

# 'Internal development' validation of EuroForMix (version 3.1.0)

Numerical tests automatically checked using *testthat* (R-package)  
Manual checks for GUI results

Carried out regarding euroformix R-package release

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# Critical to test numerical calculations done by C++

- 4 C++ functions to test

1. likelihood function for 1 replicate, no conditional references or relatedness,

- a. No stutter model `double calcLogLikGammaMarkerUnknown`

- b. Forward/backward models `double calcLogLikGammaMarkerUnknownStutter`

2. Otherwise another likelihood function is run (slower)

```
double calcLogLikGammaMarker
```

3. cumulative likelihood function (all model variants)

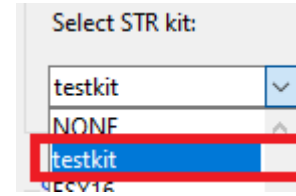
```
void calccumval
```

# “Full model” is tested

- Degradation model
- Backward stutter model
- Forward stutter model
- Dye specific settings for
  - Analytical thresholds (AT)
  - Drop-in probabilities (pC)
  - Drop-in distribution ( $\lambda$ )
  - Theta-correction (Fst)
- Non-mixtures vs mixtures (1 contributor vs more)
- Unknowns vs conditioning
- Unrelated vs relatedness for unknown (brother only)
- Stutters vs no stutters

# Example data

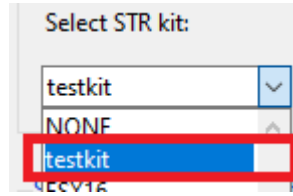
- Constructing the testkit (subset of SGMplus)
  - Two dyes only (blue and yellow)
  - TH01 renamed to 'TH 01' (white space in names)



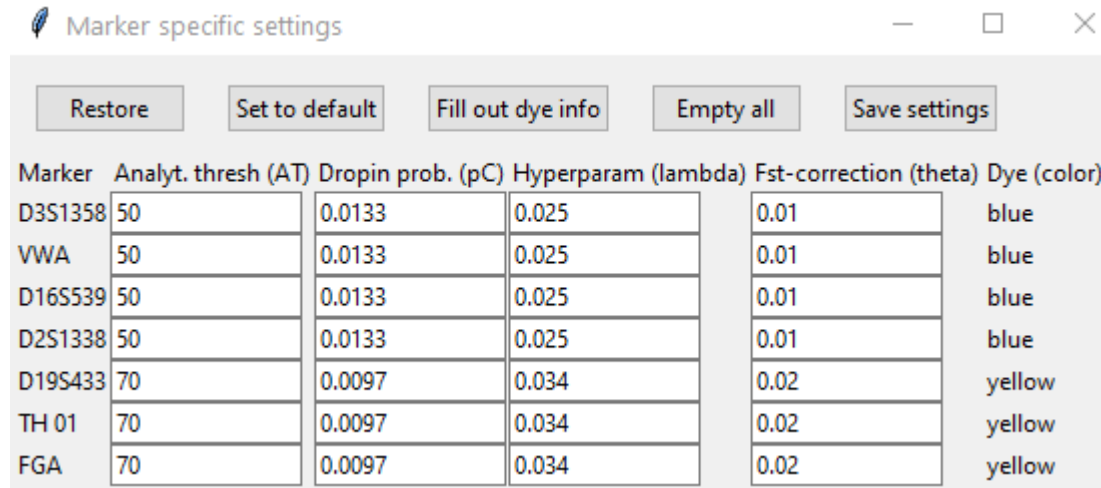
- Frequencies based on 'SGMplus\_Norway'
- 2 example data sets which includes backward and forward stutters
  1. 1 contributor, 1 replicate
  2. 2 contributors, 2 replicates
- 1 example data set including SNPs.
  - 2 contributors, 2 replicates
- Data available in R-package installation folder **euroformix**\*examples*

# Settings

- Selected kit: testkit  
(Not for SNPs)



- Dye specific settings:  
(Not for SNPs)

