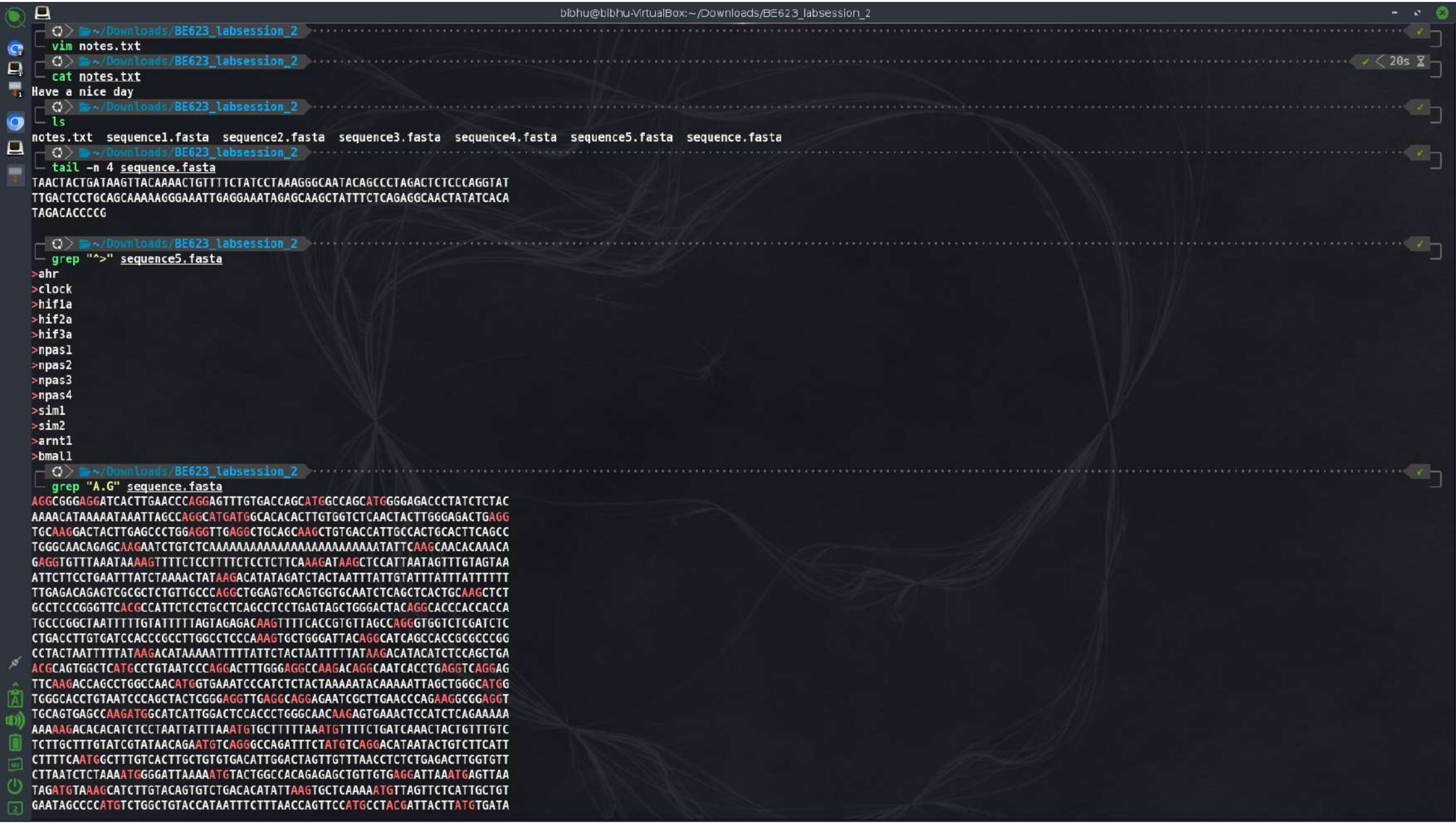
bibhu@bibhu-VirtualBox:~/Downloads/BE623_labsession_2
~/Downloads/BE623_labsession_2
vim notes.txt
~/Downloads/BE623_labsession_2
20s
cat notes.txt
Have a nice day
~/Downloads/BE623_labsession_2
ls
notes.txt sequence1.fasta sequence2.fasta sequence3.fasta sequence4.fasta sequence5.fasta sequence.fasta
~/Downloads/BE623_labsession_2
tail -n 4 sequence.fasta
TAACTACTGATAAGTTACAAAACTGTTTTCTATCCTAAAGGGCAATACAGCCCTAGACTCTCCCAGGTAT
TTGACTCCTGCAGCAAAAAGGGAAATTGAGGAAATAGAGCAAGCTATTTCTCAGAGGCAACTATATCACA
TAGACACCCCG
~/Downloads/BE623_labsession_2
grep "^>" sequence5.fasta
>ahr
>clock
>hif1a
>hif2a
>hif3a
>npas1
>npas2
>npas3
>npas4
>sim1
>sim2
>arnt1
>bmal1
~/Downloads/BE623_labsession_2
grep "A.G" sequence.fasta
AGGCGGGAGGATCACTTGAACCCAGGAGTTTGTGACCAGCATGGCCAGCATGGGGAGACCCTATCTCTAC
AAAACATAAAAATAAATTAGCCAGGCATGATGGCACACACTTGTGGTCTCAACTACTTGGGAGACTGAGG
TGCAAGGACTACTTGAGCCCTGGAGGTTGAGGCTGCAGCAAGCTGTGACCATTGCCACTGCACTTCAGCC
TGGGCAACAGAGCAAGAATCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAATATTCAAGCAACACAAACA
GAGGTGTTTAAATAAAAGTTTTCTCCTTTTCTCCTCTTCAAAGATAAGCTCCATTAATAGTTTGTAGTAA
ATTCTTCCTGAATTTATCTAAAACTATAAGACATATAGATCTACTAATTTATTGTATTTATTTATTTTTT
TTGAGACAGAGTCGCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGTGCAATCTCAGCTCACTGCAAGCTCT
GCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCACCCACCACCA
TGCCCGGCTAATTTTTGTATTTTTAGTAGAGACAAGTTTTCACCGTGTTAGCCAGGTGGTCTCGATCTC
CTGACCTTGTGATCCACCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATCAGCCACCGCGCCCGG
CCTACTAATTTTTATAAGACATAAAAATTTTTATTCTACTAATTTTTATAAGACATACATCTCCAGCTGA
ACGCAGTGGCTCATGCCTGTAATCCCAGGACTTTGGGAGGCCAAGACAGGCAATCACCTGAGGTCAGGAG
TTCAAGACCAGCCTGGCCAACATGGTGAAATCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCATGG
TGGGCACCTGTAATCCCAGCTACTCGGGAGGTTGAGGCAGGAGAATCGCTTGAACCCAGAAGGCGGAGGT
TGCAGTGAGCCAAGATGGCATCATTGGACTCCACCCTGGGCAACAAGAGTGAAACTCCATCTCAGAAAAA
AAAAAGACACACATCTCCTAATTATTTAAATGTGCTTTTTAAATGTTTTCTGATCAAACTACTGTTTGTC
TCTTGCTTTGTATCGTATAACAGAATGTCAGGGCCAGATTTCTATGTCAGGACATAATACTGTCTTCATT
CTTTTCAATGGCTTTGTCACTTGCTGTGTGACATTGGACTAGTTGTTTAACCTCTCTGAGACTTGGTGTT
CTTAATCTCTAAAATGGGGATTAAAAATGTACTGGCCACAGAGAGCTGTTGTGAGGATTAAATGAGTTAA
TAGATGTAAAGCATCTTGTACAGTGTCTGACACATATTAAGTGCTCAAAAATGTTAGTTCTCATTGCTGT
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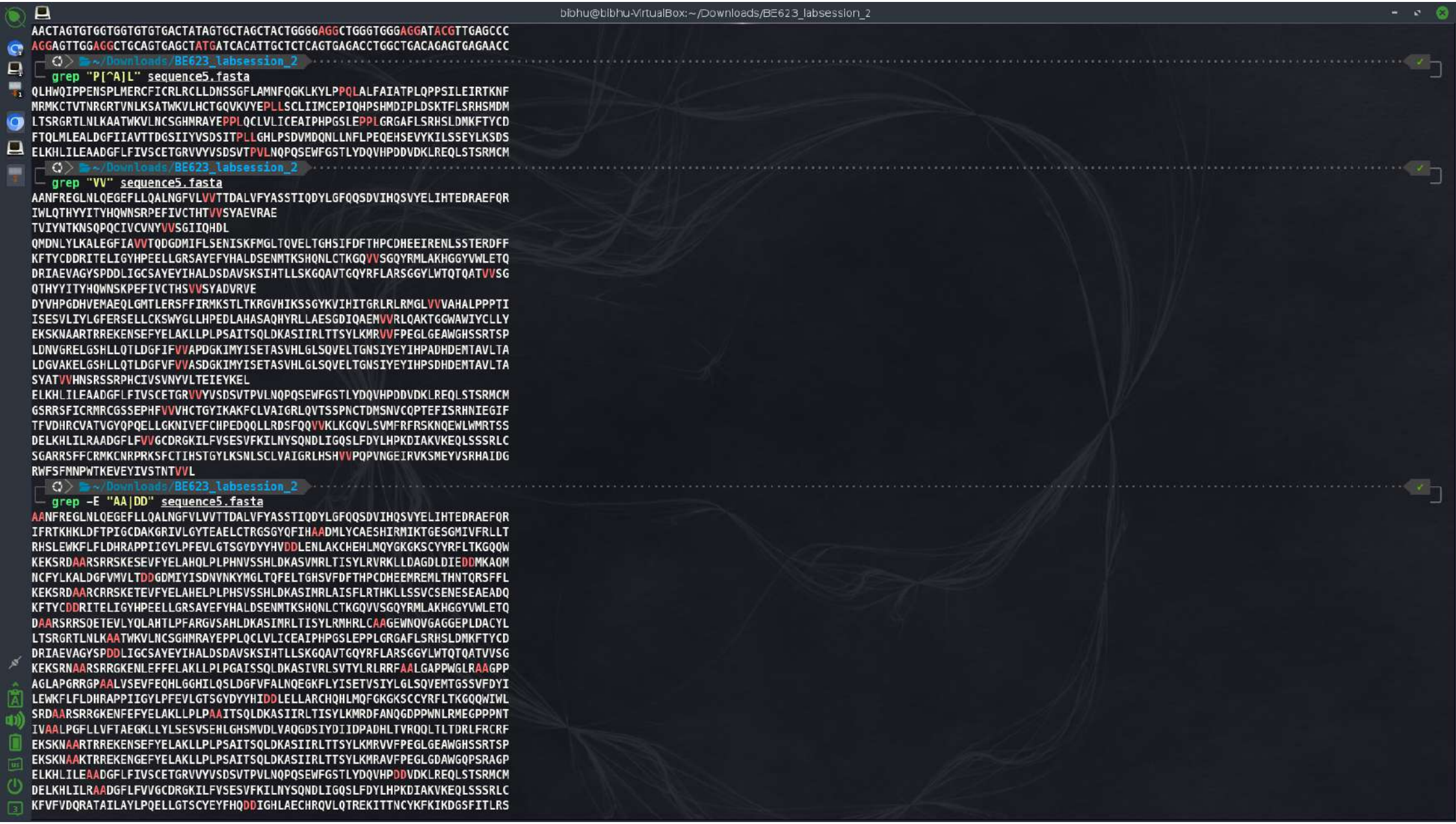
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AGGAGTTGGAGGCTGCAGTGAGCTATGATCACATTGCTCTCAGTGAGACCTGGCTGACAGAGTGAGAACC
