From: Lau, Matthew K. matthewklau@fas.harvard.edu

Subject: Re: Meeting request (was RE: ant sequences NCBI errors)

Date: June 13, 2017 at 2:08 PM

To: Aaron M Ellison aellison@fas.harvard.edu



Hey Aaron, I've got the FTP transfer running to move the genomes to Odyssey. I'm going to uzip them in a bit take a look at them.

Best,

Matt

On Jun 13, 2017, at 9:48 AM, Ellison, Aaron <aellison@fas.harvard.edu> wrote:

Matt – as long as the ftp is clear, please download this all today.

Thanks,

Aaron

From: Caroline Cusick [mailto:ccusick@broadinstitute.org]

Sent: Tuesday, June 13, 2017 9:44 AM

To: Lau, Matthew K. <matthewklau@fas.harvard.edu>; Ellison, Aaron aellison@fas.harvard.edu>

Cc: Jim Bochicchio < jboch@broadinstitute.org>

Subject: Re: Meeting request (was RE: ant sequences NCBI errors)

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Each directory will have 5 files. Foe 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

On Wed, May 31, 2017 at 4:22 PM, Lau, Matthew K. < matthewklau@fas.harvard.edu > wrote:

Hi Jim, thanks for the update.

Cheers,

Matt

On May 31, 2017, at 4:14 PM, Ellison, Aaron <aellison@fas.harvard.edu> wrote:

Thank you! Aaron

Aaron M. Ellison, Senior Research Fellow
Harvard University, Harvard Forest
324 North Main Street
Petersham, Massachusetts 01366 USA
aellison@fas.harvard.edu

@AIVIAXEII1/

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. <<u>matthewklau@fas.harvard.edu</u>>; Jennifer Wineski <<u>jwineski@broadinstitute.org</u>>; Caroline Cusick

<ccusick@broadinstitute.org>

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Hi Matt and Aaron

We wanted to send along a quick update. Our analyst Terry is going back through 5 of the assemblies you mentioned and working on trimming them. As for the other two assemblies, Terry is working with one of our engineers to put in place a pipeline they can run to look for the adapter sequencing and trim them since you didn't get an NCBI error report for those two that he can work off of.

Thanks Jim

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
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@AMaxEll17

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From: Lau, Matthew K.

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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,

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Thank you very much,

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Does Thursday June 8 in the mid-to-late afternoon work for you? If not, does Monday June 12 (any time) work?

Also, I came across this presentation on Data Sharing at Broad (http://genomicinfo.broadinstitute.org/acton/attachment/13431/f-0132/1/-/-/-/ASHG16%20Workbench%20Presentation%20-%20Final.pdf?sid=TV2:QKwcswckd).

Per my request for the code, are your analysts starting to use these Workbench methods? It seems like it would make this a whole lot easier.

Thanks!

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Postdoctoral Fellow Harvard Forest Harvard University 324 N Main St. Petersham, MA 01366 978-756-6165

"Knowledge is knowing a tomato is a fruit. Wisdom is not putting it in a fruit salad." — Miles Kingston

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On May 16, 2017, at 9:17 PM, Caroline Cusick < ccusick@broadinstitute.org > wrote:

Hi Matt,

Our analyst is going through the comments that you sent from NCBI now, and I will pass along any updates/questions he has during this and definitely keep you updated!

thanks, Caroline

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What's the status on the assemblies? And per my last email, are you reprocessing from the raw reads?

Cheers,

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Just in case it's helpful to know now, your FTP server will work fine for the data transfer.

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Our analyst had a question about whether all 7 assemblies were submitted to NCBI, or just this one (SM-AZXXM)? If the other six were returned with errors also, if you could pass that along and he will make sure to confirm that we've removed all the sites flagged by NCBI.

let me know if you have any questions! thanks,
Caroline

On Fri, May 12, 2017 at 11:21 AM, Lau, Matthew K. <<u>matthewklau@fas.harvard.edu</u>> wrote:

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ge MA

seque nce labeli ng issue? Also, is there a good soluti on to remo ving the prime rs from the asse mblie s?

