

from Monika Mehta to Everyone: 1:03 PM  
yes  
from Beatriz to Everyone: 1:03 PM  
yes  
from Chun Yang to Everyone: 1:03 PM  
yes  
from Beatriz to Everyone: 1:04 PM  
yes  
from Chun Yang to Everyone: 1:04 PM  
yes  
from sunmin to Everyone: 1:04 PM  
I missed this morning's talk. Would it be available later?  
from Zhilin Yang to Everyone: 1:04 PM  
Everything he mentioned was new to me except Galaxy. So nih doesn't  
use Galaxy much?  
from Peter Fitzgerald to Everyone: 1:05 PM  
No NIH does not have a formal support for Galaxy, but some people do  
use it  
from Des to Everyone: 1:05 PM  
Yes, the talk was recorded and the video and slides will be available  
later  
from sunmin to Everyone: 1:05 PM  
great, thank you!  
from Laurie Krug to Everyone: 1:12 PM  
can't see the terminal command line  
from Monika Mehta to Everyone: 1:12 PM  
we cannot see the terminal  
from Zhilin Yang to Everyone: 1:12 PM  
when I use makefile in the terminal, it displays both 'echo Hello' and  
Hello. Only Hello was supposed to show up right?  
from Chun Yang to Everyone: 1:12 PM  
yes  
from Monika Mehta to Everyone: 1:13 PM  
yes, can see now. thanks  
from Des to Everyone: 1:15 PM  
Zhilin Yang --that's typical behavior for "make". you can suppress  
that by using using the -s flag  
from Zhilin Yang to Everyone: 1:15 PM  
Gotcha. Thanks Des  
from Des to Everyone: 1:17 PM  
i.e. "make -s" or you can suppress output by adding a @ in front of  
the echo command in the makefile.  
from Monika Mehta to Everyone: 1:25 PM  
22 is smaller, less data?  
from Joanna Thomas to Everyone: 1:25 PM  
Because it's small?  
from Beatriz to Everyone: 1:26 PM  
yes, because is the longest one  
from Zhilin Yang to Everyone: 1:26 PM  
yes

from Laurie Krug to Everyone: 1:27 PM  
I can't hear anymore. is it just me?  
from Zhilin Yang to Everyone: 1:27 PM  
I can hear well  
from melina to Everyone: 1:27 PM  
I can also hear  
from ping xue to Everyone: 1:28 PM  
why you only see NNNN?  
from Joanna Thomas to Everyone: 1:29 PM  
Is there a way when you're downloading a file from the web using the  
curl command, to specify the folder you want it to go into?  
from Joanna Thomas to Everyone: 1:33 PM  
Thank you!  
from Zhilin Yang to Everyone: 1:35 PM  
After pasting the command, the command ran automatically in my  
terminal. is there a way that I can hold until i click 'enter' ?  
Thanks  
from Peter Fitzgerald to Everyone: 1:36 PM  
typically the command will need a return to run. Depending on how you  
cut/paste the command you may get the return as part of the paste.  
from Peter Fitzgerald to Everyone: 1:37 PM  
I believe there may be a way in the terminal preference to surpress  
the return at the end of a paste...  
from Zhilin Yang to Everyone: 1:39 PM  
Thanks Peter. I think I figured out why. i WAS copying and pasting the  
command in the terminal. Seems like if i copied the space after the  
command, the command ran automatically. But if I only copied the  
command without extra space at the end, then it is fine.  
from Chen Zhao to Everyone: 1:45 PM  
Sorry. I configured my computer but can't run seqkit  
from Chen Zhao to Everyone: 1:45 PM  
do I need to activate conda? or do something?  
from melina to Everyone: 1:47 PM  
you need to run the conda activate conda command everytime you open  
the terminal - but if you do that I dont think you need to do it again  
from Chen Zhao to Everyone: 1:47 PM  
Problem solved. Just installed.  
from Chen Zhao to Everyone: 1:47 PM  
hi melina, what is conda activation command?  
from Des to Everyone: 1:49 PM  
conda activate bioinfo  
from Ian Bettencourt (internal) to Everyone: 1:49 PM  
"conda activate bioinfo"  
from Chen Zhao to Everyone: 1:49 PM  
Thank you very much!  
from sunmin to Everyone: 2:07 PM  
yes  
from ping xue to Everyone: 2:07 PM  
yes  
from Ian Bettencourt (internal) to Everyone: 2:07 PM

yes

from Chun Yang to Everyone: 2:07 PM

yes

from Monika Mehta to Everyone: 2:07 PM

yes, was able to run, and got the output shown in the book

from Chen Zhao to Everyone: 2:08 PM

yes

from Raquel Costa to Everyone: 2:08 PM

I am able to run

from Joanna Thomas to Everyone: 2:08 PM

I couldn't but I'd forgotten to activate the environment so I will try again later

from Monika Mehta to Everyone: 2:09 PM

@Joanna - It was the same with me. Did not activate bioinfo and couldnt run anything, but after activating, there was no problem.

from Beatriz to Everyone: 2:14 PM

I as triynf to do the same with hg37

from Beatriz to Everyone: 2:14 PM

but i was not able

from Beatriz to Everyone: 2:16 PM

when you do the excercise of chr 22 with hg38, could you show us how to do it without copy paste the commands?

from Zhilin Yang to Everyone: 2:18 PM

Hi. If I want to use the biostar tools in biowulf, do I follow the 'installation for linux' instruction and install in my personal modulefiles folder? few modules in the biostar book list aren't available in biowulf. Thanks

from Zhilin Yang to Everyone: 2:19 PM

bioawk isn't aviaalbe

from Zhilin Yang to Everyone: 2:19 PM

sorry Infoseq isn't available

from Chun Yang to Everyone: 2:20 PM

Throughout the book mostly smaller genome is used (e.g. Ebola virus). When we are working on large genome such as human and mouse, is there a way to estimate the computation time, e.g. when we are doing bwa/bowtie command.

from Chun Yang to Everyone: 2:22 PM

Thanks.

from Beatriz to Everyone: 2:23 PM

yes please

from Peter Fitzgerald to Everyone: 2:23 PM

xtract -input output.xml -Pattern Taxon -first TaxId ScientificName GenbankCommonName Division

from Peter Fitzgerald to Everyone: 2:23 PM

that is the correct command for the xtract example

from Monika Mehta to Everyone: 2:27 PM

@Beatriz: it could be that you tried hg37, it should be hg19 for the previous version

from Des to Everyone: 2:28 PM

i agree with monika's answer

from Beatriz to Everyone: 2:28 PM  
i will do that  
from Zhilin Yang to Everyone: 2:29 PM  
Thanks a lot everyone.  
from Raquel Costa to Everyone: 2:29 PM  
Thank you 😊  
from Chun Yang to Everyone: 2:30 PM  
Thanks.  
from Monika Mehta to Everyone: 2:31 PM  
Thank you!  
from Beatriz to Everyone: 2:31 PM  
thank you  
from sherif to Everyone: 2:31 PM  
Thank you  
from Chun Yang to Everyone: 2:31 PM  
Thank you.  
from Milos Miljkovic to Everyone: 2:31 PM  
Thank you!  
from Joanna Thomas to Everyone: 2:32 PM  
Thank you  
from Chen Zhao to Everyone: 2:32 PM  
Thank you!