~/Downloads/BE623_labsession_2
grep "P[^A]L" sequence5.fasta
QLHWQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLPPQLALFAIATPLQPPSILEIRTKNF
MRMKCTVTNRGRTVNLKSATWKVLHCTGQVKVYEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHSMDM
LTSRGRTLNLKAATWKVLNCSGHMRAYEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
FTQLMLEALDGFIIAVTTDGSIIYVSDSITPLLGHLPSDVMDQNLLNFLPEQEHSEVYKILSSEYLKSDS
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
~/Downloads/BE623_labsession_2
grep "VV" sequence5.fasta
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IWLQTHYYITYHQWNSRPEFIVCTHTVVSYAEVRAE
TVIYNTKNSQPQCIVCVNYVVSGIIQHDL
QMDNLYLKALEGFIAVVTQDGDMIFLSENISKFMGLTQVELTGHSIFDFTHPCDHEEIRENLSSTERDFF
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLETQ
DRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
QTHYYITYHQWNSKPEFIVCTHSVVSYADVRVE
DYVHPGDHVEMAEQLGMTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRMGLVVVAHALPPPTI
ISESVLIYLGFERSELLCKSWYGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLY
EKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
LDNVGRELGSHLLQTLDGFIFVVAPDGKIMYISETASVHLGLSQVELTGNSIYEYIHPADHDEMTAVLTA
