Nabendu Das_24250059

Assignment-2

Part 1 - vi Basics & File Editing

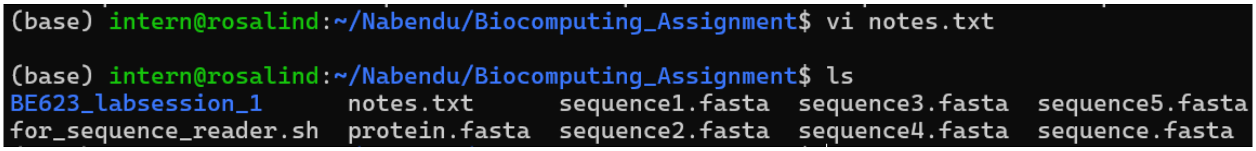
1. Open a new file called notes.txt in vi.

- Insert exactly one line of text:

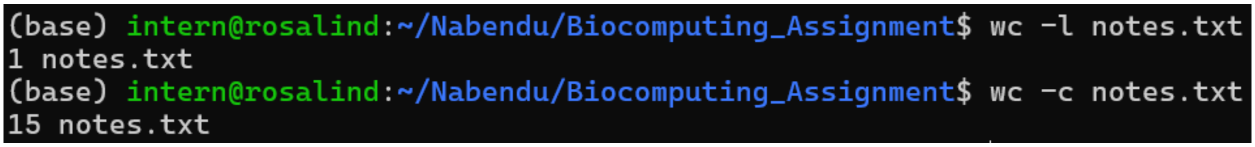
Have a nice day

(Make sure there is no trailing space at the end.)

- Save and exit.
- Verify that the file contains exactly one line and 15 characters.



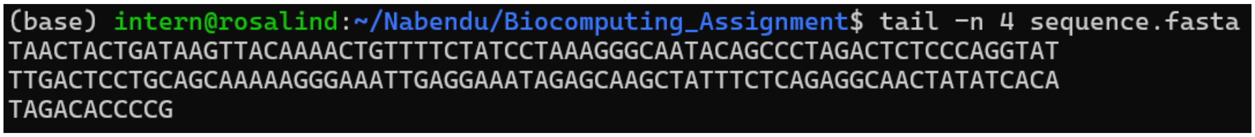
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ vi notes.txt

(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ ls
BE623_labsession_1       notes.txt      sequence1.fasta  sequence3.fasta  sequence5.fasta
for_sequence_reader.sh  protein.fasta  sequence2.fasta  sequence4.fasta  sequence.fasta
```



```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ wc -l notes.txt
1 notes.txt
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ wc -c notes.txt
15 notes.txt
```

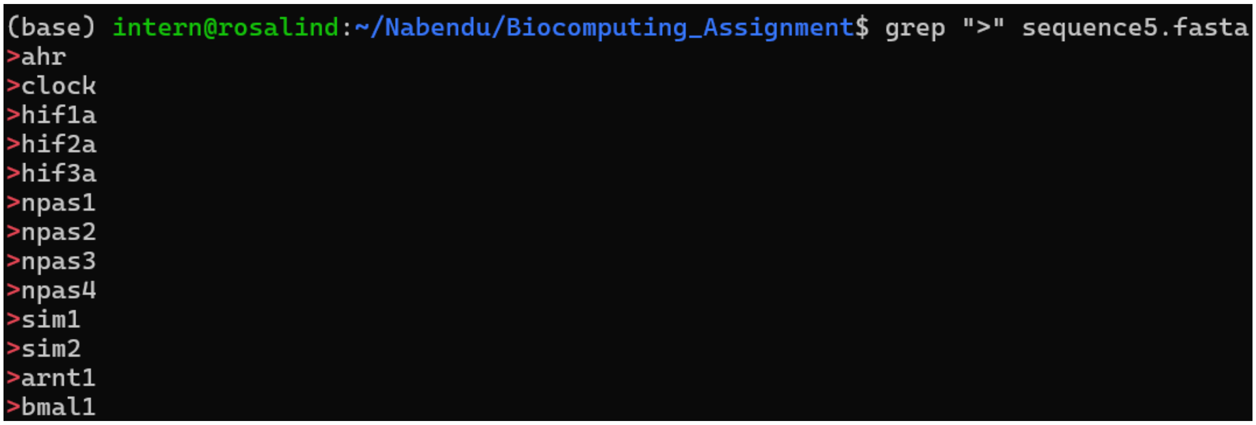
Part 2 - Pattern Matching in FASTA Files

2. Display the last four lines of sequence.fasta without opening the file in an editor.



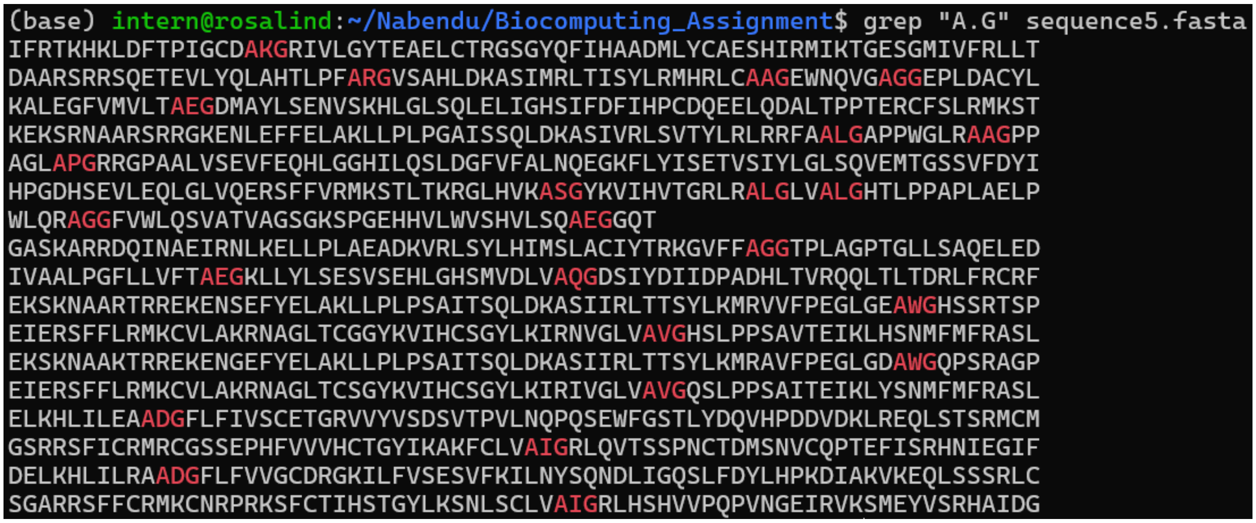
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ tail -n 4 sequence.fasta
TAACTACTGATAAGTTACAAAACTGTTTTCTATCCTAAAGGGCAATACAGCCCTAGACTCTCCCAGGTAT
TTGACTCCTGCAGCAAAAAGGGAAATTGAGGAAATAGAGCAAGCTATTTCTCAGAGGCAACTATATCACA
TAGACACCCCG
```

