

RelSearch version 0.21.0

User Manual

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2025-04-03

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Chapter 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('https://github.com/manabe0322/RelSearch/releases/download/
  ↵ v0.21.0/RelSearch_0.21.0.zip', repos = NULL, type = 'win.binary')
install.packages(c("shiny", "data.table", "dplyr", "DT", "magrittr",
  ↵ "pedtools", "Rcpp", "ribd", "shinyFeedback", "shinyjs", "shinythemes",
  ↵ "waiter"))
```

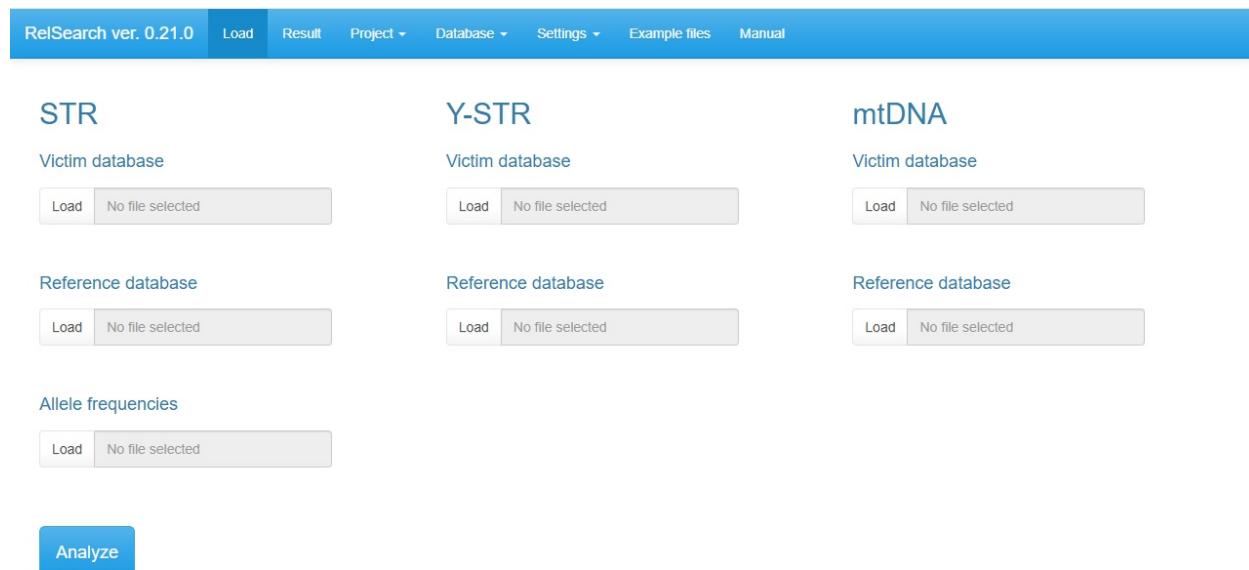
Chapter 2

Quick guide