LDGVAKELGSHLLQTLDGFVFVVASDGKIMYISETASVHLGLSQVELTGNSIYEYIHPSDHDEMTAVLTA
SYATVVHNSRSSRPHCIVSVNYVLTEIEYKEL
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
GSRRSFICRMRCGSSEPHFVVVHCTGYIKAKFCLVAIGRLQVTSSPNCTDMSNVCQPTEFISRHNIEGIF
TFVDHRCVATVGYQPQELLGKNIVEFCHPEDQQLLRDSFQQVVKLKGQVLSVMFRFRSKNQEWLWMRTSS
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIAKVKEQLSSSRLC
SGARRSFFCRMKCNRPRKSFCTIHSTGYLKSNLSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
RWFSFMNPWTKEVEYIVSTNTVVL
~/Downloads/BE623_labsession_2
grep -E "AA|DD" sequence5.fasta
AANFREGLNLQEGEFLLQALNGFVLVVTTDALVFYASSTIQDYLGFQQSDVIHQSVYELIHTEDRAEFQR
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
RHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQW
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KEKSRDAARCRRSKETEVFYELAHELPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLETQ
DAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYL
LTSRGRTLNLKAATWKVLNCSGHMRAYEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
DRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
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AGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYI
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SRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
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EKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEGLGDAWGQPSRAGP
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIAKVKEQLSSSRLC
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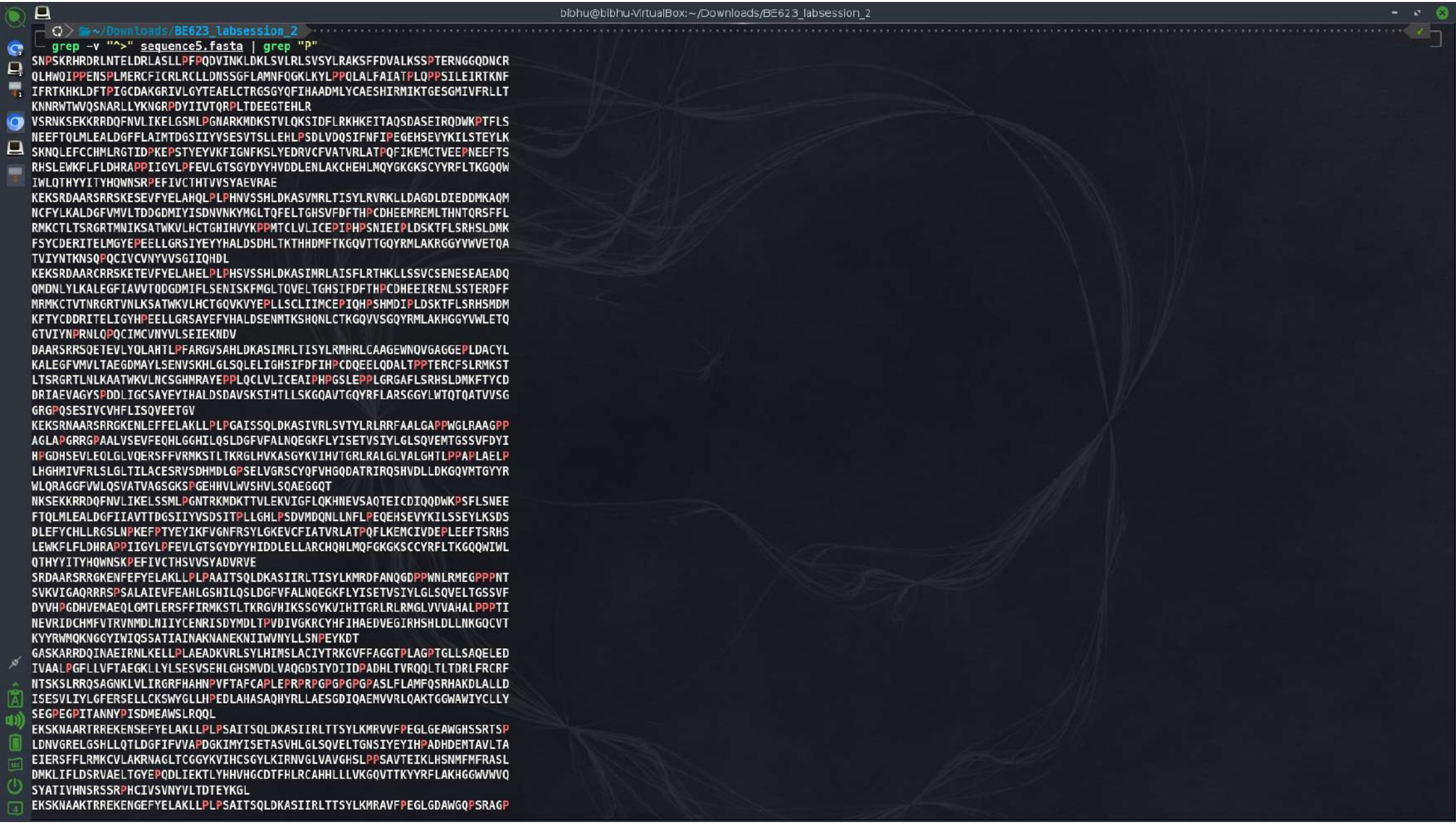
bibhu@bibhu-VirtualBox:~/Downloads/BE623_labsession_2
~/Downloads/BE623_labsession_2
grep -v "^>" sequence5.fasta | grep "P"
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QLHWQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLPPQLALFAIATPLQPPSILEIRTKNF
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
KNNRWTWVQSNARLLYKNGRPDYIIVTQRPLTDEEGTEHLR
VSRNKSEKKRRDQFNVLIKELGSMLPGNARKMDKSTVLQKSIDFLRKHKEITAQSDASEIRQDWKPTFLS
NEEFTQLMLEALDGFFLAIMTDGSIIYVSESVTSLLEHLPSDLVDQSIFNFIPEGEHSEVYKILSTEYLK
SKNQLEFCCHMLRGTIDPKEPSTYEYVKFIGNFKSLYEDRVCFVATVRLATPQFIKEMCTVEEPNEEFTS
RHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQW
IWLQTHYYITYHQWNSRPEFIVCTHTVVSYAEVRAE
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RMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMK
FSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMFTKGQVTTGQYRMLAKRGGYVWVETQA
TVIYNTKNSQPQCIVCVNYVVSGIIQHDL