3. In sequence5.fasta, print all header lines (lines starting with >).



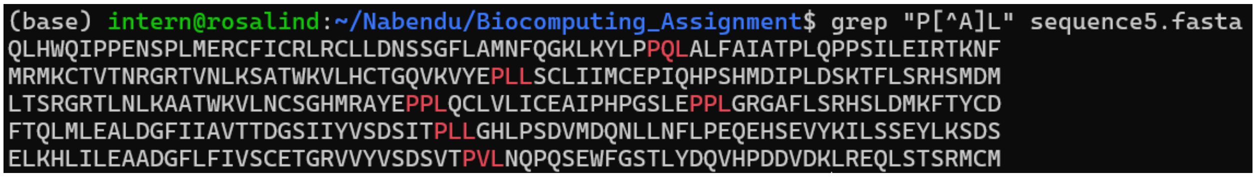
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep ">" sequence5.fasta
>ahr
>clock
>hif1a
>hif2a
>hif3a
>npas1
>npas2
>npas3
>npas4
>sim1
>sim2
>arnt1
>bmal1
```

4. Find all matches in sequence5.fasta where A is followed by any single character and then G.



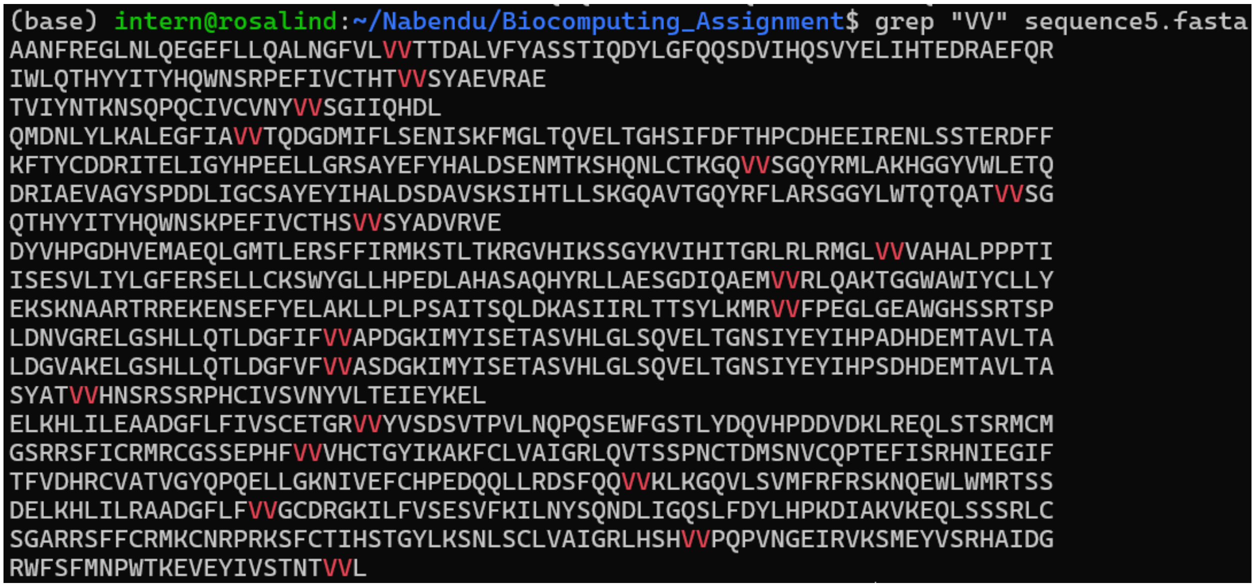
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep "A.G" sequence5.fasta
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
DAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYL
KALEGFVMVLTAEGDMAYLSENVSKHLGLSQLELIGHSIFDFIHPCDQEELQDALTPPTERCFSLRMKST
KEKSRNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPP
AGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYI
HPGDHSEVLEQLGLVQERSFFVRMKSTLTKRGLHVKASGYKVIHVTGRLRALGLVALGHTLPPAPLAELP
WLQRAGGFVWLQSVATVAGSGKSPGEHHVLWVSHVLSQAEGGQT
GASKARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYTRKGVFFAGGTPLAGPTGLLSAQELED
IVAALPGFLLVFTAEGKLLYLSESVSEHLGHSMVDLVAQGDSIYDIIDPADHLTVRQQLTLTDRLFRCRF
EKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
EIERSFFLRMKCVLAKRNAGLTCGGYKVIHCSGYLKIRNVGLVAVGHSLPPSAVTEIKLHSNMFMFRASL
EKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEGLGDAWGQPSRAGP
EIERSFFLRMKCVLAKRNAGLTCSGYKVIHCSGYLKIRIVGLVAVGQSLPPSAITEIKLYSNMFMFRASL
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
GSRRSFICRMRCGSSEPHFVVVHCTGYIKAKFCLVAIGRLQVTSSPNCTDMSNVCQPTEFISRHNIEGIF
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIAKVKEQLSSSRLC
SGARRSFFCRMKCNRPRKSFCTIHSTGYLKSNLSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
```

