



# Complex DVI cases with DIVIANA

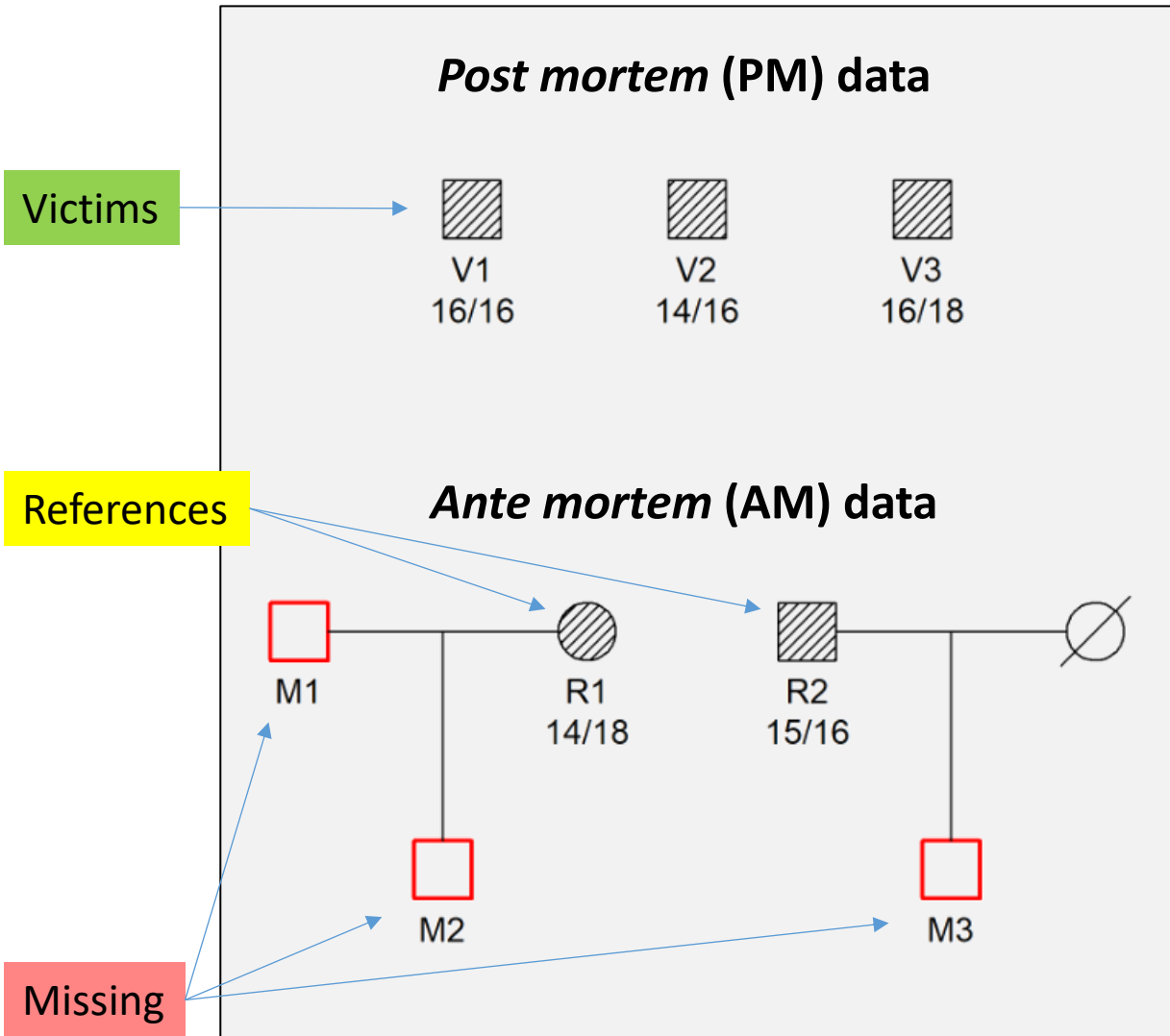
GHEP-ISFG Mexico 2026

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Dept. of Forensic Sciences, Oslo

# Outline

- Computational challenges in complex DVI cases
- The *generalized likelihood ratio* (GLR)
- A refined pipeline for complex cases
- Software: DIVIANA

# Disaster victim identification (DVI)



Complex DVI: >1 missing in a family

## Computational approaches

➤ Pairwise LR

	M1	M2	M3
V1	1	0	0.39
V2	1	16142	0
V3	1	0	6266

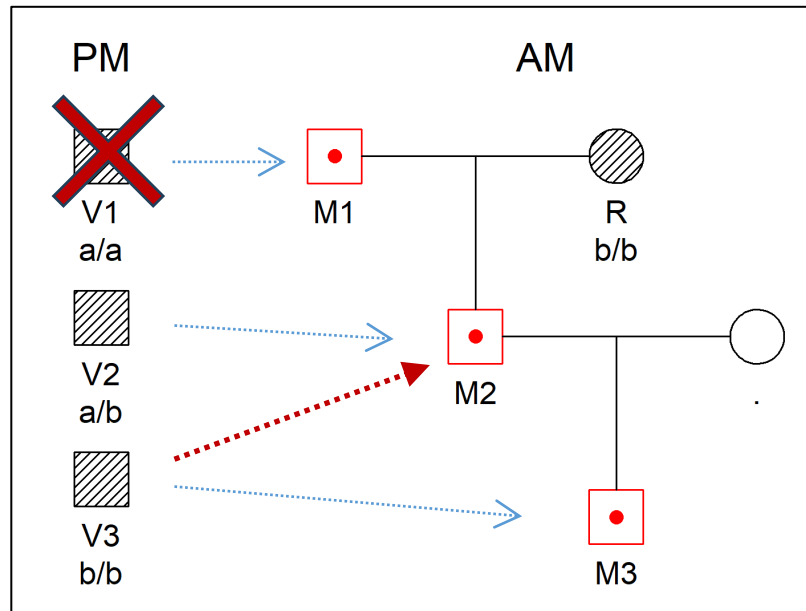
➤ Sequential (PM-driven or AM-driven)

