**Directions for Creating Tracks files from COPRO-Seq Outputs**

*Note that right now the script provided (eland2tracks\_dev.pl) is only designed to run on a single Eland output file. In the future, support will be added for multiple files whose results can be combined or reported separately.*

1. Locate the raw Eland output files (extension '.elandout') from your COPRO-Seq analysis run. These files might be deleted by the pipeline unless you specify that the software should retain intermediate analysis files (use the –a option for 'allfiles' when running batch\_coproseq.pl).
2. Create a new directory to serve as the working area for your analysis.
3. Copy the Eland output from #1 to this directory.
4. Run eland2tracks\_dev.pl with the options appropriate for your needs:  
   -l : LWGV formatted output (use this if you want to use J's viewer software)

-n : name for the sample corresponding to Eland output (specifying this is

useful when visualizing your data in LWGV later)

-z : report zeros (print all coordinates in the output, even those with no hits)

-g : directory containing genome nucleotide files (this is only required when invoking –z, for purposes of determining how many total positions are in a given genome); <new version may replace this option with -t + -m>

1. The script will create one output file for every genome found in the Eland output. For details on how to load tracks see the instructions that follow.

**Loading tracks onto J's web server**

First, copy or move the .tracks files created above for each genome of interest to your home directory on hamlet.wustl.edu (you’ll need to have J set up a new account for you along with the appropriate lightweight genome viewer folder infrastructure).

**scp \*.RNAseq nmcnulty@hamlet.wustl.edu:.**

Note the ‘:.’ at the end of the command which tells secure copy where to place the files (in your home directory).

Next, ssh into your account:

**ssh nmcnulty@hamlet.wustl.edu**

Next you’ll want to move the files from your home directory to the folder where LWGV will be looking for them:

**mv \*.RNAseq sites/CGI/lwgv\_dev**

Finally, you’ll need to update the .ann files for each genome involved (you may have to look up the accession number for your genome first). Make sure any lines describing information you don’t want to visualize are commented out with a ‘%’ and that you have a line including the new .tracks files. Note that if you've generated multiple files for the same species, you'll probably have to rename them something unique (I usually change the .tracks extension to something unique).

Here’s an example of the relevant portion of the .ann file that you’ll need to change:

% #include Graph\_Phages.NZ\_AAVO02000001.txt

#include NZ\_AAVN02000001.contig

#include NZ\_AAVN02000001.tracks

#include NZ\_AAVN02000001.genes

(In the example above, the .contig and .genes files are backbone files needed by the viewer to load genome information; only the .tracks file specifies information that will load tracks in the viewer).

Now, to view your new data in LWGV, navigate to:

hamlet.wustl.edu/~nmcnulty/microbialomics/

And then select the genome of interest from the dropdown box.