5. Find all matches in sequence5.fasta where P is followed by any character except A, then L.



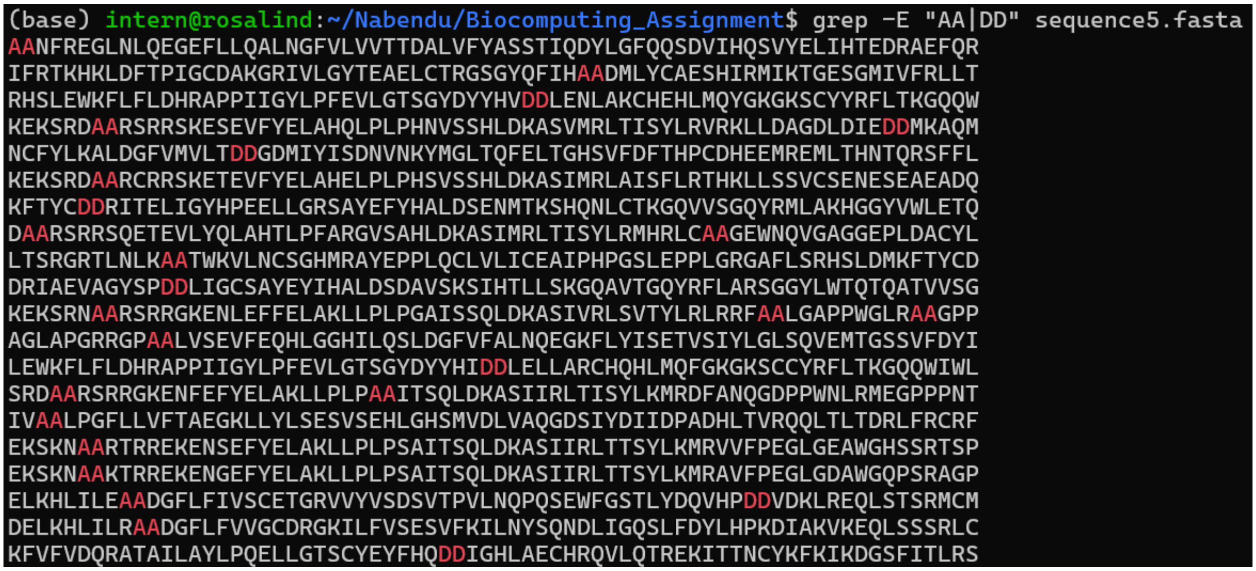
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep "P[^A]L" sequence5.fasta
QLHWQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLPPQLALFAIATPLQPPSILEIRTKNF
MRMKCTVTNRGRTVNLKSATWKVLHCTGQVKVYEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHSMDM
LTSRGRTLNLKAATWKVLNCSGHMRAYEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
FTQLMLEALDGFIIAVTTDGSIIYVSDSITPLLGHLPSDVMDQNLLNFLPEQEHSEVYKILSSEYLKSDS
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
```

6. Print all lines in sequence5.fasta that have exactly 2 consecutive Vs anywhere in the line.



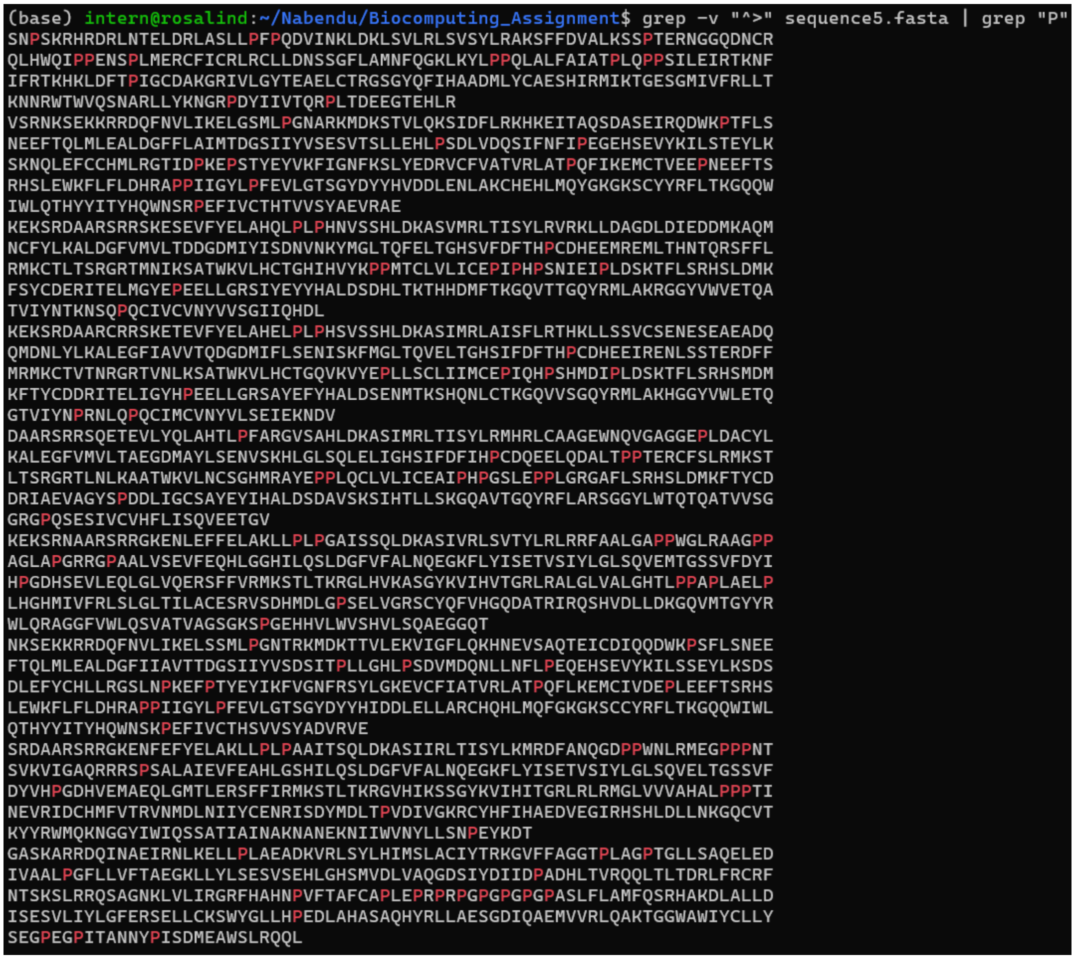
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep "VV" sequence5.fasta
AANFREGLNLQEGEFLLQALNGFVLVVTTDALVFYASSTIQDYLGFQQSDVIHQSVYELIHTEDRAEFQR
IWLQTHYYITYHQWNSRPEFIVCTHTVVSYAEVRAE
TVIYNTKNSQPQCIVCVNYVVSGIIQHDL