➤ Joint / global



# Challenge I: Pairwise LR is not robust

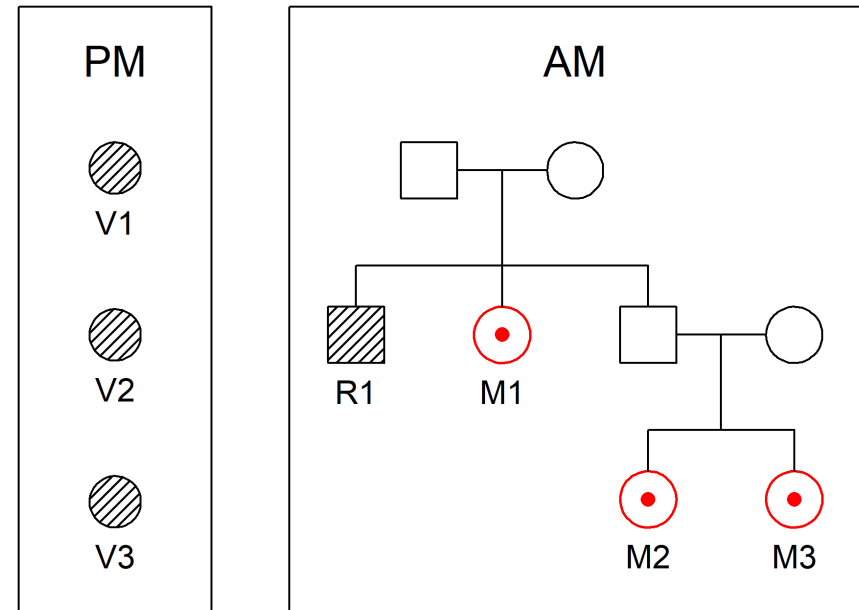
Example 1: Wrong



1 SNP marker

	M <sub>1</sub>	M <sub>2</sub>	M <sub>3</sub>
V <sub>1</sub>	1	0	0.5
V <sub>2</sub>	1	10	5.5
V <sub>3</sub>	1	20	10.5

Example 2: Weak/confusing



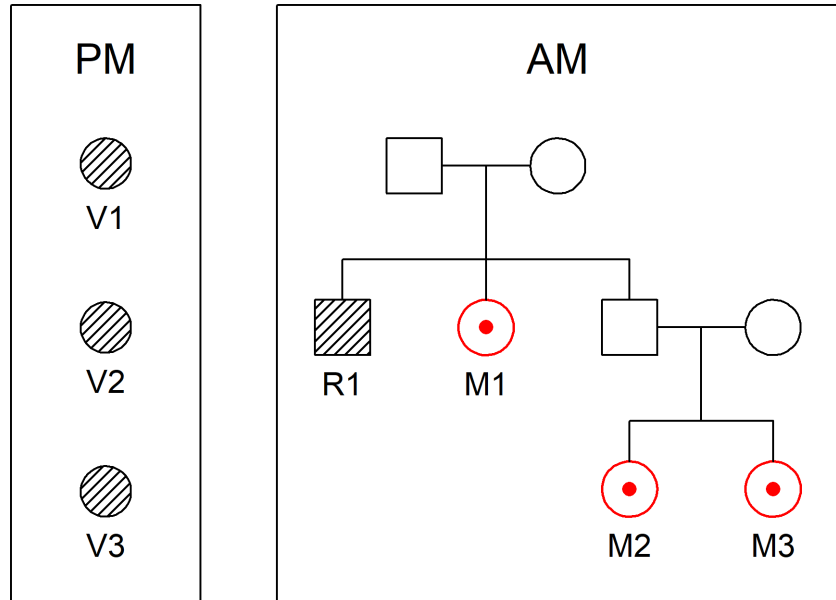
23 STR markers

	M <sub>1</sub>	M <sub>2</sub>	M <sub>3</sub>
V <sub>1</sub>	121.3	398.6	398.6
V <sub>2</sub>	0.6	36.6	36.6
V <sub>3</sub>	0.00	1.3	1.3



Thore Egeland

# Solution: Joint analysis



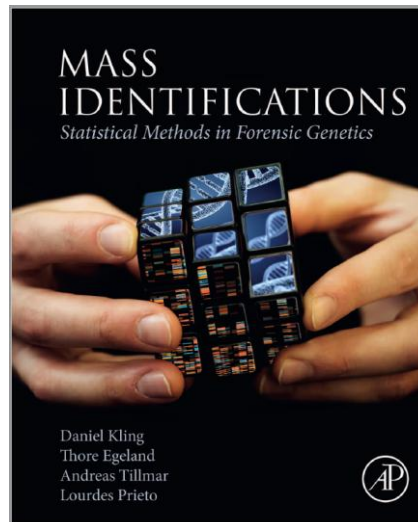
## Pairwise LR

	M1	M2	M3
V1	121.3	398.6	398.6
V2	0.6	36.6	36.6
V3	0.00	1.3	1.3

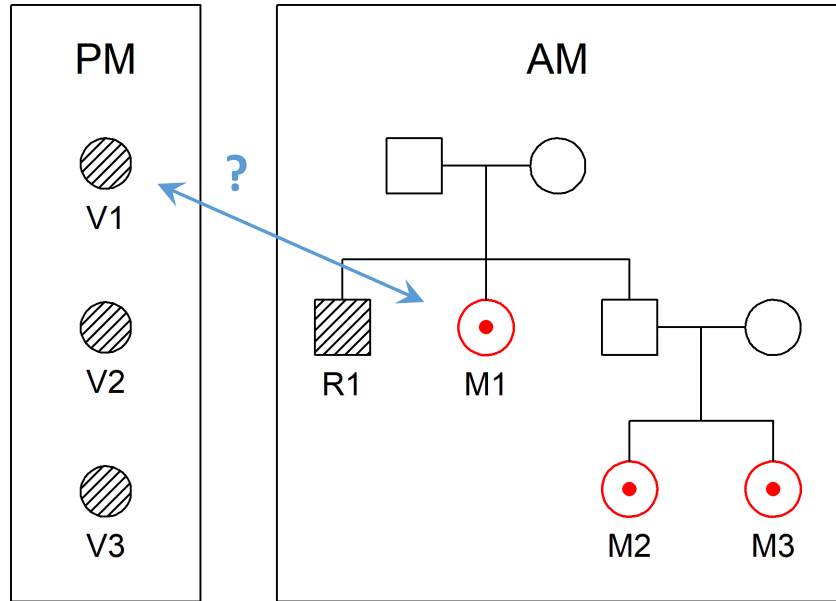
## Joint likelihoods

	V1	V2	V3	loglik
1	M1	M2	M3	-257.7
2	M1	M3	M2	-257.7
3	*	M2	M3	-268.9
4	*	M3	M2	-268.9
5	M2	M1	M3	-272.6
6	M3	M1	M2	-272.6
7	M1	*	M2	-276.5
8	M1	*	M3	-276.5
9	M2	M3	M1	-276.6
⋮				
32	*	*	*	-286.0
33	*	M1	*	-286.5
34	*	*	M1	-292.2

