CaseSolver

A program based on EuroForMix for analysing case data.

Version 1.0.0 (compiled June 2018)

by Øyvind Bleka, Oslo University Hospital
About

• A R-program with many functionalities

• Most important is profile comparisons:
  - References to evidence profiles.
  - Single source profiles to other evidence profiles.
  - Can utilize peak heights.

• Mixture comparison follows strategy given in

Forensic Science International: Genetics Supplement Series
Volume 6, December 2017, Pages e404-e406

_dnamatch2_: An open source software to carry out large scale database searches of mixtures using qualitative and quantitative models

Ø. Bleka, M. Bouzga, A. Fonneløp, P. Gill
• Suitable for cases with large amount of profiles.

• Detailed mixture analyzes using EuroForMix.
  – Advanced deconvolution module
  – Show ”Model fitted Peak heights”

• Customize friendly:
  – Design your own data import function!
  – Many kits supported.
  – Design your own strategy/report.
Installation
Requirements/Startup

- Software R installed (newer than version 3.0.1)
  [https://cran.r-project.org/](https://cran.r-project.org/)

- R-packages installed:
  - The R-package casesolver
  - The R-package euroformix (>=1.10.0)
  - Other R-packages:
    ```r
    install.packages(c("gWidgets2tcltk","R2HTML","igraph"))
    - Done only first time.
    ```

- Startup:
  - Open R and type (copy-paste command)
    ```r
    library(casesolver); gui()
    ```
Installing casesolver

Copy and run (press ENTER) these commands in the R-software (example with casesolver version 1.0.0):

```r
install.packages("devtools")
library(devtools)
install_github("oyvble/casesolver/casesolver_1.0.0")
```

You can also install euroformix in same manner (version 1.11.4):
```r
install_github("oyvble/euroformix/euroformix_1.11.4")
```
Demonstration using CaseSolver with example

A ESX17 toy example
Setting up CaseSolver for analyzing tutorial data
1) Extract folder **TutorialDataCaseSolver** from zip-file to the desktop.

2) Open R and copy-paste this command:
   ```r
   library(casesolver);gui()
   ```

3) Select CaseDirectory
4) Select ImportData function
4) Select frequency file
5) Select Kit (can be changed any time):
6) Select Model settings (use default)

7) Select Threshold settings (use default)
The user interface after importing data from a case

Click “import”
Every reference is compared to evidence profiles classified as “non-mixture”.

- Matching refs identified and labeled in MatchStatus.
  - Supports missing loci
- Otherwise assigned as an unknown
  - Added to Reference list
  - Consensus creation of unknowns
Double-clicking profiles gives EPG
Double-clicking ref-profiles to show
Multiple profiles

Hold CTRL to select multiple profile. Then press ENTER.
Functionalities

- **Compare**: Comparing all refs to mixtures.
  - Allele comparison + LR (LRmix) + LR (EuroForMix)

- **Create Report**: Creates a HTML based report (data+comparisons).

- **Add reference profile**: Add/remove reference profiles

- **Export profile(s)**: Export evidence/reference profiles to a text-file or directly to EuroForMix.

- **Calculate RMP**:
  - Random match probability calculated for all references.
  - RMNE calculated for all evidences.

- **Calculate IBS**: Gives number of shared alleles between pairwise compared reference profiles
Comparison
Compare performs 2 steps to retrieve candidate matches:

Step 1: Simple allele comparison

Step 2: LR based comparison

Step 2 can be done in 3 different variants:
- (a) LR based only on qualitative model (LRmix)
- (b) LR based only on quantitative model (EuroForMix)
- (c) Both: First (a) and then (b).

- (a) is very fast and (b) can be very slow.
- (a) is useful as a prefilter for (b).
Set threshold for candidate match

**Compare** relies on specified thresholds

**Model choice** of Step 2 can be selected here:

Variant (c) is default (Both)
Step 1

All reference profiles are allele-compared against all mixtures.
- Score = Proportion of alleles of ref which is included in a mixture (MAC)
- Score for all combination given in Match matrix (can be exported):

```
<table>
<thead>
<tr>
<th>ID</th>
<th>SampleName</th>
<th>S4</th>
<th>S6</th>
</tr>
</thead>
<tbody>
<tr>
<td>#1</td>
<td>ref1</td>
<td>1</td>
<td>0.62</td>
</tr>
<tr>
<td>#2</td>
<td>ref2</td>
<td>1</td>
<td>0.59</td>
</tr>
<tr>
<td>#3</td>
<td>ref3</td>
<td>0.65</td>
<td>1</td>
</tr>
<tr>
<td>#4</td>
<td>Unknown 1</td>
<td>0.53</td>
<td>0.55</td>
</tr>
</tbody>
</table>
```

All candidate matches (with Score>threshold) provided to step 2.
Step 2a

Calculating ML based LR for the candidate matches (Qual model)

- Addition: Estimates number of contributors in evidence.
- LR for all comparisons given in Match list (Qual LR) can be exported

All candidates with LR>threshold(qual) are candidate matches.