QMDNLYLKALEGFIAVVTQDGDMIFLSENISKFMGLTQVELTGHSIFDFTHPCDHEEIRENLSSTERDFF
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLETQ
DRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
QTHYYITYHQWNSKPEFIVCTHSVVSYADVRVE
DYVHPGDHVEMAEQLGMTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRMGLVVVAHALPPPTI
ISESVLIYLGFERSELLCKSWYGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLY
EKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
LDNVGRELGSHLLQTLDGFIFVVAPDGKIMYISETASVHLGLSQVELTGNSIYEYIHPADHDEMTAVLTA
LDGVAKELGSHLLQTLDGFVFVVASDGKIMYISETASVHLGLSQVELTGNSIYEYIHPSDHDEMTAVLTA
SYATVVHNSRSSRPHCIVSVNYVLTEIEYKEL
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
GSRRSFICRMRCGSSEPHFVVVHCTGYIKAKFCLVAIGRLQVTSSPNCTDMSNVCQPTEFISRHNIEGIF
TFVDHRCVATVGYQPQELLGKNIVEFCHPEDQQLLRDSFQQVVKLKGQVLSVMFRFRSKNQEWLWMRTSS
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIAKVKEQLSSSRLC
SGARRSFFCRMKCNRPRKSFCTIHSTGYLKSNLSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
RWFSFMNPWTKEVEYIVSTNTVVL
```