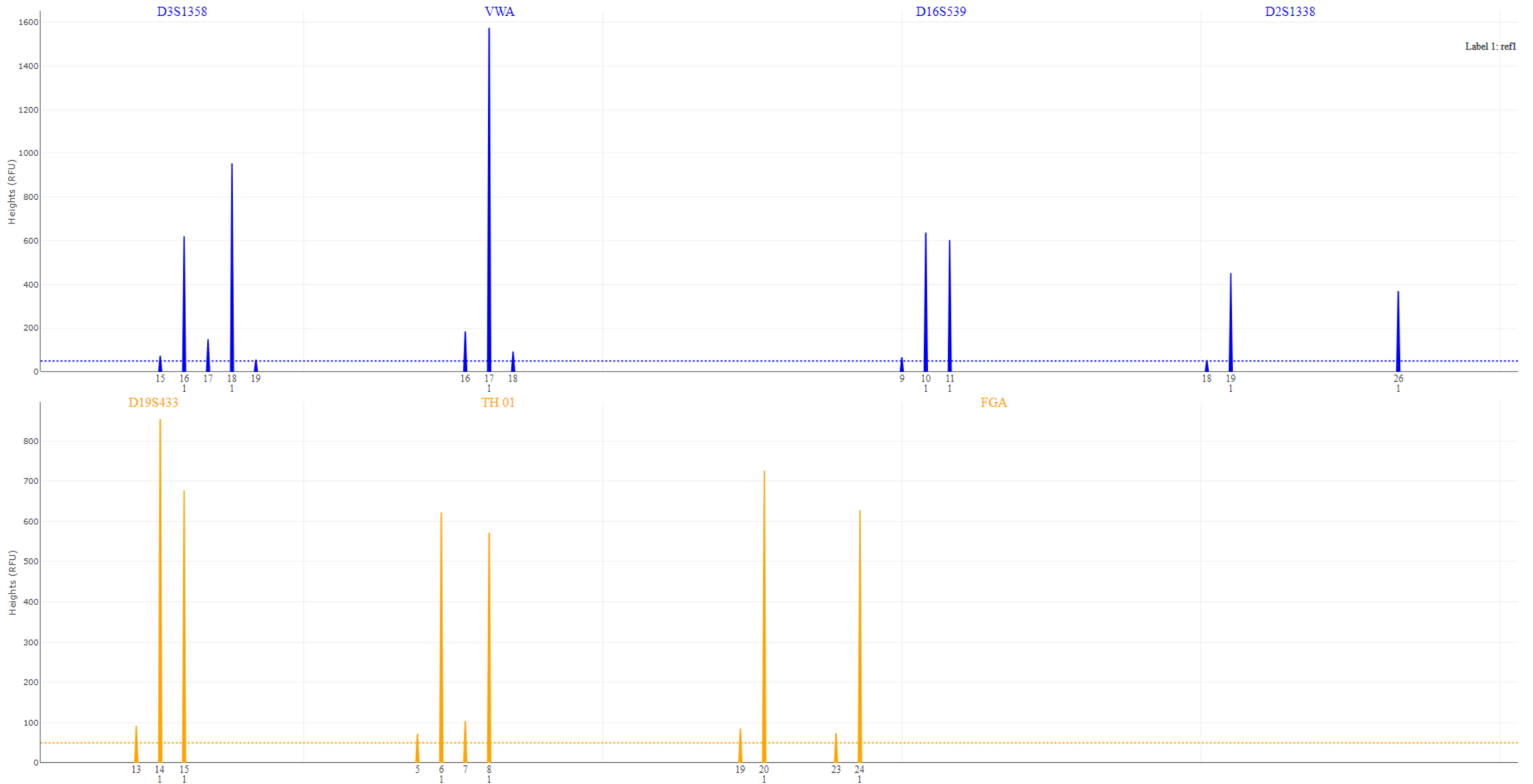
A screenshot of a "Marker specific settings" window. At the top, there are five buttons: "Restore", "Set to default", "Fill out dye info", "Empty all", and "Save settings". Below the buttons is a table with the following columns: "Marker", "Analyt. thresh (AT)", "Dropin prob. (pC)", "Hyperparam (lambda)", "Fst-correction (theta)", and "Dye (color)".

Marker	Analyt. thresh (AT)	Dropin prob. (pC)	Hyperparam (lambda)	Fst-correction (theta)	Dye (color)
D3S1358	50	0.0133	0.025	0.01	blue
VWA	50	0.0133	0.025	0.01	blue
D16S539	50	0.0133	0.025	0.01	blue
D2S1338	50	0.0133	0.025	0.01	blue
D19S433	70	0.0097	0.034	0.02	yellow
TH 01	70	0.0097	0.034	0.02	yellow
FGA	70	0.0097	0.034	0.02	yellow

