1 – Linux Terminal, PHENIX, and Coot

(handout created by Susanna Huang on August 14th, 2024, for STARS collegiate branch located at the Georgia Tech campus)

INTRODUCTION

As you may know, there are four stages of crystallography:

1. Protein expression and purification

- a. Where the desired protein manufacturing instructions (or essentially the DNA coding the desired protein) is given to bacterial strains in the form of plasmids for the bacteria to mass produce the proteins, so that the high quantities of proteins can be obtained for crystallography experiments
- b. (but if you are working with just crystallizing nucleic acids, one advantage is that you can simply purchase the nucleic acid sequences and not have to worry about the expression and purification part)



Figure 1. Left flask: an example of bacteria, which are manufacturing the desired protein, growing well in broth. Right flask: an example of bacteria that has just started to grow or is growing poorly in the broth. Source for photos and further reading: https://bitesizebio.com/28882/optimize-bacterial-protein-expression-by-considering-these-4-variables/

2. Crystallization and crystal-growth optimization

a. Where the protein and/or DNA samples are used for crystallization into beautiful crystals and where their crystal-growing conditions (experimental conditions) need to be optimized for best crystal quality growth (this is what we had worked on during the spring 2024 semester)



Figure 2. Left photo: lysozyme crystals grown for a STARS experiment (week 7, set up on March 14, 2024 by Susanna). Right photo: DNA crystals (CGCGCG) grown for an outside project (set up on 7/5/2024 and checked on 8/5/2024 by Susanna).

3. Crystal harvesting and diffraction of crystals

a. Where the good crystals are harvested, cryo-protected, and shipped off to a synchrotron facility and where the crystals are then diffracted at the beamline for X-ray diffraction data collection on the crystals' structures



Figure 3. Left photo: a lysozyme crystal being harvested onto a loop. Right photo: An example of good lysozyme diffraction data (one snap) from a different lysozyme crystal. (photo credit: Susanna Huang with the support of LBNL)

4. Diffraction data solving, model building, and model refinement

a. Where the diffraction data is scaled and integrated into electron density maps, and where these electron density maps are used in conjunction with model sequences to build the protein and/or DNA models and refine these models



Figure 4. Left photo: Example of PHENIX GUI interface. Right photo: Example of Coot GUI interface, specifically for a 12-position methionine residue on lysozyme. (Susanna Huang)

AIMS FOR THIS HANDOUT

This handout aims to:

- Contextualize PHENIX and Coot with respect to the other three steps of crystallography (INTRODUCTION)
- Provide a general introduction of model building and refinement in the crystallography process and its significance
- Guide students through the download, installation, and set-up process for a Linux subsystem
- Provide students with the basic understanding on how to navigate through a Linux subsystem, such as basic commands and typing into the Linux terminal
- Guide students through the download, installation, and set-up process for PHENIX, Coot, Python3, and Rosetta

This handout can be used for initial instruction to students and can be used for students' self-guided download of these important programs.

MODEL BUILDING AND REFINEMENT and THEIR SIGNFICANCE

You have your beautiful crystal, which is a co-crystal of HDAC6, a cancer target protein, and a small molecule inhibitor of HDAC6. You wanted to see how the small molecule inhibitor was interacting with HDAC6, in terms of its mechanism (or essentially, what is occurring at the atomic level). You had decided to go with crystallography because the other two prominent methods for structure determination: (1) Solution NMR and (2) cryoEM just did not quite seem suitable for this specific system. Solution NMR is only really good for high atomic resolution for smaller systems that are around less than 100 kDa in mass (but HDAC6 on its own is already 130-150 kDa, so Solution NMR would not be possible here). cryoEM is really good for obtaining the general structure of large macromolecular systems, requiring the studied system to be at least 50 kDa, which is good news, but only at relatively low resolution (only around 10 Å and maybe 3 Å resolution at best for most cases), which would not be useful for obtaining atomic resolution (1 Å) information of the molecular interactions occurring between the HDAC6 and the small molecule inhibitor. Xray crystallography was the best bet here because it frequently provides atomic or nearatomic resolution and can work for small systems as well as larger macromolecular systems.

You have your beautiful crystal, and you harvested it, cryoprotected it, plunged it in liquid nitrogen, and shipped it off in a black puck (a hockey puck-sized puck, which has little holes for placing the crystal pins into), packed the pucks inside of a dewar (a shipping

container that is filled with a stack of pucks and lots of liquid nitrogen to keep it cold), and shipped it off to a synchrotron facility, such as the Advanced Light Source (ALS) at the Berkeley Lab.

Several months later, when the ALS notifies you about available beamtime that you can use, you hop onto your computer, open a remote connection, obtained access to one of their macromolecular crystallography beamlines (such as 5.0.1 or 5.0.3, further reading here: https://bcsb.als.lbl.gov/beamline-overview/), and shot your crystal with X-rays to get some pretty diffraction patterns.

ALS automatically helped you integrate and scale the diffraction patterns into an electron density map. You now have the **HDAC6 sequence information** in a **.fasta file format**, your crystal **electron density information** (with phasing information as well) in a **.mtz format**.

What do you do now?

Currently, the .fasta file is a string of alphabetical numbers that are each associated with an amino acid in HDAC6. This file needs to be converted into a **.dat file format** before it can be used in conjunction with the phase information (.mtz file) by PHENIX and Coot to create a **new HDAC6 protein model** based on your HDAC6 diffraction data.

Why do we need this specific model? Other HDAC6 models will not have your special inhibitor compound, so the HDAC6 protein model may not adopt a specific conformation that we are investigating into. This HDAC6 co-crystallized with small molecule model can provide great information and insight on how the small molecule inhibitor affects HDAC6's protein and residue conformation at the atomic level, providing insight on if the small molecule may be doing its job or if the small molecule can be improved to have better binding with HDAC6 for improved protein inhibition.

DOWNLOADING LINUX SUBSYSTEMS:

Before we can do PHENIX and Coot work, we need to prepare the system format that they are compatible with: Linux.

This will be a step-by-step guide on how to download and install everything for a Windows 11 system, but each of the steps are largely applicable to Mac systems and other Windows systems as well.

Here are the main instructions websites that will be referenced:

- 1. <u>https://github.com/phenix-project/phenix_html/blob/master/wsl_instructions.md</u>
- 2. https://phenix-online.org/
- 3. <u>https://phenix-online.org/download</u>
- 4. https://phenix-online.org/documentation/install-setup-run.html
- 5. https://phenix-online.org/documentation/reference/rosetta_install.html
- 6. <u>https://rosettacommons.org/download/</u>
- 7. <u>https://downloads.rosettacommons.org/software/academic/</u>

Most of these pages are linked pages to each other. I just put them here to delineate them clearly.

