These are the steps required to use CIPRES REST from Geneious Prime. If you have questions or problems, please contact me at mmiller@ucsd.edu)

Step 1. Create an account at CIPRES REST. (one time only)

Visit: https://www.phylo.org/restusers/register.action to register.

Step 2. Install the CIPRES_Prime plugin. (one time only)

Go to http://www.phylo.org/index.php/portal/geneious_plugin

Download the CIPRES_Prime.gplugin

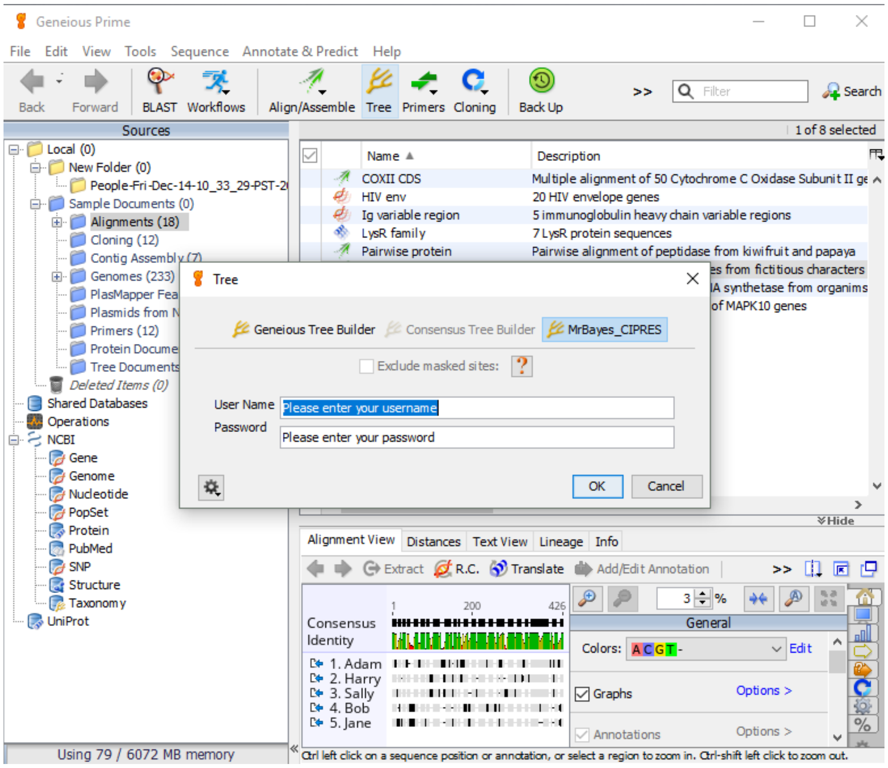
Start Geneious and drag the CIPRES_Prime plug-in onto the Geneious work area.

Geneious will prompt you as to whether or not you want to use this plug-in. Accept the add-in.

Select a data set that RAxML or MrBayes will work on.

Click Trees in the top bar.

If this is your first use of CIPRES, you will be prompted for your credentials:

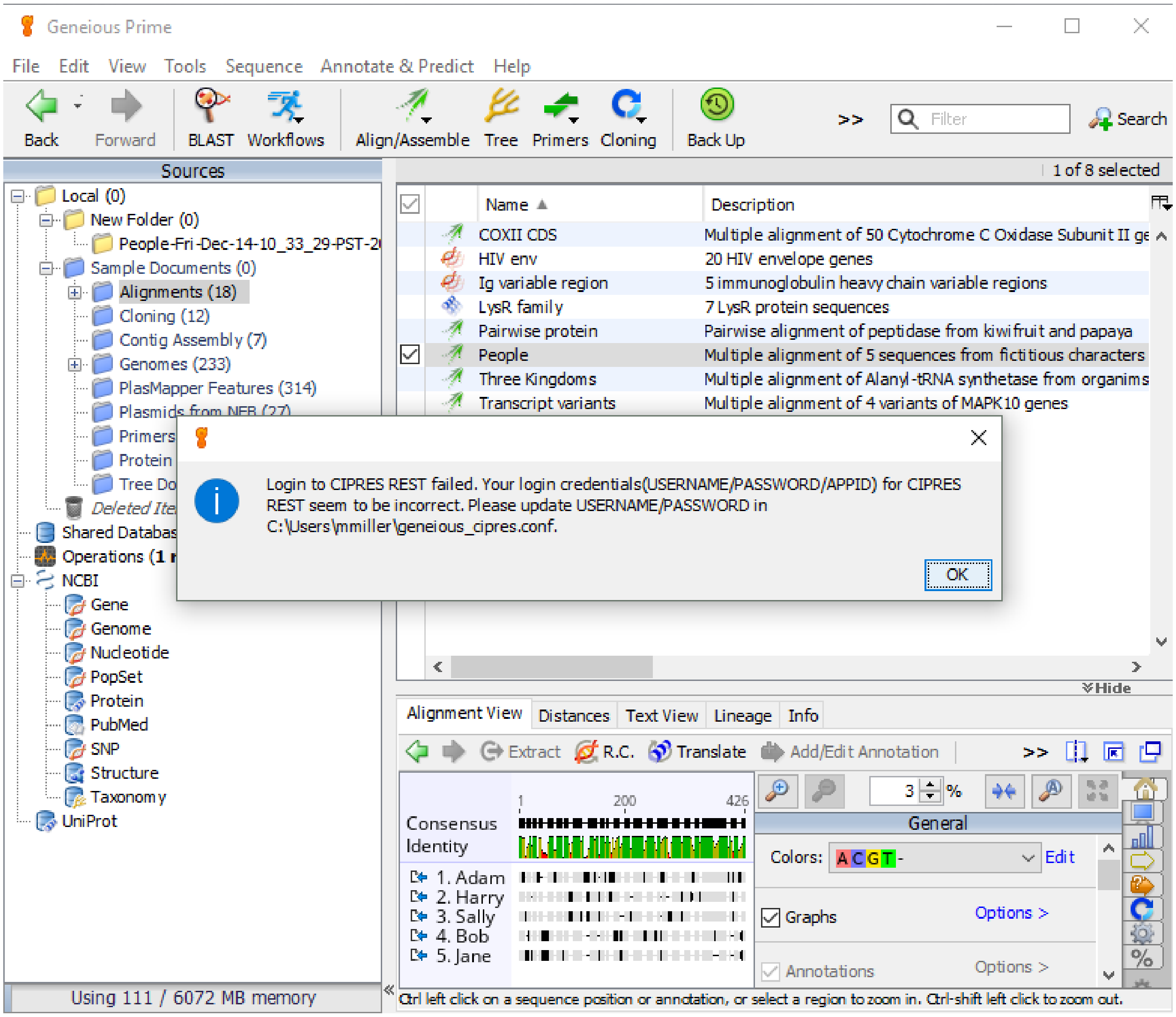


User Name: Please enter your username

Password: Please enter your password

If you enter correct credentials, you will receive a success message.
You are now ready to run jobs on CIPRES. Proceed to the next step.

If you enter incorrect credentials you will receive a message like this, with the path to your credential file:



☐	Name ▲	Description
	COXII CDS	Multiple alignment of 50 Cytochrome C Oxidase Subunit II ge
	HIV env	20 HIV envelope genes
	Ig variable region	5 immunoglobulin heavy chain variable regions
	LysR family	7 LysR protein sequences
	Pairwise protein	Pairwise alignment of peptidase from kiwifruit and papaya
☑	People	Multiple alignment of 5 sequences from fictitious characters
	Three Kingdoms	Multiple alignment of Alanyl-tRNA synthetase from organims
	Transcript variants	Multiple alignment of 4 variants of MAPK10 genes

Login to CIPRES REST failed. Your login credentials(USERNAME/PASSWORD/APPID) for CIPRES REST seem to be incorrect. Please update USERNAME/PASSWORD in C:\Users\mmiller\geneious_cipres.conf.