Provided to Step 2b if selected.
Step 2b/c

Calculating ML based LR for the candidate matches (Quan model)

- LR for all comparisons given in Match list (Quan LR) can be exported

All candidates with LR>threshold (quan) are candidate matches.

Note: Candidates can be double-clicked on to see "Model fitted Peak heights"
Evaluating candidates in match list

Double click on a row in Match list (Quan LR)
Mixtures

For all mixtures:
- Lists every mixture evidences.
- Candidate matches with LR>threshold given in “References“
- Estimated number of contributors also given.
- Can be exported.
- List can also be viewed before “comparison”.

![Image of CaseSolver v1.0.0 interface]

<table>
<thead>
<tr>
<th>Evidence</th>
<th>Reference(s)</th>
<th>Num Contr.</th>
</tr>
</thead>
<tbody>
<tr>
<td>#1 S4</td>
<td>ref2/ref1</td>
<td>2</td>
</tr>
<tr>
<td>#2 S6</td>
<td>ref3</td>
<td>2</td>
</tr>
</tbody>
</table>
A match network given:
- The width of the edge is proportional with LR

Traffic lights on profiles:
- **Green**: References
- **Orange**: 2-person mixtures
- **Red**: at least 3-person mixtures
Further evaluation*

**Double click** on row for further evaluation

*evaluation here is

1) Show “model fitted/expected peak heights”
2) Deconvolve unknown contributors

Specify your hypothesis:
- Number of contributors
- Conditional references

* CaseSolver v1.0.0

<table>
<thead>
<tr>
<th></th>
<th>Evidence</th>
<th>Reference(s)</th>
<th>Num Contr.</th>
</tr>
</thead>
<tbody>
<tr>
<td>#1</td>
<td>S4</td>
<td>ref2/ref1</td>
<td>2</td>
</tr>
<tr>
<td>#2</td>
<td>S6</td>
<td>ref3</td>
<td>2</td>
</tr>
</tbody>
</table>

Deconvolution/Show expected peak heights

- Evidence: S4
- Number of contributors: 2
- Condition on: ref2, ref1

[Calculating]
Model fitted peak heights

ESX17 - S4

Contr.1 = 0.69
Contr.2 = 0.31
Deconvolution results

Genotypes of unknown contributor(s) are automatically deduced* and presented as candidate(s) in "Deconvoluted" table.

CaseSolver v1.0.0

<table>
<thead>
<tr>
<th>Data</th>
<th>Match matrix</th>
<th>Match list (Qual LR)</th>
<th>Match list (Quan LR)</th>
<th>Mixtures</th>
<th>Deconvoluted</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

No candidates found.

*Deduction requires that \( \text{Pr}(1. \text{Top geno})/\text{Pr}(2. \text{Top geno}) > \text{threshold} \)

Also possible: Single deduced allele if \( \text{Pr}(\text{allele}) > 0.99 \)
Deducing the unknown in S6

Gives conditional references

Estimated mixture proportion for deduced component

2. allele unsure
Confirm deduced component

"Double-click" a candidate component

User can edit:
- SampleID name
- Alleles
Added deconvolved component

The deduced component is added to references.

CaseSolver supports that a reference only have one allele.

Run ”Calculate IBS” to check if the deduced ref. is similar to any others.
Save/Load project

Useful to **save** project once all comparisons/analysis are done

Restore a project by **open** project (at any time)
Report
Select what to include
Create Report
(click at any time during usage)
Directly opens the default browser
Report for Case CaseESX

CaseSolver version 1.0.0 (euroformix_1.11.4).
R version 3.5.0 (2018-04-23)
User: oyvbl
Created: 2018-06-28 14:14:08

