

RelSearch version 1.0.0 user manual

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1 Initial setup

1. Ensure that R ($\geq 4.4.0$) is installed. It is available from the [R Development Core Team website](#).
2. Begin an R session.
3. Execute the following command in R to install required packages.

```
install.packages(c("shiny", "data.table", "dplyr", "DT", "magrittr",  
  "pandoc", "pedtools", "Rcpp", "ribd", "rmarkdown", "shinyFeedback",  
  "shinyjs", "shinythemes", "waiter"))
```

4. Download "relsearch_1.0.0.zip" from the [GitHub repository page](#).
5. Install "relsearch_1.0.0.zip" from "Install package(s) from local files..."

2 Quick guide

1. Execute the following commands in R to start GUI.

```
library(relsearch)
relsearch()
```

2. Load files from each “**Browse...**” button.

The screenshot shows the relsearch ver. 0.11.0 GUI. It has a blue header bar with the version and navigation tabs: Load, Result, Project, Database, Settings, Example files, and Manual. The main area is divided into three columns: STR, Y-STR, and mtDNA. Each column has three sections: 'Victim database', 'Reference database', and 'Allele frequencies' (only in the STR column). Each section contains a 'Browse...' button (highlighted with an orange box) and a 'No file selected' status. At the bottom left of the main area is a blue 'Analyze' button.

Note See section [Files](#) for information on each file.

3. Click the “**Analysis**” button.

relsearch ver. 0.11.0

LoadResultProject ▾Database ▾Settings ▾Example filesManual

STR

Victim database

Browse...

str_victim_example.csv

Upload complete

Reference database

Browse...

str_ref_example.csv

Upload complete

Allele frequencies

Browse...

str_af_example.csv

Upload complete

Analyze

Y-STR

Victim database

Browse...

y_victim_example.csv

Upload complete

Reference database

Browse...

y_ref_example.csv

Upload complete

mtDNA

Victim database

Browse...

mt_victim_example.csv

Upload complete

Reference database

Browse...

mt_ref_example.csv

Upload complete

4. After finishing the analysis, the result window is automatically opened.

relesearch ver. 0.11.0
Load
Result
Project
Database
Settings
Example files
Manual

Result

Summary
Selected data in detail
Analysis conditions

Display setting

Default display

Identified pairs

Multiple candidates

Not support lineage

Minimum LR displayed

100

Apply

Download

Show 10 entries

Search:

Victim	Reference	Assumed relationship	LR	Estimated relationship	Paternal lineage	Maternal lineage
All	All	All	All	All	All	All
V7	R7	Father_Son	9.23e+8	Father_Son	Support	Support
V8	R8	Father_Son	6.48e+8	Father_Son	Support	Not support
V14	R14	Brother_Brother	2.85e+7	Brother_Brother	Support	Support
V9	R9	Father_Son	1.34e+7	Father_Son	Support	Not support
V11	R11	Mother_Daughter	1.25e+7			Not support
V16	R16	Brother_Sister	2.01e+6	Brother_Sister		Support
V15	R15	Brother_Sister	1.57e+6	Brother_Sister		Support
V7	R30	Brother_Brother	1.02e+5	Brother_Brother	Support	Support
V10	R10	Mother_Daughter	4.49e+4	Mother_Daughter		Support
V12	R12	Mother_Daughter	3.09e+3	Mother_Daughter		Support

Showing 1 to 10 of 12 entries

Previous 1 2 Next

Note See section [Result](#) for navigation of the result window.

5. Select **Project** ► **Save project**.

relesearch ver. 0.11.0
Load
Result
Project ▼
Database ▼
Settings ▼
Example files
Manual

New project
Load project
Save project

Result

Summary
Selected data in detail
Analysis conditions

Display setting

Default display

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Apply

Download

Show 10 entries
Search:

Victim	Reference	Assumed relationship	LR	Estimated relationship	Paternal lineage	Maternal lineage
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V7	R7	Father_Son	9.23e+8	Father_Son	Support	Support
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V14	R14	Brother_Brother	2.85e+7	Brother_Brother	Support	Support
V9	R9	Father_Son	1.34e+7	Father_Son	Support	Not support
V11	R11	Mother_Daughter	1.25e+7			Not support
V16	R16	Brother_Sister	2.01e+6	Brother_Sister		Support
V15	R15	Brother_Sister	1.57e+6	Brother_Sister		Support
V7	R30	Brother_Brother	1.02e+5	Brother_Brother	Support	Support
V10	R10	Mother_Daughter	4.49e+4	Mother_Daughter		Support
V12	R12	Mother_Daughter	3.09e+3	Mother_Daughter		Support

Showing 1 to 10 of 12 entries
Previous
1
2
Next

127.0.0.1:4409/#tab-1131-3

6. Enter the project name and click the “**Save as**” button.

relsearch ver. 0.11.0 Load Result **Project** ▾ Database ▾ Settings ▾ Example files Manual

Save project

Enter the project name

Save as

Note The saved project can be loaded from **Project ► Load project**. How to handle projects is described in section [Other functions](#).