Other documentation:

Phenix Documentation (phenix-online.org)

Main steps:

- How to download Linux
- How to use Linux subsystem
- How to download Phenix
- How to download Coot
- How to download Python3

To start, we first need WSL to run Linux on Windows:

Pin to taskbar

1. Reference website 1 (https://github.com/phenixproject/phenix_html/blob/master/wsl_instructions.md):

Ò	Installing WSL	
	To install WSL, you will need administrative access.	
	Start by launching a new Command Prompt with administraive access. This can be done by using the "Run as Adminstrator" option when right- clicking the Command Prompt icon.	
	Туре	
	wslinstall -d ubuntu-22.04	
	This will install Ubuntu 22.04 as an available linux distribution. You will be prompted for a username and password. After the process completes you should be inside a bash shell.	,
	This is the only step that requires administraive access. You can open other Command Prompts normally and enter the linux environment with	
	wsl -d ubuntu-22.04	
	Command Prompt System	
	C Open	
	Run as administrator	
	Den file location	
	Pin to Start	



Open Command Prompt and type wsl --install -d ubuntu-22.04



This will be Windows Subsystem for Linux, as the host process for Linux service on Windows.





Now it will ask for the creation of your username and password. Beware, your password will not have anything show up when you are typing into it (but the computer is remembering what you are typing).





Click enter

Lower case letters only



Click enter



Now enter a new password

We know it looks very weird when the cursor stays in the same place, but trust it, it is recording your new password, press enter

Now retype the password again, and press enter:







Now, do the second command on the website, you can enter into the Linux subsystem by typing bash into the top:



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You can also enter by going into the command prompt this way:

This is the only step that requires administraive access. You can open other Command Prompts normally and enter the linux environme	ent with
wsl -d ubuntu-22.04	₽

Follow other steps on website:



চ্য steve@StevenH: ~ option to relax this check or reconfigure NAME_REGEX. Enter new UNIX username: steve New password: Poture Retype new password: passwd: password updated successfully Installation successful! To run a command as administrator (user "root"), use "sudo <command>". See "man sudo_root" for details. Welcome to Ubuntu 22.04.3 LTS (GNU/Linux 5.15.153.1-microsoft-standard-WSL2 x86_64) * Documentation: https://help.ubuntu.com https://landscape.canonical.com https://ubuntu.com/advantage * Management: * Support: This message is shown once a day. To disable it please create the /home/steve/.hushlogin file. steve@StevenH:~\$ sudo apt-get update
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Hit:4 http://archive.ubuntu.com/ubuntu jammy-backports InRelease Get:5 http://security.ubuntu.com/ubuntu focal-security/main amd64 Packages [3125 kB] Get:6 http://security.ubuntu.com/ubuntu focal-security/main amd64 Packages [3125 kB] Get:7 http://security.ubuntu.com/ubuntu focal-security/main amd64 c-n-f Metadata [14.1 kB] Fetched 3731 kB in 3s (1077 kB/s) Reading package lists... Done Reading package lists... Done Reading package lists... Done Reading state information... Done The following NEW packages will be installed: libstl.1 0 upgraded, 1 newly installed, 0 to remove and 118 not upgraded. Need to get 1323 kB of archives. After this operation, 4131 kB of additional disk space will be used. Get:1 http://security.ubuntu.com/ubuntu focal-security/main amd64 libssl.1 amd64 1.1.1f-1ubuntu2.23 [1323 kB] Fetched 1323 kB in 1s (1918 kB/s) Preconfiguring packages ... Selecting previously unselected package libssl.1:amd64. (Reading database ... 45877 files and directories currently installed.) Preparing to unpack .../libssl1.1:.1.1f-1ubuntu2.23 ... Setting up libssl1.1:amd64 (1.1.1f-1ubuntu2.23) ... Preconsing triggers for libc-bin (2..35-0ubuntu3.4) ... Hit:1 http://security.ubuntu.com/ubuntu jammy-security InRelease Hit:2 http://archive.ubuntu.com/ubuntu jammy-security InRelease Hit:2 http://archive.ubuntu.com/ubuntu jammy-security InRelease Hit:4 http://archive.ubuntu.com/ubuntu jammy-security InRelease Hit:4 http://archive.ubuntu.com/ubuntu jammy-security InRelease Hit:4 http://archive.ubuntu.com/ubuntu jammy-backports InRelease Hit:4 http://archive.ubuntu.com/ubuntu jammy-backports InRelease Hit:4 http://archive.ubuntu.com/ubuntu jammy-backports InRelease Hit:4 http://archive.ubuntu.com/ubuntu jammy-backports InRelease Reading package lists... Done



Time for some basics:

i.

- 1. How to change directories (or go into different folders)
 - a. To go to the root directory, you simply type "cd":





- v.
- 2. How to list things out that are in a folder
 - a. To see what is in the folder, simply type **ls** to list the items out:



- iii. There is nothing in the Linux subsystem folder just yet, which is why nothing is there.
- iv. If you opened the downloads folder and wanted to go to the desktop folder, this is how you do it:
- v. Open the downloads folder in Windows, type bash at the top, **cd**.. on folder below, like so:







xiii.



xiv.



xvi. Notice that text with spaces have half quotations around them. If you wanted to cd into those folders, you would have to reference them with full quotation marks around the full term: ex: Local Settings is displaying as 'Local Settings' but if you wanted to cd into Local Settings, you would need to cd "Local Settings" with full quotation marks. Make sure to keep all the other capitalizations, punctuations exactly the same as listed.

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- xx. You can ls in the local setting folder to see what is in it

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- 3. A list of key commands in your Linux Windows subsystem:
- cd
 - \circ goes to the home directory
- ls
- \circ $\$ list out the items in the folder
- ср
 - \circ the copy file or directory function
 - o a file:
 - cd <file name> <copy-to-folder directory>
 - o an entire directory
 - cd -r <file directory name> <copy-to-folder directory>
- pwd
 - print current directory name, useful for copying the directory name for cp'ing things

- mkdr
 - o makes a new directory or folder
 - Ex: mkdr PhenixProjects
 - This makes a new directory, called PhenixProjects, in your current directory

Now you just need to download the PHENIX files:

Go to the third link.