OK

The message will tell you where to find the file you need to edit to correct your credentials at CIPRES. Look for the file geneious_cipres.conf, and use a text editor to correct your credentials.

Step 3: To run MrBayes or RAxML jobs on CIPRES:

In the top bar, select Tree

Once the Tree option opens up, select CIPRES as the tree tool. Choose a tab for MrBayes, or RAxMLBB

Configure the run using the form that opens.

For MrBayes runs, you can use the “Custom MrBayes block” option to add additional parameters.

Click OK to submit.
You will see a message saying the job is being submitted.
The message will be “Performing CIPRES”

When your job is completed, you will receive an email.

If you want to just download the results of your CIPRES REST jobs, please perform Step 4; if you want to download and import the results of your CIPRES REST jobs into Geneious, please perform Step 5 instead.

Step 4. Download your CIPRES REST results to your local machine (each time).

To download your results into your local machine, go to Tools/CIPRES

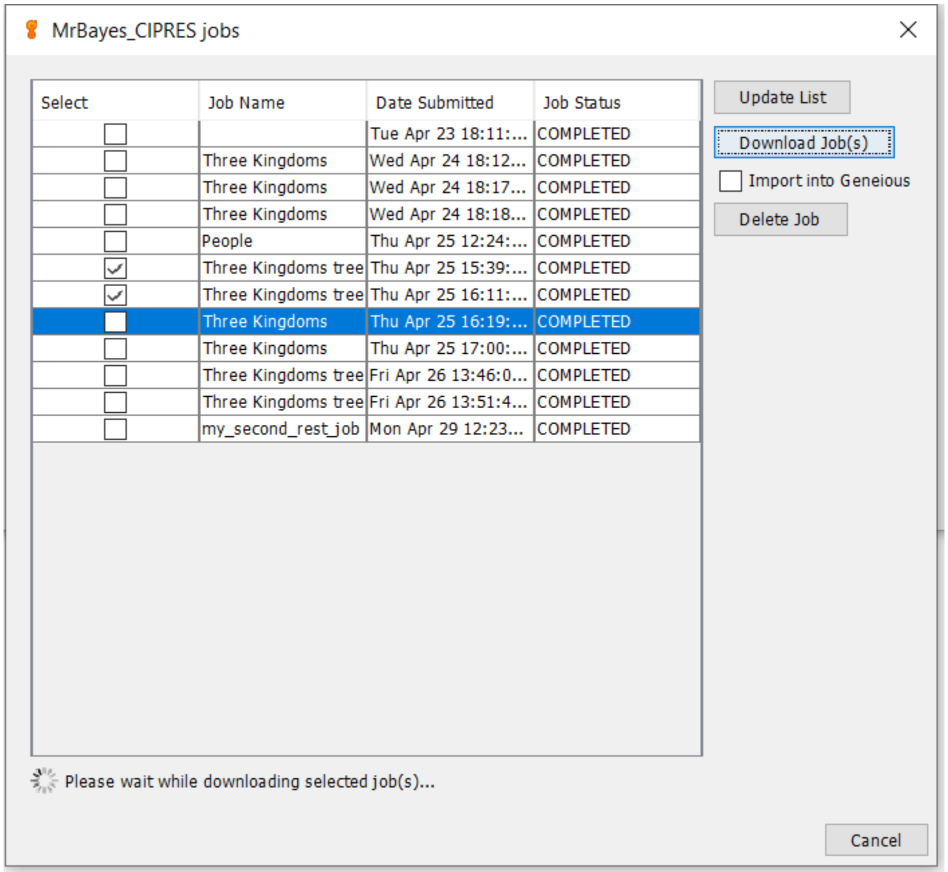
Your jobs will be displayed.

