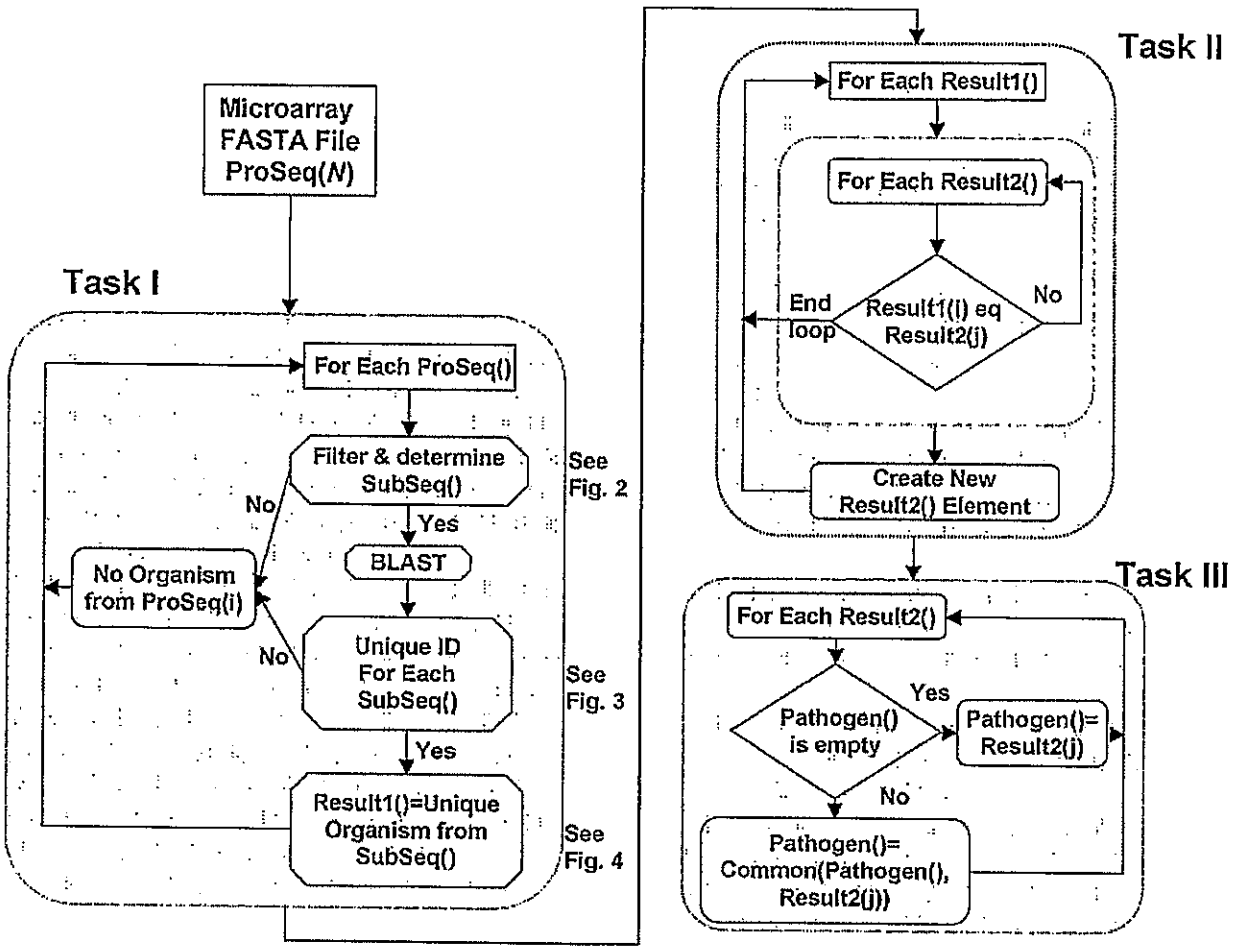

Microarray FASTA File ProSeq(N)
Task I
For Each ProSeq()
Filter & determine SubSeq()
No
Yes
BLAST
No Organism from ProSeq(i)
No
Unique ID For Each SubSeq()
Yes
Result1()=Unique Organism from SubSeq()
See Fig. 2
See Fig. 3
See Fig. 4
Task II
For Each Result1()
For Each Result2()
End loop
Result1(i) eq Result2(j)
No
Create New Result2() Element
Task III
For Each Result2()
Pathogen() is empty
Yes
Pathogen()= Result2(j)
No
Pathogen()= Common(Pathogen(), Result2(j))