7. Print all lines in sequence5.fasta that contain either AA or DD.



```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep -E "AA|DD" sequence5.fasta
AANFREGLNLQEGEFLLQALNGFVLVVTTDALVFYASSTIQDYLGFQQSDVIHQSVYELIHTEDRAEFQR
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
RHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQW
KEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQM
NCFYLKALDGFVMVLTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTHNTQRSFFL
KEKSRDAARCRRSKETEVFYELAHELPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLETQ
DAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYL
LTSRGRTLNLKAATWKVLNCSGHMRAYEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
DRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
KEKSRNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPP
AGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYI
LEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
SRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
IVAALPGFLLVFTAEGKLLYLSESVSEHLGHSMVDLVAQGDSIYDIIDPADHLTVRQQLTLTDRLFRCRF
EKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
EKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEGLGDAWGQPSRAGP
ELKHLILEAADGFLFIVSCETGRVVYVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSRMCM
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIAKVKEQLSSSRLC
KFVFVDQRATAILAYLPQELLGTSCYEYFHQDDIGHLAECHRQVLQTREKITTNCYKFKIKDGSFITLRS
```

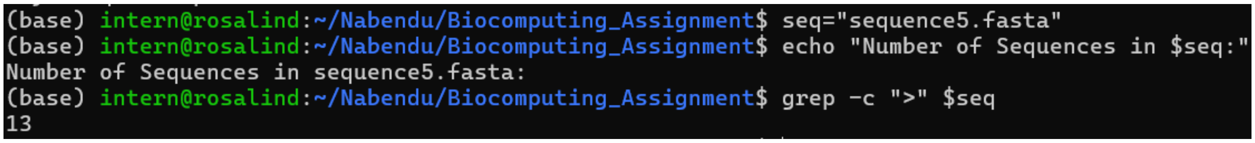
8. Print only the sequence lines (ignore headers) from sequence5.fasta that contain the letter P.



```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep -v "^>" sequence5.fasta | grep "P"
SNPSKRHRDRLNTELDRLASLLPFPQDVINKLDKLSVLRLSVSYLRAKSFFDVALKSSPTERNGGQDNCR
QLHWQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLPPQLALFAIATPLQPPSILEIRTKNF
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
KNNRWTWVQSNARLLYKNGRPDYIIVTQRPLTDEEGTEHLR
VSRNKSEKKRRDQFNVLIKELGSMLPGNARKMDKSTVLQKSIDFLRKHKEITAQSDASEIRQDWKPTFLS
NEEFTQLMLEALDGFFLAIMTDGSIIYVSESVTSLLEHLPSDLVDQSIFNFIPEGEHSEVYKILSTEYLK
SKNQLEFCCHMLRGTIDPKEPSTYEYVKFIGNFKSLYEDRVCFVATVRLATPQFIKEMCTVEEPNEEFTS
RHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQW
IWLQTHYYITYHQWNSRPEFIVCTHTVVSYAEVRAE
KEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQM
NCFYLKALDGFVMVLTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTHNTQRSFFL
RMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMK
FSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMFTKGQVTTGQYRMLAKRGGYVWVETQA
TVIYNTKNSQPQCIVCVNYVVSGIIQHDL
KEKSRDAARCRRSKETEVFYELAHELPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
QMDNLYLKALEGFIAVVTQDGDMIFLSENISKFMGLTQVELTGHSIFDFTHPCDHEEIRENLSSTERDFF
MRMKCTVTNRGRTVNLKSATWKVLHCTGQVKVYEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHSMDM
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLETQ
GTVIYNPRNLQPQCIMCVNYVLSEIEKNDV
DAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYL
KALEGFVMVLTAEGDMAYLSENVSKHLGLSQLELIGHSIFDFIHPCDQEELQDALTPPTERCFSLRMKST
LTSRGRTLNLKAATWKVLNCSGHMRAYEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
DRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
GRGPQSESIVCVHFLISQVEETGV
KEKSRNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPP
AGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYI
HPGDHSEVLEQLGLVQERSFFVRMKSTLTKRGLHVKASGYKVIHVTGRLRALGLVALGHTLPPAPLAELP
LHGHMIVFRLSLGLTILACESRVSDHMDLGPSELVGRSCYQFVHGQDATRIRQSHVDLLDKGQVMTGYYR
WLQRAGGFVWLQSVATVAGSGKSPGEHHVLWVSHVLSQAEGGQT
NKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLEKVIGFLQKHNEVSAQTEICDIQQDWKPSFLSNEE
FTQLMLEALDGFIIAVTTDGSIIYVSDSITPLLGHLPSDVMDQNLLNFLPEQEHSEVYKILSSEYLKSDS
DLEFYCHLLRGSLNPKEFPTYEYIKFVGNFRSYLGKEVCFIATVRLATPQFLKEMCIVDEPLEEFTSRHS
LEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
QTHYYITYHQWNSKPEFIVCTHSVVSYADVRVE
SRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVELTGSSVF
DYVHPGDHVEMAEQLGMTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRMGLVVVAHALPPPTI
NEVRIDCHMFVTRVNMDLNIIYCENRISDYMDLTPVDIVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVT
KYYRWMQKNGGYIWIQSSATIAINAKNANEKNIIWVNYLLSNPEYKDT
GASKARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYTRKGVFFAGGTPLAGPTGLLSAQELED
IVAALPGFLLVFTAEGKLLYLSESVSEHLGHSMVDLVAQGDSIYDIIDPADHLTVRQQLTLTDRLFRCRF
NTSKSLRRQSAGNKLVLIRGRFHAHNPVFTAFCAPLEPRPRPGPGPGPGPASLFLAMFQSRHAKDLALLD
ISESVLIYLGFERSELLCKSWYGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLY
SEGPEGPITANNYPISDMEAWSLRQQL
```

