

FIRST STEPS

BioLinux of flash Memory

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Bio-Linux 8 is a powerful, free bioinformatics workstation platform that can be installed on anything from a laptop to a large server, or run as a virtual machine.

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BL Sidebar Menu

- [Bio-Linux Software List](#)
- [Bio-Linux 8 - What's New](#)
- [Bio-Linux Remote Access Guide](#)
- [Bio-Linux Installation](#)
- [Bio-Linux Download](#)
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Bio-Linux 8 - Released July 2014

"Bio-Linux is an ideal system for scientists handling and analysing biological data."

If you use Bio-Linux in your work, please reference:
Field, D., Tiwari, B., Booth, T., Houten, S., Swan, D., Bertrand, N. and Thurston, M. 2006. Open Software for biologists: from famine to feast. *Nature Biotechnology* 24, 801 - 803.
See recent papers that have cited Bio-Linux in Google Scholar.

About Bio-Linux

Bio-Linux 8 is a powerful, free bioinformatics workstation platform that can be installed on anything from a laptop to a large server, or run as a virtual machine. Bio-Linux 8 adds more than 250 bioinformatics packages to an [Ubuntu Linux 14.04 LTS](#) base, providing around 50 graphical applications and several hundred command line tools. The [Galaxy environment](#) for browser-based data analysis and workflow construction is also incorporated in Bio-Linux 8.

Bio-Linux 8 represents the continued commitment of NERC to maintain the platform, and comes with many updated and additional tools and libraries. With this release we support pre-prepared VM images for use with VirtualBox, VMWare or Parallels. Virtualised Bio-Linux will power the [EOS Cloud](#), which is in development for launch in 2015.



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Please help us to support further development of Bio-Linux If you use Bio-Linux to analyse data for your published research, please cite [the Bio-Linux paper \(Field at al. 2006\)](#). Also, please join the [mailing list](#) to become part of the Bio-Linux users community.

ISO file for use with DVD/USB media

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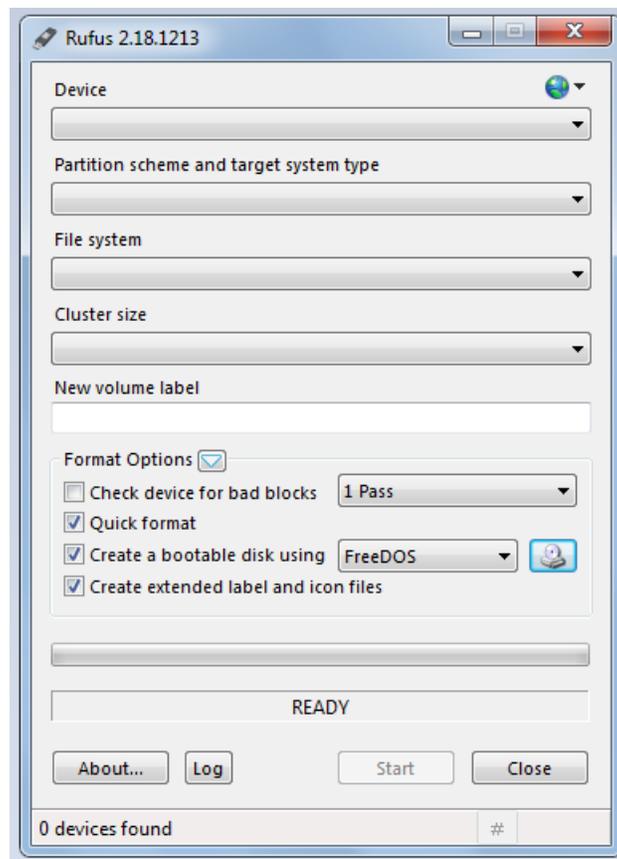
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Install Rufus on windows and open . Plug in **empty USB flash memory** to your laptop/PC :