Vigeland & Egeland. (Scientific Reports, 2021)  
**Joint DNA-based disaster victim identification**



# Challenge II: How to interpret the joint table?



## Solutions:

- Bayesian (requires priors)
- Generalised LR

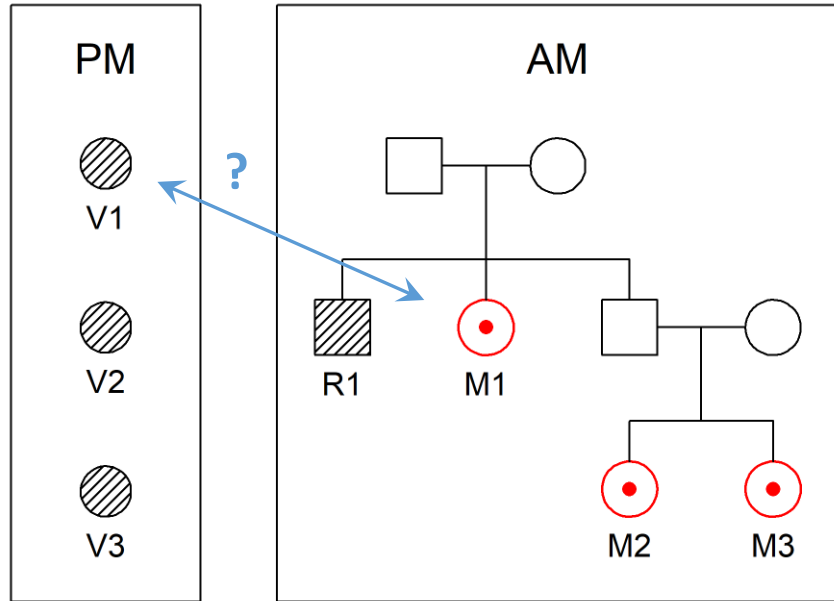
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7	M1	*	M2	-276.5
8	M1	*	M3	-276.5
9	M2	M3	M1	-276.6
⋮				
32	*	*	*	-286.0
33	*	M1	*	-286.5
34	*	*	M1	-292.2

# Generalised likelihood ratio (GLR)

Egeland & Vigeland. *Kinship cases with partially specified hypotheses*. FSI Genetics. 2025

$$\text{GLR} = \frac{\max_{i \in H_1} L_i}{\max_{j \in H_2} L_j}$$



$H_1: V1 = M1$   
 $H_2: V1 \neq M1$

$$\text{GLR}_{V1=M1} = \frac{L_1}{L_3} = \frac{e^{-257.7\dots}}{e^{-268.9\dots}} = 70\,582$$

**Strong evidence**

Joint likelihoods

	V1	V2	V3	loglik	
1	M1	M2	M3	-257.7	✓
2	M1	M3	M2	-257.7	✓
3	*	M2	M3	-268.9	✗
4	*	M3	M2	-268.9	✗
5	M2	M1	M3	-272.6	✗
6	M3	M1	M2	-272.6	✗
7	M1	*	M2	-276.5	✓
8	M1	*	M3	-276.5	✓
9	M2	M3	M1	-276.6	✗
⋮					
32	*	*	*	-286.0	✗
33	*	M1	*	-286.5	✗
34	*	*	M1	-292.2	✗

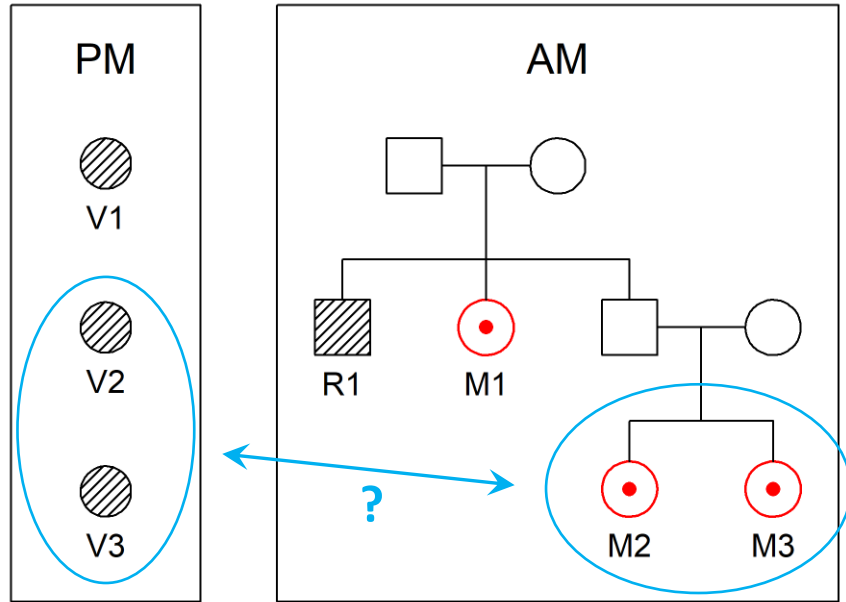
Interpretation of  $GLR = x$

$$GLR = \frac{\max_{i \in H_1} L_i}{\max_{j \in H_2} L_j}$$

*The best explanation of the data given H1  
is  $x$  times more likely  
than the best explanation given H2*



# Challenge III: Symmetric matches



Cannot separate these!

GLR to the rescue!

