

DATA WAREHOUSING AND DATA MINING LAB (CSD-421) LAB ASSIGNMENT 4

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Contents

1	Program 1	2
1.1	Question	2
1.2	Description	2
1.3	Run	2
1.4	Input Output Files	3
1.5	Check for	3
1.6	Code	4
1.7	Output	6
1.8	Result File	7
1.9	Log File	27
2	Program 2	28
2.1	Question	28
2.2	User should get	28
2.3	Server Code	28
2.4	HTML Page	29
2.5	Output	30

1 Program 1

1.1 Question

Develop a command line program to extract the features of a protein sequence file.

Input File		Output File							
Sequence	Class	SN	F1	F2	F3	F4	F5	F6	Class
PGGGKVQIVYKPV	+	1	4	0	2	3	2	1	1
PGGGKVYKPV	-	2	5	3	3	2	2	2	0
PGGGKNAEVYKPV	-	3	4	5	2	3	3	4	0
PGGGKVQIVEKPV	-	4	3	4	0	2	5	5	1
QTAPVPMPDLKNVKVY	-								
KPVDLSKVTSKCGSLGNIHLDF	-								

1.2 Description

- Input files contain only two columns: the first column is the protein sequence and the second column is the class (either -ve or +ve).
- Extract the feature of the sequence as given below rule:

SN → SN of sequence
 F1 → Count the number of N in sequence
 F2 → Count the number H in sequence
 F3 → Count the number Q in sequence
 F4 → Count the number G in sequence
 F5 → Count the number D in sequence
 F6 → Count the number T in sequence
 Class → Replace "+" with 1 and "-" with 0

1.3 Run

Run the program through the command line as

python extractFeatures.py <inputFile1> <inputFile2> n

Example:

- python extractFeatures.py inputfile1.csv
- python extractFeatures.py inputfile1.csv inputfile2.csv
- python extractFeatures.py inputfile1.csv inputfile2.csv inputfile3.csv

1.4 Input Output Files

- Input File(s) → file1.csv | file1.csv file2.txt | file1.txt file2.csv file3.txt
- Output Files → One result file and one log file
 - **Result file:**
 - It contains the extracted features for every sequence present in the input file(s).
 - Name of the result file → “result-” + str(time.time()) + “.csv”
 - e.g. → “result-20202109.csv”
 - **Logfile:**
 - It contains three columns (inputFileName, Sequence, Class) having issues with the sequences or with the class label in the input file(s).
 - Missing sequence or sequences having any numeric value
 - Missing class label
 - Name of the log file → “log-” + str(time.time()) + “.csv”
 - e.g. → “log-20200909.csv”
 - Logfile content

FileName	Sequence	Class
file1.csv	AGERT5DCT,	+
file2.csv	ARGVT,	
file3.txt	.	-
file4.txt	A4ADER,	

← Sequence contain numeric value

← Sequence class is missing

← Sequence is missing

← Sequence contain numeric value
& class is missing

1.5 Check for

- Correct number of parameters
- Show appropriate message for wrong inputs.
- Handling of “File not Found” exception
- Input file(s) contain only two columns.
- Output file name will be “result-” + str(time.time()) + “.csv”
- Log file name will be “log-” + str(time.time()) + “.csv”