## References

<table>
<thead>
<tr>
<th>SampleName</th>
<th>AMEL</th>
<th>D3S1358</th>
<th>TH01</th>
<th>D21S11</th>
<th>D18S51</th>
<th>D10S1248</th>
<th>D15S1656</th>
<th>D2S1338</th>
<th>D16S539</th>
<th>D22S1045</th>
<th>VWA</th>
<th>D8S1179</th>
<th>FGA</th>
<th>D2S441</th>
<th>D12S391</th>
<th>D19S433</th>
<th>SE33</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>ref1</td>
<td>X/X</td>
<td>16/17</td>
<td>6/8</td>
<td>30/31.2</td>
<td>12/14</td>
<td>13/16</td>
<td>16.3/17.3</td>
<td>17/18</td>
<td>11/13</td>
<td>16/16</td>
<td>17/17</td>
<td>12/14</td>
<td>11/12</td>
<td>20/22</td>
<td>13/15</td>
<td>19/34</td>
</tr>
<tr>
<td>2</td>
<td>ref2</td>
<td>X/X</td>
<td>15/16</td>
<td>6/9.3</td>
<td>28/31</td>
<td>12/15</td>
<td>13/15</td>
<td>17/17.3</td>
<td>18/23</td>
<td>9/12</td>
<td>16/16</td>
<td>15/16</td>
<td>14/14</td>
<td>19/25</td>
<td>11/14</td>
<td>15/21</td>
<td>13/13</td>
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<td>ref3</td>
<td>X/Y</td>
<td>16/18</td>
<td>6/8</td>
<td>28/28</td>
<td>14/16</td>
<td>15/16</td>
<td>10/17.3</td>
<td>16/18</td>
<td>11/12</td>
<td>15/16</td>
<td>17/17</td>
<td>12/14</td>
<td>24/25</td>
<td>10/10</td>
<td>18/24</td>
<td>13/13</td>
</tr>
<tr>
<td>4</td>
<td>Unknown 1</td>
<td>X/Y</td>
<td>16/18</td>
<td>6/7</td>
<td>30/31.2</td>
<td>14/14</td>
<td>13/16</td>
<td>12/15</td>
<td>20/23</td>
<td>9/11</td>
<td>15/17</td>
<td>14/17</td>
<td>13/14</td>
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<td>10/10</td>
<td>18/25</td>
<td>14/14</td>
</tr>
<tr>
<td>5</td>
<td>S6-C2</td>
<td></td>
<td>14/15</td>
<td>9.3</td>
<td>30/31.2</td>
<td>17/20</td>
<td>14/16</td>
<td>13/16.3</td>
<td>18/26</td>
<td>10</td>
<td>16</td>
<td>17/16</td>
<td>10/11</td>
<td>22/23</td>
<td>11/11</td>
<td>23</td>
<td>13/15</td>
</tr>
</tbody>
</table>

## Single source profiles

<table>
<thead>
<tr>
<th>SampleName</th>
<th>MatchStatus</th>
<th>AMEL</th>
<th>D3S1358</th>
<th>TH01</th>
<th>D21S11</th>
<th>D18S51</th>
<th>D10S1248</th>
<th>D15S1656</th>
<th>D2S1338</th>
<th>D16S539</th>
<th>D22S1045</th>
<th>VWA</th>
<th>D8S1179</th>
<th>FGA</th>
<th>D2S441</th>
<th>D12S391</th>
<th>D19S433</th>
<th>SE33</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>S3</td>
<td>Unknown 1</td>
<td>X/Y</td>
<td>16/18</td>
<td>6/7</td>
<td>30/31.2</td>
<td>14</td>
<td>13/16</td>
<td>12/15</td>
<td>20/23</td>
<td>11/9</td>
<td>15/17</td>
<td>14/17</td>
<td>13/14</td>
<td>23</td>
<td>10</td>
<td>18/25</td>
<td>14</td>
</tr>
<tr>
<td>2</td>
<td>S5</td>
<td>ref3</td>
<td>X/Y</td>
<td>16/18</td>
<td>6/8</td>
<td>28</td>
<td>14/16</td>
<td>15/16</td>
<td>10/17.3</td>
<td>16/18</td>
<td>11/12</td>
<td>15/16</td>
<td>17</td>
<td>12/14</td>
<td>24/25</td>
<td>10</td>
<td>18/24</td>
<td>13</td>
</tr>
<tr>
<td>3</td>
<td>S1</td>
<td>ref2</td>
<td>X</td>
<td>15/18</td>
<td>6/9.3</td>
<td>28/31</td>
<td>12/15</td>
<td>13/15</td>
<td>17/17.3</td>
<td>18/23</td>
<td>12/9</td>
<td>16</td>
<td>15/18</td>
<td>14</td>
<td>19/25</td>
<td>11/14</td>
<td>15/21</td>
<td>13</td>
</tr>
<tr>
<td>4</td>
<td>S2</td>
<td>ref1</td>
<td>X</td>
<td>16/17</td>
<td>6/8</td>
<td>30.2/31.2</td>
<td>12/14</td>
<td>13/16</td>
<td>16.3/17.3</td>
<td>17/18</td>
<td>11/13</td>
<td>16</td>
<td>17</td>
<td>12/14</td>
<td>21/23</td>
<td>11/12</td>
<td>20/22</td>
<td>13/16</td>
</tr>
</tbody>
</table>

