```
<?php

 void keyword(char str[10]) {

if(strcmp("for",str)==0||strcmp("while",str)==0||strcmp("do",str)==0||strcmp("int",s
tr)==0||strcmp("float",str)==0||strcmp("char",str)==0||strcmp("double",str)==0||strc
mp("static",str)==0||strcmp("switch",str )==0||strcmp("case",str)==0)

printf("\n%s is a keyword",str); else printf("\n%s is an identifier",str);

}

 main()

 {

 FILE *f1,*f2,*f3;

 char c,str[10],st1[10];

 int num[100],lineno=0,tokenvalue=0,i=0,j=0,k=0;

 printf("\nEnter the c program");/*gets(st1);

*/ f1=fopen("input","w");

 while((c=getchar())!=EOF) putc(c,f1);

 fclose(f1);

 f1=fopen("input","r");
```

```
 f2=fopen("identifier","w");
f3=fopen("specialchar","w");
while((c=getc(f1))!=EOF)
{
if(isdigit(c))
{
tokenvalue 2 c=getc(f1);
while(isdigit(c))
{
 tokenvalue*=10+c-'0';
c=getc(f1);
 }
num[i++]=tokenvalue;
 ungetc(c,f1);
}
 Else
```

```
 if(isalpha(c))
 {
 putc(c,f2);
c=getc(f1);
 while(isdigit(c)||isalpha(c)||c=='_'||c=='$')
 {
putc(c,f2);
 c=getc(f1);
}
 putc(' ',f2);
 ungetc(c,f1);
 }
 else if(c==' '||c=='\t') printf(" ");
else if(c=='\n') lineno++;
 else putc(c,f3);
 }
```

```
 fclose(f2);
 fclose(f3);
 fclose(f1);
 printf("\nThe no's in the program are");
 for(j=0;j<3;j++)
 {
char com[30];
int i=2,a=0;
clrscr();
printf("\n Enter comment:");
 gets(com);
if(com[0]=='/') { if(com[1]=='/') printf("\n It is a comment");
else if(com[1]=='*')
 {
 for(i=2;i<=30;i++)
 {
```

```
 if(com[i]=='*'&&com[i+1]=='/')
 {
 printf("\n It is a comment");
a=1; break;
 }
 else
continue;
 }
 if(a==0) printf("\n It is not a comment");
 }
 else printf("\n It is not a comment");
 }
 else printf("\n It is not a comment");
 getch();
}
}?>
```

1.1.1 SQL query

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 0

AND GVH = 0 AND LIP=0 AND CHG=1 AND AAC=1 AND ALM1=1 AND ALM2=1Group By CLASS_DISTRIBUTION='IM'

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 4

AND GVH = 6 AND LIP=7 AND CHG=8 AND AAC=8 AND ALM1=7 AND ALM2=0 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 0

AND GVH = 0 AND LIP=0 AND CHG=1 AND AAC=1 AND ALM1=1 AND ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=1 AND CHG=1 AND AAC=1 AND ALM1=1 AND ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 0

AND GVH = 0 AND LIP=1 AND CHG=1 AND AAC=1 AND ALM1=1 AND ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 0

AND GVH = 0 AND LIP=0 AND CHG=1 AND AAC=1 AND ALM1=1 AND ALM2=1 Group By CLASS_DISTRIBUTION

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Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=1 AND CHG=1 AND AAC=1 AND ALM1=1 AND ALM2=1 Group By CLASS_DISTRIBUTION

UNION

```
Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=0 AND CHG=0 AND AAC=1  AND ALM1=1 AND
ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=1 AND CHG=0 AND AAC=1  AND ALM1=0 AND
ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 0 AND LIP=0 AND CHG=0 AND AAC=1  AND ALM1=1 AND
ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1
```

AND GVH = 0 AND LIP=0 AND CHG=1 AND AAC=1 AND ALM1=0 AND ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 0

AND GVH = 1 AND LIP=1 AND CHG=0 AND AAC=1 AND ALM1=1 AND ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME, (Count (SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=1 AND CHG=0 AND AAC=1 AND ALM1=1 AND ALM2=1 Group by CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*) From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=1 AND CHG=0 AND AAC=0 AND ALM1=1 AND ALM2=0 Group By CLASS_DISTRIBUTION

UNION

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Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
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AND GVH = 1 AND LIP=0 AND CHG=1 AND AAC=0  AND ALM1=1 AND
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Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 1 AND LIP=1 AND CHG=1 AND AAC=0  AND ALM1=0 AND
ALM2=0 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 1

AND GVH = 0 AND LIP=0 AND CHG=0 AND AAC=1  AND ALM1=1 AND
ALM2=1 Group By CLASS_DISTRIBUTION

UNION

Select SEQUENCE_NAME,(Count(SEQUENCE_NAME)* 100 / (Select Count(*)
From ecolli)) as CLASS_DISTRIBUTION