1.6 Code

```
1  __author__ = 'Akshat Raj Vansh'
2  __version__ = '0.1.0'
3  __license__ = 'MIT'
4
5  import sys
6  import time
7
8  result = [['SN', 'F1', 'F2', 'F3', 'F4', 'F5', 'F6', 'Class']]
9  log = [['Filename', 'Sequence', 'Class']]
10
11
12 def encodeString(word):
13     return word.encode('unicode_escape')
14
15
16 def containsDigit(string):
17     return any(char.isdigit() for char in string)
18
19
20 def validateData(filename, data):
21     for x in data:
22         if (containsDigit(x[0]) or len(x[1]) == 0):
23             log.append(
24                 [filename[filename.rfind('\\')+1:], str(x[0]), str(x[1])])
25             data.remove(x)
26
27
28 def readFile(filename):
29     try:
30         file = open(encodeString(filename), "r")
31         inputFile = file.readlines()
32         data = [(x.replace('\n', '').split(',') for x in inputFile)]
33         file.close()
34         data = data[1:]
35         validateData(filename, data)
36         return data
37     except:
38         print(filename+' is not a valid file')
39         return []
40
41
42 def getTableValues(seq_no, data_item):
43     protein_sequence = data_item[0]
44     protein_class = data_item[1]
45     result = {'SN': seq_no,
46              'F1': protein_sequence.count('N'),
47              'F2': protein_sequence.count('H'),
48              'F3': protein_sequence.count('Q'),
49              'F4': protein_sequence.count('G'),
50              'F5': protein_sequence.count('D'),
51              'F6': protein_sequence.count('T'),
52              'Class': 1 if protein_class == '+' else 0}
53     return result.values()
54
55
56 def findResult(files):
```

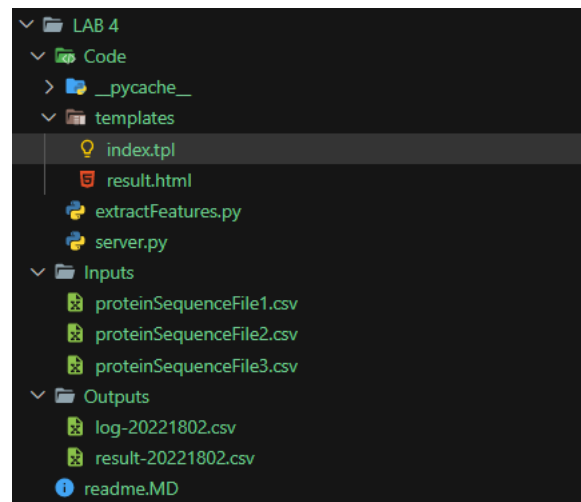
```
57     data = []
58     for i in range(len(files)):
59         data.extend(readFile(files[i]))
60     for seq_no, data_item in enumerate(data):
61         result.append(list(getTableValues(seq_no + 1, data_item)))
62
63
64 def generateLog():
65     print("Generating log...")
66     file = open('.\\Outputs\\log-'+time.strftime("%Y%d%m")+'.csv', 'w+')
67     file.writelines(','.join(str(x)
68                             for x in log[i])+'\n') for i in range(len(log)))
69     file.close()
70
71
72 def generateResult(files):
73     print('Generating result...')
74     findResult(files)
75     file = open('.\\Outputs\\result-'+time.strftime("%Y%d%m")+'.csv', 'w+')
76     file.writelines(','.join(str(x)
77                             for x in result[i])+'\n') for i in range(len(result)))
78     file.close()
79
80
81 def main(files):
82     generateResult(files)
83     generateLog()
84
85
86 def webService(string_files):
87     files = string_files.split(',')
88     main(files)
89     resultname = 'result-'+time.strftime("%Y%d%m")+'.csv'
90     logname = 'log-'+time.strftime("%Y%d%m")+'.csv'
91     output = {'result': 'Outputs\\'+ resultname,
92             'log': '\\Outputs\\'+ logname,
93             'resultname': resultname,
94             'logname': logname}
95     return output
96
97 def checkArguments(args):
98     if(len(args) == 0):
99         print('Invalid Number of argumverents')
100     else:
101         main(args)
102
103
104 if __name__ == "__main__":
105     print('Number of arguments:', len(sys.argv), 'arguments.')
106     print('Argument List:', str(sys.argv))
107     checkArguments(sys.argv[1:])
```