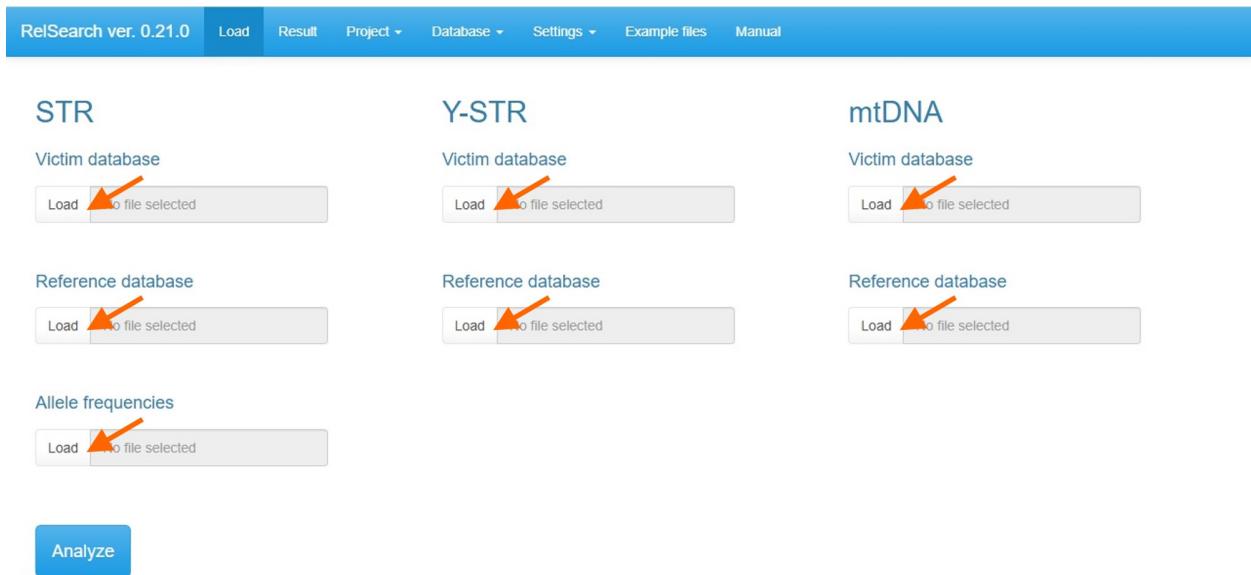
1. Execute the following commands in R to launch the software interface.

```
library(ReISearch)  
ReISearch()
```

Then, the software interface will open automatically.



2. Load files from each “Load” button.



Note

- RelSearch can analyze data for each marker type (i.e., autosomal STR, Y-STR, and mtDNA) separately as well as for all marker types together.
- For autosomal STR analysis, victim, reference, and allele frequency databases are required.
- For Y-STR analysis, victim and reference databases are required.
- For mtDNA analysis, victim and reference databases are required.
- See the [Files](#) section for information on each file.

3. Click the “Analysis” button.

STR

Victim database

Load str_victim_example.csv
Upload complete

Reference database

Load str_reference_example.csv
Upload complete

Allele frequencies

Load str_allele-freq_example.csv
Upload complete

Analyze

Y-STR

Victim database

Load y_victim_example.csv
Upload complete

Reference database

Load y_reference_example.csv
Upload complete

mtDNA

Victim database

Load mt_victim_example.csv
Upload complete

Reference database

Load mt_reference_example.csv
Upload complete

4. When the analysis is finished, the Result window opens automatically.

| Victim | Reference | Family | Assumed relationship | Estimated relationship | LR | Paternal lineage | Maternal lineage | Group of candidates |
|--------|-----------|--------|----------------------|------------------------|---------|------------------|------------------|---------------------|
| V4 | R4 | F4 | Mother_Daughter | Mother_Daughter | 6.33e+9 | All | All | All |
| V2 | R2 | F2 | Father_Daughter | Father_Daughter | 4.50e+8 | All | All | Excluded |
| V3 | R3 | F3 | Mother_Son | Mother_Son | 9.01e+7 | All | All | Not excluded |
| V1 | R1 | F1 | Father_Son | Father_Son | 4.12e+6 | Not excluded | All | Excluded |
| V19 | R19 | F19 | Father_Daughter | Father_Daughter | 3.93e+6 | All | All | Excluded |
| V5 | R5 | F5 | Brother_Brother | Brother_Brother | 2.48e+5 | Not excluded | All | Not excluded |
| V7 | R7 | F7 | Sister_Brother | Sister_Brother | 5.90e+4 | All | All | Not excluded |
| V22 | R22 | F21 | Brother_Sister | Brother_Sister | 1.77e+4 | All | All | Excluded |
| V21 | R21 | F20 | Paternal-aunt_Nephew | Paternal-aunt_Nephew | 7.95e+3 | Excluded | All | 2 |
| V21 | R21 | F20 | Sister_Brother | Sister_Brother | 3.11e+3 | All | All | Excluded |

Information

Data with LR greater than 100 is displayed.