KEKSRDAARCRRSKETEVFYELAHELPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
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DRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
GRGPQSESIVCVHFLISQVEETGV
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LHGHMIVFRLSLGLTILACESRVSDHMDLGPSELVGRSCYQFVHGQDATRIRQSHVDLLDKGQVMTGYYR
WLQRAGGFVWLQSVATVAGSGKSPGEHHVLWVSHVLSQAEGGQT
NKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLEKVIGFLQKHNEVSAQTEICDIQQDWKPSFLSNEE
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LEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
QTHYYITYHQWNSKPEFIVCTHSVVSYADVRVE
SRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
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DYVHPGDHVEMAEQLGMTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRMGLVVVAHALPPPTI
NEVRIDCHMFVTRVNMDLNIIYCENRISDYMDLTPVDIVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVT
KYYRWMQKNGGYIWIQSSATIAINAKNANEKNIIWVNYLLSNPEYKDT
GASKARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYTRKGVFFAGGTPLAGPTGLLSAQELED
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EKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
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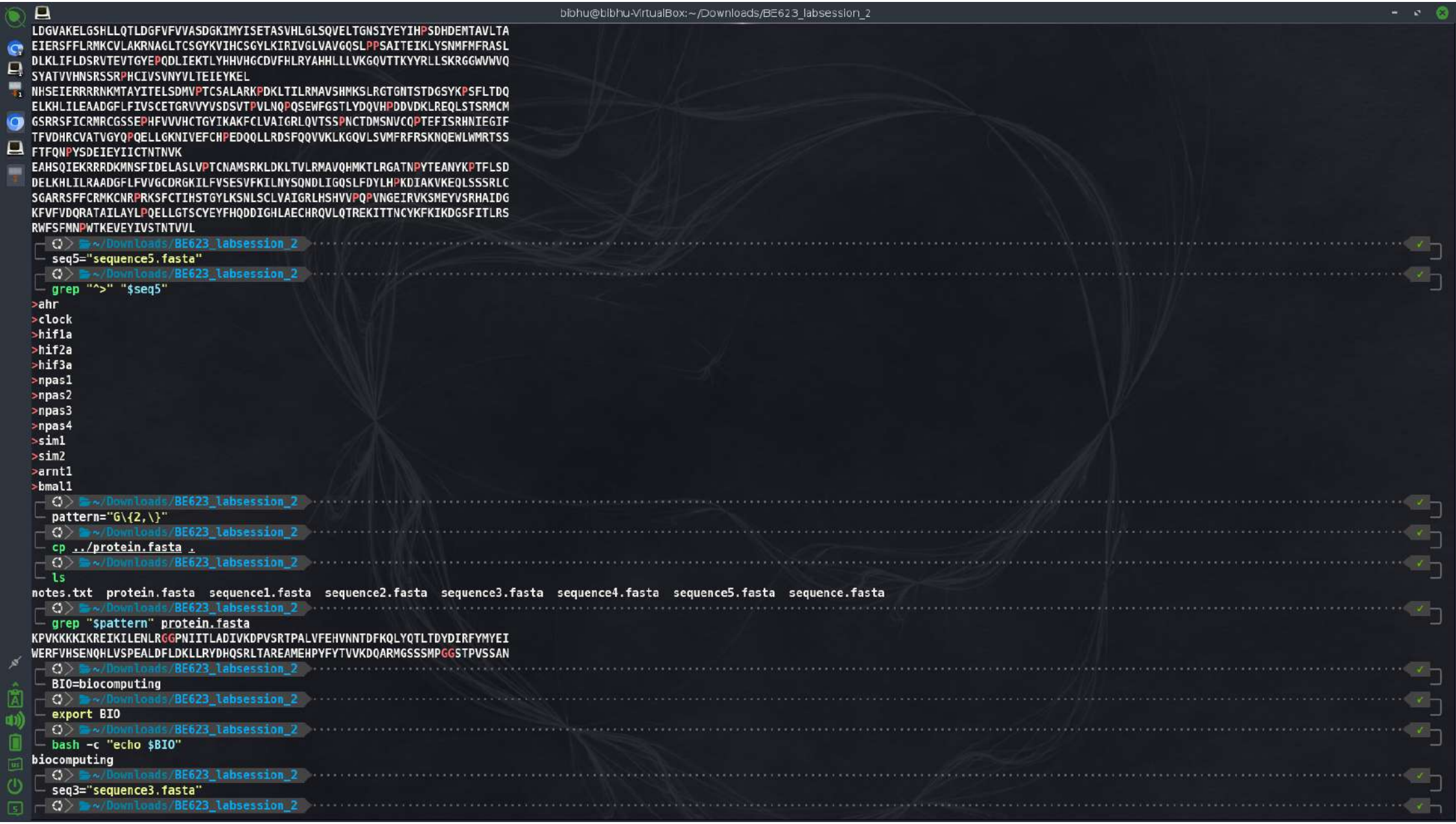