Best,

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02142, USA Phone: <u>617-</u> 714-<u>8513</u> Website https:// www.br <u>oadinsti</u> tute.org /btl Caroline Cusick
Product Coordinator
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75 Ames St | Cambridge MA 02142 USA Caroline Cusick Product Coordinator Broad Institute of MIT and Harvard 75 Ames St | Cambridge MA 02142 USA <ncbi_contam_screen.txt> Caroline Cusick
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Caroline Cusick
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Broad Institute of MIT and Harvard
75 Ames St | Cambridge MA 02142 USA

From: Lau, Matthew K. matthewklau@fas.harvard.edu

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

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<ncbi_contam_screen.txt>

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From: Jim Bochicchio jboch@broadinstitute.org

Subject: Re: Meeting request (was RE: ant sequences NCBI errors)

Date: May 31, 2017 at 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

Hi Matt and Aaron

We wanted to send along a quick update. Our analyst Terry is going back through 5 of the assemblies you mentioned and working on trimming them. As for the other two assemblies, Terry is working with one of our engineers to put in place a pipeline they can run to look for the adapter sequencing and trim them since you didn't get an NCBI error report for those two that he can work off of.

Thanks Jim

Aaron

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 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/

From: Lau, Matthew K.

Sent: Thursday, May 25, 2017 4:54 PM

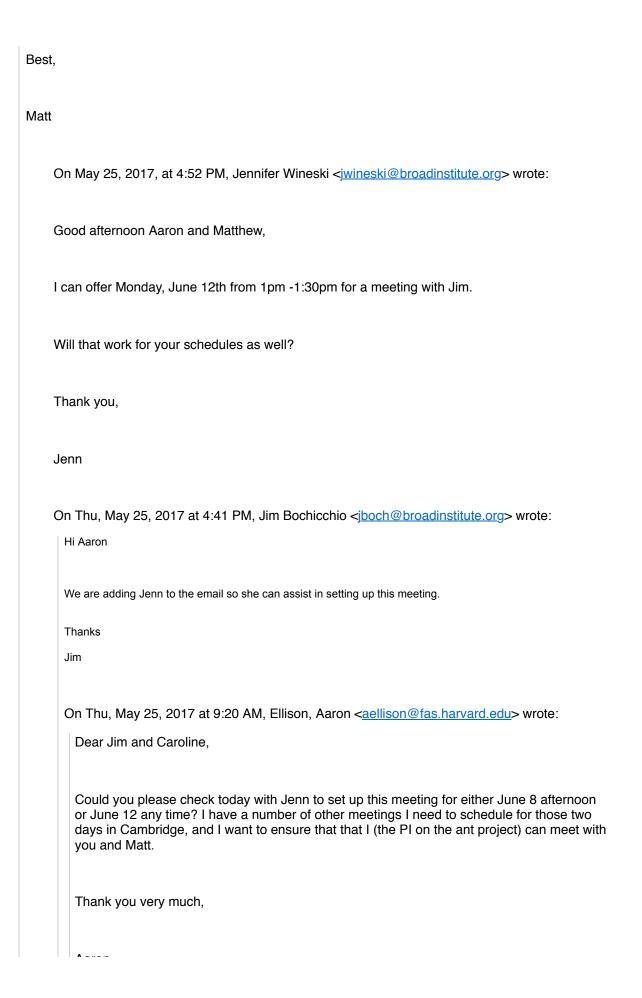
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From: Lau, Matthew K.

Sent: Wednesday, May 24, 2017 10:39 AM **To:** Jim Bochicchio <jboch@broadinstitute.org>

Cc: Caroline Cusick < ccusick@broadinstitute.org >; Ellison, Aaron

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Subject: Re: ant sequences NCBI errors

Hi Jim and Caroline, looking forward to getting something on the calendar.

Thanks!