Summary Selected data in detail Analysis conditions

Display setting

Show 10 entries Search:

Victim Reference Family Assumed relationship Estimated relationship LR Paternal lineage Maternal lineage Group of candidates

Identified

Multiple candidates

Inconclusive

Excluded

Minimum LR displayed 100

Apply

Download

Showing 1 to 10 of 19 entries Previous 1 2 Next

Note

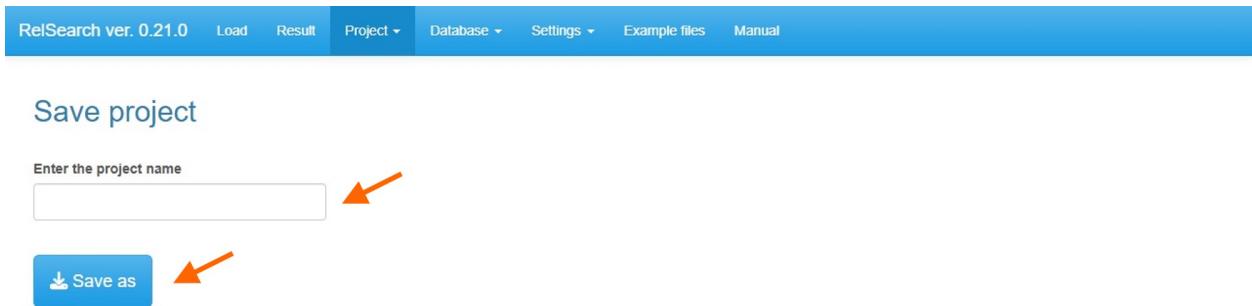
- See the **Result** section for information on navigating the Result window.

5. Select **Project ▶ Save project**.

The screenshot shows the RelSearch version 0.21.0 interface. The top navigation bar includes 'RelSearch ver. 0.21.0', 'Load', 'Result', 'Project ▾', 'Database ▾', 'Settings ▾', 'Example files', and 'Manual'. The 'Result' tab is selected, displaying a table of analysis results. The table has columns: Victim, Reference, Family, Assumed relationship, Estimated relationship, LR, Paternal lineage, Maternal lineage, and Group of candidates. The first few rows show results for V4, V2, V3, V1, V19, V5, V7, V22, V21, and V21. On the left, there's a 'Display setting' sidebar with buttons for 'Default display' (highlighted in blue), 'Identified', 'Multiple candidates', 'Inconclusive', and 'Excluded'. Below that is a 'Minimum LR displayed' input field set to 100, with an 'Apply' button. At the bottom is a 'Download' button with a download icon. A red arrow points to the 'Save project' option in the 'Project' dropdown menu.

| Victim | Reference | Family | Assumed relationship | Estimated relationship | LR | Paternal lineage | Maternal lineage | Group of candidates |
|--------|-----------|--------|----------------------|------------------------|---------|------------------|------------------|---------------------|
| V4 | R4 | F4 | Mother_Daughter | Mother_Daughter | 6.33e+9 | All | All | All |
| V2 | R2 | F2 | Father_Daughter | Father_Daughter | 4.50e+8 | All | All | Not excluded |
| V3 | R3 | F3 | Mother_Son | Mother_Son | 9.01e+7 | All | All | Not excluded |
| V1 | R1 | F1 | Father_Son | Father_Son | 4.12e+6 | Not excluded | All | Excluded |
| V19 | R19 | F19 | Father_Daughter | Father_Daughter | 3.93e+6 | All | All | 1 |
| V5 | R5 | F5 | Brother_Brother | Brother_Brother | 2.48e+5 | Not excluded | All | Not excluded |
| V7 | R7 | F7 | Sister_Brother | Sister_Brother | 5.90e+4 | All | All | Not excluded |
| V22 | R22 | F21 | Brother_Sister | Brother_Sister | 1.77e+4 | All | All | Excluded |
| V21 | R21 | F20 | Paternal-aunt_Nephew | Paternal-aunt_Nephew | 7.95e+3 | All | All | 2 |
| V21 | R21 | F20 | Sister_Brother | Sister_Brother | 3.11e+3 | All | All | Excluded |

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



Note

- The saved project can be loaded from **Project ▶ Load project**.
- How to handle projects is described in the **Other functions** section.

