hear what she has to say, offer your suggestions in a polite way and change your attitude. María does not know as much about computing as you do, but she knows the biology and what we want to achieve.

Thanks

Luis

Luis Serrano Pubul

CRG Director

EMBO member

V

On 22 Sep 2016, at 18:17, wrote:

Dear Maria,

On 22/09/16 16:31, My friends and colleagues are asking me why I didn't quit right after that. I was going to.

Dear Katerina,

Please, upload by yourself the gb (you can have them from ncbi).

The references are:

CP013921.1

CP014272.1

CP015004.1

I have been looking at your webpage and I respect your work. I did not realize about gb. instead of gbk, sorry about it.

I do not know about the place where you should see the errors....and neither how you expect we report it...simply an error message appeared

This email allegedly was written by Luis.

Although he never used ES layout,

never used to write his sweet heart's name this way.

María had full access to his desk and he wasn't in the Institute at that moment.

This histeric went out after once I said «no»

to María's manipulative «if you want to talk, as I mentioned before, we can discuss in any moment»

— see below.

That was just yet another one failed attempt of manipulative oppression.

She could easily come up to me for the questions she wanted be solved.

But in fact she barely ever even looked at the app I was making for them.

See the discussion below: she was lying, before making her «propose you to meet to discuss»

in «professional manner» — she did not even open the «webpage» to check whether it was working.

I saw it all in the logs.

My friends and colleagues are asking me why I didn't quit right after that.

I was going to.

One of the reasons — a snitch deceived me.

I am sorry, but in an adult world one does Ctrl+C of a error message and Ctrl+V to insert it to the correspondence.
Unless one wants to make a point.
As it is clear that the message of a error was not too hard to understand.

However, I do not see any of the emails that you sent respectful, starting from the first, where I tried to describe the required tasks in a professional manner and propose you to meet to discuss about them.

I am sorry I did not notice any professional manner there. You may call that spade is a spoon, but it's still a spade.
There were no proposal to meet either.
But what I clearly could see: a manipulation ending with «if you want», which I had to discard first and reacted only after you persisted.
All my answers were to the point.

Your ending sentence was not acceptable.

I can only repeat it, sorry.

I have never had any complain about my professionalism or the way to discuss or tell the things.

Your references do not shine though. So take care when asserting yourself this way.

So, please, if you want to talk, as I mentioned before, we can discuss in any moment.

Again. I do not want.
If you put «if» be ready to withstand a honest answer.
Even if you did not meet it before. Once you will have to bear it anyway.

Best regards,
Maria
If you cannot do this work let us know and we will look for another way to do that.

If you cannot communicate without cheesy manipulations you'd better to

steer clear of it whatsoever.
Especially after you have just demonstrated your own inability to perform a simplest tasks.

Regards, —
Catherine

From: Katerina Kirsanova
Sent: jueves, 22 de septiembre de 2016 15:54
To: Maria Lluch Senar <maria.lluch@crg.eu>; Luis Serrano Pubul <luis.serrano@crg.eu>
Subject: Re: Pipeline, next steps

Dear Maria,

1. I would appreciate if you would understand that you have to send the links for the information you need to be loaded.
Not several 10th Mb files of wrong format.

2. You have to send a description of a error you have met if you are really a member of the team who cares about the project and have respect to the work of the others.

3. You also have to know, that any error is seen in the logs: so I do not see any error there.

Unfortunately I have to say that the above means that you did not care to listen to me when I explained how to work with GenBank format.
You even did not care to read that I wrote many times: we work with .gb format, not gbk.

I am sure you can manage to pull it off on your own.
And I am sure you are able to learn how to put the tasks professionally and how to respect the work of the others.

Cheers, —
Catherine

On 22/09/16 15:19, Maria Lluch Senar wrote:

I tried to upload the gbk of the three species and it gives me error.
There you have the gbks. Please do asap
Thanks

From: Katerina Kirsanova
Sent: jueves, 22 de septiembre de 2016 14:43
To: Maria Lluch Senar <maria.lluch@crg.eu>; Samuel Miravet Verde <samuel.miravet@crg.eu>
Cc: Luis Serrano Pubul <luis.serrano@crg.eu>
Subject: Re: Pipeline, next steps

On 22/09/16 14:37, Maria Lluch Senar wrote:

- 2h ago the webpage was not working (today is present tense).
- About the categories: please add the classification to each gene as indicated. Also the export of the data should have the EXACT format that I have specified. We do not want to do processing by ourselves.
- When are you planning to have it?