You can monitor progress with the “Update List” button.

Highlight the completed job(s).

Click “Download Job(s)”, and specify the folder on your local machine where you would like your job results to end up.

It may take a little time for the results to download. On the bottom left corner there will be a message saying “Please wait while downloading selected job(s) …”.



Select	Job Name	Date Submitted	Job Status
☐		Tue Apr 23 18:11:...	COMPLETED
☐	Three Kingdoms	Wed Apr 24 18:12...	COMPLETED
☐	Three Kingdoms	Wed Apr 24 18:17...	COMPLETED
☐	Three Kingdoms	Wed Apr 24 18:18...	COMPLETED
☐	People	Thu Apr 25 12:24:...	COMPLETED
☑	Three Kingdoms tree	Thu Apr 25 15:39:...	COMPLETED
☑	Three Kingdoms tree	Thu Apr 25 16:11:...	COMPLETED
☐	Three Kingdoms	Thu Apr 25 16:19:...	COMPLETED
☐	Three Kingdoms	Thu Apr 25 17:00:...	COMPLETED
☐	Three Kingdoms tree	Fri Apr 26 13:46:0...	COMPLETED
☐	Three Kingdoms tree	Fri Apr 26 13:51:4...	COMPLETED
☐	my_second_rest_job	Mon Apr 29 12:23...	COMPLETED

Please wait while downloading selected job(s)...

Step 5. Download/Import your results into Geneious (each time)

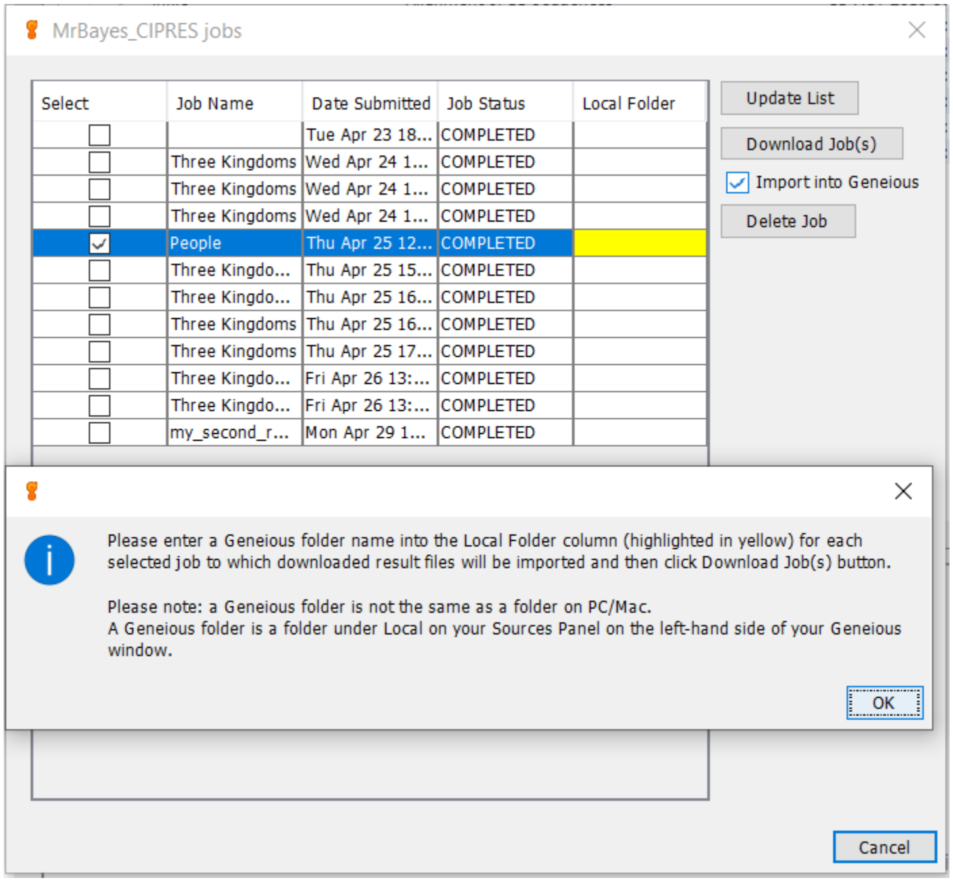
To download/import your results into Geneious, go to Tools/CIPRES

Your jobs will be displayed.