1.7 Output

Running the python script

```
PS D:\Coding\Data Mining\LAB 4> python .\Code\extractFeatures.py .\Inputs\proteinSequenceFile1.csv .\Inputs\proteinSequenceFile2.csv .\Inputs\proteinSequenceFile3.csv
Number of arguments: 4 arguments.
Argument List: ['.\\Code\\extractFeatures.py', '.\\Inputs\\proteinSequenceFile1.csv', '.\\Inputs\\proteinSequenceFile2.csv', '.\\Inputs\\proteinSequenceFile3.csv']
Generating result...
Generating log...
PS D:\Coding\Data Mining\LAB 4> █
```

Storing Output



1.8 Result File

	SN,F1,F2,F3,F4,F5,F6,Class
1	1,1,0,0,2,2,3,1
2	2,0,2,0,1,1,0,1
3	3,2,0,1,2,0,0,1
4	4,0,0,1,0,0,1,0
5	5,1,0,0,1,0,0,0
6	6,0,1,1,1,0,1,0
7	7,0,0,0,0,0,1,1
8	8,0,0,0,2,0,1,0
9	9,1,0,0,0,0,1,1
10	10,1,0,0,0,0,0,1
11	11,0,0,1,1,1,0,0
12	12,1,0,0,0,0,0,1
13	13,1,1,0,1,1,2,0
14	14,0,1,1,2,2,0,1
15	15,0,0,0,0,0,1,1
16	16,0,0,1,0,0,1,1
17	17,0,0,0,0,1,0,0
18	18,0,0,0,0,2,0,0
19	19,0,1,0,0,0,0,0
20	20,0,0,0,0,2,0,0
21	21,1,0,0,1,0,0,0
22	22,1,0,0,1,0,0,0
23	23,2,1,4,0,0,0,0
24	24,0,0,0,0,0,1,1
25	25,0,2,1,0,1,0,1
26	26,1,0,0,2,1,1,0
27	27,0,0,0,0,0,1,0
28	28,0,0,0,1,1,0,0
29	29,0,0,0,1,0,1,0
30	30,0,0,1,1,0,0,1
31	31,0,0,0,0,1,0,0
32	32,0,0,2,0,0,1,0
33	33,0,0,0,0,0,1,1
34	34,1,0,0,2,1,0,0
35	35,0,0,0,0,0,1,1
36	36,0,1,0,0,1,0,0
37	37,0,0,0,0,2,0,0
38	38,1,0,0,1,0,0,0
39	39,0,0,0,1,0,0,1
40	40,0,0,0,0,0,0,0
41	41,0,1,0,0,1,0,0
42	42,1,1,0,1,0,1,0
43	43,1,0,0,1,0,0,0
44	44,1,1,0,1,0,0,0
45	45,0,0,0,0,1,1,0
46	46,0,0,0,1,1,3,0
47	47,2,2,0,0,1,4,1
48	48,1,0,0,0,1,1,1
49	49,2,0,0,0,0,0,0
50	50,1,1,0,0,1,1,1
51	51,0,0,0,1,2,0,0
52	52,0,0,0,0,0,1,1
53	53,0,2,1,1,1,0,1
54	54,2,1,1,0,0,0,0
55	55,1,0,0,4,1,2,0


```
57 56,0,0,0,3,0,0,0
58 57,0,0,1,1,0,3,0
59 58,0,0,0,2,1,1,0
60 59,0,0,0,0,0,0,1
61 60,1,0,0,1,0,1,0
62 61,0,0,1,0,0,1,1
63 62,0,0,1,1,2,1,0
64 63,0,0,0,0,0,1,0
65 64,0,0,0,0,1,0,1
66 65,0,1,0,1,0,0,0
67 66,1,2,1,2,1,0,1
68 67,0,1,1,1,0,0,1
69 68,2,1,1,4,3,1,0
70 69,0,0,0,0,0,2,0
71 70,0,0,0,0,0,1,0
72 71,1,1,2,2,0,1,1