Chapter 3

Files

3.1 STR: Victim database

| SampleName | D3S1358 | D3S1358 | vWA | vWA | D16S539 | D16S539 | CSF1PO | CSF1PO |
|------------|---------|---------|-----|-----|---------|---------|--------|--------|
| Victim1 | 17 | 17 | 17 | | 11 | | 12 | |
| Victim2 | 17 | | 18 | 18 | | | 10 | 11 |
| Victim3 | 15 | 17 | 17 | 18 | 10 | 10 | 10 | 12 |
| Victim4 | 15 | 18 | 15 | 18 | 9 | 12 | 11 | 12 |
| Victim5 | 15 | 15 | 18 | | 9 | 9 | 10 | |

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., D16S539 of the sample “Victim2” in the above table) is ignored when calculating the likelihood ratio.
- The marker with one empty cell (e.g., vWA of the 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

| SampleName | Family | Relationship | D3S1358 | D3S1358 | vWA | vWA | D16S539 | D16S539 |
|------------|----------|-----------------|---------|---------|-----|-----|---------|---------|
| Reference1 | Family 1 | Father_Son | 17 | 17 | 14 | 17 | 10 | 10 |
| Reference2 | Family 2 | Brother_Brother | 16 | 17 | 17 | 17 | 10 | 12 |
| Reference3 | Family 3 | Brother_Brother | 16 | 17 | 14 | 18 | 9 | 9 |
| Reference3 | Family 3 | Father_Son | 16 | 17 | 14 | 18 | 9 | 9 |
| Reference4 | Family 4 | Brother_Brother | 15 | 16 | 17 | | 9 | 12 |
| Reference5 | Family 4 | Uncle_Nephew | 15 | 15 | 14 | 16 | | |

Note

- File type: .csv
- This file requires the columns “SampleName”, “Family”, “Relationship”, and columns for each marker (two columns in each).
- The names of the relationship need to be pre-defined in **Settings ▶ Relationships** (see section [Setting](#)).
- If there are multiple missing family members for a reference, add rows for each relationship of the members (e.g., Brother_Brother and Father_Son of the sample “Reference3” in the above table).
- The marker with two empty cells (e.g., D16S539 of the sample “Reference5” in the above table) is ignored when calculating the likelihood ratio.
- The marker with one empty cell (e.g., vWA of the sample “Reference4” 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

| Allele | D3S1358 | vWA | D16S539 | CSF1PO | TPOX |
|--------|---------|-----|---------|--------|------|
| 10 | | | 602 | 648 | 100 |
| 11 | | | 562 | 620 | 1072 |
| 12 | 6 | | 517 | 1267 | 114 |
| 13 | 3 | 1 | 209 | 208 | 3 |
| 14 | 79 | 586 | 26 | 52 | 2 |
| 15 | 1192 | 78 | 3 | 14 | |

Note

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

3.4 Y-STR: Victim database

| SampleName | DYS392 | DYS518 | DYS570 | DYS437 | DYS385 |
|------------|--------|--------|--------|--------|--------|
| Victim1 | 11 | 37 | 17 | 14 | 13,17 |
| Victim2 | 13 | 38 | 19 | 14 | 10,20 |
| Victim3 | 11 | 37 | 17 | 14 | 14 |
| Victim4 | 11 | 37 | 16 | 14 | 13 |
| Victim5 | | | 18 | | 13,17 |

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 in the above table).
- The marker with an empty cell (e.g., DYS392 of the sample ‘Victim5’ in the above table) is ignored for the analysis.

3.5 Y-STR: Reference database

| SampleName | Family | Relationship | DYS392 | DYS518 | DYS570 | DYS437 | DYS385 |
|------------|----------|-----------------|--------|--------|--------|--------|--------|
| Reference1 | Family 1 | Father_Son | 13 | 38 | 19 | 14 | 10,20 |
| Reference2 | Family 2 | Brother_Brother | 11 | 37 | 17 | 14 | 14,17 |
| Reference3 | Family 3 | Brother_Brother | 11 | 38 | 16 | 14 | 11 |
| Reference3 | Family 3 | Father_Son | 11 | 38 | 16 | 14 | 11 |
| Reference4 | Family 4 | Brother_Brother | 11 | 38 | 19 | 14 | 13,15 |
| Reference5 | Family 4 | Uncle_Nephew | 14 | | 18 | 14 | 13,18 |

Note

- File type: .csv
- This file requires the column "SampleName", "Family", "Relationship", and columns for each marker (one column in each).