You can monitor progress with the “Update List” button.

Highlight the completed job(s).

Tick “Import into Geneious”. Below message window will pop up.



Select	Job Name	Date Submitted	Job Status	Local Folder
☐		Tue Apr 23 18...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☑	People	Thu Apr 25 12...	COMPLETED	
☐	Three Kingdo...	Thu Apr 25 15...	COMPLETED	
☐	Three Kingdo...	Thu Apr 25 16...	COMPLETED	
☐	Three Kingdoms	Thu Apr 25 16...	COMPLETED	
☐	Three Kingdoms	Thu Apr 25 17...	COMPLETED	
☐	Three Kingdo...	Fri Apr 26 13:...	COMPLETED	
☐	Three Kingdo...	Fri Apr 26 13:...	COMPLETED	
☐	my_second_r...	Mon Apr 29 1...	COMPLETED	

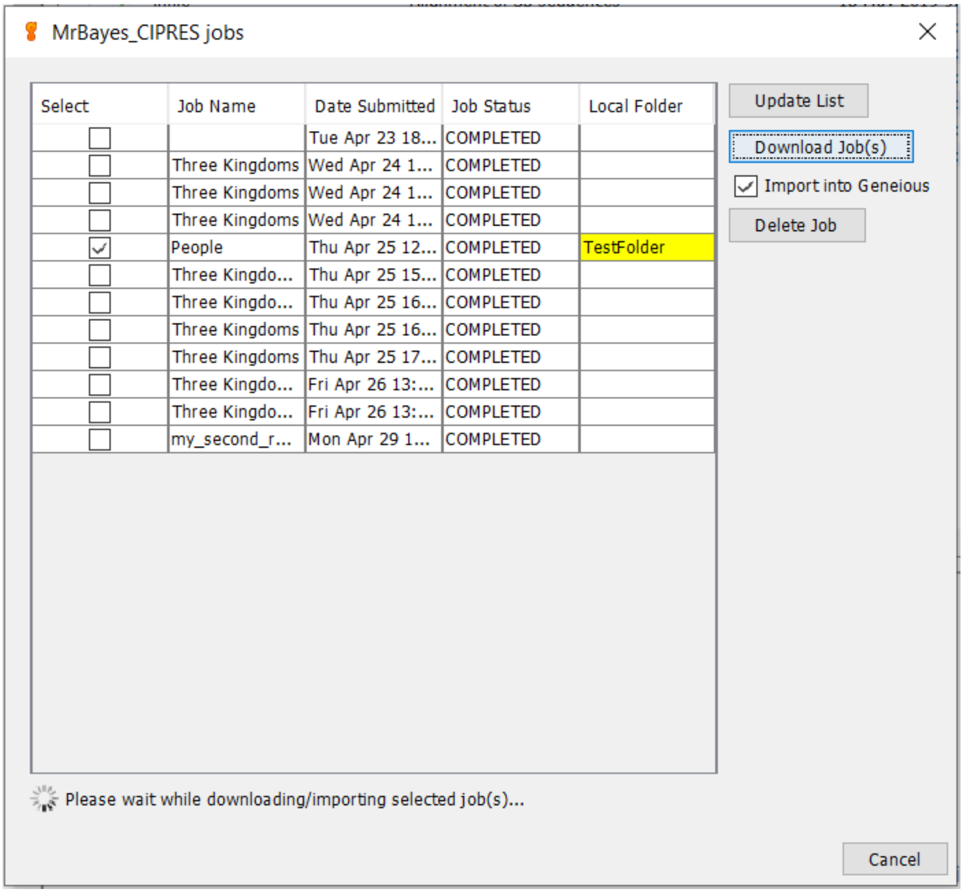
Please enter a Geneious folder name into the Local Folder column (highlighted in yellow) for each selected job to which downloaded result files will be imported and then click Download Job(s) button.