73 72,0,0,0,0,0,1,0
74 73,0,0,0,0,0,1,0
75 74,0,0,0,0,0,0,1
76 75,0,2,1,0,1,0,1
77 76,1,1,1,4,0,3,1
78 77,1,0,1,3,0,2,1
79 78,0,0,1,0,0,1,1
80 79,1,0,0,1,1,0,0
81 80,0,0,1,0,0,1,0
82 81,0,0,0,0,0,1,0
83 82,0,1,1,1,0,5,0
84 83,0,0,0,0,0,0,0
85 84,0,0,0,0,0,1,0
86 85,0,0,0,1,0,2,1
87 86,0,0,0,1,1,1,0
88 87,0,1,0,1,0,0,0
89 88,0,0,2,1,1,1,0
90 89,0,0,1,0,0,0,0
91 90,0,0,0,0,0,1,0
92 91,1,2,0,5,0,1,0
93 92,0,0,0,0,0,2,0
94 93,1,0,3,0,0,1,0
95 94,0,0,1,0,0,1,1
96 95,0,0,1,0,0,0,0
97 96,2,0,0,1,1,2,0
98 97,1,1,0,1,2,0,0
99 98,0,0,0,0,0,0,1
100 99,0,0,1,0,0,1,0
101 100,0,0,1,0,0,1,0
102 101,0,0,0,0,0,1,1
103 102,2,1,2,0,2,0,1
104 103,0,0,0,0,1,0,0
105 104,1,0,0,1,0,0,1
106 105,0,0,0,0,1,1,0
107 106,0,2,0,2,1,0,1
108 107,0,0,0,0,0,1,1
109 108,0,0,0,0,0,1,0
110 109,0,0,0,0,1,0,0
111 110,0,0,1,0,0,1,0
112 111,0,1,2,0,1,0,0
113 112,0,0,0,0,0,1,0
114 113,1,1,0,0,0,0,0
```

```
115 114,0,1,0,2,0,0,0
116 115,0,0,0,0,0,0,1
117 116,0,1,2,0,0,1,0
118 117,1,0,0,3,0,3,1
119 118,1,1,1,0,0,3,0
120 119,1,0,0,1,0,1,0
121 120,0,0,0,0,0,2,1
122 121,0,0,0,0,0,1,1
123 122,0,0,0,1,2,5,1
124 123,0,0,1,1,1,1,0
125 124,1,1,2,3,0,1,0
126 125,0,0,0,0,0,1,0
127 126,1,0,1,2,0,0,1
128 127,0,0,0,0,0,0,1
129 128,1,0,1,1,2,0,0
130 129,2,0,0,0,0,0,0
131 130,0,0,0,0,0,1,0
132 131,1,0,0,1,0,1,0
133 132,3,1,0,2,1,0,1
134 133,0,0,0,0,2,0,1
135 134,0,0,1,0,1,0,0
136 135,0,0,0,0,0,0,1
137 136,1,0,1,3,0,3,1
138 137,0,0,0,1,1,0,1
139 138,0,0,0,4,0,0,0
140 139,3,0,1,1,3,2,1
141 140,0,1,0,0,0,0,0
142 141,1,0,1,0,0,0,0
143 142,0,0,0,0,1,0,0
144 143,0,0,0,0,0,1,1
145 144,0,0,0,0,0,1,1
146 145,2,0,0,1,0,2,0
147 146,0,0,0,0,1,0,1
148 147,1,1,1,0,0,0,0
149 148,0,0,0,0,0,0,1
150 149,0,0,0,0,0,1,0
151 150,1,0,2,1,0,0,1
152 151,0,1,2,1,1,1,1
153 152,0,0,0,1,0,1,0
154 153,0,0,0,0,0,1,0
155 154,1,0,1,1,0,0,0
156 155,1,0,0,1,0,0,0
157 156,3,0,1,0,1,0,0
158 157,1,0,1,1,0,1,0
159 158,0,1,0,0,0,1,0
160 159,0,2,2,3,2,0,1
161 160,0,0,0,1,1,0,0
162 161,2,1,2,1,0,0,0
163 162,0,0,0,0,0,0,0
