

From: Lau, Matthew K. matthewklau@fas.harvard.edu
Subject: Re: FTP information for assembly data
Date: December 13, 2016 at 10:04 AM
To: Caroline Cusick ccusick@broadinstitute.org
Cc: James Bochicchio jboch@broadinstitute.org



Awesome, thanks Caroline.

Cheers,

Matt

On Dec 13, 2016, at 9:24 AM, Caroline Cusick
<ccusick@broadinstitute.org> wrote:

Hi Matt,

These should be all set and in the folder for the FTP (the file names will be XXX.tar.gz, and will match the key). If you could just let me know when you're all set, I'll make sure to remove the compressed duplicates.

thanks!
Caroline

On Thu, Dec 8, 2016 at 2:14 PM, Caroline Cusick
<ccusick@broadinstitute.org> wrote:

Hi Matt,

I'm queueing the tarballs up now, I'll send you another email when they're complete.

thanks!
Caroline

On Wed, Dec 7, 2016 at 3:27 PM, Lau, Matthew K.
<matthewklau@fas.harvard.edu> wrote:

Hi Caroline, when you get a chance, would you compress the raw data files?

Thanks!

Matt

On Dec 6, 2016, at 5:20 PM, Lau, Matthew K.
<matthewklau@fas.harvard.edu> wrote:

Hi Caroline, thanks! I'll move those over onto my server tomorrow morning.

Best,

Matt

On Dec 6, 2016, at 4:42 PM, Caroline Cusick
<ccusick@broadinstitute.org> wrote:

Hi Matt,

I just wanted to follow up with the FTP log in for the Raw Data. I've also re-attached the key that indicates the library type for each sequencing run. Let me know if you run into any issues

access by: <ftp://ftp.broadinstitute.org/>
username: SSF-1728
password: f3aexw29

thanks!
Caroline

On Mon, Nov 21, 2016 at 11:25 AM, Lau, Matthew K.
<matthewklau@fas.harvard.edu> wrote:

Great, thanks Terry!

I was able to access the files. I'll grab those and get them off your FTP server ASAP.

Thanks for your hard work on this.

Happy T-Day,

Matt

On Nov 18, 2016, at 4:14 PM, Terrance Shea
<tshea@broadinstitute.org> wrote:

Hello again-

It was a pleasure to meet you in the meeting today. Below described the contents of the assembly handoff and how to access it.

The assembly data is available via <ftp://aadata@ftp.broadinstitute.org> with the following username and password:

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

You should see the following folder:

<image.png>

and then within this "lau-ant" folder 7 folders, one for each sample, for example:

<image.png>

I have attached the assembly metrics sheet which was reviewed in the meeting. The "pre_post_pilon" tab shows the assembly metrics before and after running Pilon (assembly improvement tool that is run after ALLPATHS-LG assembly). The "filtered_assembly_stats" shows the metrics after likely contaminant contigs/scaffolds were removed

Removal

There are two versions of the assembly in each sample directory, pre- and post- contamination filtering.

Each sample directory contains a contigs file (contigs.fasta), scaffolds file (scaffolds.fasta), and agp file (assembly.agp). These are pre-contamination removal. The agp file describes how contigs are linked within scaffolds.

Each sample directory contains a "gaemr" analysis directory and within this is a "chart", "table", and "html" subdirectory. The "index.html" file (within gaemr/html folder) may be opened in a browser to view. The GAEMR analysis corresponds to the previously described "contigs.fasta" and "scaffolds.fasta" files. One additional gaemr file is found in the "chart" directory and that is a blast bubble plot done at the superkingdom level (default level is genus). This plot gives an approximation for the number of bacterial and viral contigs found.

Likely contaminants (generally either Wolbochia and/or Mycoplasma) were found during the analysis of the GAEMR output. Contaminants scaffolds were removed and these are listed in the "remove.txt" file. The assembly with contaminants removed is found in the "filtered.contigs.fasta", "filtered.scaffolds.fasta", and "filtered.agp" set of files. The contigs/scaffolds removed (not in the filtered.contigs.fasta file) may be found in the "filtered.removed.fasta" file. GAEMR was not re-run on the contamination-filtered assembly.

Please let us know if you encounter any problems in accessing the data. Also, if all goes smoothly, please let us know once you have all of this as we can then remove it from the FTP area.

I gather that Caroline or Jim will be in touch once back from their break regarding raw data handoff.

Terry

<SSF-1728_basic_assembly_stats_20161118.xlsx>

--

Caroline Cusick

Product Coordinator

Broad Institute of MIT and Harvard

75 Ames St | Cambridge MA 02142 USA

<SSF-1728_KeyforCollaborator.xlsx>

--

Caroline Cusick

Product Coordinator

Broad Institute of MIT and Harvard

75 Ames St | Cambridge MA 02142 USA

--

Caroline Cusick

Product Coordinator

Broad Institute of MIT and Harvard

75 Ames St | Cambridge MA 02142 USA