Please note: a Geneious folder is not the same as a folder on PC/Mac.
A Geneious folder is a folder under Local on your Sources Panel on the left-hand side of your Geneious window.

Click OK and enter a Geneious folder name into the Local Folder column highlighted in yellow (please note: a Geneious folder is not the same as a folder on PC/Mac. A Geneious folder is a folder under Local on your Source Panel on the left hand side of your Geneious window.)

Click “Download Job(s)”, and specify the folder on your local machine where you would like your job results to end up (the plugin keeps a copy of the results under the specified folder on your local machine and then import them into Geneious for you).

It may take a little time for the results to download/import. On the bottom left corner there will be a message saying “Please wait while downloading/importing selected job(s) …”.

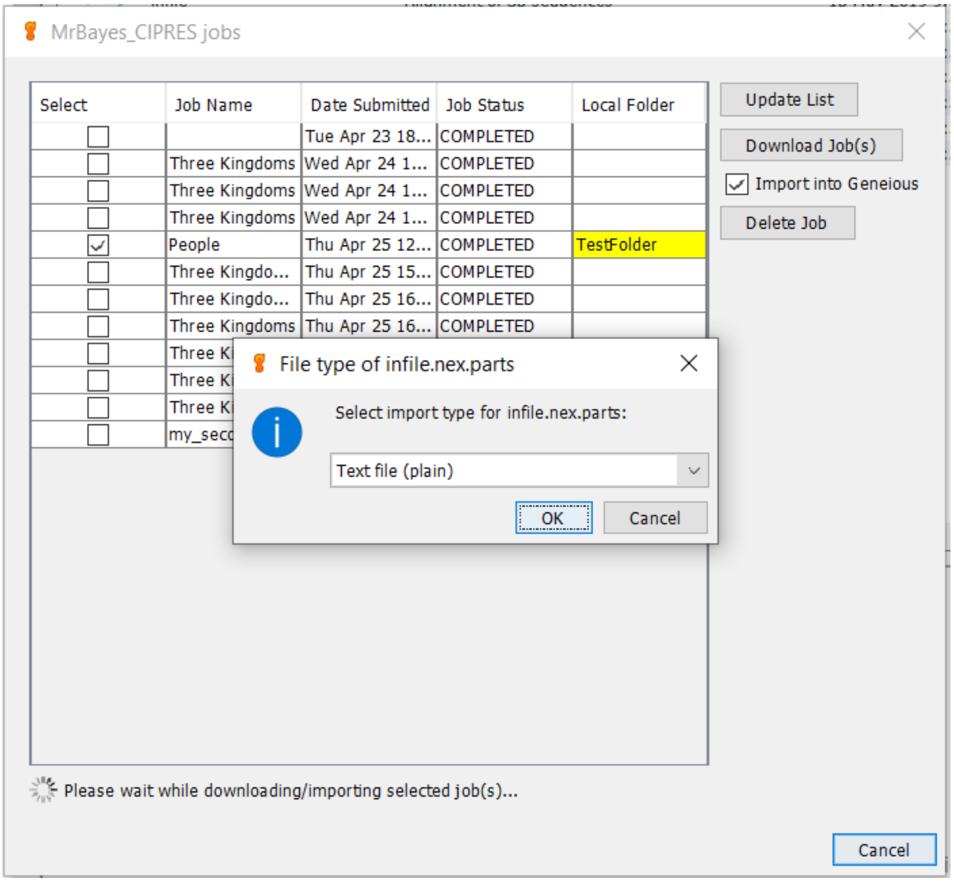


Select	Job Name	Date Submitted	Job Status	Local Folder
☐		Tue Apr 23 18...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☑	People	Thu Apr 25 12...	COMPLETED	TestFolder
☐	Three Kingdo...	Thu Apr 25 15...	COMPLETED	
☐	Three Kingdo...	Thu Apr 25 16...	COMPLETED	
☐	Three Kingdoms	Thu Apr 25 16...	COMPLETED	
☐	Three Kingdoms	Thu Apr 25 17...	COMPLETED	
☐	Three Kingdo...	Fri Apr 26 13:...	COMPLETED	
☐	Three Kingdo...	Fri Apr 26 13:...	COMPLETED	
☐	my_second_r...	Mon Apr 29 1...	COMPLETED	

☑ Import into Geneious

Please wait while downloading/importing selected job(s)...

If Geneious doesn't recognize any file during importing, it will pop up a window asking you to select an import file type for that file. You can select a file type from the drop-down list and then click OK or you can just click Cancel to skip importing of that particular file.



Select	Job Name	Date Submitted	Job Status	Local Folder
☐		Tue Apr 23 18...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☐	Three Kingdoms	Wed Apr 24 1...	COMPLETED	
☑	People	Thu Apr 25 12...	COMPLETED	TestFolder
☐	Three Kingdo...	Thu Apr 25 15...	COMPLETED	
☐	Three Kingdo...	Thu Apr 25 16...	COMPLETED	
☐	Three Kingdoms	Thu Apr 25 16...	COMPLETED	
☐	Three Ki			
☐	Three Ki			
☐	Three Ki			
☐	my_seco			

