

@AMaxEll17

<http://harvardforest.fas.harvard.edu/aaron-ellison/>

From: Jim Bochicchio [<mailto:jboch@broadinstitute.org>]
Sent: Wednesday, May 31, 2017 3:56 PM
To: Ellison, Aaron <aellison@fas.harvard.edu>
Cc: Lau, Matthew K. <matthewklau@fas.harvard.edu>; Jennifer Wineski <jwineski@broadinstitute.org>; Caroline Cusick <ccusick@broadinstitute.org>
Subject: Re: Meeting request (was RE: ant sequences NCBI errors)

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We'll be there.

Thank you,
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Aaron M. Ellison, *Senior Research Fellow*

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Subject: Re: Meeting request (was RE: ant sequences NCBI errors)
Date: June 13, 2017 at 1:47 PM
To: Caroline Cusick ccusick@broadinstitute.org
Cc: Aaron M Ellison aellison@fas.harvard.edu, Jim Bochicchio jboch@broadinstitute.org



Hi Caroline, thanks for putting those on the FTP server. I'm grabbing those right now.

Best,

Matt

On Jun 13, 2017, at 9:43 AM, Caroline Cusick <ccusick@broadinstitute.org> wrote:

Hi Matt and Aaron,

Terry has moved all the information to the FTP (we will still create the Aspera backup) and has provided the information on the new assemblies below:

The assembly data is available via <ftp://aadata@ftp.broadinstitute.org> with the following username and password, you should be able to access the directory /lau/ant:

- username **aadata**
- password **CILanalysis154**

Each directory will have 5 files. For example using this folder, SM-AJDMW/

SM-AJDMW/remove.txt
SM-AJDMW/assembly.agp
SM-AJDMW/scaffolds.fasta
SM-AJDMW/assembly.removed.fasta
SM-AJDMW/contigs.fasta

The contigs.fasta and scaffolds.fasta are the updated assembly files and the assembly.agp is the updated AGP corresponding to the updated fasta files. The "remove.txt" file is the table of directives instructing modify_assembly.py where to remove adapter sequence. Finally, assembly.removed.fasta is the fasta sequence of the removed adapter.

We're working on the methods and scripts, and I'll follow up with those as soon as we have them. Let me know if you have any questions or have any issues accessing the data.

thanks!
Caroline

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Cheers,

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Best,

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<ncbi_contam_screen.txt>

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Cc: Jim Bochicchio jboch@broadinstitute.org

CC

Hi Matt and Aaron,

Terry has moved all the information to the FTP (we will still create the Aspera backup) and has provided the information on the new assemblies below:

The assembly data is available via <ftp://aadata@ftp.broadinstitute.org> with the following username and password, you should be able to access the directory /lau/ant:

- username **aadata**
- password **CILanalysis154**

Each directory will have 5 files. For example using this folder, SM-AJDMW/

SM-AJDMW/remove.txt
SM-AJDMW/assembly.agp
SM-AJDMW/scaffolds.fasta
SM-AJDMW/assembly.removed.fasta
SM-AJDMW/contigs.fasta

The contigs.fasta and scaffolds.fasta are the updated assembly files and the assembly.agp is the updated AGP corresponding to the updated fasta files. The "remove.txt" file is the table of directives instructing `modify_assembly.py` where to remove adapter sequence. Finally, assembly.removed.fasta is the fasta sequence of the removed adapter.

We're working on the methods and scripts, and I'll follow up with those as soon as we have them. Let me know if you have any questions or have any issues accessing the data.

thanks!
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617-

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Website

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<https://>

www.broadinstitute.org/btl

[oadinstitute.org](https://www.broadinstitute.org/btl)

[/btl](https://www.broadinstitute.org/btl)

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75 Ames St | Cambridge MA 02142 USA

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Aaron M. Ellison, Senior Research Fellow

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thank!

THANKS:

Caroline

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wrote:

Hi Caroline, just pinging you again
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radar.

Thanks!

Matt

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quick question, if
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Date: May 25, 2017 at 5:03 PM
To: Ellison, Aaron aellison@fas.harvard.edu
Cc: Lau, Matthew K. matthewklau@fas.harvard.edu, Jim Bochicchio jboch@broadinstitute.org, Caroline Cusick ccusick@broadinstitute.org

JW

Thank you. I will send an invitation shortly!

On Thu, May 25, 2017 at 5:01 PM, Ellison, Aaron <aellison@fas.harvard.edu> wrote:

Works for me, too.

We'll be there.

Thank you,

Aaron

Aaron M. Ellison, Senior Research Fellow

Harvard University, Harvard Forest

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aellison@fas.harvard.edu

@AMaxEll17

<http://harvardforest.fas.harvard.edu/aaron-ellison/>

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Email: jwineski@broadinstitute.org

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Subject: Re: Meeting request (was RE: ant sequences NCBI errors)
Date: May 25, 2017 at 4:53 PM
To: Jim Bochicchio jboch@broadinstitute.org
Cc: Ellison, Aaron aellison@fas.harvard.edu, Lau, Matthew K. matthewklau@fas.harvard.edu, Caroline Cusick ccusick@broadinstitute.org

JW

Good afternoon Aaron and Matthew,

I can offer Monday, June 12th from 1pm -1:30pm for a meeting with Jim.

Will that work for your schedules as well?

Thank you,

Jenn

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@AMaxEll17

From: Lau, Matthew K.
Sent: Wednesday, May 24, 2017 10:39 AM
To: Jim Bochicchio <jboch@broadinstitute.org>
Cc: Caroline Cusick <ccusick@broadinstitute.org>; Ellison, Aaron <aellison@fas.harvard.edu>
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From: Jim Bochicchio jboch@broadinstitute.org
Subject: Re: Meeting request (was RE: ant sequences NCBI errors)
Date: May 25, 2017 at 4:42 PM
To: Ellison, Aaron aellison@fas.harvard.edu, Jennifer Wineski jwineski@broadinstitute.org
Cc: Lau, Matthew K. matthewklau@fas.harvard.edu, Caroline Cusick ccusick@broadinstitute.org

JB

Hi Aaron

We are adding Jenn to the email so she can assist in setting up this meeting.

Thanks
Jim

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Dear Jim and Caroline,

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Thank you very much,

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Aaron M. Ellison, Senior Research Fellow

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@AMaxEll17

<http://harvardforest.fas.harvard.edu/aaron-ellison/>

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