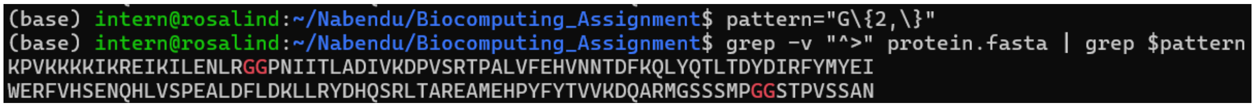
Part 3 - Using Variables

9. Store the filename sequence5.fasta in a variable called seq and print the number of sequences in it (headers count as sequences).



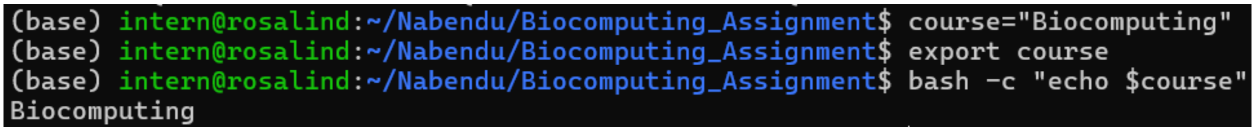
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ seq="sequence5.fasta"
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ echo "Number of Sequences in $seq:"
Number of Sequences in sequence5.fasta:
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep -c ">" $seq
13
```

10. Store the pattern G\{2,\} in a variable and search protein.fasta for sequence lines (ignore headers) with 2 or more consecutive Gs.



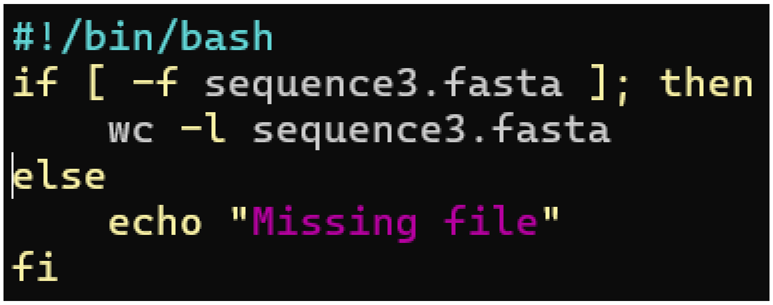
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ pattern="G\{2,\}"
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep -v "^>" protein.fasta | grep $pattern
KPVKKKKIKREIKILENLRGGPNIITLADIVKDPVSRTPALVFEHVNNTDFKQLYQTLTDYDIRFYMYEI
WERFVHSENQHLVSPEALDFLDKLLRYDHQSRLTAREAMEHPYFYTVVKDQARMGSSSMPGGSTPVSSAN
```

11. Store "Biocomputing" in a variable, export it, and verify that it is available inside a new shell started using:
bash -c 'echo $VARIABLE_NAME'

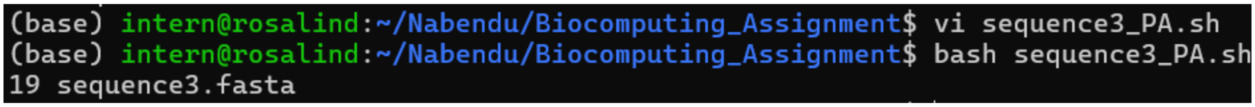


```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ course="Biocomputing"
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ export course
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ bash -c "echo $course"
Biocomputing
```

12. Write a shell script that checks if sequence3.fasta exists in the current folder. If yes, print the number of lines. If no, print "Missing file".