- The names of the relationship need to be pre-defined in **Settings ▶ Relationships** (see section [Setting](#)).
- If there are multiple missing family members for a reference, add rows for each relationship of the members (e.g., Brother_Brother and Father_Son of the sample "Reference3" 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 in the above table).
- The marker with an empty cell (e.g., DYS518 of the sample 'Reference5' in the above table) is ignored for the analysis.

3.6 mtDNA: Victim database

| SampleName | Range | Haplotype |
|------------|----------------------------|--|
| Victim1 | 73-340 16024-16365 | 16183C 16189C 16217C 16311C 73G 263G 309.1C 315.1C |
| Victim2 | 73-340 16024-16365 | 16093C 16114A 16223T 16362C 73G 263G 309.1C 315.1C |
| Victim3 | 73-167 240-340 16024-16365 | 16095T 16189C 16223T 16265C 16274A 16362C 73G 263G |
| Victim4 | 73-265 16024-16284 | 16223T 73G 152C 263G |
| Victim5 | | |

Note

- File type: .csv
- This file requires the column "SampleName", "Range", and "Haplotype".
- In the 'Range' column, the first and the last positions in each readable sequence must be written with a hyphen between these positions (e.g., 73-340). The readable sequences must be separated by a single blank space.
- In the 'Haplotype' column, the mtDNA types are expressed as the differences to a reference sequence such as the revised Cambridge Reference Sequence [1] (e.g., 73G, 315.1C, and so on). Each mtDNA type must be separated by a single blank space.
- The empty cells in the 'Range' and 'Haplotype' columns (e.g., the sample 'Victim5' in the above table) mean that there is no readable sequence.

3.7 mtDNA: Reference database

| SampleName | Family | Relationship | Range | Haplotype |
|------------|----------|-----------------|--------------------|-------------------------------|
| Reference1 | Family 1 | Mother_Daughter | 73-340 16024-16365 | 16223T 73G 263G 309.1C 315.1C |
| Reference2 | Family 2 | Mother_Daughter | 73-340 16024-16365 | 16172C 16223T 73G 150T 263G |
| Reference3 | Family 3 | Brother_Brother | 73-340 16024-16365 | 16172C 16189C 16223T 73G 263G |
| Reference3 | Family 3 | Father_Son | 73-340 16024-16365 | 16172C 16189C 16223T 73G 263G |
| Reference4 | Family 4 | Sister_Sister | 73-340 16024-16365 | 16223T 16362C 73G 263G 315.1C |
| Reference5 | Family 4 | Aunt_Niece | | |

Note

- File type: .csv
- This file requires the column "SampleName", "Family", "Relationship", "Range", and "Haplotype".
- The names of the relationship need to be pre-defined in **Settings ▶ Relationships** (see section [Setting](#)).
- If there are multiple missing family members for a reference, add rows for each relationship of the members (e.g., Brother_Brother and Father_Son of the sample "Reference3" in the above table).
- In the 'Range' column, the first and the last positions in each readable sequence must be written with a hyphen between these positions (e.g., 73-340). The readable sequences must be separated by a single blank space.
- In the 'Haplotype' column, the mtDNA types are expressed as the differences to a reference sequence such as the revised Cambridge Reference Sequence [1] (e.g., 73G, 315.1C, and so on). Each mtDNA type must be separated by a single blank space.
- The empty cells in the 'Range' and 'Haplotype' columns (e.g., the sample 'Reference5' in the above table) mean that there is no readable sequence.

Chapter 4

Setting

4.1 Criteria

In RelSearch, users can set some criteria to identify or exclude the assumed relationship for each victim-reference pair. For autosomal STR, RelSearch calculates LR values for each victim-reference pair and investigates whether these LR values are greater than an LR threshold or not. For Y-STR, RelSearch analyzes the number of mismatched loci and the total mismatched steps between victim and reference Y-STR profiles to search paternal lineages. For mtDNA, RelSearch investigates the number of mismatched nucleotides between the victim and the reference sequences to search maternal lineages.

To set criteria, select **Setting ▶ Criteria**.