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SYATVVHNSRSSRPHCIVSVNYVLTEIEYKEL
NHSEIERRRRNKMTAYITELSDMVPTCSALARKPDKLTILRMAVSHMKSLRGTGNTSTDGSYKPSFLTDQ
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
GSRRSFICRMRCGSSEPHFVVVHCTGYIKAKFCLVAIGRLQVTSSPNCTDMSNVCQPTEFISRHNIEGIF
TFVDHRCVATVGYQPQELLGKNIVEFCHPEDQQLLRDSFQQVVKLKGQVLSVMFRFRSKNQEWLWMRTSS
FTFQNPYSDEIEYIICTNTNVK
EAHSQIEKRRRDKMNSFIDELASLVPTCNAMSRKLDKLTVLRMAVQHMKTLRGATNPYTEANYKPTFLSD
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIAKVKEQLSSSRLC
SGARRSFFCRMKCNRPRKSFCTIHSTGYLKSNLSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
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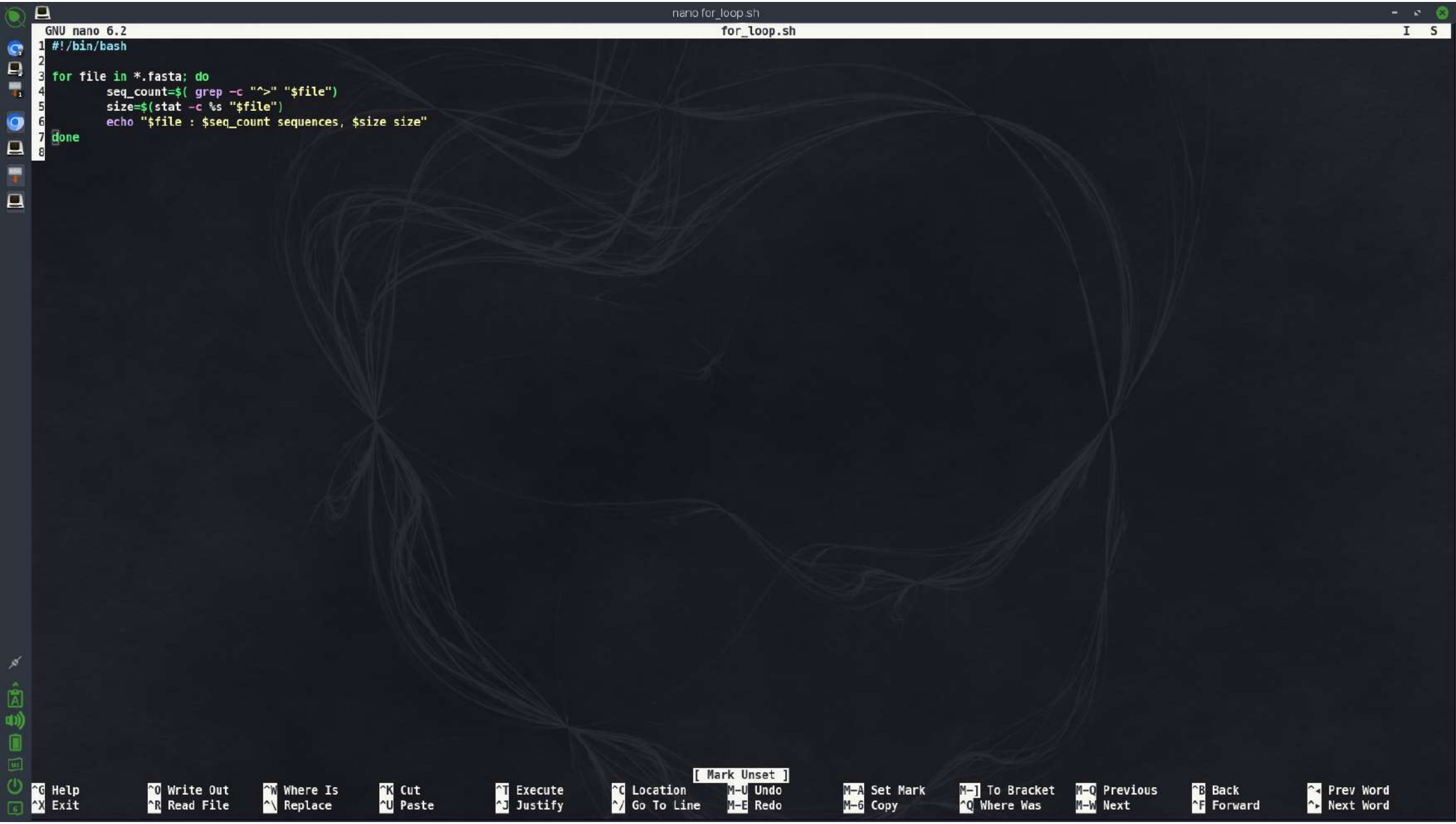
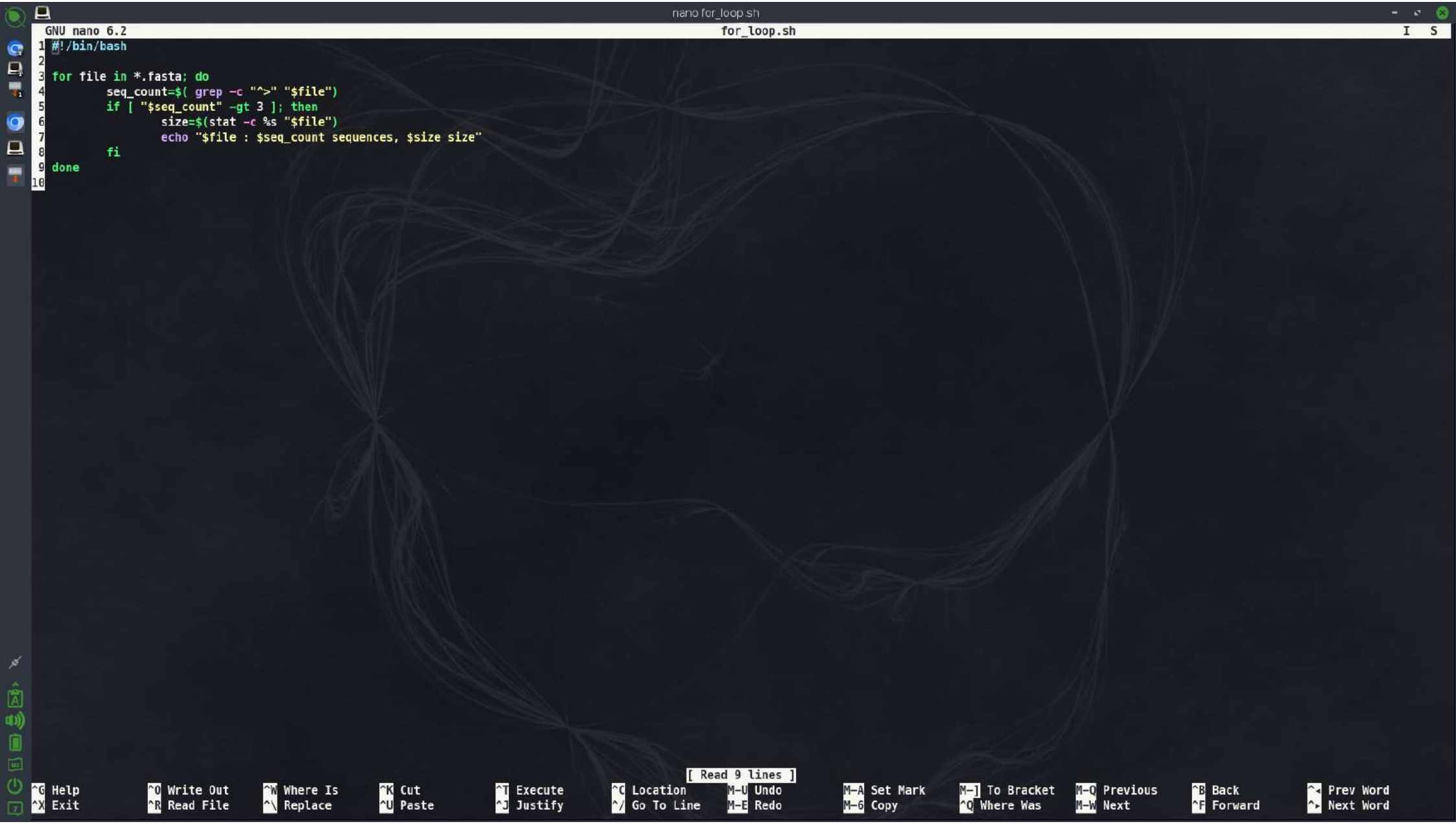
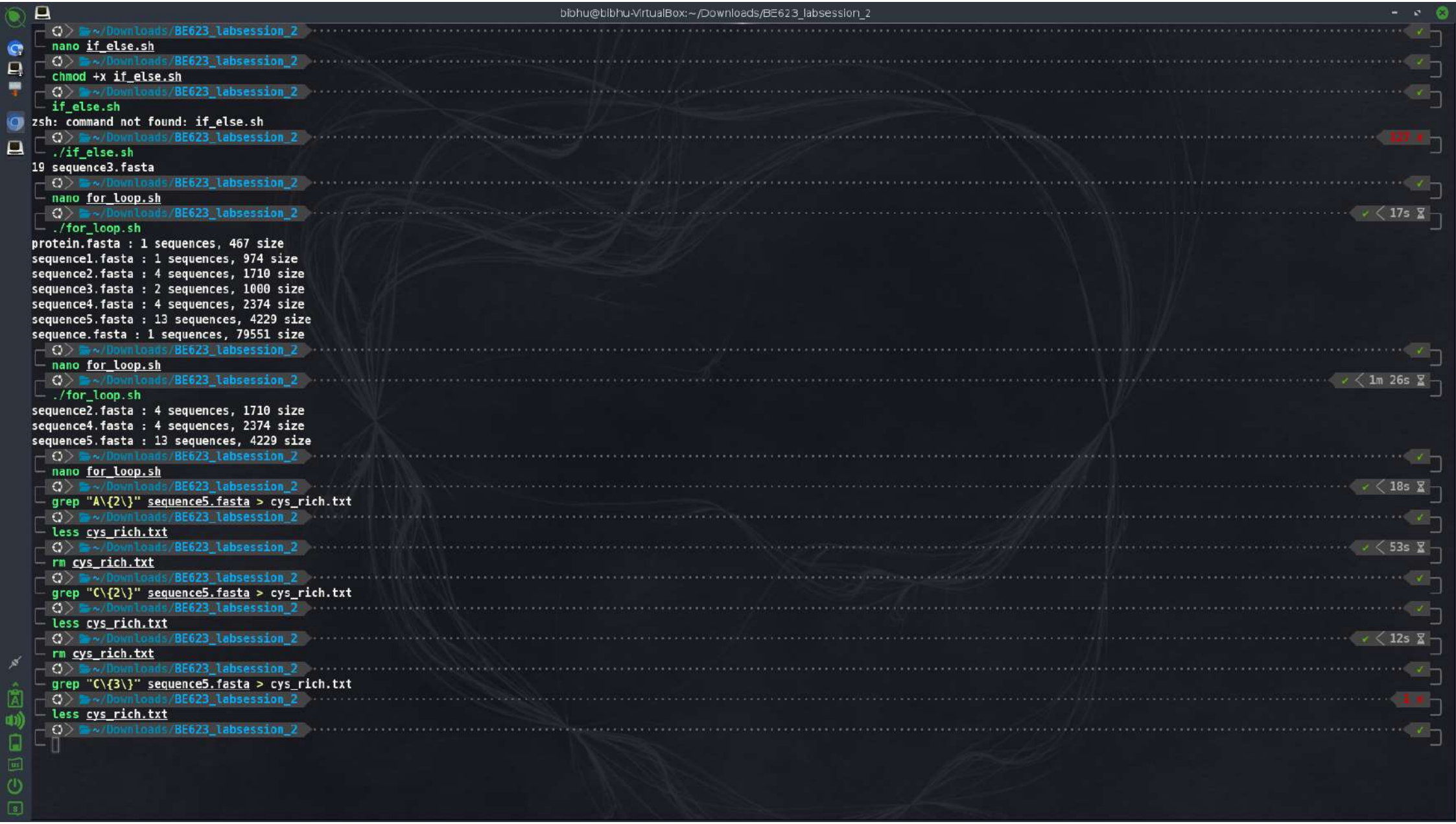
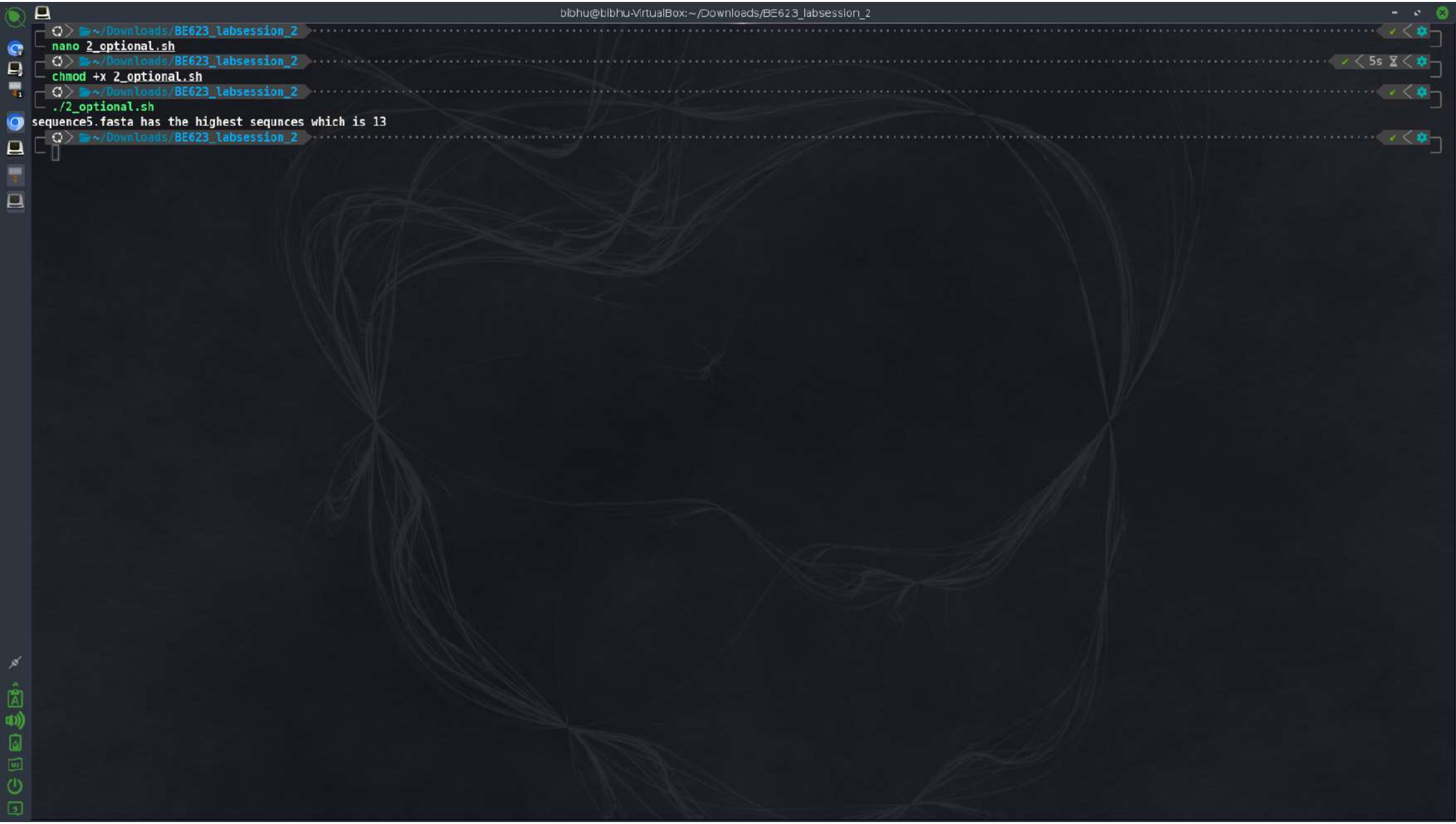
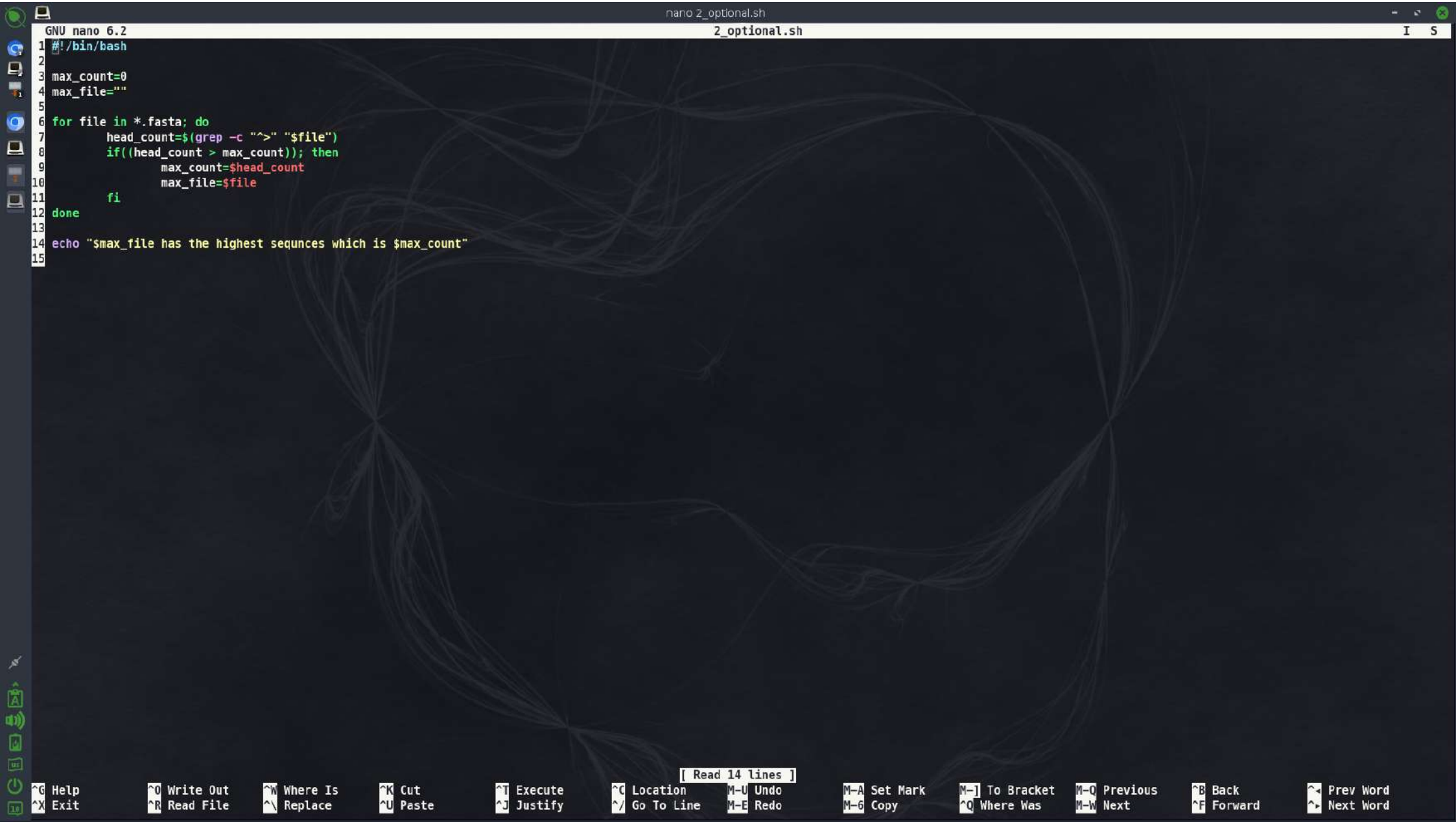
RWFSFMNPWTKEVEYIVSTNTVVL
~/Downloads/BE623_labsession_2
seq5="sequence5.fasta"
~/Downloads/BE623_labsession_2
grep "^>" "$seq5"
>ahr
>clock
>hif1a
>hif2a
>hif3a
>npas1
>npas2
>npas3
>npas4
>sim1
>sim2
>arnt1
>bmal1
~/Downloads/BE623_labsession_2
pattern="G\{2,\}"
~/Downloads/BE623_labsession_2
cp ../protein.fasta .