Fig. 1

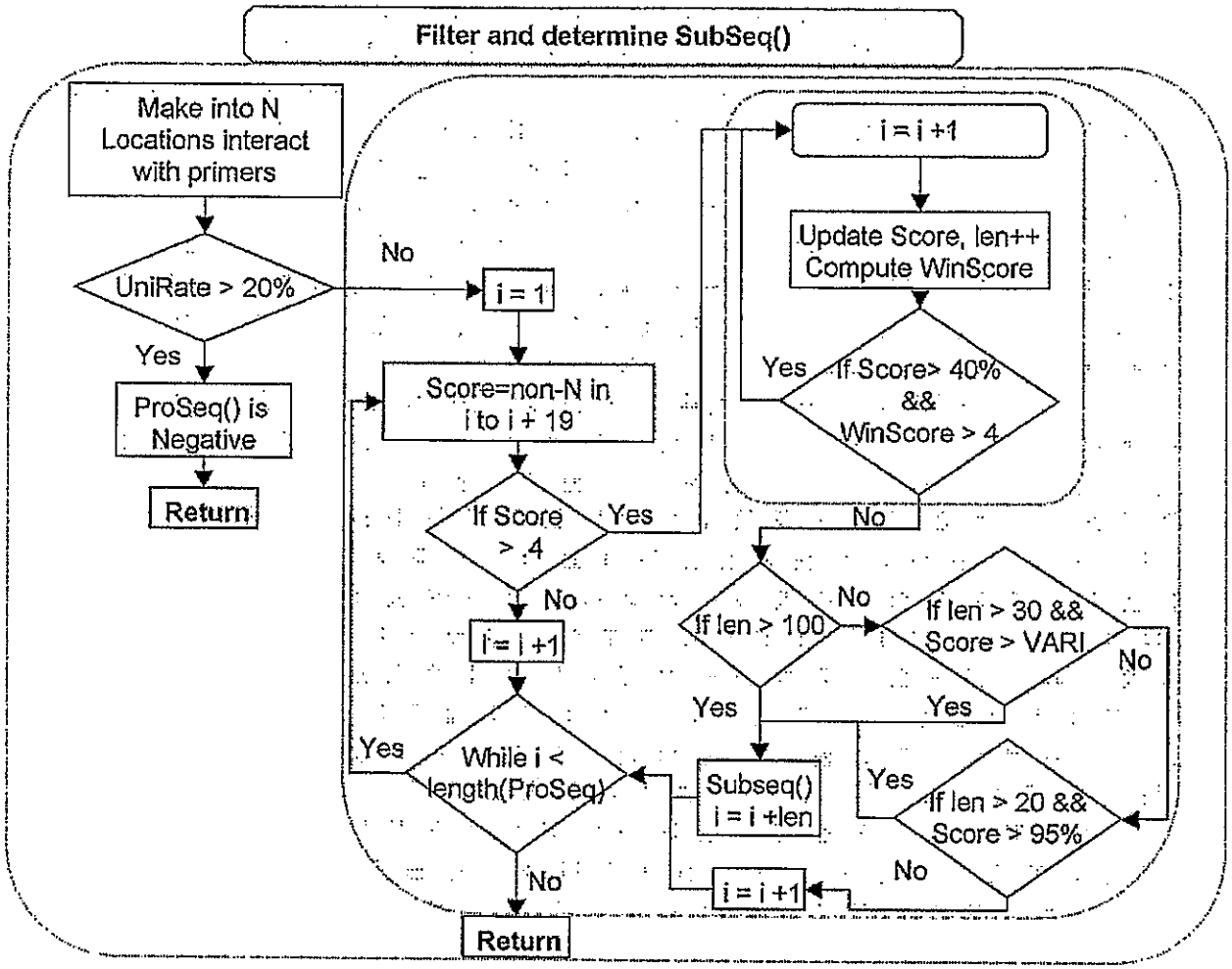

Filter and determine SubSeq()
Make into N Locations interact with primers
UniRate > 20%
No
Yes
ProSeq() is Negative
Return
i = 1
Score=non-N in i to i + 19
If Score > 4
Yes
No
i = i +1
While i < length(ProSeq)
Yes
No
Return
i = i +1
Update Score, len++ Compute WinScore
If Score> 40% && WinScore > 4
Yes
No
If len > 100
No
If len > 30 && Score > VARI
No
Yes
Yes
Subseq() i = i +len
Yes
If len > 20 && Score > 95%
No
i = i +1