164 163,0,0,0,0,0,3,0
165 164,1,0,0,0,0,0,1
166 165,0,0,0,0,0,1,1
167 166,0,0,1,1,0,0,0
168 167,1,0,0,1,0,2,1
169 168,3,1,1,0,1,0,0
170 169,1,0,1,0,0,0,0
171 170,0,0,1,0,0,1,1
172 171,0,0,1,0,0,1,0
```

```
173 172,0,0,0,0,1,1,1
174 173,0,0,0,0,0,2,0
175 174,0,0,0,0,0,1,0
176 175,0,1,0,0,0,0,0
177 176,0,1,0,0,2,0,0
178 177,0,2,1,1,1,0,1
179 178,0,1,0,0,0,1,0
180 179,0,0,0,0,0,2,1
181 180,0,1,0,1,0,0,0
182 181,0,0,0,0,0,0,0
183 182,0,0,1,0,0,1,1
184 183,0,0,0,1,0,0,0
185 184,1,0,0,0,1,0,0
186 185,0,1,0,1,0,0,0
187 186,0,0,0,0,1,1,0
188 187,0,1,0,2,1,2,0
189 188,0,0,1,0,0,1,1
190 189,0,0,0,0,0,0,0
191 190,0,0,0,0,1,0,0
192 191,1,1,1,0,0,0,0
193 192,1,0,0,0,2,0,0
194 193,0,0,0,0,1,1,0
195 194,0,0,0,0,1,1,0
196 195,1,1,0,1,0,0,1
197 196,0,0,0,0,0,1,1
198 197,0,0,0,1,1,0,1
199 198,2,0,0,1,1,0,0
200 199,0,0,0,0,0,1,1
201 200,0,0,0,0,0,1,1
202 201,0,0,0,0,0,1,1
203 202,0,0,0,0,0,0,0
204 203,0,0,0,3,1,0,1
205 204,0,0,0,1,2,1,0
206 205,0,0,0,0,0,1,1
207 206,0,0,1,0,0,0,1
208 207,0,0,1,0,0,1,0
209 208,0,0,2,1,0,0,0
210 209,1,1,1,0,0,1,0
211 210,0,0,0,0,0,1,0
212 211,0,0,0,2,1,1,0
213 212,0,0,0,0,0,0,0
214 213,1,1,0,0,1,0,0
215 214,1,1,2,0,0,0,0
216 215,0,0,0,0,0,1,1
217 216,0,0,0,0,0,0,1
218 217,1,1,0,0,0,1,0
219 218,0,1,1,1,3,0,0
220 219,0,0,0,0,0,1,1
221 220,2,1,0,0,1,0,0
222 221,0,0,0,0,1,0,0
223 222,2,0,1,2,0,3,1
224 223,1,0,0,0,0,1,1
225 224,0,0,0,0,0,0,0
226 225,0,0,0,1,0,1,1
227 226,0,0,1,1,1,1,0
228 227,1,1,0,1,0,1,0
229 228,1,0,1,3,2,0,0
230 229,0,0,0,2,0,0,0
```

```
231 230,0,0,1,0,0,1,0
232 231,0,0,1,0,0,1,0
233 232,0,0,0,0,0,0,0
234 233,1,0,0,1,0,0,0
235 234,0,0,2,2,1,0,0
236 235,0,0,0,3,1,0,0
237 236,1,0,0,1,0,1,0
238 237,0,0,0,0,0,0,0
239 238,0,1,0,1,0,0,0
240 239,0,0,0,0,0,0,0
241 240,0,0,1,0,0,0,0
242 241,1,1,1,1,0,2,1
243 242,0,2,1,0,1,0,1
244 243,0,0,0,1,0,0,1
245 244,0,0,0,1,2,3,1
246 245,3,1,0,1,0,0,0
247 246,0,0,0,0,0,1,0
248 247,0,0,0,0,1,3,1
249 248,0,0,0,0,0,2,0
250 249,2,0,0,0,1,0,0
251 250,0,2,1,1,1,0,1