~/Downloads/BE623_labsession_2
ls
notes.txt protein.fasta sequence1.fasta sequence2.fasta sequence3.fasta sequence4.fasta sequence5.fasta sequence.fasta
~/Downloads/BE623_labsession_2
grep "$pattern" protein.fasta
KPVKKKKIKREIKILENLRGGPNIITLADIVKDPVSRTPALVFEHVNNTDFKQLYQTLTDYDIRFYMYEI
WERFVHSENQHLVSPEALDFLDKLLRYDHQSRLTAREAMEHPYFYTVVKDQARMGSSSMPGGSTPVSSAN
~/Downloads/BE623_labsession_2
BIO=biocomputing
~/Downloads/BE623_labsession_2
export BIO
~/Downloads/BE623_labsession_2
bash -c "echo $BIO"
biocomputing
~/Downloads/BE623_labsession_2
seq3="sequence3.fasta"
~/Downloads/BE623_labsession_2


nano for_loop.sh
GNU nano 6.2
for_loop.sh
I S
#!/bin/bash
for file in *.fasta; do
seq_count=$(grep -c "^>" "$file")
size=$(stat -c %s "$file")
echo "$file : $seq_count sequences, $size size"
done
[Mark Unset]
^G Help
^X Exit
^O Write Out
^R Read File
^W Where Is
^\ Replace
^K Cut
^U Paste
^T Execute
^J Justify
^C Location
^/ Go To Line
M-U Undo
M-E Redo
M-A Set Mark
M-6 Copy
M-] To Bracket
^Q Where Was
M-Q Previous
M-W Next
^B Back
^F Forward
^◂ Prev Word
^▸ Next Word


nano for_loop.sh
GNU nano 6.2
for_loop.sh
I S
#!/bin/bash
for file in *.fasta; do
seq_count=$(grep -c "^>" "$file")
if ["$seq_count" -gt 3]; then
size=$(stat -c %s "$file")
echo "$file : $seq_count sequences, $size size"
fi
done
[Read 9 lines]
^G Help ^O Write Out ^W Where Is ^K Cut ^T Execute ^C Location M-U Undo M-A Set Mark M-] To Bracket M-Q Previous ^B Back ^◂ Prev Word
^X Exit ^R Read File ^\ Replace ^U Paste ^J Justify ^/ Go To Line M-E Redo M-6 Copy ^Q Where Was M-W Next ^F Forward ^▸ Next Word


bibhu@bibhu-VirtualBox:~/Downloads/BE623_labsession_2
~/Downloads/BE623_labsession_2
nano if_else.sh
~/Downloads/BE623_labsession_2
chmod +x if_else.sh
~/Downloads/BE623_labsession_2
if_else.sh
zsh: command not found: if_else.sh
~/Downloads/BE623_labsession_2
127
./if_else.sh
19 sequence3.fasta
~/Downloads/BE623_labsession_2
nano for_loop.sh
~/Downloads/BE623_labsession_2
17s
./for_loop.sh
protein.fasta : 1 sequences, 467 size
sequence1.fasta : 1 sequences, 974 size
sequence2.fasta : 4 sequences, 1710 size
sequence3.fasta : 2 sequences, 1000 size
sequence4.fasta : 4 sequences, 2374 size
sequence5.fasta : 13 sequences, 4229 size
sequence.fasta : 1 sequences, 79551 size
~/Downloads/BE623_labsession_2
nano for_loop.sh
~/Downloads/BE623_labsession_2
1m 26s
./for_loop.sh
sequence2.fasta : 4 sequences, 1710 size
sequence4.fasta : 4 sequences, 2374 size
sequence5.fasta : 13 sequences, 4229 size
~/Downloads/BE623_labsession_2
nano for_loop.sh
~/Downloads/BE623_labsession_2
18s
grep "A\{2\}" sequence5.fasta > cys_rich.txt
~/Downloads/BE623_labsession_2
less cys_rich.txt
~/Downloads/BE623_labsession_2
53s
rm cys_rich.txt
~/Downloads/BE623_labsession_2
grep "C\{2\}" sequence5.fasta > cys_rich.txt
~/Downloads/BE623_labsession_2
less cys_rich.txt
~/Downloads/BE623_labsession_2
12s
rm cys_rich.txt
~/Downloads/BE623_labsession_2
grep "C\{3\}" sequence5.fasta > cys_rich.txt
~/Downloads/BE623_labsession_2
1
less cys_rich.txt
~/Downloads/BE623_labsession_2


bibhu@bibhu-VirtualBox:~/Downloads/BE623_labsession_2
~/Downloads/BE623_labsession_2
nano 2_optional.sh
~/Downloads/BE623_labsession_2
5s
chmod +x 2_optional.sh
~/Downloads/BE623_labsession_2
./2_optional.sh
sequence5.fasta has the highest sequnces which is 13
~/Downloads/BE623_labsession_2


nano 2_optional.sh
GNU nano 6.2
2_optional.sh
#!/bin/bash
max_count=0
max_file=""
for file in *.fasta; do
head_count=$(grep -c "^>" "$file")
if((head_count > max_count)); then
max_count=$head_count
max_file=$file
fi
done
echo "$max_file has the highest sequnces which is $max_count"
[Read 14 lines]
^G Help ^O Write Out ^W Where Is ^K Cut ^T Execute ^C Location M-U Undo M-A Set Mark M-] To Bracket M-Q Previous ^B Back ^◂ Prev Word
^X Exit ^R Read File ^\ Replace ^U Paste ^J Justify ^/ Go To Line M-E Redo M-6 Copy ^Q Where Was M-W Next ^F Forward ^▸ Next Word