## Mixtures w/peak heights

**S4**

<table>
<thead>
<tr>
<th>AMEL</th>
<th>D3S1358</th>
<th>TH01</th>
<th>D21S11</th>
<th>D18S51</th>
<th>D10S1248</th>
<th>D15S1656</th>
<th>D2S1338</th>
<th>D16S539</th>
<th>D22S1045</th>
<th>VWA</th>
<th>D8S1179</th>
<th>FGA</th>
<th>D2S441</th>
<th>D12S391</th>
<th>D19S433</th>
<th>SE33</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>X (8892)</td>
<td>15</td>
<td>(4514)</td>
<td>6 (2775)</td>
<td>28 (3139)</td>
<td>12 (3248)</td>
<td>13 (5577)</td>
<td>16.3 (2434)</td>
<td>17 (1832)</td>
<td>9 (2122)</td>
<td>16 (14730)</td>
<td>15 (3363)</td>
<td>12 (495)</td>
<td>19 (3563)</td>
<td>11 (2711)</td>
<td>15 (3246)</td>
</tr>
<tr>
<td>2</td>
<td>16 (1953)</td>
<td>8</td>
<td>(1203)</td>
<td>30.2 (1119)</td>
<td>14 (453)</td>
<td>15 (5468)</td>
<td>17 (3545)</td>
<td>18 (3532)</td>
<td>11 (1011)</td>
<td>17 (2470)</td>
<td>14 (6654)</td>
<td>21 (3087)</td>
<td>12 (1806)</td>
<td>20 (782)</td>
<td>16 (299)</td>
<td>29.2 (742)</td>
</tr>
<tr>
<td>3</td>
<td>17 (3027)</td>
<td>9.3</td>
<td>(5086)</td>
<td>31 (2846)</td>
<td>15 (1931)</td>
<td>16 (2767)</td>
<td>17.3 (3940)</td>
<td>23 (3777)</td>
<td>12 (3154)</td>
<td>18 (2372)</td>
<td>23 (560)</td>
<td>14 (3300)</td>
<td>21 (2216)</td>
<td>31.2 (1014)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>18 (3992)</td>
<td>31.2</td>
<td>(1065)</td>
<td></td>
<td>13 (477)</td>
<td></td>
<td>25 (2743)</td>
<td></td>
<td></td>
<td>22 (1286)</td>
<td></td>
<td>34 (569)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
**Comparisons**

**Comparison matrix**

<table>
<thead>
<tr>
<th>SampleName</th>
<th>S4</th>
<th>S6</th>
</tr>
</thead>
<tbody>
<tr>
<td>ref1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>ref2</td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>ref3</td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>Unknown</td>
<td></td>
<td>1</td>
</tr>
</tbody>
</table>

**Match list (Qual LR)**

<table>
<thead>
<tr>
<th>Evidence</th>
<th>Reference</th>
<th>MAC</th>
<th>log10LR</th>
<th>numContr</th>
</tr>
</thead>
<tbody>
<tr>
<td>S4</td>
<td>ref1</td>
<td>1</td>
<td>14.58</td>
<td>2</td>
</tr>
<tr>
<td>S6</td>
<td>ref3</td>
<td>1</td>
<td>13.65</td>
<td>2</td>
</tr>
<tr>
<td>S4</td>
<td>ref2</td>
<td>1</td>
<td>13.43</td>
<td>2</td>
</tr>
</tbody>
</table>

**Match list (Quan LR)**

<table>
<thead>
<tr>
<th>Evidence</th>
<th>Reference</th>
<th>MAC</th>
<th>log10LR</th>
<th>numContr</th>
</tr>
</thead>
<tbody>
<tr>
<td>S4</td>
<td>ref2</td>
<td>1</td>
<td>20.16</td>
<td>2</td>
</tr>
<tr>
<td>S6</td>
<td>ref3</td>
<td>1</td>
<td>19.01</td>
<td>2</td>
</tr>
<tr>
<td>S4</td>
<td>ref1</td>
<td>1</td>
<td>18.73</td>
<td>2</td>
</tr>
</tbody>
</table>