From ecolli WHERE MCG = 0
```

AND GVH = 1 AND LIP=0 AND CHG=1 AND AAC=0 AND ALM1=0 AND ALM2=1 Group By CLASS_DISTRIBUTION

6.1.2 A Modified fuzzy rules for E.COLI datasets

1. If(GVH=low)AND(LIP=low)AND(CHG=low)AND(AAC=low)AND(ALM1=low)AND(ALM2=low)THEN class distribution is CP.

2. If(GVH=medium)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=high)THEN class distribution is CP.

3. If(GVH=low)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=high)AND(ALM2=high)THEN class distribution is CP.

4. If(GVH=medium)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=high)THEN class distribution is CP.

5. If(GVH=low)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=high)THEN class distribution is CP.

6. If(GVH=low)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=medium)THEN class distribution is IM.

7. If(GVH=low)AND(LIP=medium)AND(CHG=low)AND(AAC=high)AND(ALM1=high)AND(ALM2=high)THEN class distribution is IM.

8. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=high)AND(ALM2=high)THEN class distribution is IM.

9. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=low)AND(ALM1 =high)AND(ALM2=high)THEN class distribution is IM.

10. If(GVH=medium)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(A LM1=high)AND(ALM2=high)THEN class distribution is IM.

11. If(GVH=low)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1 =medium)AND(ALM2=high)THEN class distribution is IM.

12. If(GVH=medium)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(A LM1=high)AND(ALM2=high)THEN class distribution is IMS.

13. If(GVH=low)AND(LIP=high)AND(CHG=high)AND(AAC=high)AND(AL M1=medium)AND(ALM2=medium)THEN class distribution is IML.

14. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM 1=medium)AND(ALM2=medium)THEN class distribution is IML.

15. If(GVH=medium)AND(LIP=low)AND(CHG=low)AND(AAC=medium)AND (ALM1=high)AND(ALM2=high)THEN class distribution is IMU.

16. If(GVH=medium)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(A LM1=medium)AND(ALM2=high)THEN class distribution is IMU.

17. If(GVH=high)AND(LIP=high)AND(CHG=low)AND(AAC=medium)AND(ALM1=high)AND(ALM2=high)THEN class distribution is IMU.

18. If(GVH=low)AND(LIP=high)AND(CHG=low)AND(AAC=medium)AND(ALM1=high)AND(ALM2=high)THEN class distribution is IMU.

19. If(GVH=medium)AND(LIP=high)AND(CHG=low)AND(AAC=low)AND(ALM1=high)AND(ALM2=low)THEN class distribution is OM.

20. If(GVH=medium)AND(LIP=high)AND(CHG=low)AND(AAC=medium)AND(ALM1=medium)AND(ALM2=high)THEN class distribution is OM.

21. If(GVH=high)AND(LIP=high)AND(CHG=low)AND(AAC=high)AND(ALM1=high)AND(ALM2=medium)THEN class distribution is OM.

22. If(GVH=low)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=low)THEN class distribution is OM.

23. If(GVH=low)AND(LIP=high)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=low)THEN class distribution is OM.

24. If(GVH=low)AND(LIP=high)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=high)THEN class distribution is OML.

25. If(GVH=low)AND(LIP=high)AND(CHG=low)AND(AAC=high)AND(ALM1=high)AND(ALM2=medium)THEN class distribution is OML.

26. If(GVH=high)AND(LIP=high)AND(CHG=low)AND(AAC=high)AND(ALM1=medium)AND(ALM2=high)THEN class distribution is OML.

27. If(GVH=medium)AND(LIP=high)AND(CHG=low)AND(AAC=high)AND(ALM1=high)AND(ALM2=low)THEN class distribution is OML.

28. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=low)AND(ALM1=medium)AND(ALM2=low)THEN class distribution is PP.

29. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=medium)AND(ALM1=high)AND(ALM2=low)THEN class distribution is pp.

30. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=low)AND(ALM1=high)AND(ALM2=low)THEN class distribution is PP.

31. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=low)AND(ALM1=low)AND(ALM2=low)THEN class distribution is PP.

32. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=high)AND(ALM1=low)AND(ALM2=low)THEN class distribution is PP.

33. If(GVH=high)AND(LIP=low)AND(CHG=low)AND(AAC=medium)AND(ALM1=low)AND(ALM2=low)THEN class distribution is PP.

34. If(GVH=medium)AND(LIP=medium)AND(CHG=medium)AND(AAC=medium)AND(ALM1=low)AND(ALM2=low)THEN class distribution is PP.

35. If(GVH=medium)AND(LIP=medium)AND(CHG=medium)AND(AAC=medium)AND(ALM1=medium)AND(ALM2=low) THEN class distribution is PP.

36. If (GVH=medium) AND (LIP=medium) AND (CHG=medium) AND (AAC=medium) AND (ALM1=medium) AND (ALM2=high) THEN class distribution is PP.

37. If (GVH=high) AND (LIP=medium) AND (CHG=medium) AND (AAC=medium) AND (ALM1=medium) AND (ALM2=high) THEN class distribution is PP.

38. If (GVH=medium) AND (LIP=medium) AND (CHG=medium) AND (AAC=high) AND (ALM1=medium) AND (ALM2=high) THEN class distribution is PP.