Not very long after you load E. coli, Lactobacillus and B. subtilis into DB :)

From: Katerina Kirsanova
Sent: jueves, 22 de septiembre de 2016 14:31
To: Maria Lluch Senar <maria.lluch@crg.eu>; Samuel Miravet Verde <samuel.miravet@crg.eu>
Cc: Luis Serrano Pubul <luis.serrano@crg.eu>
Subject: Re: Pipeline, next steps

On 22/09/16 14:11, Maria Lluch Senar wrote:

Hi Katerina,
See my answers bellow

From: Katerina Kirsanova
Sent: jueves, 22 de septiembre de 2016 13:41
To: Maria Lluch Senar <maria.lluch@crg.eu>; Samuel Miravet Verde <samuel.miravet@crg.eu>

Cc: Luis Serrano Pubul
[<luis.serrano@crg.eu>](mailto:luis.serrano@crg.eu)
Subject: Re: Pipeline, next steps

Dear All,

On 22/09/16 12:58, Maria Lluch Senar wrote:

Dear Katerina,
I've just tried to enter in the
webpage and it is not working J

it was down since last week.
Can you solve it? please

It was simple past tense in English.

We have been discussing with
Samuel which other aspects could
be implemented in the pipeline.

- 1) For the genomes that we
sent (for doing translation
of genomes and
comparative analysis). By
default for E.coli and
different bacteria from
Mycoplasma the
correspondent codon usage
should be considered.

You can chose it while loading .gb file.
we want that by default in E. coli and b.
subtilis you put the code 11 of gbk

As I said you can chose it in the corresponding
interface, if 11 is a default for E.coli in .gb file: you
chose «Take from GenBank file»

- 2) Then for the comparative.
We need a different output file. We would like having an excel file with this information:
 - a. id of gene
 - b. number of compared genomes where the protein has been found
 - c. Category of conservation:
 - i. Mycoplasma: if it is conserved in other Mycoplasmas different to M. pneumoniae
 - ii. Gram positive: if it appears conserved in Bacillus subtilis and or Lactobacillus
 - iii. Gram negative: if it appears conserved in E. coli

This information exists in the exported table.

The information is not in this format (please read what I have written) the groups and categories are not in the

output file as I have defined J

J

It's a matter of looking into the table: these categories/data are seen straight away. If you need export data to be automatically processed further or you need to sort data by these categories, say it as it is please.

3) Also, the last section that we discussed long time ago about the pipeline is the representation of the results.

a. There should be a section of Analysis of smORFs and it should represent in histograms or pies the results of:

i.
Conservation
of smORFs
(%of the total
putative
smORFs that
can be
classified in
any of the
three
categories)

ii.
Transcriptionally
active (% of
the total

putative
smORFs that
show
significant
levels of RNA)

iii. ncRNAs
(% of ncRNAs
that could
encode for
proteins (ORF
inside); % of
real ncRNAs).
Of each
section of the
pie there
should be two
subpies
representing
for each
category: the
% that overlap
in antisense
with annotated
ORFs (A) the %
that overlap in
sense (S) and
the % that are
in intergenic
regions (IR).

I can make dynamic graphical
representation of all information
presented in the tables.
I would be great!!!

Please, let us know if you want to
meet to discuss about it

Most of all I want being outside, doing a
lot of different things on my own.
But while inside here 9.30-17.30 I am
available anytime which suits you best.

Re: Pipeline, next steps

Let us know if you need information for doing
what we said J and if you want we can meet
inside or outside ;p

Quite frankly: if you do ask whether I want to meet:
No, I do not.
Sorry.

Cheers, —
Catherine

Cheers, —
Catherine.

Thank you very much
Cheers
Maria