**Final match list (w/all mixtures)**

<table>
<thead>
<tr>
<th>Evidence</th>
<th>Reference(s)</th>
<th>Num Contr.</th>
</tr>
</thead>
<tbody>
<tr>
<td>S4</td>
<td>ref2/ref1</td>
<td>2</td>
</tr>
<tr>
<td>S6</td>
<td>ref3</td>
<td>2</td>
</tr>
</tbody>
</table>
Settings:

Thresholds:

MAC threshold=0.9
Qual. LR threshold=10
Quan. LR threshold=1000
Minimum loci=7
Deconv. ratio=10
Deconv. alleleProb=0.99

Model:

Frequency file=C:/Users/oyvbl/Desktop/tutorialdata/ESX17_Norway.csv

Qualitative (LRmix):

Drop-in prob=0.05

Quantitative (EuroForMix):

Detection threshold=50
Kit=ESX17
Degradation model=ON
Stutter model=OFF
Drop-in prob=0.05
Other functionalities
Note: Inserting minimum allele freq of 0.001 if not seen.

<table>
<thead>
<tr>
<th>ID</th>
<th>SampleName</th>
<th>RMNE</th>
</tr>
</thead>
<tbody>
<tr>
<td>#1</td>
<td>S1</td>
<td>2.71e-23</td>
</tr>
<tr>
<td>#2</td>
<td>S3</td>
<td>8.35e-27</td>
</tr>
<tr>
<td>#3</td>
<td>S4</td>
<td>2.96e-23</td>
</tr>
<tr>
<td>#4</td>
<td>S5</td>
<td>8.72e-16</td>
</tr>
<tr>
<td>#5</td>
<td>S2</td>
<td>1.23e-15</td>
</tr>
<tr>
<td>#6</td>
<td>S6</td>
<td>1.87e-15</td>
</tr>
</tbody>
</table>

Note: Inserting minimum allele freq of 0.001 if not seen.
Details about

“setting up CaseSolver for the first time”
Setting up CaseSolver for the first time*

The user must specify the following:

1) **ImportData function**: A R-script converting profiles in datafiles to “casesolver format”.

2) **Case directory**: A directory with case-folders (which includes datafiles).

3) **Population frequencies**
   - Necessary for LR calculations

4) **Kit selection**
   - Necessary for EPGs/LR calcs.

5) **Model settings**

6) **Threshold settings**

*Settings are stored permanently
2) Case directory:

A specified directory where a folder for each case are given (by its casename).

- CaseSolver applies the R-function `importData` to every existing file in the selected CaseFolder.
- CaseSolver accepts that some files are non-data.

Selected directory includes casefolders:

```
Name      Date modified    Type         Size
-------    -----------    -------      ------
CaseESX    12/20/2017 5:41 PM File folder  
CaseFusion 3/4/2018 2:00 PM    File folder  
```

Casefolder includes data files:

```
Name       Date modified    Type         Size
-------    -----------    -------      ------
evids.csv  3/4/2018 1:59 PM CSV File     7 KB
other.txt  3/5/2018 10:39 AM Text Document 0 KB
refs.csv   3/4/2018 1:59 PM CSV File     2 KB
```
1) ImportData function

- Select a file which includes a R-function named "importData".

- `importData` MUST take one filename as parameter, read the file, and convert the data to the following output format:

  The output MUST be a list with the elements "markers", "mix" and "ref":

Example of output from a file with only evidence profiles:

```
$mix
SampleName Markers   Alleles   Heights
"S1"     "AMEL"   "X"       "2043"
"S1"     "D3S1358" "14/17" "729/1053"
"S1"     "D1S1656" "12/17.3" "613/1013"
"S1"     "D2S441" "10/16" "677/525"
"S1"     "D10S1248" "13/16" "238/559"
"S1"     "D13S317" "11/12" "624/777"
"S1"     "Penta E" "10/15" "712/645"
```

"mix" must be a matrix with markers given per row. Allele info must be collapsed with "/"

The column order is important, but the column names are not.

```
$ref
numeric(0)
```

```
$markers
"AMEL"  "D3S1358" "D1S1656" "D2S441" "D10S1248" "D13S317" "Penta E"
```

The vector in "markers" will decide what markers (and the order) are presented in the GUI
1) `ImportData` function (continue)

