*** This is where I think the problem is ****

indivdual 74,91,55,93

We have a sample that has 4 contributors we use sim.mix to make the repliste in step 8 and the list of alleles for prosecutor and the defense. Later we use noncom.sus alleles to calculate LRs. That doesn't seem right.

Sample: Sim.Mix



Alleles: for sim.mix @ K



Alleles for noncom.sus @ k



For non contributors:

FUNCTION is CALLED:

- 1) A file is input by the user
- 2) Genotypes are simulated using simugeno with respect to the tabfreq object == sim.genotypes

3) The non contributor suspect data is generated using simumix object and sim.genotypes == noncom.sus

4) A Matrix that holds allele frequencies according to the input file is generated == pop.afs.matrix

Beginning of loop: else if (non.or.truecontrib == 1)

5) Sim.mix is created. When the function was called the number of contributors was set to four, so four of the 100 generated individuals are randomly selected and saved to sim.mix.

```
CSF1PO D3S1358 D5S818 D7S820 D8S1179 D13S317 D16S539 D18S51 D21S11
                                                                                FGA
                                                                                           TH01
                                                                                                          VWA
nd74 "13/13" "15/15" "13/11" "11/10" "13/14" "12/11" "12/12" "17/15" "28/27'
                                                                                 "24/20"
                                                                                           "7/9"
                                                                                                   "9/9"
                                                                                                          "19/18"
nd91 "10/13" "17/18" "11/12" "8/9"
                                     "15/13" "12/11" "12/11" "23/18" "28/31.2"
                                                                                                  "11/9"
                                                                                 "21/22"
                                                                                           "9.3/9"
                                                                                                          "17/17'
     "10/12" "14/16" "8/13" "11/8"
                                     "14/13" "11/8"
                                                     "9/12"
                                                             "13/19" "27/30'
                                                                                 "26/24"
```

6) We initiate an empty vector to hold LRs for each loci at a given simulation == singleLR vector <- c()

Beginning of while loop: while (k < 14)

7) We save the alleles at a given K to the empty vector prosecutor.all.atk.

```
> prosecutor.all.atk
[1] 11 10 8 9 11 8 10 8
> defense.all.atk
  [1] 8 11 13 9 11 8 11 10 8 9 11 8
>
```

8) A single LR is calculated at the current loci (4) using the

single_LR <- LR(Repliste = c(sim.mix\$mix.all[[k]])</pre>

```
"8" "9" "10" "11"
 Tp = c(prosecutor.all.atk,
     as.numeric(strsplit(noncon.sus$mix.prof[1,k], "/")[[1]])),
12 11
 Td = c(defense.all.atk),
8 11 13 9 11 8 11 10 8 9 11 8
 Vp = 0,
 Vd = c(as.numeric(strsplit(noncon.sus$mix.prof[1,k], "/")[[1]])),
12 11
 xd = 1,
 xp = 0,
 theta = 0,
 prDHet = c(0.2, 0.2),
 prDHom = c(0.04, 0.04),
 prC = 0,
 freq = pop.afs.matrix[[k,1]]
```