252 251,0,0,0,0,0,0,1
253 252,1,2,1,2,1,0,1
254 253,0,0,0,0,0,1,1
255 254,0,0,0,1,0,1,0
256 255,0,0,1,0,0,1,0
257 256,0,0,0,0,0,1,0
258 257,0,0,1,0,0,1,0
259 258,0,2,1,1,0,0,1
260 259,0,0,0,0,0,0,1
261 260,0,0,0,0,0,1,1
262 261,0,0,0,4,1,0,0
263 262,2,0,0,1,0,0,0
264 263,0,0,0,0,0,2,0
265 264,0,0,0,1,0,0,0
266 265,0,0,0,0,1,0,1
267 266,2,1,0,0,1,0,0
268 267,1,0,1,0,0,0,1
269 268,0,0,1,1,1,1,0
270 269,0,1,1,1,1,0,1
271 270,0,0,0,0,0,0,1
272 271,0,0,0,0,1,1,0
273 272,0,0,0,1,0,1,0
274 273,1,1,1,0,0,0,0
275 274,2,1,1,4,3,1,0
276 275,1,0,0,1,0,2,1
277 276,1,1,0,1,0,0,0
278 277,1,2,1,5,0,1,0
279 278,1,0,0,0,1,2,0
280 279,0,0,0,0,0,1,0
281 280,1,0,0,3,3,2,1
282 281,0,0,0,0,0,1,0
283 282,0,0,0,0,0,1,1
284 283,0,0,1,0,0,0,0
285 284,0,0,0,0,1,0,1
286 285,0,1,1,0,0,0,0
287 286,0,0,0,0,0,1,0
288 287,0,0,0,0,1,2,1
```

```
289 288,1,0,0,1,0,0,0
290 289,1,1,0,0,3,0,0
291 290,0,0,0,0,0,1,1
292 291,0,0,0,0,0,1,0
293 292,0,0,1,0,2,0,0
294 293,1,2,1,3,2,0,1
295 294,0,0,0,0,0,1,0
296 295,0,0,1,0,0,0,1
297 296,0,0,0,0,0,1,0
298 297,2,1,0,1,0,0,0
299 298,2,1,0,1,0,0,0
300 299,0,0,0,1,0,1,0
301 300,0,0,0,0,0,2,0
302 301,0,0,1,0,0,1,0
303 302,0,1,0,1,2,3,0
304 303,0,0,0,0,1,1,1
305 304,0,0,1,0,0,1,0
306 305,0,1,0,0,0,0,0
307 306,0,0,1,0,0,1,0
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1100 1099,0,0,0,0,0,0,1
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1103	1102,0,0,0,0,1,0,0
1104	1103,0,0,1,0,0,1,1
1105	1104,1,0,0,0,1,0,0
1106	1105,0,2,0,1,1,0,1
1107	1106,0,1,2,1,1,1,1
1108	1107,0,0,0,0,0,0,1
1109	1108,0,2,1,0,1,0,1
1110	1109,0,0,0,0,1,0,0
1111	1110,0,0,0,0,1,0,0
1112	1111,0,1,0,1,0,0,0
1113	1112,1,1,0,0,0,1,0
1114	1113,0,0,0,1,0,2,1
1115	1114,0,0,0,0,0,1,0
1116	1115,0,0,0,0,1,0,0
1117	1116,0,0,0,0,0,1,1
1118	1117,0,0,0,0,0,1,1
1119	1118,1,0,0,0,1,2,0
1120	1119,1,0,0,1,0,0,0
1121	1120,1,1,1,0,0,0,0
1122	1121,0,0,1,0,1,1,0
1123	1122,0,0,0,2,1,1,0
1124	1123,1,0,2,1,0,0,1
1125	1124,1,0,2,0,1,0,0
1126	1125,0,0,0,0,0,2,1