< > C : 🔒 phe	nix-online.org/phenic_request/index.cgi 😢 💿 🗢 😇 🕹 🗯 🕹
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If the password has exp Current Institutional E-	ired, to download a new version of Phenix please complete this form again. shuang466@gatech.edu
First Name	Susanna
Last Name	Hung
Institution Name	Georgia Institute of Technology
Department	School of Chemistry and Biochemistry
Department URI	http://chemistry.gatech.edu
Institution Street	Allanta, GA 3032
Address	
ZIP or Post Code	30332
Country	Unied States
VON-COMMERCIAL END USER	
Software: PHENIX (LBNL Version: 1 General	Ref. (R-1770)
Software: LABELIT (LBNL Version: 1.1.4	Ref. (R-1960)
IMPORTANT - READ CAREFU	LLY: This License Agreement ("Agreement") is a
 I have read and acc I will only use the s I am not a military Submit Phenix request form 	ept the license terms stated above. oftware for non-profit research. end user in a country other than the US and will not use the software for non-US military purposes.
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	Pequest Confirmed
We are able to accept	your online request for Phenix. An e-mail message will be sent to you with a password and instructions for downloading the Phenix software.
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The information way as	download@phenix-online.org
Email shuang466@gat	vided. echedu
FirstName Susanna	
LastName Huang	nstitute of Technology
Department School of	Chemistry and Biochemistry
URL https://chemistry.g	atechedu
StreetAddress Atlanta, City Atlanta	GA 30332
Post_Code 30332	
Country US	

Email that is received:

To download the Phenix distribution with a web browser go to:

https://phenix-online.org/download

When prompted for a user name and password enter:

User Name: download

Password: 3c55hyu

The password is changed on the 1st of each month at 00:05 PST/PDT.

If the password is expired, simply request a new one at: https://phenix-online.org/

This is an automatically generated message. Please do not reply to this email. If you experience problems please contact:

download@phenix-online.org

Citing Phenix:

Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. Liebschner D., Afonine P.V., Baker M.L., Bunkoczi G., Chen V.B., Croll T.I., Hintze B., Hung L.W., Jain S., McCoy A.J., Moriarty N.W., Oeffner R.D., Poon B.K., Prisant M.G., Read R.J., Richardson J.S., Richardson D.C., Sammito M.D., Sobolev O.V., Stockwell D.H., Terwilliger T.C., Urzhumtsev A.G., Videau L.L., Williams C.J., and Adams P.D. Acta Cryst. D75, 861-877 (2019).

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With the temporary username and password, you can now go back to website 3 and click "Download official release" and paste the login information inside





It will bring you to the below page. Click on the Linux download command-line installer at the top of the page.



For Phenix I.20.1 and before, the Phenix GUI will crash on macOS Sonoma (14). Please download this fix to fix your Phenix installation. Extract the tarball and run "sudo ./fix_wxpython.sh /Applications/phenix-1.20.1-4487". You will need administrative access to modify files in /Applications.

Windows (partially supported)

For full functionality, you should run the Python 2.7 linux installer on Windows using WSL. Instructions for setting up Phenix with WSL can be found here.

A native Windows build is only available for Python 3, but you will encounter crashes. See below for the link to the Windows installer.

The next official release of Phenix will be in Python 3 and Windows will have a working installer again.

Python 3.9 (Alpha) - For testing and development, do not expect full functionality

Save the downloaded tar.gz file into the downloads folder:

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	ACLib	4/20/2024 12:51 PM	File folder	
🛄 Desktop	*			
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Documents ;	*			
- e				
File name:	phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-cento	s6.tar		~
Save as type:	Compressed Archive Folder			
∧ Hide Folders			Save	Cancel



Meanwhile, while we get the phenix thing working, we can go ahead and download Coot:

https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/binaries/release/coot-0.9.8binary-Linux-x86_64-ubuntu-20.04.4-python-gtk2.tar.gz and save it into the downloads folder. This link will directly download the Coot directory

While that is installing

go to the downloads folder



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games	/home/steve/.hushlogin file. steve@StevenH:/mnt/c/Users/steve/Downloads\$									

Now, type **pwd** into the terminal to print the working directory (essentially the directory that you are currently in)

We need this working directory so that when we go to the root directory, we can extract the tar ball file (which is currently in the downloads directory) into the root directory, where the PHENIX program can reside in the Linux subsystem and operate correctly.



In this case, the operating directory is /mnt/c/Users/steve/Downloads

This will be used in the next step:

Go to the root directory, this is where you will extract your PHENIX file into.



There most likely is nothing in it right now:



While you are in this root directory, extract the Linux installer:

tar -xf /mnt/c/Users/<Windows username>/Downloads/<Phenix installer file>

where <Windows username> would be "steve" in this case.

Where <Phenix installer file> is ... well we don't know

How do we find the file name?

Go to the downloads folder and type "ls":


In this case, it was listed as "phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6.tar.gz"

Copy the name of this directory (which in this case is /mnt/c/Users/steve/Downloads), the name of the file (which in this case is phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6.tar.gz)

Next, navigate back to the root directory and type in this into the terminal:

cd

tar -xf /mnt/c/Users/<Windows username>/Downloads/<Phenix installer file>

or in this specific case:

tar -xf /mnt/c/Users/steve/Downloads/phenix-installer-1.21.1-5286-intel-linux-2.6x86_64-centos6.tar.gz

छ steve@StevenH: ~ × + ∽	-	o ×
<pre>'opinon writing.docx' pattern.ai pct_free_easeus.exe.temp pct_free_installer_20240709.1-17205423117937b14590.exe 'pencil2d=win640=0.6.6.zip phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6.tar.gz pjgstep_minecraft.mp3 positive-uplifting=music-for-youtube-videos-166946.mp3 powerful-beat-121791.mp3 roblox-death-sound-effect.mp3 scan-combined.pdf scan0007-combined.pdf scan0007-combined.pdf scan0009-merged.pdf 'song for scratch - Made with Clipchamp.mp4' stomping-rock-four-shots-111444.mp3 summer-adventures-115949.mp3 sunsine-jaunt-163686.mp3 'truth or dare.txt' typing.txt ven_diagram.docx vine-boom.mp3 war.txt wraffle.wheel 'writing show.pdf' steve@StevenHi*M_I/c/Users/steve/Downloads\$ cd steve@StevenHi*M_I/c/Users/steve/Downloads\$ cd</pre>		
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<pre>pct_free_easeus.exe.temp pct_free_installer_20240709.1-17205423117937b14590.exe 'pencil2d-win64-0.6.6 (1).zip' pencil2d-win64-0.6.6.zip phenix-installer_1.21.1-5286-intel-linux-2.6-x86_64-centos6.tar.gz pigstep_minecraft.mp3 positive-uplifting-music-for-youtube-videos-166946.mp3 powerful-beat-121791.mp3 roblox-death-sound-effect.mp3 scan-combined.pdf scan.0009-merged.pdf 'song for scratch - Made with Clipchamp.mp4' stomping-rock-four-shots-111444.mp3 summer-adventures-115949.mp3 sunsine-jaunt-163686.mp3 'truth or dare.txt' typing.txt vern_diagram.docx vine-boom.mp3 war.txt wraffle.wheel 'writing show.docx' 'writing show.docx' /home/steve steve@StevenH:-\$ pwd /home/steve steve@StevenH:-\$ pwd</pre>		