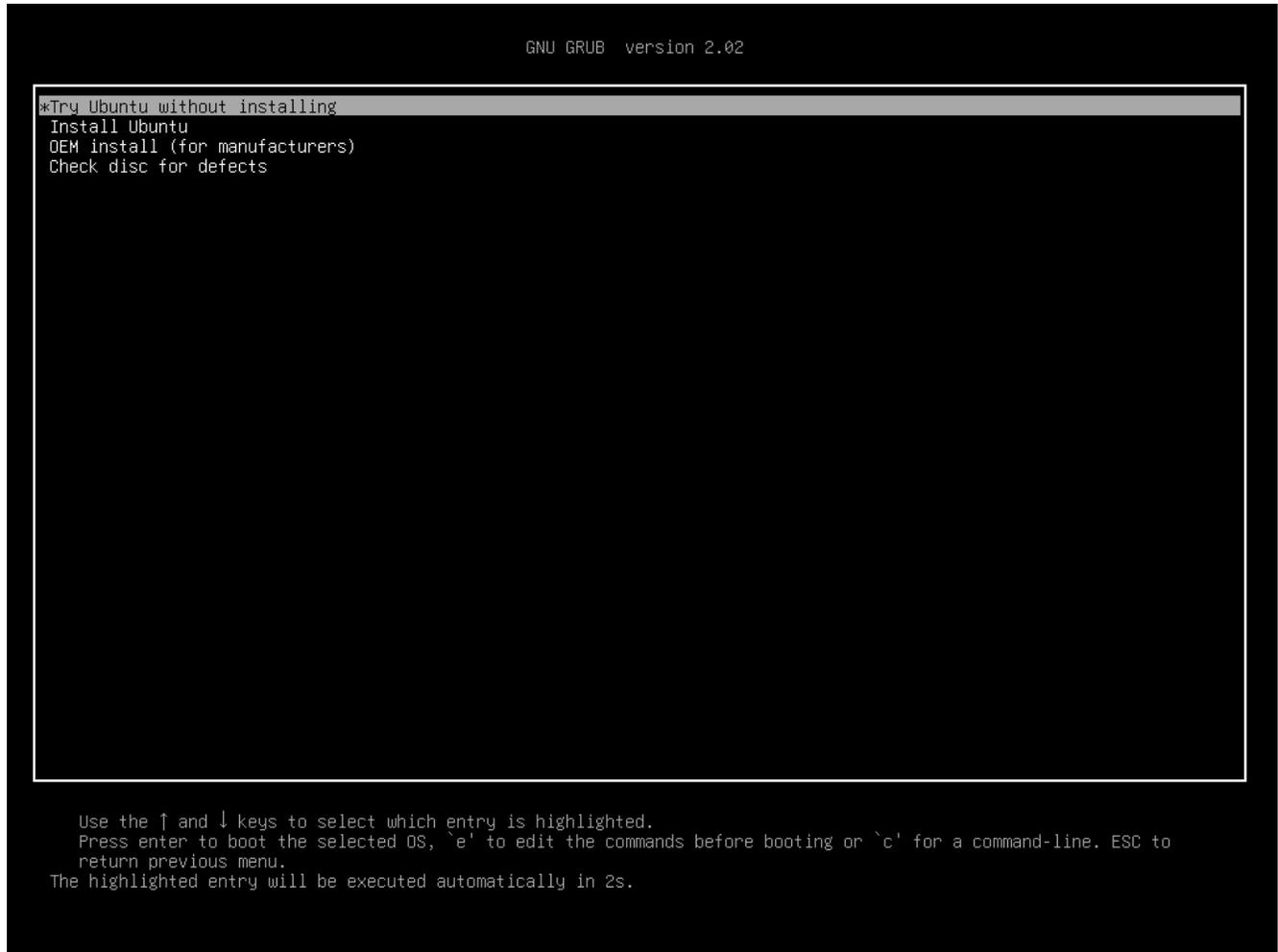


Note : The USB flash memory should be empty because the previous process the clear all files stored on it.

From Device choose the USB name , press on the CD icon  the chose the LINUX ISO file which you have downloaded and **Press START.**

After Finishing of **rufus** restart your computer .

Try to boot from USB; this depend on your computer type but most PCs press F12 or F10 or F8 and select the USB drive. The following page will appear.



Choose Try Ubuntu without installing

Note : If boot error contains (gfxboot.c32:not a valid COM32R image) press TAB button on keyboard and write live and press ENTER. Such error could appear by bad rufus installation.

INSIDE BIOLINX

Press on this Icon on desktop:



USAGE: This is the documentation home page of BioLinux

Press on this icon :



USAGE: This is the documentation home page for BioLinux installed software which well open in your browser e.g, Google chrome.

About :

Browse by Application/ Package Name

[List all applications/packages](#)

Browse by Category

[List all categories](#)

USAGE: The first option contains documentation for every software by name
The second option contains programs by category i.e. , Sequence Alignment, or protein analysis.

By Selecting :

Browse by Category

Alignment ▾ View Category

Press View Category this would appear :

Alignment

Category	Applications
Alignment	FastTree dialign
SubCategory	Applications
Consensus	cons consambig gap4 megamerger merger spin
Differences	act diffseq
Dot_plots	dotmatcher dotpath dotter dottup polydot
Editing	clcsequenceviewer jalview squint
Global	est2genome fasta ggsearch gsearch needle needleall stretcher swat
Graphical	blixem clcsequenceviewer clustalx dotter jalview jprofilegrid mummerplot nucmer2xfig seaview squint
Local	arb bl2seq bowtie bwa cross_match dba fasta fastf fastm fasts fastx fasty flalign glsearch lalign lfasta matcher plalign pfasta prenucl prfx prss psw psbdb seqmatchall sibsim4 sim4 ssearch supermatcher swat tfastf tfastm tfasts tfastx tfasty water wordfinder wordmatch
Multiple	annotate clustalw clustalx combineMUMs dialign edialign emma exact-tandems gaps hmalign infoalign jalview lalign2list mapview mgaps mocca mummer mummerplot muscle nucmer nucmer2xfig plotcon postnuc postpro prank prepro prettyplot PROmer repeat-match run-mummer1 run-mummer3 seaview show-aligns show-coords show-tiling showalign squint t-coffee tranalign yamap
Profiles	jprofilegrid profit profit prophecy prophecy prophet prophet
Statistics	alistat pfscale prfx prss weight