1127	1126,0,0,2,0,0,1,0
1128	1127,0,1,0,0,2,0,0
1129	1128,1,0,2,5,0,3,1
1130	1129,0,0,1,0,0,1,1
1131	1130,0,0,0,0,1,0,0
1132	1131,1,0,1,2,1,1,0
1133	1132,0,0,1,0,0,1,0
1134	1133,0,0,0,0,0,0,1
1135	1134,0,0,0,0,1,1,0
1136	1135,0,1,0,0,0,0,0
1137	1136,0,0,2,0,0,1,0
1138	1137,0,0,0,0,1,2,1
1139	1138,0,0,1,1,2,1,0
1140	1139,1,1,0,1,0,0,0
1141	1140,0,0,0,0,0,1,1
1142	1141,1,0,0,1,0,0,1
1143	1142,1,0,0,0,0,1,1
1144	1143,0,0,1,1,0,0,1
1145	1144,2,0,0,0,0,0,0
1146	1145,0,0,0,0,0,1,0
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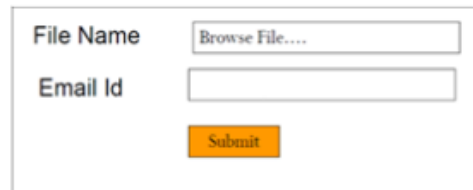
1.9 Log File

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4 proteinSequenceFile1.csv,PG33GKVQIVEKPV,-
5 proteinSequenceFile1.csv,KDRVQSKIGSLDNITHVPGGGN,
6 proteinSequenceFile1.csv,QTAPVPMPDLKNVSKIGSTE,
7 proteinSequenceFile1.csv,KPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLD,
8 proteinSequenceFile1.csv,PGGGKN8EVYKPV,-
9 proteinSequenceFile1.csv,QTAPVPMPDLKNVSKIGS67ENLKHQPGGGKVQIVY,-
10 proteinSequenceFile1.csv,PGGG5VQIVYKPV,+
11 proteinSequenceFile2.csv,QTAPVPMPDLKNVSKIGSTE,
12 proteinSequenceFile2.csv,PGGGKN8EVYKPV,-
13 proteinSequenceFile2.csv,PGGG5VQIVYKPV,+
14 proteinSequenceFile2.csv,QTAPVPMPDLKNVSKIGS67ENLKHQPGGGKVQIVY,-
15 proteinSequenceFile2.csv,PG33GKVQIVEKPV,-
16 proteinSequenceFile2.csv,NLKHQPGGGKVQIVYKPVDSLKVTSKCGSLGNIHHKPGGGQVE,
17 proteinSequenceFile2.csv,KDRVQSKIGSLDNITHVPGGGN,
18 proteinSequenceFile2.csv,PGGGKV3KPV,-
19 proteinSequenceFile2.csv,KPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLD,
20 proteinSequenceFile3.csv,PGGGKN8EVYKPV,-
21 proteinSequenceFile3.csv,QTAPVPMPDLKNVSKIGS67ENLKHQPGGGKVQIVY,-
22 proteinSequenceFile3.csv,KDRVQSKIGSLDNITHVPGGGN,
23 proteinSequenceFile3.csv,KPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLD,
24 proteinSequenceFile3.csv,PGGG5VQIVYKPV,+
25 proteinSequenceFile3.csv,PGGGKV3KPV,-
26 proteinSequenceFile3.csv,PG33GKVQIVEKPV,-
27 proteinSequenceFile3.csv,QTAPVPMPDLKNVSKIGSTE,
```