Now type in your command



This might take a quick second or a bit of a while. It is just extracting the zip file (or in the case of Linux, the tar file) into the root directory. This process may be fast or slow depending on your computer (this example computer had Windows 11, 6 cores, 8 processors, 8 GB of memory, 4 GB of dedicated GPU and it only took a couple of minutes)

You will know when it is done when the "\$" comes back again:



Now you can check to see if it successfully copied over by typing ls



If it copied over successfully, now you can run the installation process:

cd phenix-installer-<version>-<platform>

./install --prefix \${HOME}

You need to cd into this folder. You can do so by typing "cd phenix" and then click tab to autofill the rest. If you don't want to autofill, you can simply type the full folder name.



steve@StevenH:-/phenix-ins × + v - - - × *
steve@StevenH:-/phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6.tar.gz
steve@StevenH:-*\$ tar -xf /mnt/c/Users/steve/Downloads/phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6.tar.gz
steve@StevenH:-*\$ cd
steve@St

If you hold it down, this accidently happens:



But don't worry if that happens, there is nothing wrong with it.

Now that you are in the correct folder, start the installation process by typing:

./install --prefix \${HOME}



₨ steve@StevenH: ~/phenix-ins × + ∨		×
<pre>steve@StevenH:~/phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6\$</pre>		
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steve@stevenH:~/phenix-installer_1.21.1-528b-intel-Linux-2.b-X86_b4-Centos6\$		
steve@stevenH:~/phenix-installer_1.21.1-528b-intel-Linux-2.b-X80_b4-Centos6\$		
steve@stevenH:~/phenix-installer_1.21.1-5280-intel-linux-2.6-x80_04-Centos65		
steve@stevenh:~/phenix-installer_1.21.1-5200-intel_linux_2.6-x00_04-Centosos		
steve@stevent:~/phenix=instatter=1.21.1=5200=intel=linux=2.6=x06_04-Centosos		
stevens:~/phenix-instatter-1.21.1-3200-intet-tinux-2.0-x00_04-centoso\$./instattprefix \$thone;		
Phenix Installation		
version: 1.21.1-5286		
machine type: intel-linux-2.6-x86_64		
OS version: 5.15.153.1-microsoft-standard-WSL2		
destination: /home/steve/phenix-1.21.1-5286		
# of processors: 8		

Esteve@StevenH: ~/phenix-ins × + ∨	– c	> X
<pre>steve@StevenH:~/phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6\$ steve@StevenH:~/phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6\$ steve@StevenH:~/phenix-installer-1.21.1</pre>		
Phenix Installation		
version: 1.21.1-5286 machine type: intel-linux-2.6-x86_64 OS version: 5.15.153.1-microsoft-standard-WSL2 destination: /home/steve/phenix-1.21.1-5286 # of processors: 8		
Configuring Phenix components		
🖾 steve@StevenH: ~/phenix-ins X + ~		

Log file: /home/steve/phenix-installer-1.21.1-5286-intel-linux-2.6-x86_64-centos6/base_tmp/install_finalize.lo Generating Phenix environment setup scripts Generating Phenix environment additions for dispatchers Calling write_gui_dispatcher_include args ['build_dir=/home/steve/phenix-1.21.1-5286/build', 'base_dir=/home/steve/phenix-1.21.1-5286/conda_b uffix=phenix', 'gtk_version=2.10.0', 'quiet', 'use_conda', 'ignore_missing_dirs'] prologue export PHENIX="/home/steve/phenix-1.21.1-5286" export PHENIX_VERSION=1.21.1-5286 export PHENIX_VERSION=1.21.1-5286 export PHENIX_VERSION=1.21.1-5286 export PHENIX_MIYPE=intel-linux-2.6-x86_64 epilogue if [! -z "\$QB_PYTHONPATH"]; then export PYHONPATH=\$PYTHONPATH:\$QB_PYTHONPATH	g ase',	's
if [! -z "\$QB_LD_LIBRARY_PATH"]; then export LD_LIBRARY_PATH=\$LD_LIBRARY_PATH:\$QB_LD_LIBRARY_PATH fi if [-z "\$QB_DYLD_LIBRARY_PATH"]: then		
<pre>if [: -2 _4V5_DILD_LIBRARY_PATH], then export DYLD_LIBRARY_PATH=\$DYLD_LIBRARY_PATH:\$QB_DYLD_LIBRARY_PATH fi if ["\$PHENIX_MTYPE" != "macintel-osx"] && \ ["\$PHENIX_MTYPE" != "macintel-osx-"] && \ ["\$PHENIX_MTYPE" != "macintel-osx-x86_64"]; then export PYMOL_PATH=\$PHENIX/pymol fi</pre>		
Configuring Phenix components Precompiling .py files		



So, now if you want to open PHENIX, you just bash into any folder, for this example, type:

source /home/steve/phenix-1.21.1=5286/phenix_env.sh

Then type **phenix**



If it doesn't work, **cd** to the root directory, go into the phenix folder and find out the list of items in the directory.



It seems that it is here:



You just need to make sure that the directory is correct, in the first command, an equals sign was used when a dash was supposed to be used. When you fix this error, it can be fixed:

Get the new one: source /home/steve/phenix-1.21.1-5286/phenix_env.sh

And then type **phenix**

This time it worked because there was no error:



Now type phenix

The Phenix GUI shows up, but not the full screen. This may be because it is missing code or may be because of limited memory space.

We are just going to go ahead and install coot:

cd

tar -xf /mnt/c/Users/<Windows username>/Downloads/coot-0.9.8-binary-Linuxx86_64-ubuntu-20.04.4-python-gtk2.tar.gz

cd

tar -xf /mnt/c/Users/steve/Downloads/coot-0.9.8-binary-Linux-x86_64-ubuntu-20.04.4-python-gtk2.tar.gz



It has extracted the files successfully into the root directory you can check:



Coot is extracted now.



As you can see, it says no lib libstdc++ available, so we are going to download this library.

Actually no it is because the *<phenix directory* > was not replaced.

In -s -f /usr/lib/x86_64-linux-gnu/libstdc++.so.6 <User>/conda_base/lib/libstdc++.so.6



In -s -f /usr/lib/x86_64-linux-gnu/libstdc++.so.6 /home/steve/phenix-1.21.1-

5286/conda_base/lib/libstdc++.so.6



It has to be the full phenix folder

So that is done.