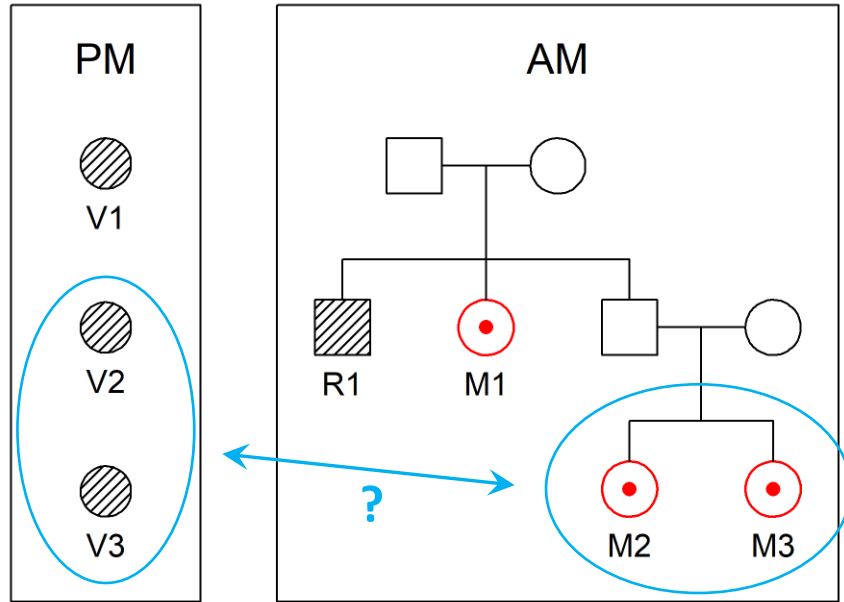
Joint likelihoods

	V1	V2	V3	loglik
1	M1	M2	M3	-257.7
2	M1	M3	M2	-257.7
3	*	M2	M3	-268.9
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5	M2	M1	M3	-272.6
6	M3	M1	M2	-272.6
7	M1	*	M2	-276.5
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⋮				
32	*	*	*	-286.0
33	*	M1	*	-286.5
34	*	*	M1	-292.2



# Challenge III: Symmetric matches

$$\text{GLR} = \frac{\max_{i \in H_1} L_i}{\max_{j \in H_2} L_j}$$



$H_1: \{V2, V3\} = \{M2, M3\}$   
 $H_2: \{V2, V3\} \neq \{M2, M3\}$

$$\text{GLR} = 2.9 \times 10^6$$

**Strong evidence!**

Joint likelihoods

	V1	V2	V3	loglik	
1	M1	M2	M3	-257.7	✓
2	M1	M3	M2	-257.7	✓
3	*	M2	M3	-268.9	✓
4	*	M3	M2	-268.9	✓
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32	*	*	*	-286.0	✗
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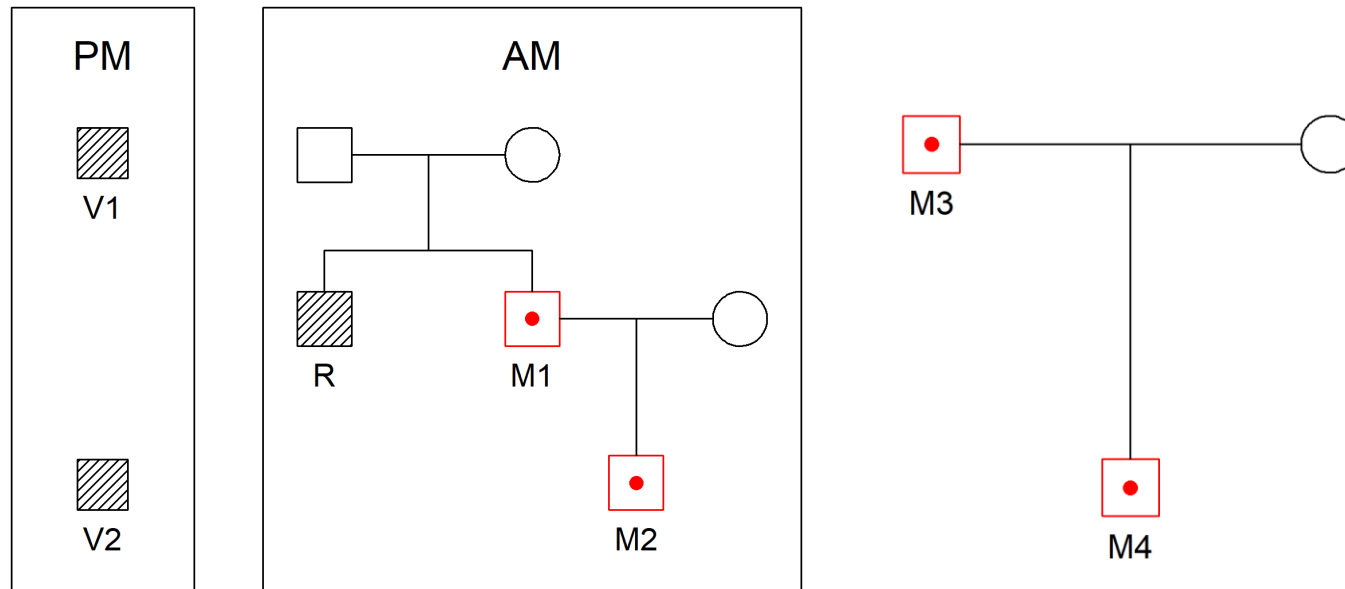
Conclusion: V2 and V3 are M2 and M3 (but we don't know who-is-who)

# Challenge IV:

## False identifications of related victims



Klaas Slooten (NFI)  
+ Aafko Boonstra



V1	V2	LR	GLR	LR0
M1	M2	4.8E+8	1.1E+8	4E+10

$LR_0 > LR \Rightarrow$  evidence *against* relationship with R

- V1, V2 are father and son, but unrelated to R.
- Misidentified as M1, M2
- Diagnostic: compare with a **reference-free LR0**.