☑ Import into Geneious

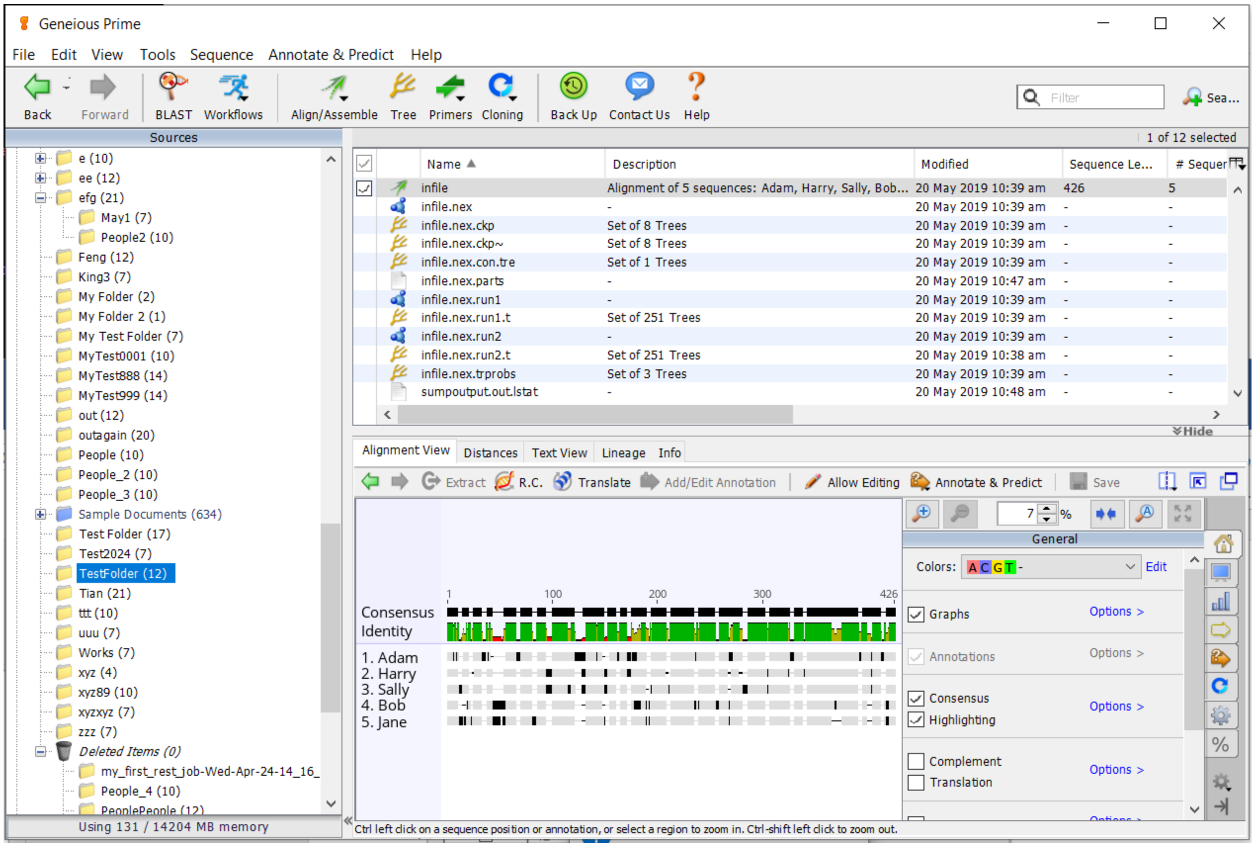
File type of infile.nex.parts

Select import type for infile.nex.parts:

Text file (plain)

Please wait while downloading/importing selected job(s)...

Once the download/import is complete, locate the job results under the folder name you enter into Local Folder column at the beginning of this step (for example, on above screenshot, “TestFolder”) on Sources Panel on the left hand side of your Geneious window. Click on it and the imported files should be shown on the main panel.



- e (10)
- ee (12)
- efg (21)
  - May1 (7)
  - People2 (10)
- Feng (12)
- King3 (7)
- My Folder (2)
- My Folder 2 (1)
- My Test Folder (7)
- MyTest0001 (10)
- MyTest888 (14)
- MyTest999 (14)
- out (12)
- outagain (20)
- People (10)
- People_2 (10)
- People_3 (10)
- Sample Documents (634)
- Test Folder (17)
- Test2024 (7)
- TestFolder (12)
- Tian (21)
- ttt (10)
- uuu (7)
- Works (7)
- xyz (4)
- xyz89 (10)
- xyzxyz (7)
- zzz (7)