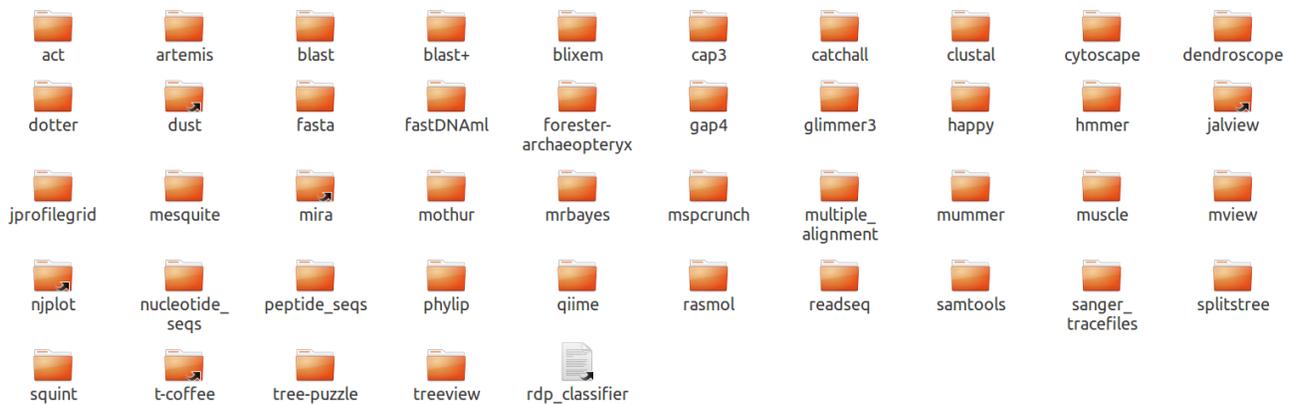
USAGE: These are different tools for sequence alignment , these tools are already installed on BioLinux and you can use.

SAMPLE DATA

On Desktop you will find this folder :



Open previous folder . The following window will appear :

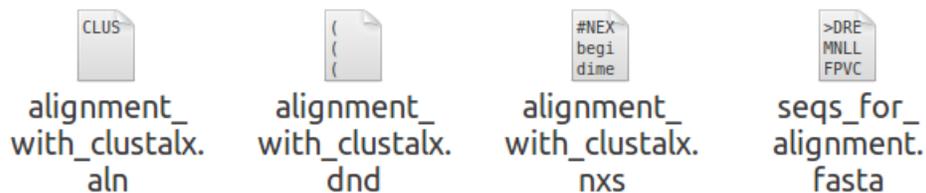


USAGE: These folders contain different sample data for BioLinux tools as input.

Open the next folder:



This window will appear :



USAGE: These files are output and input files for tool called “clustalw”. The first three files are the input and the last file is the output.

Press on this file :



This window will appear:

A screenshot of a gedit window titled 'seqs_for_alignment.fasta (~/Desktop/Sample Data/clustal) - gedit'. The window shows the following content:

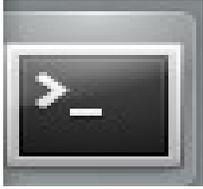
```
>DRERSOX9A
MNLDPYLKMTDEQEKCLSDAPSPMSSEDSAGSPCPSASGSDTENTRPAENSLLAADGTLGDFKKDEEDK
FPVCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKT
LGKLWRLLENEVEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQSESEEDGSEQTHISPNAIFKALQ
QADSPASSMGEVHSPSEHSGSQGPPTPPTTPKTDTPGKADLKREARPLQENTGRPLSINFQVDIGEL
SSDVIETFDVNEFDQYLPPNGHQNAPYAGGYAAWMTKPQNGSPQSSQLTPLNPAEPDQPRTTTHIKTEQLS
PSHYNEQQGSPQHISYGSFNVQHLQHYSTSFPSITRAQYDYSDSHQGGASSYYTHAGGQSSGLYSTFSYM
SSSQRPMTPIADSTGVPSIPQSNHSPQHWDQQPVYTQLSRP
>CAURS0X9A
MNLDPYLKMSDEQDKGLSDAPSLMSSEDSAGSPCPSGSGSDTENTRPEEHLGEFKKDEDKFPVCIRDAV
SQVLKGYDWTLPMPVVRVNGAHKSKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLN
EGEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQSESEEDGSEQTHISPNAIFKALQQADSPASSM
GEVHSPGEGHSGSQGPPTPPTTPKTDVQPGKVDLKRERPLQENTGRPLNIDFREVDIGELSNDVIETFD
VNEFDQYLPPNGHATNASYVGGYATWMGKPQNGSPSSSTQLTPLGTGGSGDQDQPRTTTHIKTEQLSPSHYN
EQQQGSPQHASYGSFNVQHLQHYSTSFPSITRAQYEYSDHQGGANSYYTHAGGQSSGLYSTFSYMSPSQR
PMYTPPIADSTGVPSIPQSNHSPQHWDQQPVYTQLSRP
```

The status bar at the bottom indicates 'Plain Text', 'Tab Width: 8', 'Ln 1, Col 1', and 'INS'.