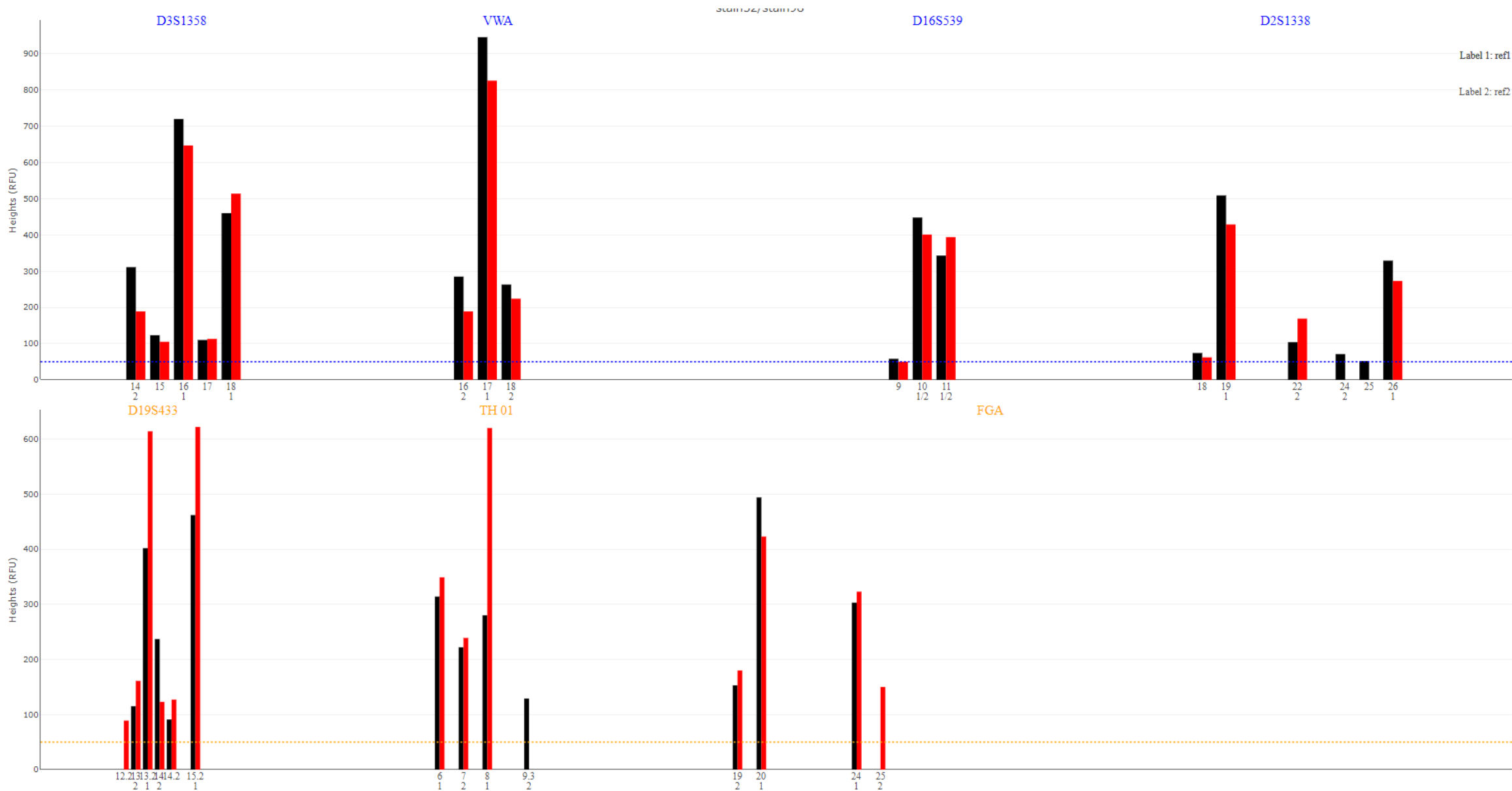
- Optimization settings:

```
-----Optimalisation setting-----  
Required number of (identical) optimizations: 2  
Accuracy of optimisations (steptol): 0.001  
Seed for optimisations: 1
```