Example of output from a file with only reference profiles:

```bash
$mix
numeric(0)

$ref
SampleName Markers   Alleles
"ref1"    "AMEL"     "X/X"
"ref1"    "D3S1358"  "16/17"
"ref1"    "D1S1656"  "17/18.3"
"ref1"    "D2S441"   "10/15"
"ref1"    "D10S1248" "13/14"
"ref1"    "D13S317"  "9/12"
"ref1"    "Penta E"  "12/16"
"ref3"    "AMEL"     "X/X"
"ref3"    "D3S1358"  "16/18"
"ref3"    "D1S1656"  "15.3/17"
"ref3"    "D2S441"   "14/14"
"ref3"    "D10S1248" "13/14"
"ref3"    "D13S317"  "12/14"
"ref3"    "Penta E"  ""

$markers
"AMEL"    "D3S1358"  "D1S1656" "D2S441" "D10S1248" "D13S317" "Penta E"
```

Important notes for reference profiles:
- 1) "Empty markers” must be given as ”".
- 2) Homozygous variants must given as ”10/10”
- 3) Single alleles like ”12” is possible (like for Y-STRs variants for instance)

The 2 and 3 variants are sometimes treated differently in the program:
  - See slide ”Handling single allele”
1) ImportData function (optional)

An additional list element "meta" with metadata can be given in the output:

```
$meta
$meta$`Sample type`
  Sample Type
  [1,] "S1"  "Blood"
  [2,] "S2"  "Saliva"

$meta$`Negative samples`
  Sample Status
  [1,] "S7"  "Negative"
  [2,] "S8"  "Negative"
```

"meta" must contain list elements (with names given as strings) which again contains matrix elements.

The information will be presented in the generated report:

**Metadata**

<table>
<thead>
<tr>
<th>Sample</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>S1</td>
<td>Blood</td>
</tr>
<tr>
<td>S2</td>
<td>Saliva</td>
</tr>
</tbody>
</table>

**Negative samples**

<table>
<thead>
<tr>
<th>Sample</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>S7</td>
<td>Negative</td>
</tr>
<tr>
<td>S8</td>
<td>Negative</td>
</tr>
</tbody>
</table>
3) Kit selection
- Necessary for
  - Showing EPGs
  - Calculating LR in comparison.

The kit-info is necessary in order for CaseSolver to get the basepair information.
- Used for showing EPGs
- Used for applying the degradation model (always on).
4) Population frequencies
- Necessary for LR, RMNE and RMP calculations
- User must select a file including allele frequencies
  - LRmix/EuroForMix format

User can choose to include AMEL:
(Marker name must be AMEL)
Included: X = 0.75, Y = 0.25

This enables that the peak heights in AMEL is utilized in the analysis.
5) Model settings

These values are settings used in the LR calculations

- **Detection threshold (EFM only):**
  - The peak height threshold used in the analysis.

- **Dropin probability:**
  - The allele dropin probability (using by both models)

- **Dropin peak height Lambda (EFM only):**
  - The parameter used to model the dropin peak heights
6) Thresholds settings

In Import:
- **Minimum loci for being SS match:**
  - In situation of missing markers (in SingleSource-evid/ref comparison). This threshold is the required minimum compared non-missing loci.

In Comparison:
- **MAC threshold**
  - The required number of proportion of alleles of a reference to be included in a compared mixture profile. All candidates above this threshold are further analysed with LR calculation.
- **LR threshold (for Qual or Quan model)**
  - The required LR value for that a reference is assigned as a ”match” to the compared mixture profile.

In Calculate IBS:
- **Minimum IBS for being relative candidate**
  - The required number of sharing alleles between two references to be assigned as a candidate.

In Deconvolution:
- **Prob-ratio to next**
  - The threshold gives how ”sure” a top ranked genotype must be in order to be a deduced genotype.
  - $\text{Pr(1st ranked geno)}/\text{Pr(2nd ranked geno)} > \text{threshold}$
- **Prob. Single allele**
  - The threshold gives how ”sure” a top ranked allele must be in order to be a deduced allele. This is in case when deducing a genotype fails.
• Haned 2011: *Forensim: an open-source initiative for the evaluation of statistical methods in forensic genetics*

• Bleka et al. 2016: *EuroForMix: An open source software based on a continuous model to evaluate STR DNA profiles from a mixture of contributors with artefacts*

• Bleka et al. 2017: *dnamatch2: An open source software to carry out large scale database searches of mixtures using qualitative and quantitative models*