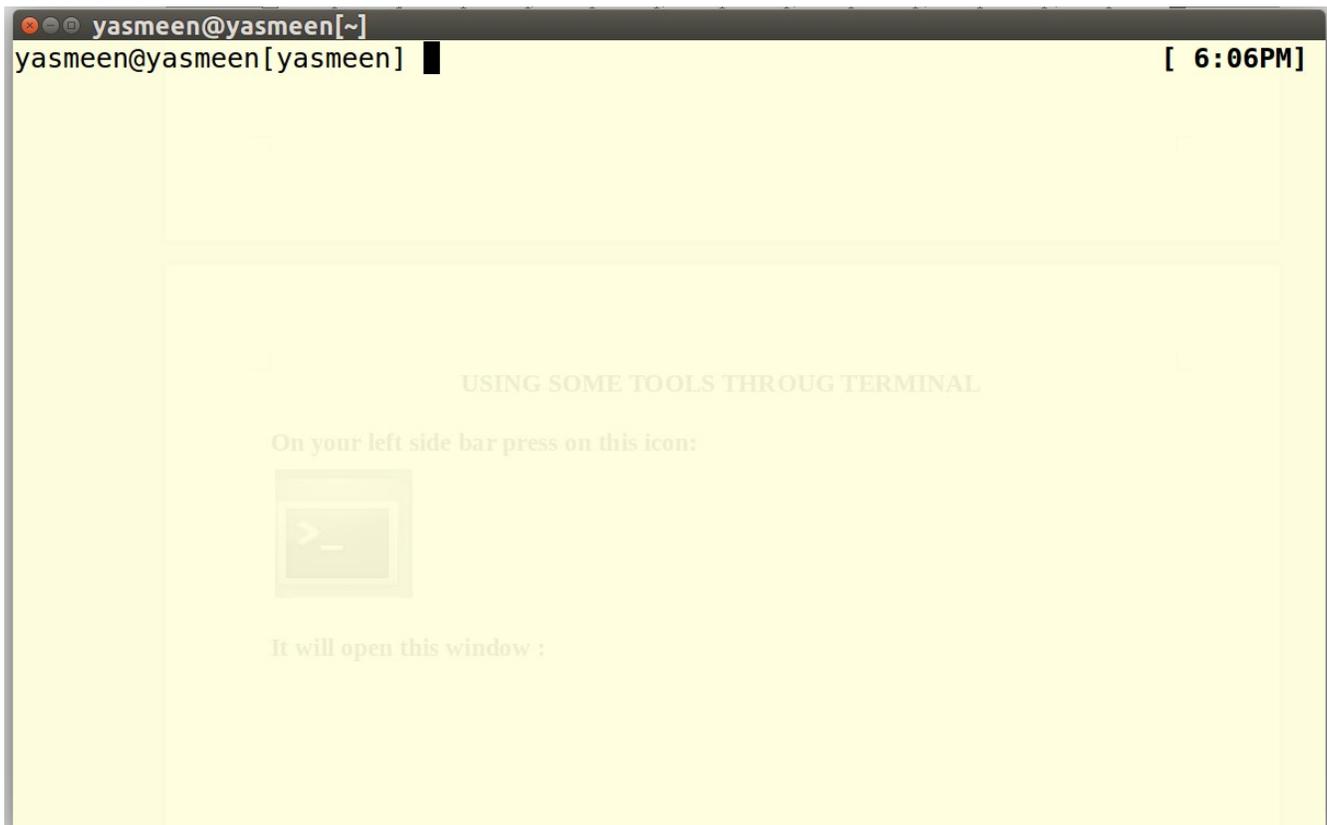
USAGE: These are amino acid sequences in FASTA file format and could be used for crystalw input.

SIMPLE DATA ANALYSIS

On your left side bar press on this icon:



It will open this window :



USAGE: This is the terminal of Linux, its the connection between you and your system which you can use to call any tool.

In previous window write :

echo hello

```
yasmeen@yasmeen[yasmeen] echo hello
```

Press Enter and the result would be:

```
yasmeen@yasmeen[yasmeen] echo hello  
hello
```

USAGE : “echo” is a tool in Linux to print text on the terminal end.

In previous window write :

mkdir Desktop/bioinfo

```
yasmeen@yasmeen[yasmeen] mkdir Desktop/bioinfo
```

USAGE : “mkdir” is a tool in Linux to create a folder.

Minimize terminal and look at Desktop you will find an empty folder called bioinfo:



Go to SAMPLE DATA FOLDER on Desktop:



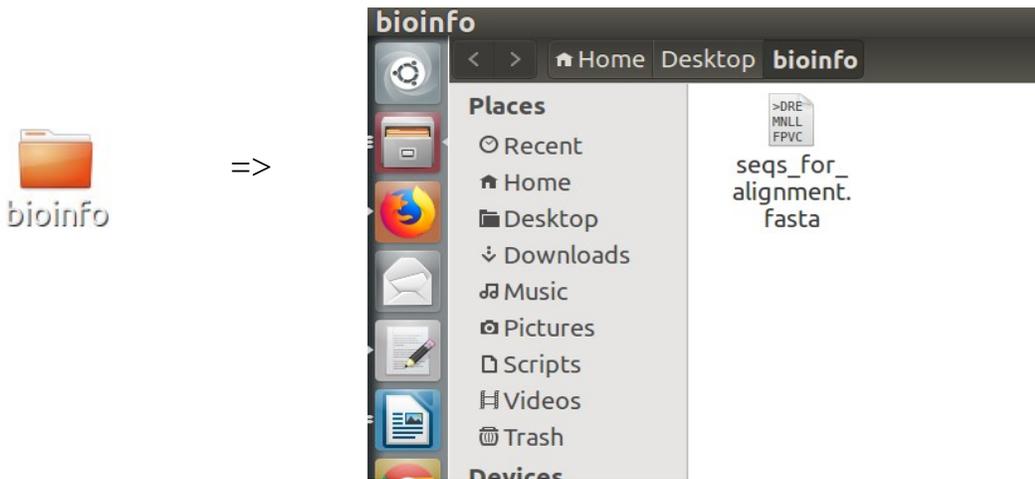
Open this folder next :



Using mouse and right click, copy this file :

```
>DRE  
MNL  
FPVC  
seqs_for_  
alignment.  
fasta
```

Minimize window and open bioinfo folder on desktop and paste the previous file copy :



Maximize the terminal or reopen:



Inside the terminal write the following command and press enter:

cd Desktop/bioinfo

```
yasmeen@yasmeen[yasmeen] cd Desktop/bioinfo
```

USAGE : “cd” is a tool in Linux change your current working directory to another .

You will notice that terminal current directory has changed from your home folder e.g. “yasmeen” to your target folder “bioinfo”:

```
yasmeen@yasmeen[yasmeen] cd Desktop/bioinfo [ 6:41PM]
yasmeen@yasmeen[bioinfo] █ [ 6:43PM]
```

USING SOME BIOLINUX TOOLS

In terminal write the following command and press ENTER:

```
clustalw seqs_for_alignment.fasta
```

```
yasmeen@yasmeen[bioinfo] clustalw seqs_for_alignment.fasta
```

USAGE : clustalw is tool used for sequence alignment (1) . As I showed previously Bio-Linux has some bioinformatics tools installed (go to INSIDE BIOLINUX section) . These tools could be accessed through terminal.

After pressing ENTER this would happen in terminal:

```
yasmeen@yasmeen[bioinfo] clustalw seqs_for_alignment.fasta [ 6:49PM]

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: DRERSOX9A 462 aa
Sequence 2: CAURS0X9A 457 aa
Sequence 3: OMYKS0X9 488 aa
Sequence 4: OLATS0X9B 476 aa
Sequence 5: TNIGUnk 495 aa
Sequence 6: XTRPS0X9 481 aa
Sequence 7: RRUGS0X9A 482 aa
Sequence 8: DRERS0X9B 360 aa
Sequence 9: CCARS0X9B 428 aa
Sequence 10: CAURS0X9B 416 aa
Sequence 11: TNIGUnm 484 aa
Sequence 12: ASTUS0X9 432 aa
Sequence 13: HSAPS0X9 509 aa
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 90
Sequences (1:3) Aligned. Score: 80
Sequences (1:4) Aligned. Score: 77
Sequences (1:5) Aligned. Score: 78
Sequences (1:6) Aligned. Score: 76
Sequences (1:7) Aligned. Score: 77
Sequences (1:8) Aligned. Score: 62
```

After few seconds the program will finish analysis and terminal would return to normal state.

```
There are 12 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences: 2      Score:9416
Group 2: Sequences: 2      Score:10155
Group 3: Sequences: 3      Score:9782
Group 4: Sequences: 4      Score:8362
Group 5: Sequences: 2      Score:9790
Group 6: Sequences: 3      Score:9417
Group 7: Sequences: 7      Score:8497
Group 8: Sequences: 9      Score:8422
Group 9: Sequences: 10     Score:8525
Group 10: Sequences: 11    Score:7842
Group 11: Sequences: 2     Score:6511
Group 12: Sequences: 13    Score:6255
Alignment Score 148754

CLUSTAL-Alignment file created [seqs_for_alignment.aln]
yasmeen@yasmeen[bioinfo]
```

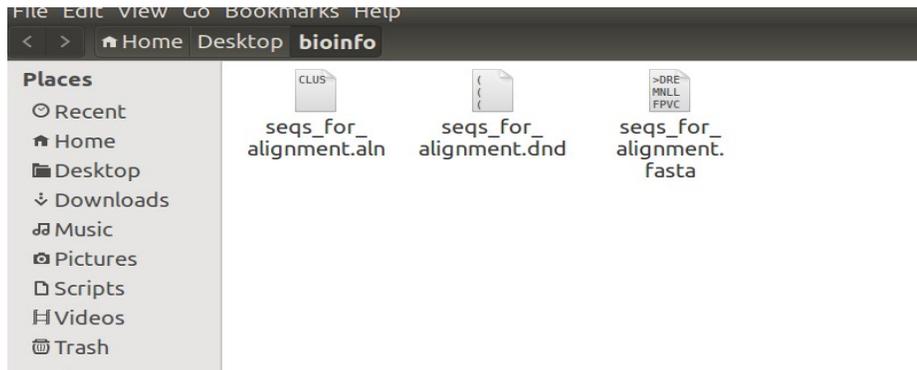
On terminal write the following command and press ENTER:

clear

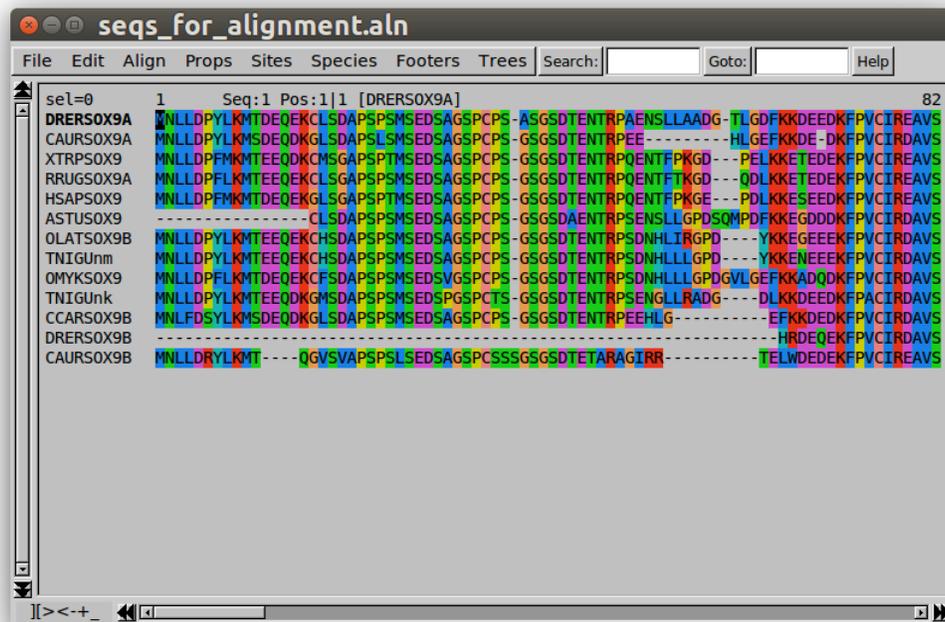
```
yasmeen@yasmeen[bioinfo] clear
```

USAGE : clear is Linux tool to clean terminal window from previous commands outputs.

Open bioinfo folder you can see the following three files :

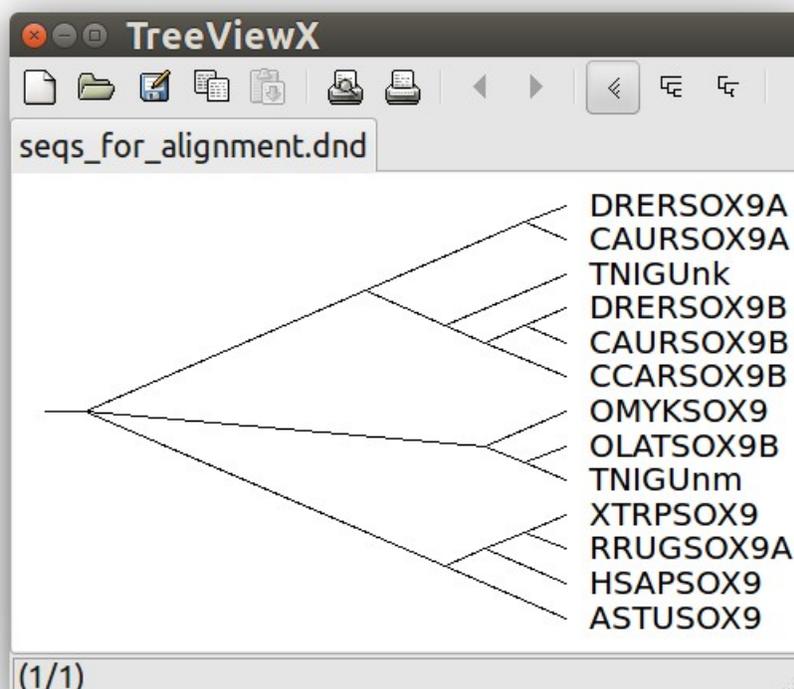


USAGE : These files are the input of clustalw program (seqs_for_alignment.fasta) and the output files (seqs_for_alignment.aln and seqs_for_alignment.dnd). Using mouse right click choose to open seqs_for_alignment.aln using Seaview. The following window will appear:



UASGE : Sea View is a bioinformatics tool to show sequence alignment output see their paper (2).

Click on the seqs_for_alignment.dnd file and choose open with and choose Tree View X , the following window will open :



USAGE : Tree View X is a tool for drawing phylogenetic analysis.