3 Files

3.1 STR: Victim database

SampleName	D3S1358	D3S1358.1	vWA	vWA.1	D16S539	D16S539.1	CSF1PO	CSF1PO.1	TPOX	TPOX.1
Victim1	17	17	17		11		12			
Victim2	17		18	18			10	11	8	
Victim3	15	17	17	18	10	10	10	12	8	11
Victim4	15	18	15	18	9	12	11	12	8	8
Victim5	15	15	18		9	9	10		9	11
Victim6	16	16	17				10	13	8	8
Victim7	14	15	17	18	12				8	8
Victim8	16	18	17	18	11		9	12	8	
Victim9	15	15	16	18	11	11	12	12	8	11
Victim10	15	16	18	19	9	10	12	12	8	11

Note

- File type: .csv
- This file requires the column “SampleName” and columns for each marker (two columns in each).
- The marker with two empty cells (e.g., TPOX of sample “Victim1” in the above table) is ignored when calculating the likelihood ratio.
- The marker with one empty cell (e.g., vWA of sample “Victim1” in the above table) can be regarded as both homozygote (i.e., no drop-out) and heterozygote with drop-out of one allele when calculating the likelihood ratio.

3.2 STR: Reference database

Note

- File type: .csv
- This file requires the columns “SampleName”, “Relationship”, and columns for each marker (two columns in each).
- The relationship of a missing family member should be designated in the column “Relationship”. The names of the relationship need to be pre-defined in **Settings Relationships** (see section **Setting**).
- If a reference has multiple missing family members, add rows for each relationship of the members (e.g., sibling and parent-child of the sample “Reference7” in the above table).

- The marker with two empty cells (e.g., CSF1PO of sample “Reference10” in the above table) is ignored when calculating the likelihood ratio.
- The marker with one empty cell (e.g., vWA of sample “Reference10” in the above table) can be regarded as both homozygote (i.e., no drop-out) and heterozygote with drop-out of one allele when calculating the likelihood ratio.

3.3 STR: Allele frequencies

Note

- File type: .csv
- This file requires the columns “Allele” and columns for each marker (one column in each).

3.4 Y-STR: Victim database

Note

- File type: .csv
- This file requires the column “SampleName” and columns for each marker (one column in each).
- In the marker with more than one allele, each allele must be separated by a comma without any spaces (e.g., DYS385).
- The marker with an empty cell (e.g., DYS456 of sample ‘Victim6’) is ignored for analysis.

3.5 Y-STR: Reference database

Note

- File type: .csv
- This file requires the column “SampleName”, “Relationship”, and columns for each marker (one column in each).
- The relationship of a missing family member should be designated in the column “Relationship”. The name of the relationship should be defined in Settings > Relationships.
- If a reference has multiple missing family members, add rows for each relationship of the members (e.g., sibling and parent-child of the sample “Reference7” in the above table).

- In the marker with more than one allele, each allele must be separated by a comma without any spaces (e.g., DYS385).
- The marker with an empty cell (e.g., DYS518 of sample ‘Reference10’) is ignored for analysis.

3.6 mtDNA: Victim database

Note

- File type: .csv
- This file requires the column “SampleName”, “Range”, and “Haplotype”.

3.7 mtDNA: Reference database

Note

- File type: .csv
- This file requires the column “SampleName”, “Relationship”, “Range”, and “Haplotype”.
- The relationship of a missing family member should be designated in the column “Relationship”. The name of the relationship should be defined in Settings > Relationships.
- If a reference has multiple missing family members, add rows for each relationship of the members (e.g., sibling and parent-child of the sample “Reference7” in the above table).

4 Setting

4.1 Criteria

You can set the following criteria to support the assumed relationship. Press the **Save** button to reflect the changes. Press the **Reset** button if you want to return to default values.

4.1.1 STR

- Minimum LR: The minimum likelihood ratio that supports the assumed relationship

4.1.2 Y-STR

- Maximum number of mismatched loci: The upper limit of the number of mismatched loci between victim and reference profiles to support paternal lineage.
- Maximum total mutational steps: The upper limit of total mutational steps (i.e., sum of mutational steps of all loci) between victim and reference profiles to support paternal lineage.

4.1.3 mtDNA

- Maximum number of inconsistency: The upper limit of inconsistency between victim and reference profiles to support maternal lineage.

4.2 Relationship

4.3 Mutation rate

4.4 Other parameters

You can set the minimum allele frequency which is used for the unobserved alleles. Press the **Save** button to reflect the changes. Press the **Reset** button if you want to return to the default value.

5 Result

6 Other functions

6.1 Project

6.2 View database

6.3 Example files

Example files for each database can be downloaded from the **Example files** tab.

7 Computational principle

7.1 STR

7.1.1 Likelihood ratio

The likelihood ratio (LR) is calculated for each victim-reference pair by assuming the following two hypotheses:

H_1 : The victim and the reference are a certain relationship,

H_2 : The victim and the reference are unrelated.

The equation of the LR is as follows:

$$LR = \frac{Pr(G_v, G_r | H_1)}{Pr(G_v, G_r | H_2)}$$

where G_v and G_r denote the genotypes of the victim and the reference, respectively.

In RelSearch, users can set the minimum threshold of the LR to support H_1 . The default threshold is 100, which is determined based on the verbal scale “Moderate Support” written in the Scientific Working Group on DNA Analysis Methods (SWGDAM) guideline[1].

The LR without considering allelic drop-out and mutations is calculated based on the method of Wenk et al[2].

7.2 Y-STR

7.3 mtDNA

Reference

- [1] Scientific Working Group on DNA Analysis Methods, Recommendations of the SWG-DAM ad hoc working group on genotyping results reported as likelihood ratios., (2018).
- [2] R.E. Wenk, M. Traver, F.A. Chiafari, Determination of sibship in any two persons, Transfusion 36 (1996) 259–262.