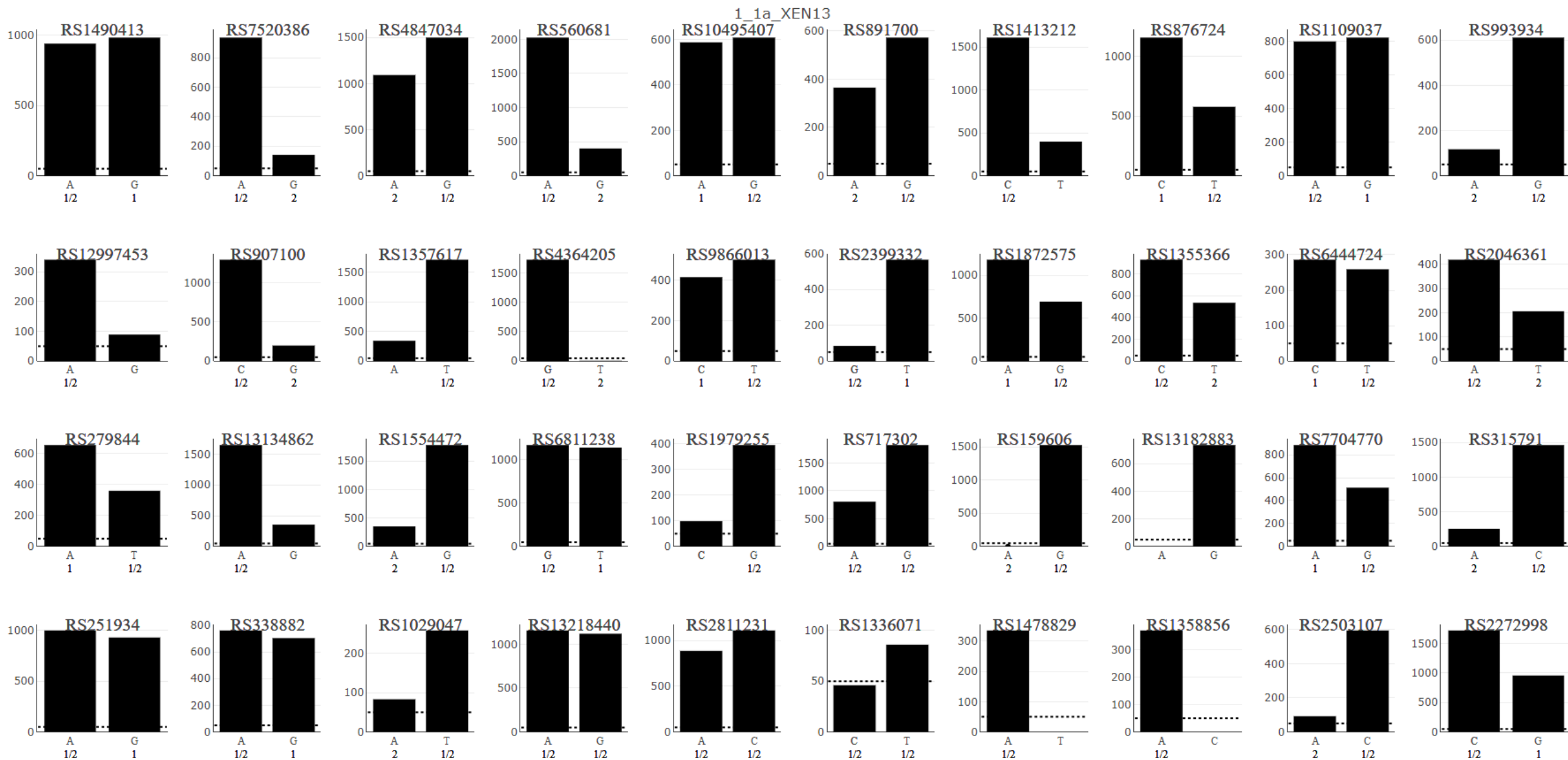
# Example data 1: stain34



# Example data 2: stain52/stain98



# Example data 3: 1\_1a\_XEN13/ 1\_1b\_XEN13 (SNPs)





# Checking R-functions depending on C++

- contLikMLE: Obtain maximum likelihood value/parameter estimates
- logLiki: Calculate per-marker likelihood
- validMLEmodel: Calculates cumulative probabilities (of PHs)
- deconvolve: Calculates posterior probabilities of unknown genotypes
- contLikINT: Bayesian approach (integration)
- contLikMCMC: MCMC simulation
- Functions which are indirectly checked:
  - tableReader: Imports tables from files
  - freqImport: Imports allele frequencies
  - sample\_tableToList: Converts table data to list format
  - prepareData: Restructures the data prepared as input
  - calcRMPfst: Used to obtain “Upper boundary” of LR
  - Qassignate: Performs allele frequency imputation and Q-designation
  - prepareC: Used to prepare data for running C++ code.