# A large example: ICMP workshop 2017

**PM**



V1



V2



V3

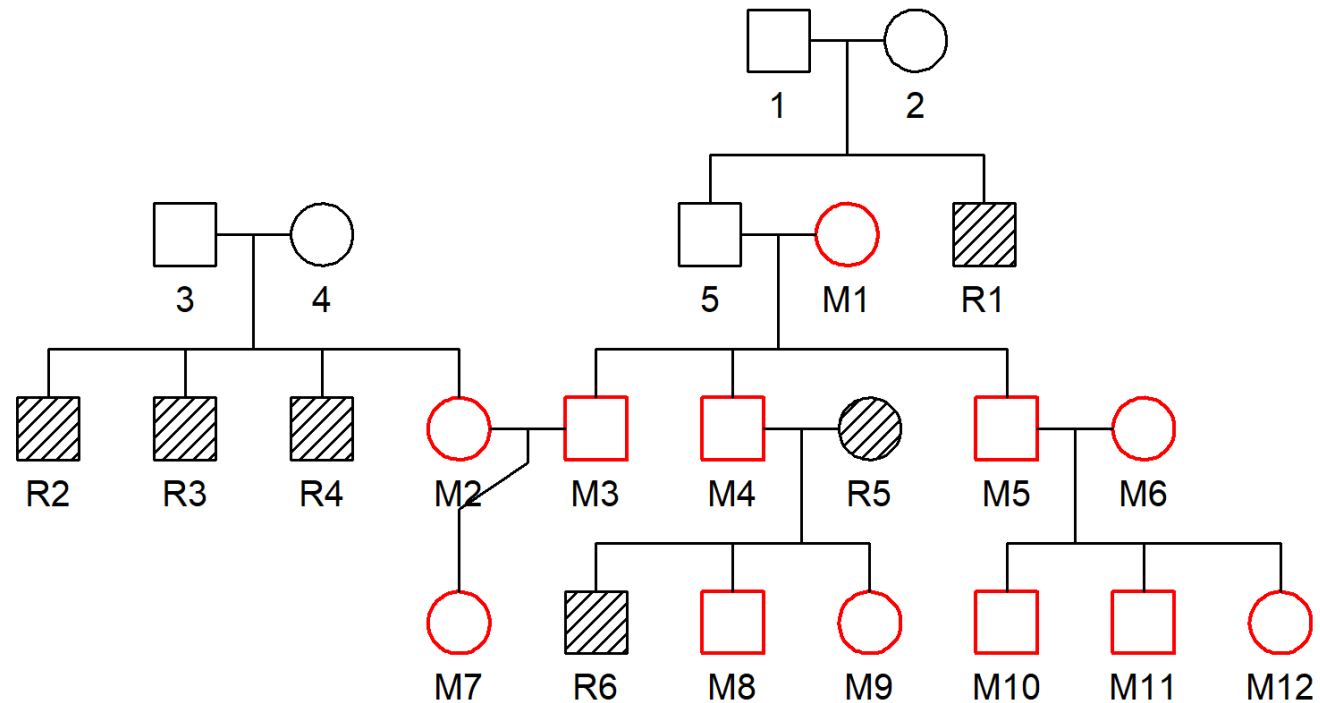


V4



V5

**AM**

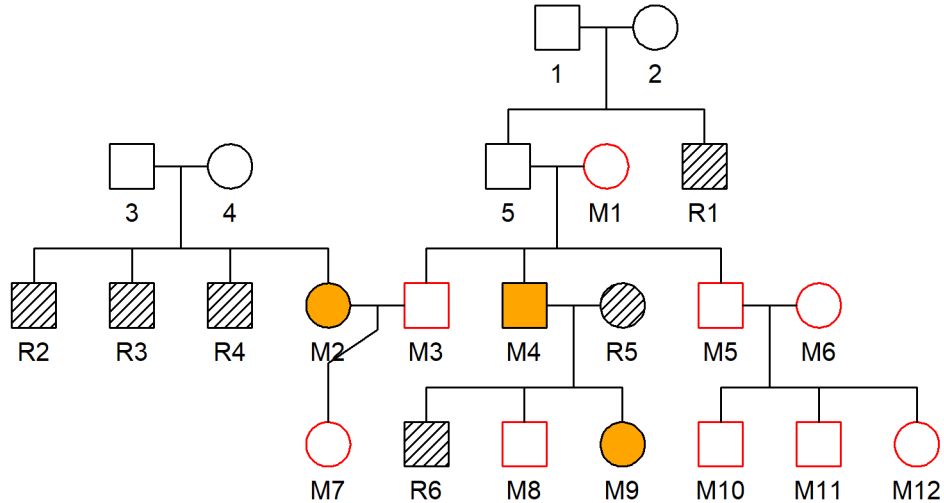


# A refined DVI pipeline

PM



AM



## 1. Exclusion matrix

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12
V1	0	8	-	-	-	0	0	-	3	-	-	0
V2	-	-	0	5	0	-	-	6	-	0	0	-
V3	0	6	-	-	-	0	0	-	3	-	-	0
V4	-	-	0	3	0	-	-	0	-	0	0	-
V5	0	5	-	-	-	0	0	-	7	-	-	0

R code

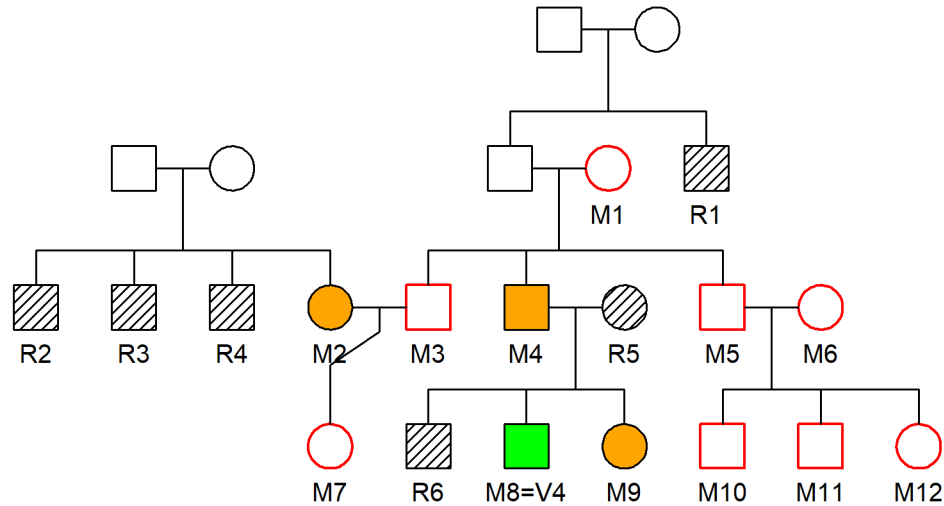
```
1. findExcluded()
```

# A refined DVI pipeline

PM



AM



## 1. Exclusion matrix

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12
V1	0	8	-	-	-	0	0	-	3	-	-	0
V2	-	-	0	5	0	-	-	6	-	0	0	-
V3	0	6	-	-	-	0	0	-	3	-	-	0
V4	-	-	0	3	0	-	-	0	-	0	0	-
V5	0	5	-	-	-	0	0	-	7	-	-	0