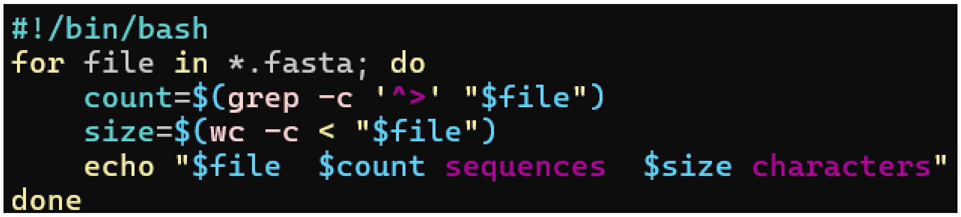


```
#!/bin/bash
if [ -f sequence3.fasta ]; then
    wc -l sequence3.fasta
else
    echo "Missing file"
fi
```

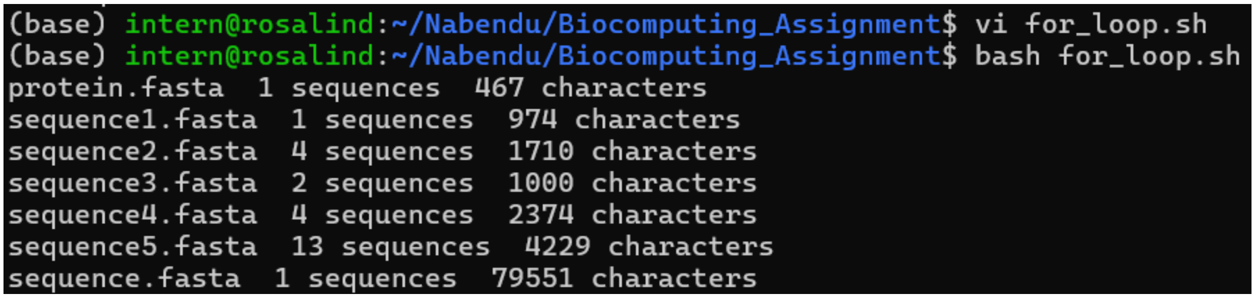


```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ vi sequence3_PA.sh
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ bash sequence3_PA.sh
19 sequence3.fasta
```

13. Using a for loop, go through all .fasta files in the current directory and print: filename, number of sequences, and file size in characters.

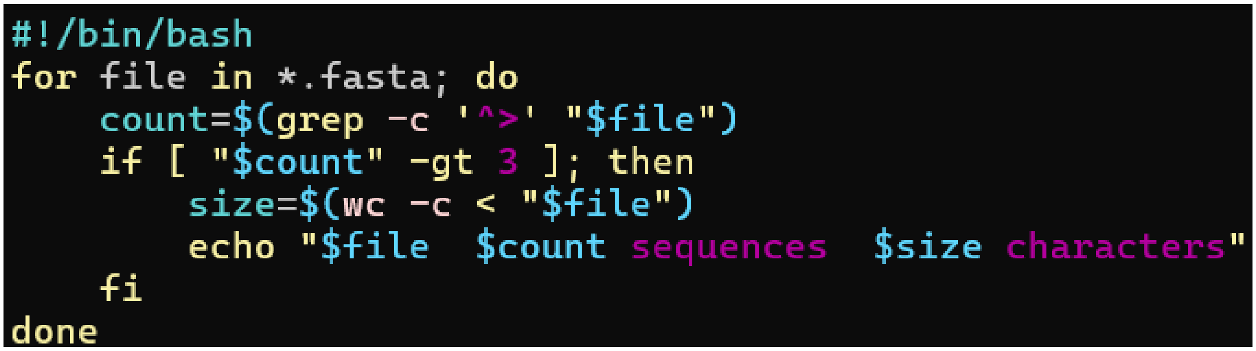


```
#!/bin/bash
for file in *.fasta; do
    count=$(grep -c '^>' "$file")
    size=$(wc -c < "$file")
    echo "$file  $count sequences  $size characters"
done
```

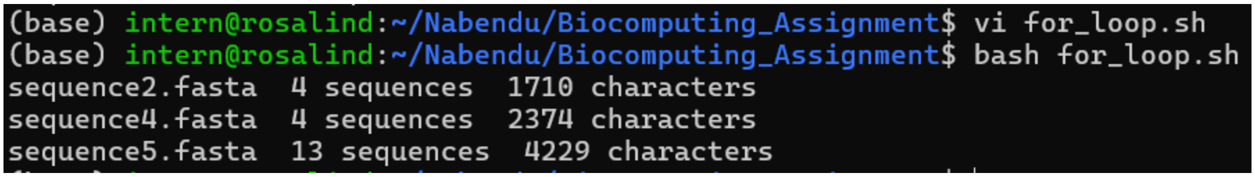


```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ vi for_loop.sh
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ bash for_loop.sh
protein.fasta  1 sequences  467 characters
sequence1.fasta  1 sequences  974 characters
sequence2.fasta  4 sequences  1710 characters
sequence3.fasta  2 sequences  1000 characters
sequence4.fasta  4 sequences  2374 characters
sequence5.fasta  13 sequences  4229 characters
sequence.fasta  1 sequences  79551 characters
```