# Propositions tested for dataset 1: *test\_logLik1contr*

- Hyp 1: ref1 is contributor
- Hyp 2: 1 (unrelated) unknown is contributor, ref1 is known non-contributor
- Hyp 3: 1 unknown sibling of ref1 is contributor, ref1 is known non-contributor

# GUI check Hp: Hyp 1 vs Hd: Hyp 2

**Model specification**

Contributor(s) under Hp:

ref1

#unknowns (Hp): 0

Contributor(s) under Hd:

ref1

#unknowns (Hd): 1

1st unknown is

Unrelated

to

**Data selection**

Loci: stain34 ref1

VWA

D16S539

D2S1338

D19S433

TH 01

FGA

D3S1358

**Model options**

Degradation:  YES  NO

BW Stutter:  YES  NO

FW Stutter:  YES  NO

**Estimates under Hd**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	1.00000	0.00000
P.H.expectation	921.88777	39.71914
P.H.variability	0.09886	0.01377
Degrad. slope	0.77117	0.03573
BWstutt-prop.	0.10357	0.01005
FWstutt-prop.	0.05100	0.01014

Maximum Likelihood value

logLik= -155.3

adj.loglik= -160.3

Lik= 3.4e-68

**Estimates under Hp**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	1.00000	0.00000
P.H.expectation	921.88130	39.71892
P.H.variability	0.09886	0.01377
Degrad. slope	0.77117	0.03573
BWstutt-prop.	0.10357	0.01005
FWstutt-prop.	0.05100	0.01014

Maximum Likelihood value

logLik= -134.1

adj.loglik= -139.1

Lik= 5.8e-59

**Joint LR**

LR= 1.69e+09

log10LR= 9.228

Upper boundary= 9.228

**Non-contributor analysis**

Select reference to replace with non-contributor:

ref1

Sample maximum based

Sample integrated based

**LR for each locus**

VWA	9.465
D16S539	26.03
D2S1338	141.3
D19S433	7.256
TH 01	22.84
FGA	20.49
D3S1358	14.3

## Under Hp:

Theta=921.88130259,0.09885783,0.77117149,0.10356833,0.05099810

logLik=-134.0967859

## Under Hd:

Theta=921.88777210,0.09885714,0.77116993, 0.10356872,0.05099952

logLik=-155.344653303007

Upper boundary: 9.22783157308603

# GUI check Hp: Hyp 1 vs Hd: Hyp 3

**Model specification**

Contributor(s) under Hp:  
 ref1  
 #unknowns (Hp): 0

Contributor(s) under Hd:  
 ref1  
 #unknowns (Hd): 1

1st unknown is  
 Sibling

to  
 ref1

**Data selection**

Loci: stain34 ref1

VWA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D16S539	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D2S1338	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D19S433	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
TH 01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
FGA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D3S1358	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

**Model options**

Degradation:  YES  NO  
 BW Stutter:  YES  NO  
 FW Stutter:  YES  NO

Estimates under Hd			Estimates under Hp			Joint LR		LR for each locus	
Parameter estimates:			Parameter estimates:			LR=	log10LR=	Upper boundary= 9.228	
param	MLE	Std.Err.	param	MLE	Std.Err.	Select reference to replace with non-contributor: ref1			
Mix-prop. C1	1.00000	0.00000	Mix-prop. C1	1.00000	0.00000	Sample maximum based			
P.H.expectation	921.81772	39.70668	P.H.expectation	921.88130	39.71892	Sample integrated based			
P.H.variability	0.09884	0.01377	P.H.variability	0.09886	0.01377	VWA	2.29		
Degrad. slope	0.77121	0.03573	Degrad. slope	0.77117	0.03573	D16S539	2.843		
BWstutt-prop.	0.10356	0.01005	BWstutt-prop.	0.10357	0.01005	D2S1338	3.486		
FWstutt-prop.	0.05101	0.01014	FWstutt-prop.	0.05100	0.01014	D19S433	2.361		
Maximum Likelihood value			Maximum Likelihood value			TH 01 2.926			
logLik=	-141.2		logLik=	-134.1		FGA	2.93		
adj.loglik=	-146.2		adj.loglik=	-139.1		D3S1358	2.751		
Lik=	4.6e-62		Lik=	5.8e-59					

Under Hp:

Theta=921.88130259,0.09885783,0.77117149,0.10356833,0.05099810  
 logLik=-134.0967859

**Under Hd:**

Theta=921.81771878,0.09883688,0.77120574,0.10356310,0.05100558  
 logLik=-141.239022451048

# Propositions tested for dataset 2: *test\_logLik2contr2Rep*

- Hyp 1: ref1 + ref2 are contributors
- Hyp2: ref 1 + 1 (unrelated) unknown are contributors, ref2 is known non-contributor
- Hyp3: ref 1 + 1 related (sibling) unknown of ref2 are contributors, ref2 is known non-contributor