Fig. 2

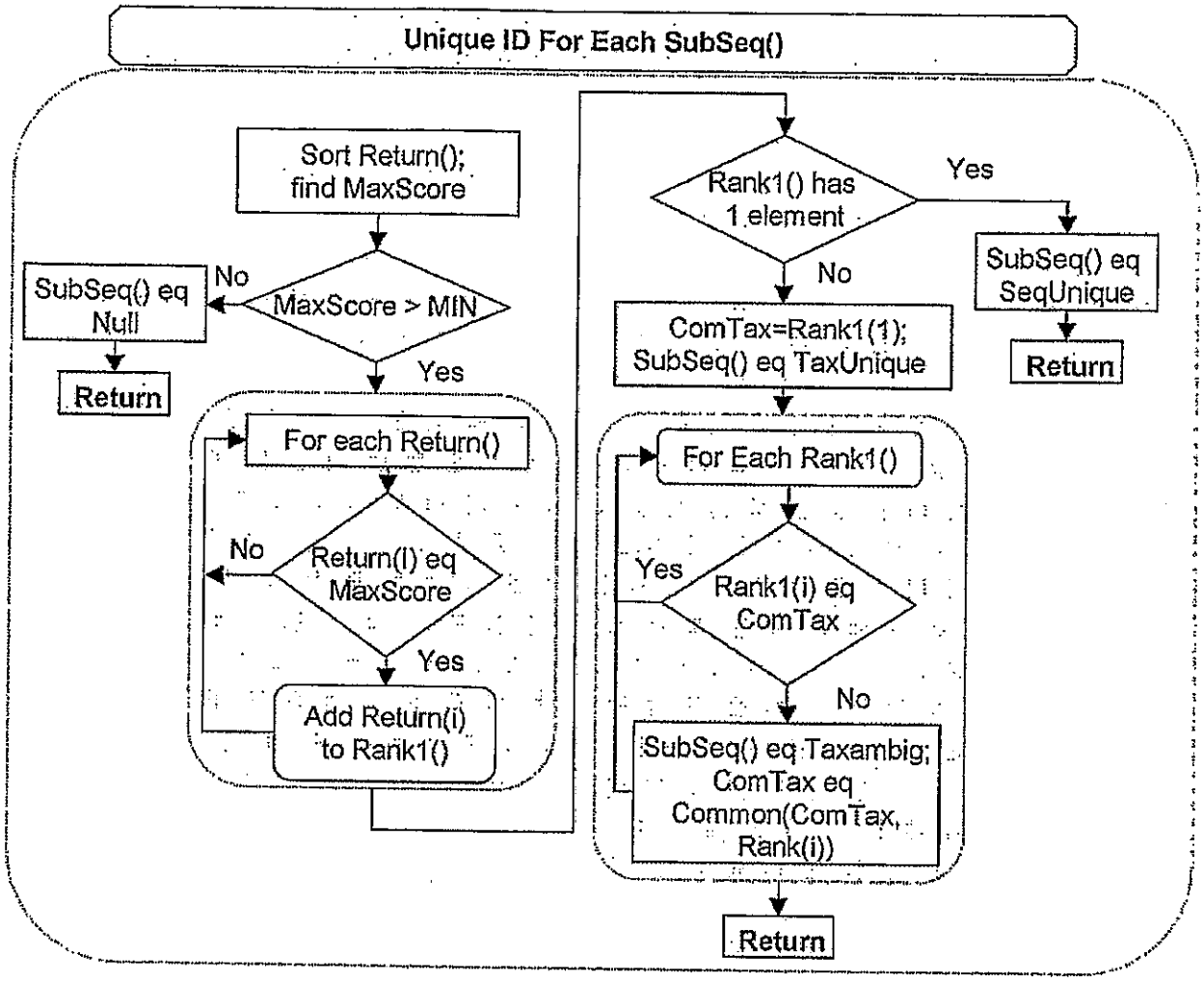

Unique ID For Each SubSeq()
Sort Return(); find MaxScore
SubSeq() eq Null
No
MaxScore > MIN
Yes
Return
For each Return()
No
Return(I) eq MaxScore
Yes
Add Return(i) to Rank1()
Rank1() has 1 element
Yes
SubSeq() eq SeqUnique
Return
No
ComTax=Rank1(1); SubSeq() eq TaxUnique
For Each Rank1()
Yes
Rank1(i) eq ComTax
No
SubSeq() eq Taxambig; ComTax eq Common(ComTax, Rank(i))
Return