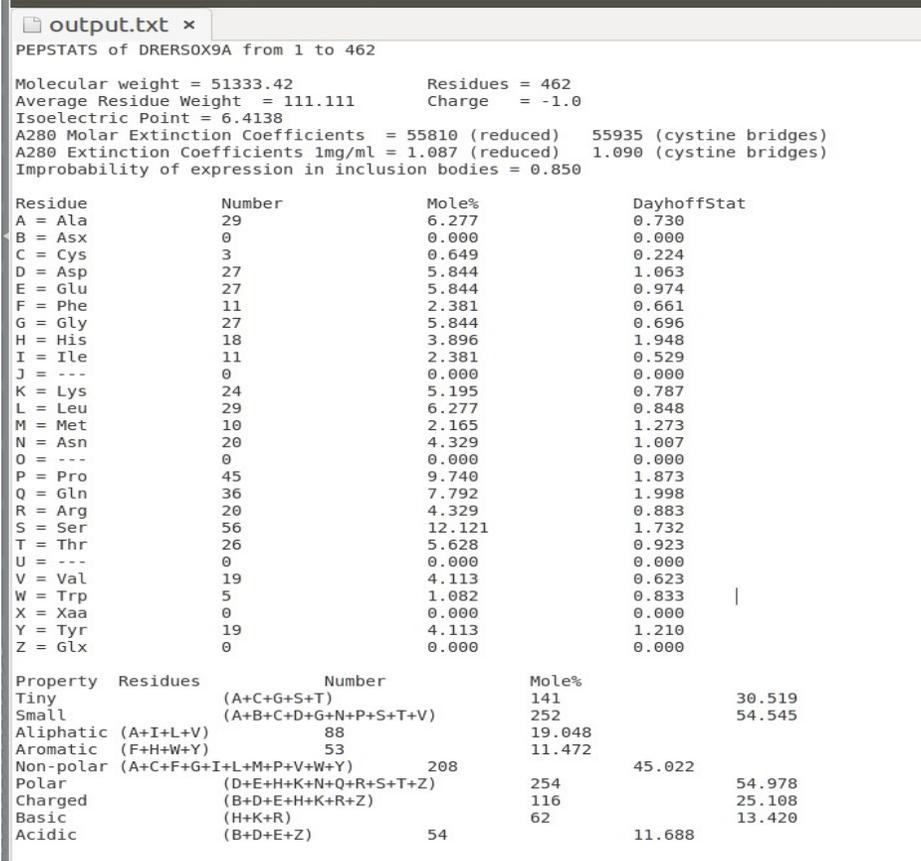
Using Other tools

Some BioLinux tools need to inputs . The input file and the output destination . For example pepstat is a tool you can use to study the amino acid sequence different properties. Using the following command

```
yasmeen@yasmeen[bioinfo] pepstats seqs_for_alignment.fasta output.txt
```

USAGE: The first word is the program name “pepstat” , the second is the input file (seqs_for_alignment.fasta) and the final is the output file (output.txt).

Click on the output.txt and open you will see the following output:



```
PEPSTATS of DRERSOX9A from 1 to 462
Molecular weight = 51333.42      Residues = 462
Average Residue Weight = 111.111  Charge = -1.0
Isoelectric Point = 6.4138
A280 Molar Extinction Coefficients = 55810 (reduced)  55935 (cystine bridges)
A280 Extinction Coefficients 1mg/ml = 1.087 (reduced)  1.090 (cystine bridges)
Improbability of expression in inclusion bodies = 0.850

Residue      Number      Mole%      DayhoffStat
A = Ala      29          6.277      0.730
B = Asx      0           0.000      0.000
C = Cys      3           0.649      0.224
D = Asp      27          5.844      1.063
E = Glu      27          5.844      0.974
F = Phe      11          2.381      0.661
G = Gly      27          5.844      0.696
H = His      18          3.896      1.948
I = Ile      11          2.381      0.529
J = ---      0           0.000      0.000
K = Lys      24          5.195      0.787
L = Leu      29          6.277      0.848
M = Met      10          2.165      1.273
N = Asn      20          4.329      1.007
O = ---      0           0.000      0.000
P = Pro      45          9.740      1.873
Q = Gln      36          7.792      1.998
R = Arg      20          4.329      0.883
S = Ser      56          12.121     1.732
T = Thr      26          5.628      0.923
U = ---      0           0.000      0.000
V = Val      19          4.113      0.623
W = Trp      5           1.082      0.833
X = Xaa      0           0.000      0.000
Y = Tyr      19          4.113      1.210
Z = Glx      0           0.000      0.000

Property  Residues      Number      Mole%
Tiny      (A+C+G+S+T)   141         30.519
Small     (A+B+C+D+G+N+P+S+T+V)  252         54.545
Aliphatic (A+I+L+V)   88          19.048
Aromatic  (F+H+W+Y)     53          11.472
Non-polar (A+C+F+G+I+L+M+P+V+W+Y)  208         45.022
Polar    (D+E+H+K+N+O+R+S+T+Z)  254         54.978
Charged  (B+D+E+H+K+R+Z)  116         25.108
Basic    (H+K+R)       62          13.420
Acidic   (B+D+E+Z)     54          11.688
```

Some tools need you to direct their output to out files. For example ; **revcomp** is tool you can use to convert sequences to its reverse complement .

```
yasmeen@yasmeen[bioinfo] revcomp seqs_for_alignment.fasta > REV-OUT.fasta
```

