(matWelcome to the Metagenomics Summer School Etherpad!

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 Course Resources: https://github.com/GenomicsAotearoa/metagenomics_summer_school

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/nesi/nobackup/nesi02659/MGSS_Intro/animals.txt
/nesi/nobackup/nesi02659/MGSS_Intro/names.txt

sed -i 's/[dD]ogs/cats/g' animals.txt <-- covers both cases, and -i overwrites the file

for loop that seems to be working:
for filename in *.fastq
 do
 name=$(basename ${filename} .fastq)
 echo ${name}
 done

Copying files from HPC to your computer
1. Copying files from ga-vl01 to Mac &Linux Downloads directory

-
    - scp ga-vl01:~/MGSS_Intro/Test_1.fastq ./

2. Copying files from ga-vl01 Windows

-
    - scp ga-vl01:~/MGSS_Intro/Test_1.fastq /mnt/c/Users/
      yourWindowsUsername/Downloads
    - scp **yourNesiUsername**@ga-vl01:~/MGSS_Intro/Test_1.fastq /mnt/c/Users/
      yourWindowsUsername/Downloads

copy the files for fastqc runs from following location:
/scale_wlg_nobackup/filesets/nobackup/nesi02659/MGSS_U/<YOURUSERNAME>/
2.fastqc

If you have windows 10, to see where you copied your Test_1.fastq file to type:

explorer.exe .
into your local ubuntu terminal

Resources for fast QC exercise
Files: https://drive.google.com/open?id=108WKgX_FQAMas3pHr0WSxpRltxsl6Z3T
FastQC: https://www.bioinformatics.babraham.ac.uk/projects/fastqc/

Location of files to be used for this course

/nesi/nobackup/nesi02659/MGSS_U/Your_User_Name

tetramer calculation for esomana (untested)
https://github.com/tetramerFreqs/Binning

Useful website to expain shell commands. Enter the command and switches (eg "ls -l") and
explainshell tells you what it means. https://explainshell.com/

If Micropia can turn science into art with whole genomes, Kim can do it with
metegenomes
https://www.micropia.nl/en/discover/news/2016/4/21/new-tree-of-life/

Leighton Pritchard is a genius!
http://armchairbiology.blogspot.com/2013/11/ani-are-you-okay-are-you-okay-ani.html

count your genes - gives you number of lines
if in fasta file then need to divide by 4
grep '>' <filename> | wc -l

extract entries from a multi-FASTA file with samtools given a text file of sequence names,
works with wrapped sequences (sequences with line breaks): **xargs samtools faidx big.fasta
< names.txt**

- May you please fill this survey before you leave to help us improve our work.
POST_WORKSHOP SURVEY: https://www.surveymonkey.com/r/TFCX8VD

Thank you so much for being part of the Metagenomics Summer School 2019. Wish you all
the best as you go back to your working place.
*******************************THE
END***

Illustration tools/icons
Good (free) website for choosing colours!
https://color.adobe.com/create
A good (and much cheaper) alternative to Illustrator: Affinity Designer. One-time pay, no

subscription. Macs only

Icons for nice scientific illustrations:

https://biorender.com/ (free for educational purposes)

https://thenounproject.com/ (free, but need to make an account)

https://nanx.me/ggsci/ <-- colour palettes in R, including default colour sets for publications

https://github.com/karthik/wesanderson <-- A Wes Anderson color palette for R!