The screenshot shows the RelSearch software interface. At the top, there is a navigation bar with tabs: RelSearch ver. 0.21.0, Load, Result, Project, Database, Settings, Example files, and Manual. The 'Settings' tab is currently active, and a dropdown menu is open next to it. The 'Criteria' option in this menu is highlighted with a blue background and white text. An orange arrow points from the text 'To set criteria, select **Setting ▶ Criteria**.' to this 'Criteria' option. Below the navigation bar, there are sections for STR, Y-STR, and mtDNA analysis. Each section includes fields for 'Victim database' and 'Reference database', both with 'Load' and 'No file selected' buttons. There is also a section for 'Allele frequencies' with similar loading options. At the bottom left, there is a large blue 'Analyze' button.

Then the criteria setting window will open automatically.

The screenshot shows the RelSearch software interface with a blue header bar containing the version "RelSearch ver. 0.21.0" and navigation links: Load, Result, Project, Database, Settings, Example files, and Manual. Below the header are four main sections:

- LR Criteria**: Minimum LR to support the assumed relationship (input: 100), Maximum LR to exclude the assumed relationship (input: 0.01).
- Y-STR Usage Criteria**: Minimum number of loci with genotypes (input: 10).
- mtDNA Usage Criteria**: Minimum read length (bp) (input: 300).
- Paternal Lineage Criteria**: Maximum number of mismatched loci (input: 4), Upper limit of the total mutational steps (input: 5).
- Maternal Lineage Criteria**: Maximum number of inconsistency (input: 1).

At the bottom left are two buttons: "Save" and "Reset".

4.1.1 LR Criteria

- Minimum LR to support the assumed relationship: If the LR is greater than the set value, the victim-reference pair is supported as the assumed relationship.
- Maximum LR to exclude the assumed relationship: If the LR is less than the set value, the victim-reference pair is excluded from the assumed relationship.

Note

If the LR is between the above two values, the relationship of the victim-reference pair is considered inconclusive.

4.1.2 Y-STR Usage Criteria

- Minimum number of loci with genotypes: To adopt the Y-STR analysis result of a victim-reference pair, the number of loci where genotypes of both individuals are obtained must be greater than the set value. If the number is less than the set value, the paternal lineage of the victim-reference pair is considered inconclusive.

Note

The victim-reference pair that does not meet the following Paternal Lineage Criteria is excluded from the paternal lineage even if the pair does not meet the Y-STR Usage Criteria.

4.1.3 Paternal Lineage Criteria

- Maximum number of mismatched loci: If the number of mismatched loci in a victim-reference pair is greater than the set value, the pair is excluded from the paternal lineage.
- Upper limit of the total mutational steps: If the total mutational steps in a victim-reference pair is greater than the set value, the pair is excluded from the paternal lineage.

4.1.4 mtDNA Usage Criteria

- Minimum read length (bp): To adopt the mtDNA analysis result of a victim-reference pair, the read length in both individuals must be greater than the set value. If the number is less than the set value, the maternal lineage of the victim-reference pair is considered inconclusive.

Note

The victim-reference pair that does not meet the following Maternal Lineage Criteria is excluded from the maternal lineage even if the pair does not meet the mtDNA Usage Criteria.