# GUI check Hp: Hyp 1 vs Hd: Hyp 2

**Model specification**

**Contributor(s) under Hp:**

- ref1
- ref2
- #unknowns (Hp): 0

**Contributor(s) under Hd:**

- ref1
- ref2
- #unknowns (Hd): 1

**Data selection**

Loci:	stain52	stain98	ref1	ref2
VWA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D16S539	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D2S1338	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D19S433	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
TH 01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
FGA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D3S1358	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

**Estimates under Hd**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.76348	0.02215
Mix-prop. C2	0.23652	0.02215
P.H.expectation	796.61088	38.26642
P.H.variability	0.14807	0.01688
Degrad. slope	0.73973	0.03988
BWstutt-prop.	0.11937	0.01770
FWstutt-prop.	0.05045	0.01966

Maximum Likelihood value

logLik= -349.6  
adj.loglik= -355.6  
Lik= 1.5e-152

**Estimates under Hp**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.79608	0.01631
Mix-prop. C2	0.20392	0.01631
P.H.expectation	794.83757	38.66065
P.H.variability	0.15097	0.01437
Degrad. slope	0.74679	0.04040
BWstutt-prop.	0.11872	0.01521
FWstutt-prop.	0.05499	0.01735

Maximum Likelihood value

logLik= -330.5  
adj.loglik= -336.5  
Lik= 3e-144

**Joint LR**

LR= 1.99e+08  
log10LR= 8.299  
Upper boundary= 9.668

**Non-contributor analysis**

Select reference to replace with non-contributor: ref2

Sample maximum based  
Sample integrated based

**LR for each locus**

VWA	7.085
D16S539	15.15
D2S1338	164.9
D19S433	7.156
TH 01	6.249
FGA	64.69
D3S1358	3.887

## Under Hp:

Theta=0.79607926,0.20392074,794.83757183,0.15096867,  
0.74678609, 0.11871766,0.05499105  
logLik=-330.464144513856

## Under Hd:

Theta=0.763477081556841,0.236522918443159,796.610875241322,  
0.148066384014808,0.739731359928258,0.119369627520945,0.050450  
8269641699  
logLik=-349.572712290044

# GUI check Hp: Hyp 1 vs Hd: Hyp 3

**Model specification**

**Contributor(s) under Hp:**

ref1  
 ref2  
 #unknowns (Hp): 0

**Contributor(s) under Hd:**

ref1  
 ref2  
 #unknowns (Hd): 1

1st unknown is  
 Sibling

to  
 ref2

**Model options**

Degradation:  YES  NO  
 BW Stutter:  YES  NO  
 FW Stutter:  YES  NO

**Data selection**

Loci:	stain52	stain98	ref1	ref2
VWA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D16S539	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D2S1338	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D19S433	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
TH 01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
FGA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D3S1358	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

**Estimates under Hd**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.78181	0.03289
Mix-prop. C2	0.21819	0.03289
P.H.expectation	794.66771	38.92441
P.H.variability	0.15170	0.01478
Degrad. slope	0.74564	0.04075
BWstutt-prop.	0.11894	0.01600
FWstutt-prop.	0.05137	0.01908

Maximum Likelihood value

logLik= -337.2  
 adj.loglik= -343.2  
 Lik= 3.6e-147

**Estimates under Hp**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.79608	0.01631
Mix-prop. C2	0.20392	0.01631
P.H.expectation	794.83757	38.66065
P.H.variability	0.15097	0.01437
Degrad. slope	0.74679	0.04040
BWstutt-prop.	0.11872	0.01521
FWstutt-prop.	0.05499	0.01735

Maximum Likelihood value

logLik= -330.5  
 adj.loglik= -336.5  
 Lik= 3e-144

**Joint LR**

LR= 832.8  
 log10LR= 2.921  
 Upper boundary= 9.668

**Non-contributor analysis**

Select reference to replace with non-contributor:  
 ref2

Sample maximum based  
 Sample integrated based

**LR for each locus**

VWA	2.295
D16S539	2.523
D2S1338	3.813
D19S433	2.215
TH 01	1.971
FGA	3.404
D3S1358	2.537

## Under Hp:

Theta=0.79607926,0.20392074,794.83757183,0.15096867,  
 0.74678609, 0.11871766 , 0.05499105  
 logLik=-330.464144513856

## Under Hd:

Theta=0.781811348820458,0.218188651179542,794.667708593774,0.151698  
 944113907,0.745636804143434,0.118944752922951,0.0513713668220271  
 logLik=-337.188990585992