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On May 22, 2017, at 8:25 PM, Jim Bochicchio <<u>jboch@broadinstitute.org</u>> wrote:

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We'll check with Jenn our admin to set up a meeting. She's currently out of the office but should be back on Wednesday.

Thanks

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From: Jennifer Wineski jwineski@broadinstitute.org

Subject: Re: Meeting request (was RE: ant sequences NCBI errors)

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

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	Thank you very much,
	Could you please check today with Jenn to set up this meeting for either June 8 afternoon or June 12 any time? I have a number of other meetings I need to schedule for those two days in Cambridge, and I want to ensure that that I (the PI on the ant project) can meet with you and Matt.
	Dear Jim and Caroline,
	On Thu, May 25, 2017 at 9:20 AM, Ellison, Aaron <aellison@fas.harvard.edu> wrote:</aellison@fas.harvard.edu>
	Jim
	Thanks
	We are adding Jenn to the email so she can assist in setting up this meeting.
	Hi Aaron
0	n Thu, May 25, 2017 at 4:41 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:</jboch@broadinstitute.org>
Je	enn
TI	nank you,
W	fill that work for your schedules as well?
lo	can offer Monday, June 12th from 1pm -1:30pm for a meeting with Jim.
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Cc: Jim Bochicchio <jboch@broadinstitute.org>; Ellison, Aaron <aellison@fas.harvard.edu>; Caroline Cusick <ccusick@broadinstitute.org>

Subject: Re: Meeting request (was RE: ant sequences NCBI errors)

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Aaron M. Ellison, Senior Research Fellow Harvard University, Harvard Forest 324 North Main Street Petersham, Massachusetts 01366 USA ΑE

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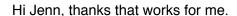
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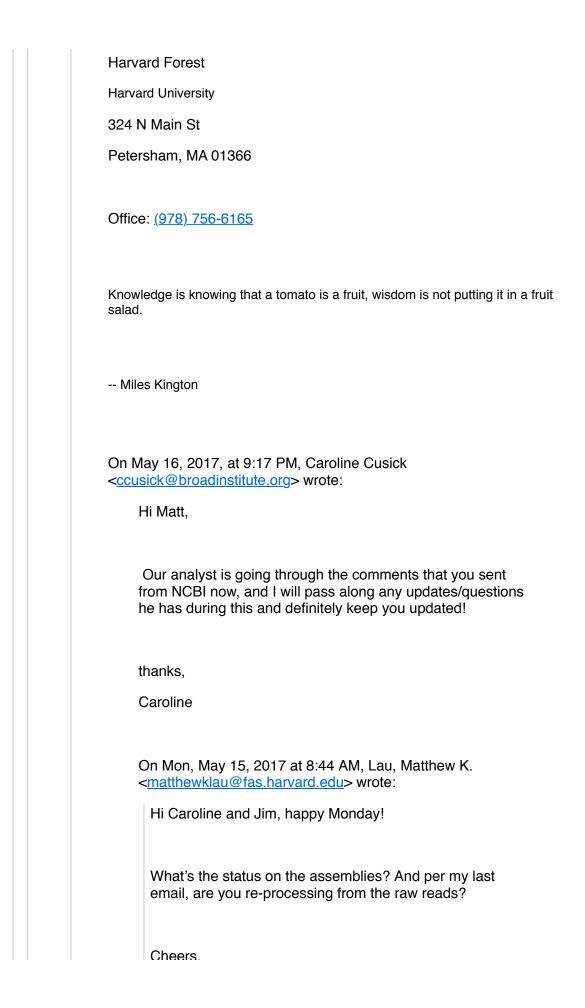
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Cc: Lau, Matthew K. matthewklau@fas.harvard.edu, Caroline Cusick ccusick@broadinstitute.org

Thank you.

Aaron

Aaron M. Ellison, Senior Research Fellow
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aellison@fas.harvard.edu
@AMaxEll17

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Sent: Thursday, May 25, 2017 4:42 PM

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