Fig. 3

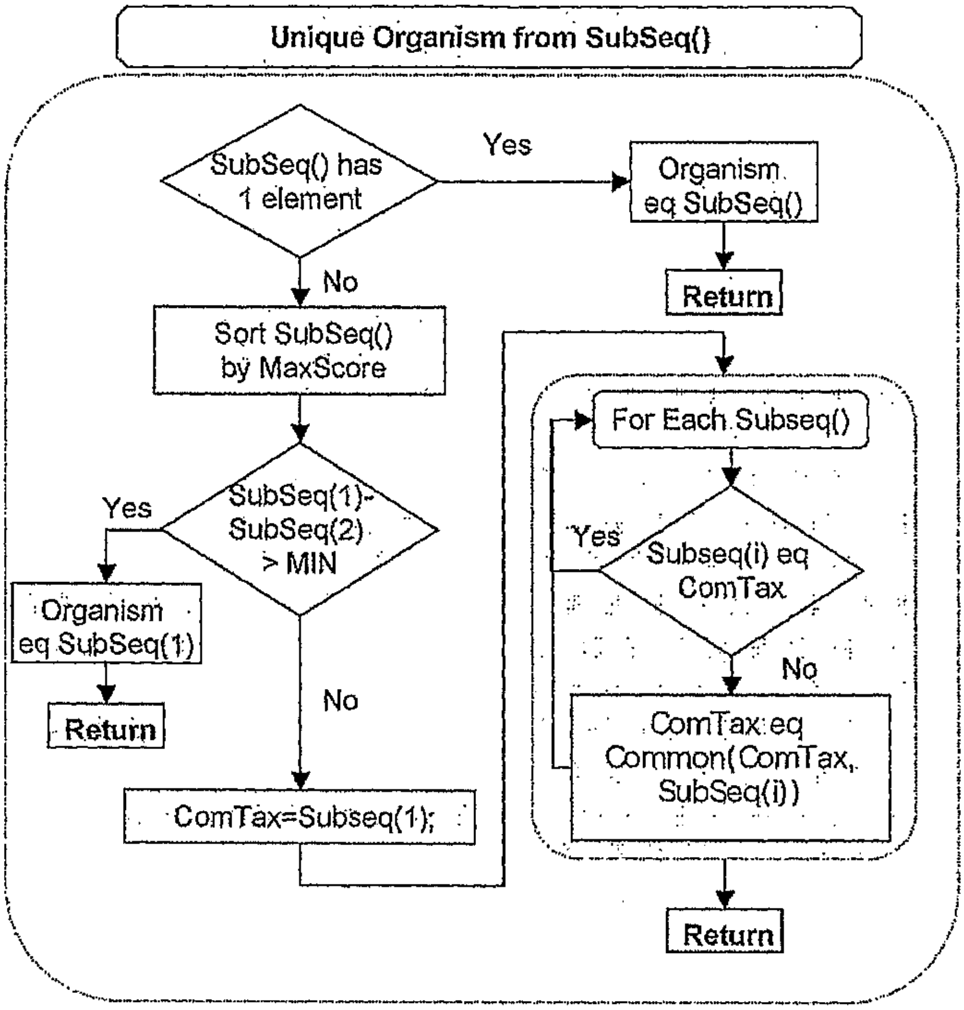


Fig. 4

```
                  *****                                                     ***
     FluANA1_Tile CTGGGTAAATCAAACATATGTCAATATTAACAACACTAACGTTGTTGCTGGAAAGGACACA 184
      A/Weiss/43 CTGGGTAAATCAAACATATGTTAATATTAGCAACACTAACGTTGTTGCTGGAAAAGGCACA 179
A/PuertoRico/8/34 CTGGGTAAA---------------------------------------------GGACACA 199
      Sample_Raw CTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGNCGTTGTTGCTGGAAAGGNCACA 184
 Sample_filtered CTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACA 184
```

Fig. 5