Then this part:

export LIBGL_ALWAYS_INDIRECT=0

source <Phenix directory>/phenix_env.sh

export LIBGL_ALWAYS_INDIRECT=0

source /home/steve/phenix-1.21.1-5286/phenix_env.sh



 steve@StevenH:~\$ ^C
 Pofinement

 steve@StevenH:~\$ export LIBGL_ALW
 Current directory: /nome/steve/p9-build
 Browse...

 source /home/steve/phenix-1.21.1 A new Phenix nightly build is available (version dev-5420)
 Project: p9-build

And you may have to set up tutorial data first before you can open the phenix window, but now the phenix window is working perfectly fine.

And now you just need to link Coot to Phenix:

/home/<linux username>/coot-Linux-x86_64-ubuntu-20.04.4-gtk2-python/bin/coot

/home/steve/coot-Linux-x86_64-ubuntu-20.04.4-gtk2-python/bin/coot



	Phenix home	×
<u>F</u> ile Projects <u>U</u> tilities <u>H</u>	Phenix preferences	×
Quit Preferences	General Projects Process Refine Wizards Graphics Files User info Col	lors p Server
Actions Job history Projects Show group: All groups ✓ Select ⊘ Delete ID Last n ✓ p9-build Aug 17	Image: Constraint intervent of the end of the	dev-5420 now click to download directly from oad credentials.) Is with Crystals or Cry manipulation ap-based comparisons sing ment nipulate, compare) older, FEM, density-n
/home	e/steve/p9-build Browse	
A new Phenix nightly build is	s available (version dev-5420) Project	ct: p9-build ///

To check to see if Phenix is running properly, you can run the p9 build tutorial data model building project.

	Create project	×
Please choose a characters only) overlap with a pr store settings an named '.phenix'.	simple project ID (alphanumeric and underscore and project directory. The directory should not reviously defined project directory. Phenix will d files specific to this project in a subdirectory	
Project ID :	123	
Project directory :	/home/steve	Browse Q
Sequence file :	/home/steve/p9-build/seq.dat	Browse
Add to group :	None	
	Switch to this project	
	Set up tutorial data	
		<mark>∦ C</mark> ancel ∉ <u>O</u> K

	Create project	×
Please choose a characters only) overlap with a pr store settings an named '.phenix'.	simple project ID (alphanumeric and underscore and project directory. The directory should not reviously defined project directory. Phenix will d files specific to this project in a subdirectory	
Project ID :	123	
Project directory :	/home/steve/PhenixProjects	Browse
Sequence file :	/home/steve/PhenixProjects/p9-build/seq.dat	Browse Q
Add to group :	None	
	✓ Switch to this project	
	Set up tutorial data	
	💥 <u>C</u> ancel	<u>ер</u> к
ह्य steve@StevenH: ~ ×	+ ~	- o x
steve@StevenH:/mnt/c/Users steve@StevenH:~\$ ls Phenix coot-Linux-x86_64-ubuntu-2 p9-build steve@StevenH:~\$ mkdir Phe	:/steve/Downloads\$ cd phenix-1.21.1-5286 :0.04.4-gtk2-python phenix-installer-1.21.1-5286-intel-linux-2.6- :nixProjects	x86_64-centos6

And you can see that while you were doing the Phenix stuff, there were errors that occurred:



This PhenixProjects folder is where you will put your PHENIX projects into (because they cannot be out in the open in your root directory)

You cane make a new directory in your root directory by typing: mkdir PhenixProjects

Now your new directory is called PhenixProjects. You can save your Phenix Project folders in here.

		Tutorial setup	×		
Phenip Phenip select will be	x comes with several ex a tutorial to run and a d created automatically.	ample datasets used for training purpose estination directory for the project; a new and the files copied to the final location.	es. Please v project The		
destin directe	ation directory may con ory itself.	tain other projects, but it should not be a	project	ystals or Cryo-EM	
Tutorial data:	Please select a datas	et		ation	
		1		comparisons	
Destination:	/home/steve		Browse	Create project	×
	Append user name	(steve) to project ID	cel <u>elo</u> K	e a simple project ID (alphanumeric and underscore ily) and project directory. The directory should not a previously defined project directory. Phenix will a and files specific to this project in a subdirectory nix'.	
		Model pullul		p9 build	
		Refinement	Project directory	/home/steve/PhenixProjects	Browse Q
		Ligands	Sequence file :		Browse Q
		Cryo-EM: Map analysis,	: Add to group :	None	
		Validation an	d	✓ Switch to this project	
		Map improver	r	Set up tutorial data	
		Docking, mod	E	Cance	е Серк
		Refinement			

The only tutorial data under BUILDING:

		Tutorial setup 🛛 🗙								
]]]	Phenix comes with several example datasets used for training purposes. Please select a tutorial to run and a destination directory for the project; a new project will be created automatically, and the files copied to the final location. The destination directory may contain other projects, but it should not be a project directory itself.									
	Tutorial data: P. aerophilum translation initiation-factor 5a (building from experimental pha									
	Destination:	/home/steve/PhenixProjects Browse								
		Append user name (steve) to project ID								
		View README								
		<mark>і С</mark> апсеl Сак								

	Phenix home					
<u>File</u> Projects <u>U</u> tilities <u>H</u> elp						
Quit Preferences Help Citations Coot	デーダ AS					
Actions Job history						
Projects	Download Phenix version dev-5420 now					
Show group: All groups	A new Phenix installer is available - click to download directly from our server. (Requires prior registration or download credentials.)					
Select 🤣 Delete 📣 New project 📣 Import project	Favorites					
ID Last modified # of jobs R-free	AlphaFold: Predicted models with Crystals or Cryo-EM					
y9-build_0 Aug 17 2024 03:50 PM 0	Crystals: Data analysis and manipulation					
	Validation and map-based comparisons					
	Experimental phasing					
	Molecular replacement					
	Maps (create, manipulate, compare)					
	Enhanced maps (Polder, FEM, density-modified)					
	Model building					
	Refinement					
	Ligands					
	Cryo-EM: Map analysis, symmetry, manipulation					
	Validation and map-based comparisons					
	Man improvement					

Now click ok and go to this one, double click.