The first word is the tool name **revcomp** , the second is the input file name (**seqs_for_alignment.fasta**) and the third “>” is the direction sign used to direct the output of the tool to out file and the final is the output file . If you didn't use the last two words (> and output file name) the tool output (**revcomp**) will be printed to the terminal window. If you open the REV-OUT.fasta you will see the following :



```
output.txt x seqs_for_alignment.fasta x
->DRERSOX9A
MNLLDPYLKMTDEQEKCLSDAPSPSMSSEDSAGSPSPSAGSGSDTENTRPAENSLAADGTLGDFKKDEEDK
FPVCCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKT
LGKLRWLLNEVEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQSESEDSGEQTHISPNAIFKALQ
QADSPASSMGEVHSPSEHSGSQGPPPTPTTPKTDVQPGKADLKREARPLQENTGRPLSINFQDQVDIGEL
SSDVIETFDVNEFDQYLPNGHQNAPYAGGYAAMTKPQNGSPQSSQLTPLNPAEPDQPRTTTHIKTEQLS
PSHYNEQQGSPQHISYGSFNVQHLQHYSTSFPSITRAQYDYSDSHQGGASSYTHAGGQSSGLYSTFSYMS
SSSQRPMTPIADSTGVPSIPQSNHSPQHWDQQPVTQLSRP
->CAURS0X9A
MNLLDPYLKMSDEQDKGLSDAPSLSMSSEDSAGSPSPSAGSGSDTENTRPEEHLGEFKKDEKFPVCIIRDAV
SQVLKGYDWTLPMPVVRVNGAHSKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKT LGKLRWLLN
EGEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQSESEDSGEQTHISPNAIFKALQQADSPASSM
GEVHSPGEHSGSQGPPPTPTTPKTDVQPGKVDLKRTRPLQENTGRPLNIDFREVDIGELSNVDIETFD
VNEFDQYLPNGHATNASYVGGYATWVGKQNGSPSSQTLTPLGTGGSGDQDQPRTTTHIKTEQLSPSHYN
EQQQGSPQHASYGSFNVQHLQHYSTSFPSITRAQYSDHQGGANSYTHAGGQSSGLYSTFSYMSPSQR
PMTPIADSTGVPSIPQSNHSPQHWDQQPVTQLSRP
->OMYKS0X9
MNLLDPFLKMTDEQEKCFSDAPSPSMSSEDSVGSPPSPSAGSGSDTENTRPSDNHLLGPDGVLGEFKKADQD
KFPVCIIRDAVSQVLKGYDWTLPMPVRLNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSK
TLGKLRWLLNEGEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQSEPEDGEQTHISSGDIKALQ
QADSPASSMGEVHSPSEHSGSQGPPPTPTTPKTDLAVGKADLKREGRPLQEGTGRQLNIDFRVDIGEL
SSDVISNIEAFDVHEFDQYLPNGHPGMPGINGAQTSTYGSYRGISSNIGVAGGHWMSKQQQQQPIIS
ILSGGGGTGGEQGSQGRTTQIKTEQLSPSHYSEQQGSPQHVTYGSFNLQHYSSASSYPSITRTQDYSD
HQGGANSYSHAGAQSGLYSFSSYMSPSQRPMYTPIDPTGVPSVPTQTHSQHWEQQQPVTQLSRP
->OLATS0X9B
MNLLDPYLKMTTEQEKCHSDAPSPSMSSEDSAGSPSPSAGSGSDTENTRPSDNHLIRGPDYKKEGEEKFPV
CIRDAVSQVLKGYDWTLPMPVVRVNGSSKSKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGK
LRWLLNEVEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQSEAEDEPHTISPNAIFKALQQADS
PASSMGEAHSPEHSGSQGPPPTPTTPKTDLSSSKADLKREGRPVQEGTSRQLNIDFGAVDIGELSSDV
ISNIGSFVDVDFDQYLPNGHQAAGMTGTAQTSYSSNYVINSSAVGQATNVGAHAWMPKQHQHSLATIGGGGD
QSQQQQRTTQIKTEQLSPSHYSEQQSSPQHVSYSFNLQHYSTSSYPSITRAQYDYSHQHNSANSYSSH
AAGQGSNMYSTFSYMSPSQRPMYTPIDSTGVPSVPQTHSPQHWEQQPIYQLSRP
->TNIGunK
MNLLDPYLKMTTEQDKGMSDAPSPSMSSEDSVGSPPSPSAGSGSDTENTRPSENGLLRADGDLKDEEDKFFPA
CIRDAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGK
LRWLLNEVEKRPFVEEAERLRVQHKKDHPDYKYQPRRRKSVKNGQNESDDGGGEQTHISPNAIFKALQQAD
SPASSMGEVHSPGEHSGSQGPPPTPTTPKTDVTSVKIDLKREGLRLTLDGPGGRQLNIDFRVDVIGELS
SDVISHIETFDVNEFDQYLPNGHPGANSATPVSYSGTYSISSGVPSPQAGGVAAWLTKPNQNOQQGQQQ
QQHTLTTLVGSGSEAQHRITQIKTEQLSPSHYNDQQGSPQHITYSPFNLQHYSPSPYPAISRQQDYSE
HQGANNSGGTNTSYSHAGAQSGLYSTFSYVSSPSQRPMYTPIDNTGVPTIPQSSPQHWEQAPVYT
QLTRP
```