# Propositions tested for dataset 2' *test\_logLik2contr1RepNoStutter*

- Considering 1 replicate (stain52 only)
- Stutter models are turned off, degrad still turned on.
- Hyp 1: ref1 and ref2 are contributor
- Hyp 2: 2 (unrelated) unknowns are contributors, ref1 and ref2 are known non-contributors



# GUI check Hd: Hyp 1 versus Hd: Hyp 2

**Model specification**

**Contributor(s) under Hp:**

ref1  
 ref2  
 #unknowns (Hp): 0

**Contributor(s) under Hd:**

ref1  
 ref2  
 #unknowns (Hd): 2  
 1st unknown is: Unrelated  
 to:

**Data selection**

Loci:	stain52	ref1	ref2
VWA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D16S539	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D2S1338	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D19S433	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
TH 01	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
FGA	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
D3S1358	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

**Model options**

Degradation:  YES  NO  
 BW Stutter:  YES  NO  
 FW Stutter:  YES  NO

**Estimates under Hd**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.71856	0.03466
Mix-prop. C2	0.28144	0.03466
P.H.expectation	699.01859	71.26387
P.H.variability	0.23119	0.04118
Degrad. slope	0.77082	0.08450

Maximum Likelihood value

logLik= -234.1  
 adj.loglik= -238.1  
 Lik= 2.2e-102

Further Action

**Estimates under Hp**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.72364	0.02812
Mix-prop. C2	0.27636	0.02812
P.H.expectation	688.46525	59.93876
P.H.variability	0.20350	0.03046
Degrad. slope	0.77411	0.07047

Maximum Likelihood value

logLik= -203.6  
 adj.loglik= -207.6  
 Lik= 3.7e-89

Further Action

**Joint LR**

LR= 1.695e+13  
 log10LR= 13.23  
 Upper boundary= NA

**Non-contributor analysis**

Select reference to replace with non-contributor: ref1

**LR for each locus**

VWA 58.93  
 D16S539 2.049  
 D2S1338 6650  
 D19S433 1817  
 TH 01 150.2  
 FGA 97.67  
 D3S1358 0.7918

## Under Hp:

Theta=0.723637935771717,0.276362064228283,688.465246180605,  
 0.203496638155194,0.774111003592664  
 logLik= -203.634478762721

## Under Hd:

Theta=0.718560679161608,0.281439320838392,699.01859159150,  
 0.231186789294128,0.7708186860514  
 logLik= -234.095699644915

# Propositions tested for dataset 3 (SNPs):

## *test\_logLik2contr1RepSNP*

Global settings for all markers:

Easy mode:	<input checked="" type="radio"/> NO <input type="radio"/> YES
Default detection threshold	500
Default fst-correction	0.02
Default probability of drop-in	0.05
Default drop-in hyperparam (lambda)	0.01

Note: Profile P1 has missing markers  
RS13182883 and RS576261  
(substituting with additional unknown)

Only 1<sup>st</sup> replicate

- Hyp 1: P1 + 1U are contributors
- Hyp2: 1U + 2U (unrelated) unknowns are contributors, P1 is known non-contributor

# GUI check Hp: Hyp 1 vs Hd: Hyp 2

The screenshot displays the software interface for a forensic analysis. It is divided into several sections:

- Model specification:** Includes settings for 'Contributor(s) under Hp' (P1 checked, #unknowns = 1) and 'Contributor(s) under Hd' (P1 unchecked, #unknowns = 2). It also has a '1st unknown is' dropdown set to 'Unrelated' and 'Model options' for degradation and stutter.
- Data selection:** A 'Show selected data' section with 'Evidence(s)' containing '1\_1a\_XEN13' and a 'Show' button.
- Estimates under Hd:** A table of parameter estimates and a 'Maximum Likelihood value' box.
- Estimates under Hp:** A table of parameter estimates and a 'Maximum Likelihood value' box.
- Joint LR:** A box showing 'LR= 2.935e+26', 'log10LR= 26.47', and 'Upper boundary= 50.85'.
- Non-contributor analysis:** A section with a 'Select reference to replace with non-contributor:' dropdown set to 'P1' and two buttons: 'Sample maximum based' and 'Sample integrated based'.