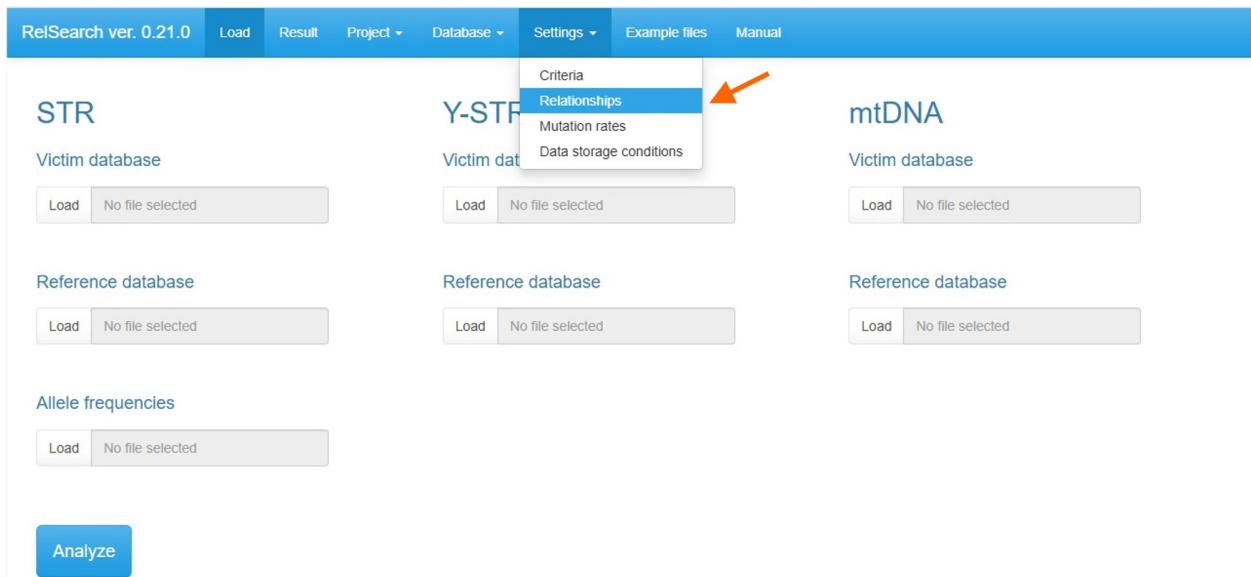
4.1.5 Maternal Lineage Criteria

- Maximum number of inconsistency: If the number of inconsistency in a victim-reference pair is greater than the set value, the pair is excluded from the maternal lineage.

After changing the criteria, press the **Save** button to reflect the changes. Press the **Reset** button if you want to return to default values.

4.2 Relationship

The names of the relationship in each reference profile need to be pre-defined. To define the relationship names, select **Setting ▶ Relationships**.



Then the relationship setting window will open automatically.

| Relationships | | | | | | | |
|-----------------|--------------|-----------------|--------------|--------------|--------------|------------------|------------------|
| Show 10 entries | | | | | | | |
| Relationship | Sex (Victim) | Sex (Reference) | Pr (IBD = 2) | Pr (IBD = 1) | Pr (IBD = 0) | Paternal lineage | Maternal lineage |
| Father_Son | M | M | 0 | 1 | 0 | Yes | No |
| Father_Daughter | M | F | 0 | 1 | 0 | No | No |
| Mother_Son | F | M | 0 | 1 | 0 | No | Yes |
| Mother_Daughter | F | F | 0 | 1 | 0 | No | Yes |
| Son_Father | M | M | 0 | 1 | 0 | Yes | No |
| Son_Mother | M | F | 0 | 1 | 0 | No | Yes |
| Daughter_Father | F | M | 0 | 1 | 0 | No | No |
| Daughter_Mother | F | F | 0 | 1 | 0 | No | Yes |
| Brother_Brother | M | M | 0.25 | 0.5 | 0.25 | Yes | Yes |
| Brother_Sister | M | F | 0.25 | 0.5 | 0.25 | No | Yes |

Showing 1 to 10 of 44 entries

Previous 1 2 3 4 5 Next

There are 44 pre-defined victim-reference relationships as the default. The names of these relationships are determined in the order of victim_reference (e.g., Father_Son means that a victim is the father and a reference is the son). You are free to change these names.

Information on the table is as follows.

- **Sex (Victim):** The biological sex of the victim
- **Sex (Reference):** The biological sex of the reference
- **Pr(IBD = 2):** The probability that two alleles are identity by descent (IBD).
- **Pr(IBD = 1):** The probability that one allele is identity by descent (IBD).
- **Pr(IBD = 0):** The probability that zero allele is identity by descent (IBD).
- **Paternal lineage:** Information on whether each relationship is paternal lineage or not.
- **Maternal lineage:** Information on whether each relationship is maternal lineage or not.

You can edit, add, and delete the relationships from the left sidebar.

4.2.1 Edit

You can edit the relationship names from the **Edit** button.