Then click Model Building and go to AutoBuild:

<u>F</u> ile Projects <u>U</u> tilities <u>H</u> elp		
Quit Preferences Help	Coot	🚀 🚾 🕺 🔅 📔 😳 🔛 PyMOL KING Tools Help Server
Actions Job history		
Projects		
Show group: All answer		validation and map-based comparisons
All groups Manag		Experimental phasing
Select 🧭 Delete 🖕 New project 🖕 Ir	nport project	Molecular replacement
ID Last modified # of	obs R-free	Maps (create, manipulate, compare)
p9-build Aug 17 2024 03:50 PM 0		Enhanced maps (Polder, FEM, density-modified)
> ps-build_0 Aug 17 2024 03.39 PM 0		Model building
		Predict and Build: Crystallography
		Iterative AlphaFold prediction, MR/docking, and rebuilding
		AutoBuild Automated model-building and refinement
		Phase and build Faster auto-building combined with density modification

and click on it

		Phenix home	
Ele Projects Utilities Help			
🙆 🔏 ? 📄 🛫	🦟 🔀 🌾	AutoBuild (Project: p9-build_0)	. – ×
Quit Preferences Help Citations Coot	PyMOL KING Tools	Eile Actions Settings Utilities Help	
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Follow the tutorial here: <u>https://youtu.be/og3TM9Cwve0?si=iqtepsk4G8bu0VZ1</u> or follow along on this document as well:

	AutoBuild (Project: p9-build_0)										_ 🗆	X			
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	🛅 steve 🛛 Ph	enixProjects	p9-build_0]			Save	_ ,	(triage	Coot	PyMOL		C Help	
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And click open

		Auto	oBuild (Pro	oject	: p9-build_0)				_ 🗆 🗙
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Q /home/steve/Phenix	Projects/p9-build_(0/seq.dat			Sequence		Sequence		-
Add file Remove	file Modify file d	ata type	Input file o	ptions	3				¥
🕒 Idle						Proje	ct: p9-build_0		

Now you will modify the file data type so that the pd_data_and_phases.mtz will be the experimental data (where the phases are)

And change the setting so that the p9_hires.mtz will be the high resolution map data type:

AutoB	uild (Project:	9-build_0)				_	×
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/home/steve/PhenixProjects/p9-build_0/p9_hires.mtz		ccp4_mtz		High-resol	ution data		
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	AutoBuild (Project: p9-bu	ild_0)	_ 🗆 🗙
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Crystal info and general parameters			
Space group : ▼ Unit cell : 113.949 11	3.949 32.474 90 90 90		
High-resolution limit : 0.0 NCS copie	s : Solvent fra	ction :	
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Quick mode I Map file has been density-modifie	d		
Model-building and refinement			
Refinement cycles : 3 Aax. iterative b	uild cycles : 6 🖡 Ma	ax. iterative rebuild cycles : 15	
Chain type : Auto	: Auto 🔽		
□ Skip free R flags hexdigest R-free flag value :			
☑ Include input model	d strands only	Morph input model into density	
☑ Build outside model	dues	Refine input model before rebuilding	
☑ Refine model during building ☑ Place waters in	refinement	Use simulated annealing	
Twin law : Use 2Fo-Fc map	in rebuilding (try with twin law))	
Model building Refinement All parameters			
● Idle		Project: p9-build_0	

This is the original

Just check "quick mode"

Change the "max iterative build cycles" to 1 from 6

Change the "max iterative rebuild cycles" to 1 from 15

Un-check "build outside model"

AutoBuild (Project: p9-buil	d_0)							
<u>File Actions Settings U</u> tilities <u>H</u> elp								
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Number of processors : 4 A Map file FOM :								
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Chain type : Auto 🔽 Rebuild in place : Auto 🔽								
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☑ Include input model	Morph input model into density							
Build outside model Build SeMet residues	Refine input model before rebuilding							
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Twin law : Use 2Fo-Fc map in rebuilding (try with twin law)								
Model building Refinement All parameters								
● Idle	Project: p9-build_0							

AutoBuild (Project: p9-build	
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High-resolution limit : 0.0 NCS copies : Solvent fraction	on :
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☑ Quick mode ☑ Map file has been density-modified	
Model-building and refinement Refinement cycles : 3 A Max. iterative build cycles : 1 A	iterative rebuild cycles :
Chain type : Auto 💌 Rebuild in place : Auto 💌	
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Build outside model Build SeMet residues	Refine input model before rebuilding
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Model building Refinement All parameters	
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Now click run

				AutoB	uild (P	roject: p	o9-bu	ild_0)					_ 🗆 X
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		ADOI	View	log					Project	ng_h	uild 0		

While this is loading, you can check the terminal, and there might be a lot of errors:



	AutoBuild (Project: p9-build_0)							
<u>F</u> ile <u>A</u> ctions <u>S</u> ettings <u>U</u> tilities <u>H</u> elp								
Preferences Help Run Abort	Save Xtriage Coot PyMOL	CD Help						
Configure AutoBuild_run_1_		4 ▷ ×						
Status Summary		4 ⊳						
Output files Directory: /home/steve/PhenixProjects/p9-bui	ld_0/AutoBuild_run_1_							
File name	Contents	🥑 Open in Coot						
্ AutoBuild_run_1_1.log	AutoBuild log	Open in PyMOL						
Data analysis AutoBuild has analyzed your X-ray data with Xtriage. This will indicate whether you have any pathologies such as twinning or pseudosymmetry, as well as providing information on data quality and anomalous signal. Image log file Image log file								
1 job(s) running	Project: p9	-build_0 //						

	AutoBuild (Project: p9-build_0)	
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Status Summary Model-building Structure state	IS	4 ⊅
Output files Directory: /home/steve/PhenixProjects/p9-bu	ild_0/AutoBuild_run_1_	
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Data analysis AutoBuild has analyzed your X-ray data with Xtriage. pseudosymmetry, as well as providing information on Xtriage log file	This will indicate whether you have any pathologies such as data quality and anomalous signal. and graphs	twinning or
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	AutoBuild (Project: p9-build_0)
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Configure AutoBuild_run_1_	4 ⊳ ×
Status Summary Model-building Structure status	4 Þ
Wizard status Running	
Creating overall_best files Refining AutoBuild_run_1_/cycle_best_1.p exptl_fobs_phases_freeR_flags.mtz Setting refinement resolution to 1.7443 Using test_flag_value of 1 in refinement Starting phenix on Sat Aug 17 16:16:52 2024 by steve	ے b against original data in AutoBuild_run_1_/
	-
Pause XAbort View Ic	9
 1 job(s) running 	Project: p9-build_0

And now you can go to summary and open Coot to see what is going on to the model in Coot:

AutoBuild	l (Project: p9-build_0)
<u>File Actions Settings Utilities H</u> elp	
🕺 🤊 🖄 🔛 🗌	🚺 (🛫 🚿 (🛟
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Output files Directory: /home/steve/PhenixProjects/p9-build_0/AutoBu	ild_run_1_
File name Contents	🔮 Open in Coot
د AutoBuild_run_1_1.log AutoBuild lo	g
	🦗 Open in PyMOL
	Starting Coot
Data analysis	
AutoBuild has analyzed your X-ray data with Xtriage. This will indic pseudosymmetry, as well as providing information on data quality a	Coot is being started with the Phenix extensions pre-loaded. Depending on computer speed, it may take several seconds for the program to open.
	Don't show this message again
Xtriage log file	Cancel @OK
● 1 job(s) running	Project: p9-build_0





This run on average only takes around 20 to 30 minutes:

	AutoBuild (Project: p9-build_0)		_ 🗆 🗙
<u>File Actions</u> <u>Settings</u> <u>U</u> tilities <u>H</u> elp			
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File name	Contents	A Oper	n in Coot
Q AutoBuild_run_1_1.log	AutoBuild log		
Q overall_best_refine_map_coeffs.mtz	Best refined maps (2Fo-Fc, Fo-Fc)	0per	n in PvMOI
Q overall_best_denmod_map_coeffs.mtz	Best density-modified map	l we ober	, mit yn oe
Q overall_best_refine_data.mtz	Original data, exptl phases, R-fre		
\bigcirc overall_best_placed.pdb	Best model (docked sequence onl	-1	
Data analysis AutoBuild has analyzed your X-ray data with Xtriage. pseudosymmetry, as well as providing information on	This will indicate whether you have any data quality and anomalous signal.	pathologies such as twinning or	
Xtriage log file	and graphs		
● 1 job(s) running		Project: p9-build_0	//
		· · -	

AutoBuild (Project: p9-build_0)	_ 🗆 X				
<u>File Actions Settings U</u> tilities <u>H</u> elp					
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Preferences Help Run Abort Save Xtriage Coot PyMOL Help					
Configure AutoBuild_run_1_	× 4 P				
Status Summary Model-building Structure status	4 Þ				
Protein chains					
Double-click on any residue or secondary structure element to zoom in on that region in Coot or PyMOL.					
Select chain: A 🔽 Clear selection					
1 XXXXXXXXXXVEAGELKEGSYVVIDGEPXXXXXXXXXXXXXAKARI 50					
51 VAVGVFDGGKRTLSLPVDAQVEVPIIEKFTAQILSVSGDVIQLMDMRDYK 100					
101 TIEVPMKYVEEEAKGRLAPGAEVEVWOILDRYKII 150					
• 1 job(s) running Project: p9-build_0					
	toBuild (Project: p9-build_0)				
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<u>File Actions</u> <u>Settings</u> <u>U</u> tilities <u>H</u> elp					
Image: New York Image: New York Image: New York Preferences Help Run Abort	ve Xtriage Coot PyMOL Help				
Configure AutoBuild_run_1_	4 ≬ X				
Status Summary Model-building Structure status	4 Þ				
Wizard status Running					
Log output					
Re-using input PDB coordinates in build this cycle Density modifying image of refine.pdb_2 - refine.pdb_2 ->resolve_denmod_3.log Unit cell: (113.949, 113.949, 32.474, 90, 90, 90) Space group: I 4 (No. 79) Unit cell: (113.949, 113.949, 32.474, 90, 90, 90) Space group: I 4 (No. 79)					
Running standard build/extend Starting with current best model of working_best.pdbsetting it to starting_model.pdb Including parts of this model if best Starting best model from starting_model.pdb Building 1 RESOLVE models Model 1: Residues built=116 placed=108 Chains=1 Model-map CC=0.67 (Build_1.pdb)					
1 job(s) running	Project: p9-build_0				

AutoBuild (Project: p9-build_0)	_ 🗆 X				
<u>F</u> ile <u>A</u> ctions <u>S</u> ettings <u>U</u> tilities <u>H</u> elp					
X ? Image Image Image Image Image Image Preferences Help Run Abort Save Xtriage Coot PyMOL Help					
Configure AutoBuild_run_1_	4 Þ ×				
Status Summary Model-building Structure status	4 Þ				
Running					
Log output 'refinement.output.export_final_f_model=True' Moving refinement file AutoBuild_run_1_/TEMP0/refine_1_001_f_model.mtz to AutoBuild_run_1_/TEMP0/ refine_f_model.mtz Moving refinement file AutoBuild_run_1_/TEMP0/refine_1_001.mtz to AutoBuild_run_1_/TEMP0/ refine_map_coeffs_1.mtz Model: AutoBuild_run_1_/TEMP0/refine_1.pdb R/Rfree=0.28/0.30 Maps from refinement will be filled (2F0FCWT PH2F0FCWT) Set refine map coeffs file best_refine_map_coeffs to refine_map_coeffs_1.mtz					
Model completion cycle 1 Models to combine and extend: ['starting_model.pdb', 'Build_1.pdb', 'refine_1.pdb'] Model 2: Residues built=121 placed=113 Chains=1 Model-map CC=0.80 (Build_combine_extend_2.pdb) Pause X Abort View log	Ţ				
● 1 job(s) running Project: p9-build_0					

	AutoBuild (Pro	oject: p9-bui	ld_0)			_ 🗆 X
<u>F</u> ile <u>A</u> ctions <u>S</u> ettings <u>U</u> tilities <u>H</u> elp						
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Configure AutoBuild_run_1_						4 Þ 🗙
Status Summary Model-building Structure status						4 Þ
Wizard status FINISHED Log output 'cycle_best_1.log_refine', 'helices_only 'working_best_refine_map_coeffs.mtz', 't 'aniso_data_PHX.mtz', 'refinement_PHX.mt 'cycle_best_1.mtz', 'exptl_phases_for_dm 'cycle_best_3.log_refine', 'AutoBuild_Fa 'cycle_best_1.log_eval', 'cycle_best_1.l 'autoBuild_inp', 'seq_from_file_dat', 'c 'AutoBuild_summary.dat', 'exptl_fobs_pha 'working_best_denmod_map_coeffs.mtz', 'A AutoBuild_run_1_/working_files Done_cleaning_up Wiew log View log	_model.log', itle.dat', 'wd z_xtriage_graf _aniso.mtz', al', 'refinemd cts.dat', 'cyd og', 'working ycle_best_ref: ses_freeR_flad utoBuild_warn:	'hires_PHX orking_bes phs.log', 'working_b ent_PHX.mt ccle_best_3 _best.pdb' ine_map_co gs.mtz', ' ings.dat',	.mtz', t.log', ' 'AutoBuil est.log_e z_triage .log', 'n ; 'cycle_ effs_1.m cycle_bes 'refinem	'helices_on Ld_run_1_1.1 eval', 'worl elog.pkl', refinement_f best_3.log tz', 'cycle st_1.pdb', nent_PHX.mt;	Ly_model.pdb', Log', king_best_placed.pd PHX.mtz', denmod', _best_3.pdb', z_xtriage.log']) to	db',
• Idle				Project: p9-b	ouild_0	