## 2. Pairwise LR matrix

	M1	M3	M5	M6	M7	M8	M10	M11	M12
V1	0.1	0.0	0.0	1	0	0	0.0	0.0	0.2
V2	0.0	0.2	0.2	0	0	0	1.2	1.2	0.0
V3	0.1	0.0	0.0	1	0	0	0.0	0.0	2.3
V4	0.0	0.8	0.8	0	0	2850564	3.1	3.1	0.0
V5	17.5	0.0	0.0	1	0	0	0.0	0.0	2.8

## R code

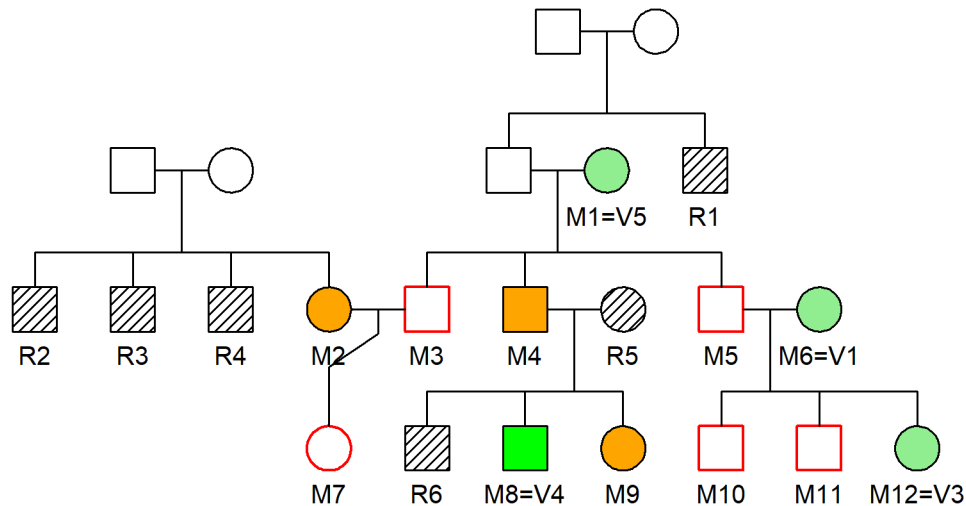
1. `findExcluded()`
2. `findUndisputed()`

# A refined DVI pipeline

PM

AM

V2



## R code

1. `findExcluded()`
2. `findUndisputed()`
3. `jointDVI()`

## 1. Exclusion matrix

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12
V1	0	8	-	-	-	0	0	-	3	-	-	0
V2	-	-	0	5	0	-	-	6	-	0	0	-
V3	0	6	-	-	-	0	0	-	3	-	-	0
V4	-	-	0	3	0	-	-	0	-	0	0	-
V5	0	5	-	-	-	0	0	-	7	-	-	0

## 2. Pairwise LR matrix

	M1	M3	M5	M6	M7	M8	M10	M11	M12
V1	0.1	0.0	0.0	1	0	0	0.0	0.0	0.2
V2	0.0	0.2	0.2	0	0	0	1.2	1.2	0.0
V3	0.1	0.0	0.0	1	0	0	0.0	0.0	2.3
V4	0.0	0.8	0.8	0	0	2850564	3.1	3.1	0.0
V5	17.5	0.0	0.0	1	0	0	0.0	0.0	2.8

## 3. Joint + GLR

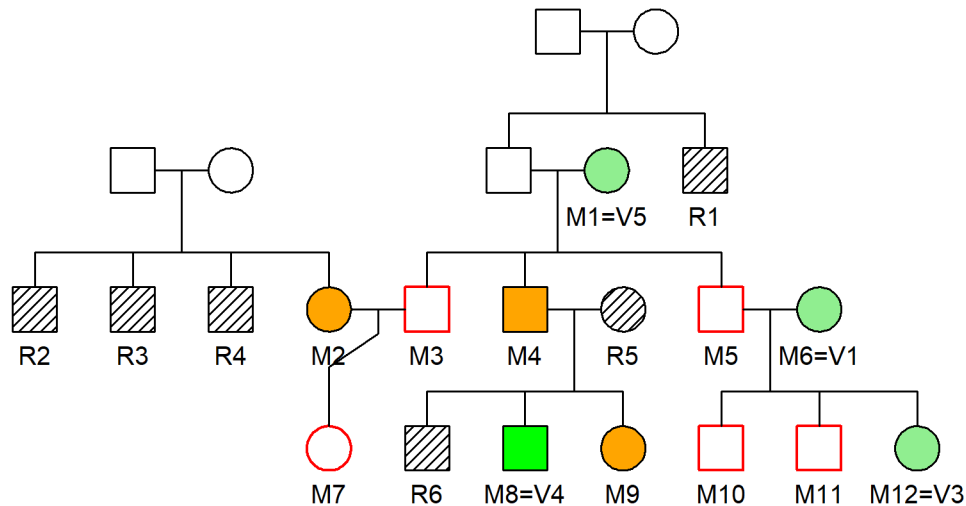
	V1	V2	V3	V5	loglik	LR posterior	
1	M6	M10	M12	M1	-312.98	3.98e+17	0.5
2	M6	M11	M12	M1	-312.98	3.98e+17	0.5
3	M6	M10	M12	M7	-327.16	2.76e+11	0.0
4	M6	M11	M12	M7	-327.16	2.76e+11	0.0
5	M6	*	M12	M1	-327.74	1.54e+11	0.0
6	M6	M10	M7	M1	-329.12	3.91e+10	0.0

# A refined DVI pipeline

PM

AM

 V2



## R code

1. `findExcluded()`
2. `findUndisputed()`
3. `jointDVI()`
4. `findSymmetric()`

## 1. Exclusion matrix

	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12
V1	0	8	-	-	-	0	0	-	3	-	-	0
V2	-	-	0	5	0	-	-	6	-	0	0	-
V3	0	6	-	-	-	0	0	-	3	-	-	0
V4	-	-	0	3	0	-	-	0	-	0	0	-
V5	0	5	-	-	-	0	0	-	7	-	-	0