2 Program 2

2.1 Question

Develop a webservice for program 1



2.2 User should get

- Result File
- Log File

2.3 Server Code

```

1  from black import out
2  import extractFeatures
3  from bottle import Bottle, template, request
4
5  app = Bottle()
6  output = {}
7
8  @app.route('/')
9  def index():
10     """Home Page"""
11     return template("./templates/index.tpl", result="", log="", resultname="", logname="")
12
13  @app.route('/', method="POST")
14  def formhandler():
15     """Handle the form submission"""
16
17     files = request.forms.get('files')
18     print(files)
19     output = extractFeatures.webService(files)
20     return template("./templates/index.tpl",
21                    result=output['result'],
22                    log=output['log'],
23                    resultname=output['resultname'],
24                    logname=output['logname'])
25
26  if __name__ == '__main__':
27     app.run(debug=True)

```

2.4 HTML Page

```

1  <!DOCTYPE html>
2  <html>
3  <head>
4      <title>LAB ASSIGNMENT 4</title>
5      <meta name="viewport" content="width=device-width, initial-scale=1">
6  <style>
7  * {
8      box-sizing: border-box;
9  }
10 .column {
11     float: left;
12     width: 50%;
13     padding: 10px;
14     height: 600px;
15     overflow-x: hidden;
16         overflow-y: auto;
17         text-align: justify;
18 }
19
20 .row:after {
21     content: "";
22     display: table;
23     clear: both;
24 }
25 </style>
26 </head>
27
28 <body>
29     <form method="post" action="/">
30         <fieldset>
31             <legend>DATA MINING AND WAREHOUSING LAB ASSIGNMENT 4</legend>
32             <center>
33                 <ul>
34                     <label for="files">Select files : </label>
35                     <input type="file" id="files" name="files" multiple /> Email ID:
36                     <input name="first" />
37                 </ul>
38
39                 <input type="submit" value="Generate Result" />
40             </center>
41         </fieldset>
42     </form>
43     <br />
44
45 </div>
46 <div class="row">
47     <div class="column" style="background-color:#aaa;">
48         <h2>{{resultname}}</h2>
49         <p>{{result}}</p>
50     </div>
51     <div class="column" style="background-color:#bbb;">
52         <h2>{{logname}}</h2>
53         <p>{{log}}</p>
54     </div>
55 </div>
56

```

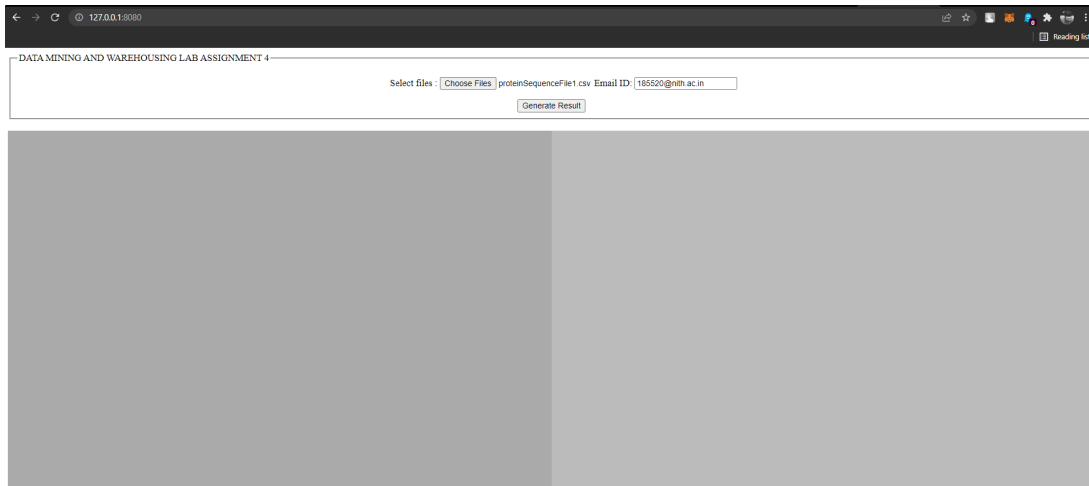
57 </body>

58

59 </html>

2.5 Output

Before Selecting the files



After submitting the selected files