14. Modify the above loop so that it only prints files with more than 3 sequences.



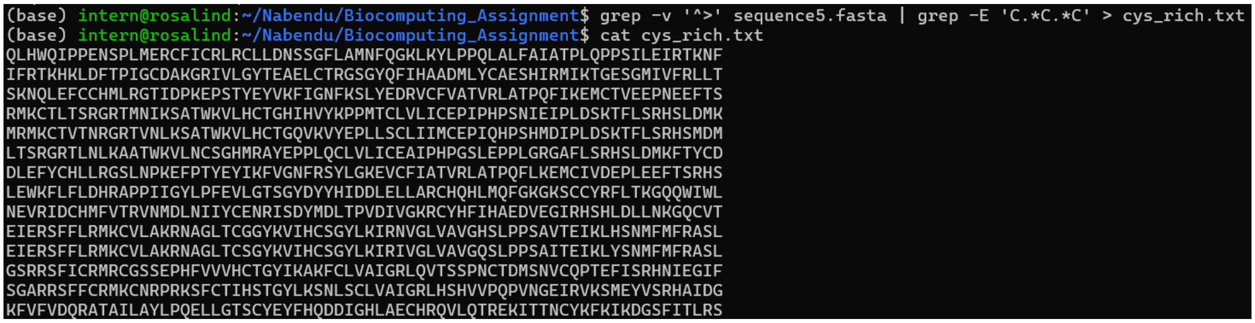
```
#!/bin/bash
for file in *.fasta; do
    count=$(grep -c '^>' "$file")
    if [ "$count" -gt 3 ]; then
        size=$(wc -c < "$file")
        echo "$file  $count sequences  $size characters"
    fi
done
```



```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ vi for_loop.sh
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ bash for_loop.sh
sequence2.fasta  4 sequences  1710 characters
sequence4.fasta  4 sequences  2374 characters
sequence5.fasta  13 sequences  4229 characters
```

Part 5 - Applied Data Extraction

15. From sequence5.fasta, extract only the sequence lines (no headers) that contain 3 or more cysteines (C). Save the output to a file named cys_rich.txt. Ensure the output file contains no empty lines.



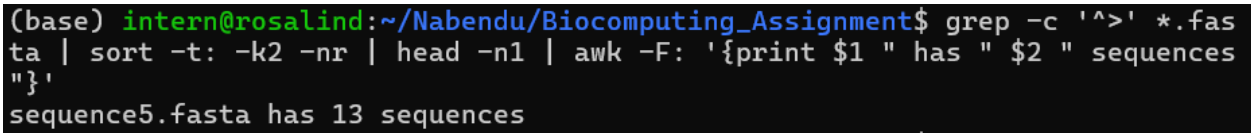
```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep -v '^>' sequence5.fasta | grep -E 'C.*C.*C' > cys_rich.txt
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ cat cys_rich.txt
QLHWQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLPPQLALFAIATPLQPPSILEIRTKNF
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
SKNQLEFCCHMLRGTIDPKEPSTYEYVKFIGNFKSLYEDRVCFVATVRLATPQFIKEMCTVEEPNEEFTS
RMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMK
MRMKCTVTNRGRTVNLKSATWKVLHCTGQVKVYEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHSMDM
LTSRGRTLNLKAATWKVLNCSGHMRAYEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
DLEFYCHLLRGSLNPKEFPTYEYIKFVGNFRSYLGKEVCFIATVRLATPQFLKEMCIVDEPLEEFTSRHS
LEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
NEVRIDCHMFVTRVNMDLNIIYCENRISDYMDLTPVDIVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVT
EIERSFFLRMKCVLAKRNAGLTCGGYKVIHCSGYLKIRNVGLVAVGHSLPPSAVTEIKLHSNMFMFRASL
EIERSFFLRMKCVLAKRNAGLTCSGYKVIHCSGYLKIRIVGLVAVGQSLPPSAITEIKLYSNMFMFRASL
GSRRSFICRMRCGSSEPHFVVVHCTGYIKAKFCLVAIGRLQVTSSPNCTDMSNVCQPTEFISRHNIEGIF
SGARRSFFCRMKCNRPRKSFCTIHSTGYLKSNLSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
KFVFVDQRATAILAYLPQELLGTSCYEYFHQDDIGHLAECHRQVLQTREKITTNCYKFKIKDGSFITLRS
```

Extra Challenge (Optional)

Write a single shell command that finds the file in the current directory with the largest number of sequences (by header count) and prints:

<filename> has <count> sequences

Hint: You will likely need wc, grep, sort, and head.



```
(base) intern@rosalind:~/Nabendu/Biocomputing_Assignment$ grep -c '^>' *.fas
ta | sort -t: -k2 -nr | head -n1 | awk -F: '{print $1 " has " $2 " sequences
"}'
sequence5.fasta has 13 sequences
```