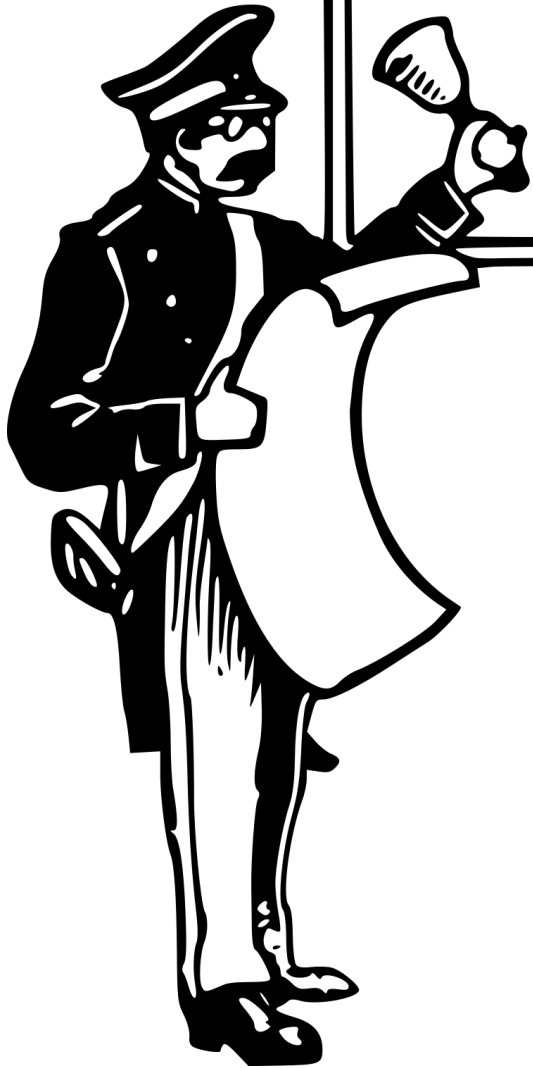
## 2. Pairwise LR matrix

	M1	M3	M5	M6	M7	M8	M10	M11	M12
V1	0.1	0.0	0.0	1	0	0	0.0	0.0	0.2
V2	0.0	0.2	0.2	0	0	0	1.2	1.2	0.0
V3	0.1	0.0	0.0	1	0	0	0.0	0.0	2.3
V4	0.0	0.8	0.8	0	0	2850564	3.1	3.1	0.0
V5	17.5	0.0	0.0	1	0	0	0.0	0.0	2.8

## 3. Joint + GLR

	V1	V2	V3	V5	loglik	LR posterior	
1	M6	M10	M12	M1	-312.98	3.98e+17	0.5
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3	M6	M10	M12	M7	-327.16	2.76e+11	0.0
4	M6	M11	M12	M7	-327.16	2.76e+11	0.0
5	M6	*	M12	M1	-327.74	1.54e+11	0.0
6	M6	M10	M7	M1	-329.12	3.91e+10	0.0