	AutoBuild (P	Project: p9-build_0)		- 🗆 ×			
<u>F</u> ile <u>A</u> ctions <u>S</u> ettings <u>U</u> tilities <u>H</u> e	lp						
Preferences Help	EXAPORT Abort Save	Xtriage Coot	🧩 🛛 🗘 PyMOL Help				
Configure AutoBuild_run_1_				4 Þ 🗙			
Status Summary Model-building	Structure status			4 Þ			
Output files Directory: /home/steve/PhenixP	rojects/p9-build_0/AutoBuild	i_run_1_					
File name	Contents			Open in Coot			
্ AutoBuild_run_1_1.log	AutoBuild log			•			
্ overall_best_refine_map_coeffs.m	ntz Best refined ma	ps (2Fo-Fc, Fo-Fc)		Open in PvMOL			
্ overall_best_denmod_map_coeffs	s.mtz Best density-mo	odified map		, , , , , , , , , , , , , , , , , , , ,			
् overall_best_refine_data.mtz	Original data, e	xptl phases, R-fre					
♀ overall_best_placed.pdb	Best model (doo	Best model (docked sequence onl					
Data analysis AutoBuild has analyzed your X-ray data with Xtriage. This will indicate whether you have any pathologies such as twinning or pseudosymmetry, as well as providing information on data quality and anomalous signal. Image log file Image Results and graphs							
Warnings NOTE: Free R Flag (FreeR_flag) in input data file will not be used as a hires or refinement file is present							
Final model							
R-work: 0.2384	R-free:	0.2571	cc:				
Residues: 121 Idle	Fragments:	3	Waters: Project: p9-build_0	110			

If you would like to, you can try phenix.refine as well (to test Coot further)

As we can see though, there were those errors that happened when clicking in PHENIX, but no errors when we were running coot:



So, to fix this, let us see if downloading python3 will fix the PHENIX errors (also at this point **nano** already works)

https://docs.python-guide.org/starting/install3/linux/

as you can see, it already has python3



\$ sudo apt-get update

\$ sudo apt-get install python3.6



园 steve@StevenH: /mnt/c/Wind × + ~	-		×
<pre>Fetched 1387 kB in 1s (928 kB/s) Selecting previously unselected package libboost-python1.74.0. (Reading datbase 45887 files and directories currently installed.) Preparing to unpack/libboost-python1.74.0_1.74.0-14ubuntu3_amd64.deb Unpacking libboost-python1.74.0 (1.74.0-14ubuntu3) Selecting previously unselected package libcasa-casa6:amd64. Preparing to unpack/libcasa-casa6.3.4.0-2build1_amd64.deb Unpacking libcasa-casa6:amd64 (3.4.0-2build1) Selecting previously unselected package libcasa-python3-6:amd64. Preparing to unpack/libcasa-cysa6.3.4.0-2build1_amd64.deb Unpacking libcasa-casa6:amd64 (3.4.0-2build1) Selecting previously unselected package libcasa-python3-6:amd64. Preparing to unpack/libcasa-python3-6.3.4.0-2build1_amd64.deb Unpacking libcasa-python3-6:amd64 (3.4.0-2build1) Setting up libcasa-casa6:amd64 (3.4.0-2build1) Setting up libcasa-cypthon3-6:amd64 (3.4.0-2build1) Setting up libcasa-python3-6:amd64 [2.4.0-2build1] Setting up libcasa libc-bin (2.35-0ubuntu3.</pre>			
Steve@StevenH: /mnt/c/Wind × + →	-		×
<pre>[1817 kB] Get:6 https://ppa.launchpadcontent.net/deadsnakes/ppa/ubuntu jammy/main amd64 python3.8 amd64 3.8.19-1+jammy1 Fetched 5103 kB in 55 (1045 kB/s) Selecting previously unselected package libpython3.8-minimal:amd64. (Reading database 45901 files and directories currently installed.) Preparing to unpack/0-libpython3.8-minimal_3.8.19-1+jammy1_amd64.deb Unpacking libpython3.8-minimal:amd64 (3.8.19-1+jammy1) Selecting previously unselected package python3.8-minimal. Preparing to unpack/1-python3.8-minimal_3.8.19-1+jammy1_amd64.deb Unpacking python3.8-minimal (3.8.19-1+jammy1) Selecting previously unselected package mailcap. Preparing to unpack/2-mailcap_3.70+nmulubuntu1_all.deb Unpacking mailcap (3.70+nmulubuntu1) Selecting previously unselected package mime-support. Preparing to unpack/3-mime-support_3.66_all.deb Unpacking mailcap (3.70+nmulubuntu1) Selecting previously unselected package libpython3.8-stdlib:amd64. Preparing to unpack/4-libpython3.8-stdlib_3.8.19-1+jammy1_amd64.deb Unpacking mime-support (3.66) Selecting previously unselected package libpython3.8-stdlib:amd64. Preparing to unpack/4-libpython3.8_s19-1+jammy1_amd64.deb Unpacking libpytho3.8_stdlib.a.8.19-1+jammy1_amd64.deb Unpacking python3.8 (3.8.19-1+jammy1) Selecting previously unselected package python3.8. Preparing to unpack/5-python3.8_3.8.19-1+jammy1_amd64.deb Unpacking python3.8 (3.8.19-1+jammy1) Setting up libpython3.8-minimal:amd64 (3.8.19-1+jammy1) Setting up python3.8-minimal:amd64 (3.8.19-1+jammy1) Setting up python3.8-minimal:amd64 (3.8.19-1+jammy1)</pre>	[439	kB]	

Setting up mine-support (3.66) ... Setting up libpython3.8-stdlib:amd64 (3.8.19-1+jammy1) ... Setting up python3.8 (3.8.19-1+jammy1) ... Processing triggers for man-db (2.10.2-1) ... steve@StevenH:/mnt/c/Windows/system32\$ |



So now let us try doing the same p9 and see if the errors are still there:



Now there are no more errors!!



To check if Coot is running fine, you can take the p9 build and run .refine:

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p9-build Aug 17 2024 03:5 0	Molecular replacement					
	Maps (create, manipulate, compare)					
	Enhanced maps (Polder, FEM, density-modified)					
	Model building					
	Refinement					
	Automated refinement using diffraction data (X-ray, neutron,)					

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If you press space and you can go from amino acid to amino acid, then that means Coot is successfully working!

And no more errors in the terminal for PHENIX!!



Congratulations you have successfully download PHENIX and Coot!!!!