## Under Hp:

Param=0.800719189324181,0.199280810675819,730.581491903075,0.631339725096235  
logLik=-1409.45126218041

## Under Hd:

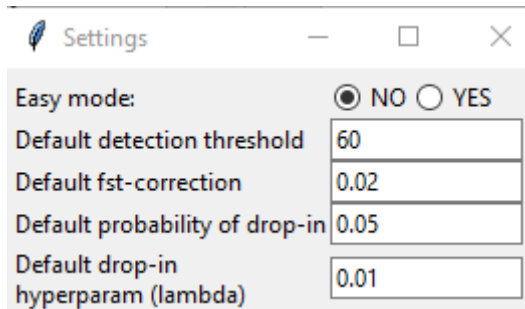
Param=0.5000401203235,0.49999598796765,743.962888261923,0.668780008839223  
logLik=-1470.39533062578

# Propositions tested for dataset 3 (SNPs):

## *test\_logLik2contr2RepSNP*

Note: Profiles P1+P3 are missing markers RS13182883 and RS576261 (substituting with additional unknown)

Global settings for all markers:



Easy mode:	<input checked="" type="radio"/> NO <input type="radio"/> YES
Default detection threshold	60
Default fst-correction	0.02
Default probability of drop-in	0.05
Default drop-in hyperparam (lambda)	0.01

Using **both** replicates

- Hyp 1: P1 + P3 are contributors
- Hyp2: P1 + 1 (unrelated) unknown are contributors, P3 is known non-contributor

# GUI check Hp: Hyp 1 vs Hd: Hyp 2

**Model specification**

Contributor(s) under Hp:

P1  
 P3  
#unknowns (Hp): 0

Contributor(s) under Hd:

P1  
 P3  
#unknowns (Hd): 1  
1st unknown is: Unrelated  
to:

**Model options**

Degradation:  YES  NO  
BW Stutter:  YES  NO  
FW Stutter:  YES  NO

**Show selected data**

Evidence(s)

1\_1a\_XEN13  
 1\_1b\_XEN13

Show

Data selection

**Estimates under Hd**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.66610	0.02502
Mix-prop. C2	0.33390	0.02502
P.H.expectation	815.87512	17.95501
P.H.variability	0.51310	0.01641

Maximum Likelihood value

logLik= -3807.2  
adj.loglik= -3810.2  
Lik= 3.7e-1654

**Estimates under Hp**

Parameter estimates:

param	MLE	Std.Err.
Mix-prop. C1	0.78429	0.01706
Mix-prop. C2	0.21571	0.01706
P.H.expectation	797.88513	20.22211
P.H.variability	0.59090	0.01844

Maximum Likelihood value

logLik= -3980.1  
adj.loglik= -3983.1  
Lik= 3.1e-1729

## Under Hp:

Param=0.784287340610599,0.215712659389401,797.885130883847,0.590903414911386  
logLik=-3980.05359609996

## Under Hd:

Param=0.666100819168908,0.333899180831092,815.87511749016,0.5130965438557  
logLik=-3807.17711247693

# Additional: Testing the **qualitative** model (tested for dataset 2, using both replicates)

Different drop-out probability models are tested:

- Hyp 1: Ref1 + Ref2, common drop-out parameter
- Hyp 2: Ref1 + Ref2, Ref1 drop-out parameter set to 0.
- Hyp 3: Ref1 + Ref2, 2 drop-out parameters

Ref2 known non-contr for hyps Hyp '4-6':

- Hyp 4: Ref1 + 1U, common drop-out parameter.
- Hyp 5: Ref1 + 1U, Ref1 drop-out parameter set to 0.
- Hyp 6: Ref1 + 1U, 2 drop-out parameters

# GUI check

Only common drop-out parameter implemented in GUI

Model specification

Contributor(s) under Hp:

ref1  
 ref2

#unknowns (Hp): 0

Contributor(s) under Hd:

ref1  
 ref2

#unknowns (Hd): 1

1st unknown is  
Unrelated

Confirm

Results of MLE based LR:  
LR=2.62e-08  
log10LR=-7.582  
Estimated pD under Hp=0.07301  
Estimated pD under Hd=0.0381

Do you want to export the results?

Yes No

Hyp 1 (Hp) : R1+R2 (common drop-out parameter):  
logLik = -95.1168543762792  
d = 0.0730126, 0.0730126

Hyp 4 (Hd): R1+1U (common drop-out parameter):  
logLik = -77.6593191143117  
d = 0.03809141, 0.03809141

log10LR = -7.581711

# Additional validation of EFM GUI

- The GUI is manually inspected for concise results whenever new versions are released – based on following data:
  - The output from the manual (tutorial data)
    - Also covers the Bayesian approach
  - Workshop material:
    - ENFSI exercises (ENFSI1 and ENFSI2)
    - EFMexercise26