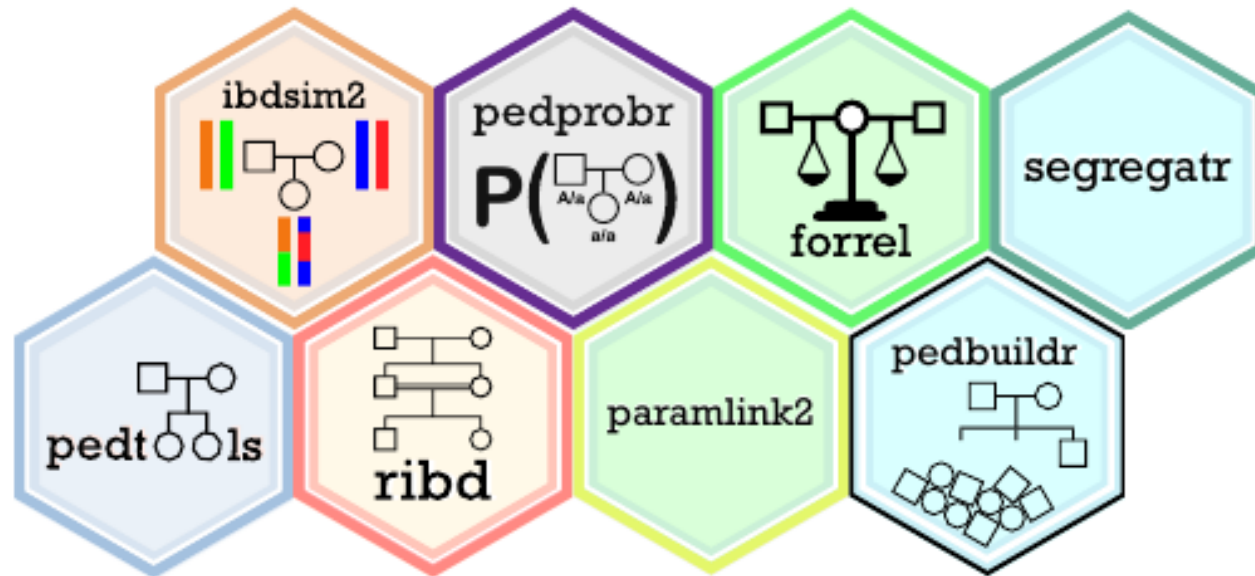
# Software: DIVIANA



*Diviana eudoreella*

# Behind the wings of DIVIANA: The **pedsuite**

A collection of packages for pedigree analysis in R



Home page: <https://magnusdv.github.io/pedsuite>

Source code: <https://github.com/magnusdv>

Developers: Magnus D. Vigeland, Thore Egeland

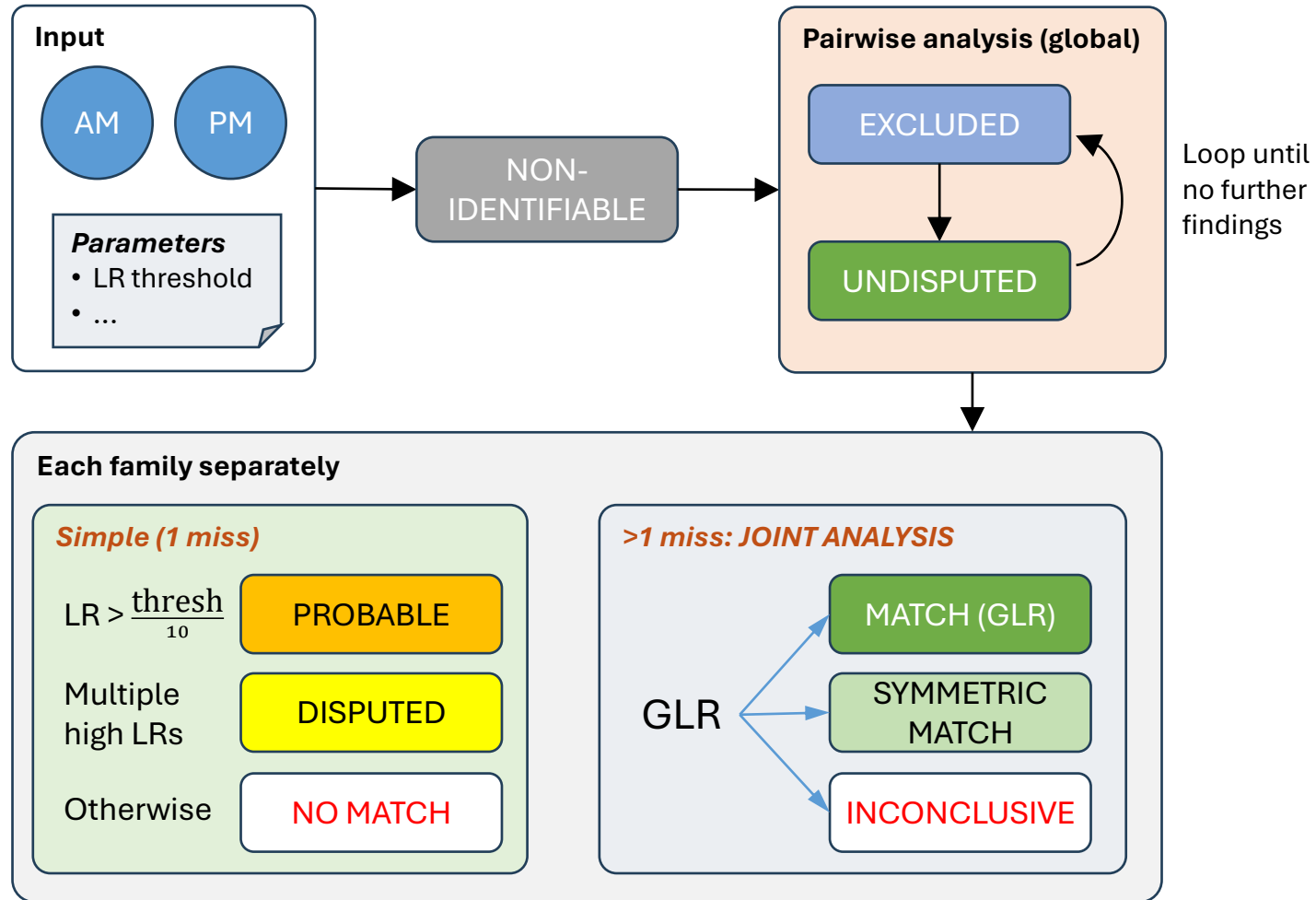
## PEDIGREE ANALYSIS IN R



Magnus Dehli Vigeland



# The DIVIANA pipeline



# Installation in R



## **1) Install from GitHub (only once)**

With 'pak':

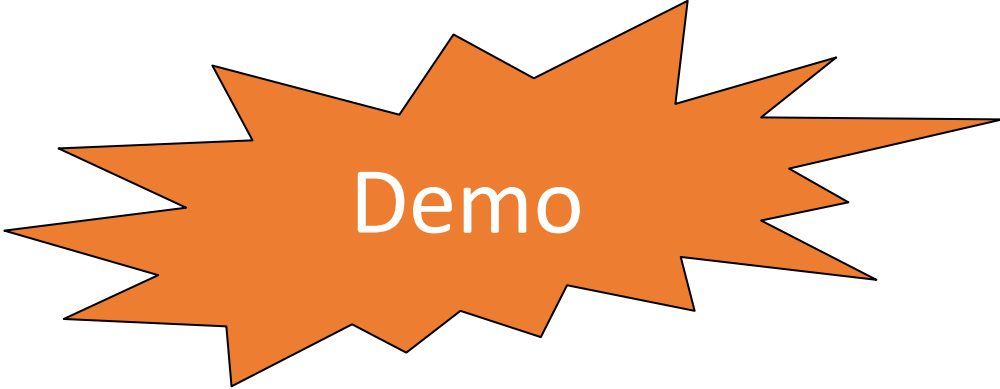
- `library(pak) # if error: install.packages("pak")`
- `pak("magnusdv/diviana", dep = T)`

Or with 'remotes':

- `library(remotes) # if error: install.packages("remotes")`
- `install_github("magnusdv/diviana", dep = T)`

## **2) Start the app**

- `diviana::launchApp()`



# Biased selection of references



Thore Egeland



Lourdes Prieto



Article | [Open Access](#) | Published: 01 July 2021

## Joint DNA-based disaster victim identification

Magnus D. Vigeland [✉](#) & Thore Egeland

*Scientific Reports* **11**, Article number: 13661 (2021) | [Cite this article](#)

> *Forensic Sci Int Genet.* 2025 Jun

## Kinship cases with partially specified hypotheses

Thore Egeland <sup>1</sup>, Magnus Dehli Vigeland <sup>2</sup>

> *BMC Bioinformatics.* 2022 Jun 7;23(1):220.  
doi: 10.1186/s12859-022-04759-y.

## QuickPed: an online tool for drawing pedigrees and analysing relatedness

Magnus D Vigeland <sup>1</sup>

The **pedsuite** R packages:  
<https://magnusdv.github.io/pedsuite>

relatedness and IBD: tribd, ibdlink2  
pedigree likelihoods: pedprobr, pedmut  
medical genetics: paramlink2, segregatr  
forensic genetics: pedtools, forrel, dvir, pedbuilder