- *Deleted Items (0)*
  - my_first_rest_job-Wed-Apr-24-14_16_
  - People_4 (10)
  - PeoplePeople (12)

Using 131 / 14204 MB memory

	Name ▲	Description	Modified	Sequence Le...	# Sequer
☑	infile	Alignment of 5 sequences: Adam, Harry, Sally, Bob...	20 May 2019 10:39 am	426	5
	infile.nex	-	20 May 2019 10:39 am	-	-
	infile.nex.ckp	Set of 8 Trees	20 May 2019 10:39 am	-	-
	infile.nex.ckp~	Set of 8 Trees	20 May 2019 10:39 am	-	-
	infile.nex.con.tre	Set of 1 Trees	20 May 2019 10:39 am	-	-
	infile.nex.parts	-	20 May 2019 10:47 am	-	-
	infile.nex.run1	-	20 May 2019 10:39 am	-	-
	infile.nex.run1.t	Set of 251 Trees	20 May 2019 10:39 am	-	-
	infile.nex.run2	-	20 May 2019 10:39 am	-	-
	infile.nex.run2.t	Set of 251 Trees	20 May 2019 10:38 am	-	-
	infile.nex.trprobs	Set of 3 Trees	20 May 2019 10:39 am	-	-
	sumpoutput.out.lstat	-	20 May 2019 10:48 am	-	-

☑ Graphs
☐ Annotations
☑ Consensus
☑ Highlighting
☐ Complement
☐ Translation

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.