The screenshot shows the RelSearch software interface. At the top, there is a navigation bar with options: RelSearch ver. 0.21.0, Load, Result, Project, Database, Settings, Example files, and Manual. Below the navigation bar, the main window has a title 'Relationship' and several buttons: Edit, Add, Delete, Reset, and Family tree. A modal dialog box is open over the main window, titled 'Edit the name of the relationship'. Inside the dialog, there is a dropdown menu labeled 'Select a relationship' containing the option 'Father_Son'. Below it is a text input field labeled 'Enter a new name' with an empty text box. At the bottom right of the dialog are two buttons: 'Save' and 'Cancel'. In the background, there is a table with columns: Mother_Daughter, Father_Son, Son_Mother, Daughter_Father, Daughter_Mother, Brother_Brother, and Brother_Sister. The table contains data such as gender (M or F), counts (0 or 1), and lineage (Yes or No). The table also includes a 'Maternal lineage' column with values 'No', 'No', 'Yes', 'Yes', 'Yes', 'No', and 'Yes'. At the bottom of the table, it says 'Showing 1 to 10 of 44 entries' and has a page navigation section with buttons for Previous, Next, and page numbers 1, 2, 3, 4, 5.

In the pop-up window, select a relationship from the defined relationships, and enter a new name of the selected relationship. Press the **Save** button to reflect the new name.

4.2.2 Add

You can define a new relationship from the **Add** button. Then, the following pop-up window will open.

Add information on a relationship

Relationship

Family tree

Incorrect setting of the family tree!

Set a family tree

[Add a person](#)[Delete a person](#)[View family tree](#)

| Person | Sex | Father | Mother | Founder |
|--------|-----|--------|--------|---------|
| Victim | M | Victim | Victim | No |
| Ref | M | Victim | Victim | No |

[Save](#) [Cancel](#)

The procedure is as follows.

1. Enter a relationship name.
2. Make a family tree to define the relationship between a victim and a reference. The following is a list of functions to make a family tree.
 - **Add a person:** The function to add an unknown person (UK) to the list of persons.
 - **Delete a person:** The function to delete an unknown person (UK) from the list of persons.
 - **Sex:** The function to select a biological sex (male: M or female: F).
 - **Father:** The function to select a person who is the father.
 - **Mother:** The function to select a person who is the mother.
 - **Founder:** The function to select whether the person is a founder of the family tree or not.

Here is an example of defining the brother-brother relationship for the victim-reference pair.

- 2.1. Press the **Add** button twice to add the untyped father and mother. UK1 and UK2 are assumed to be the father and mother, respectively.
- 2.2. Set the sex of the Victim, Ref, UK1, and UK2 to "M", "M", "M", and "F", respectively.
- 2.3. In the Founder column, select "No" for Victim and Ref, and select "Yes" for UK1 and UK2.
- 2.4. In the Father column, select "UK1" for Victim and Ref.
- 2.5. In the Mother column, select "UK2" for Victim and Ref.

Set a family tree

| Add a person | Delete a person | View family tree | | |
|--------------|-----------------|------------------|--------|---------|
| Person | Sex | Father | Mother | Founder |
| Victim | M | UK1 | UK2 | No |
| Ref | M | UK1 | UK2 | No |
| UK1 | M | Victim | Victim | Yes |
| UK2 | F | Victim | Victim | Yes |

3. Press the **View family tree** button to check whether the relationship between a victim and a reference is correctly defined or not.

Add information on a relationship

| | |
|---|---|
| Relationship <input type="text"/> | Family tree Incorrect setting of the family tree! |
|---|---|

Set a family tree

Add a person

Delete a person

View family tree



Person

Sex

Father

Mother

Founder

Victim

M

UK1

UK2

No

Ref

M

UK1

UK2

No

UK1

M

Victim

Victim

Yes

UK2

F

Victim

Victim

Yes

Save

Cancel

If the relationship between a victim and a reference is correctly defined, the family tree will be displayed.

Add information on a relationship

Relationship

Family tree

```
graph TD; UK1[UK1] --- Bar[ ]; Bar --- Ref[Ref]; Bar --- Victim[Victim]
```

Set a family tree

[Add a person](#)

[Delete a person](#)

[View family tree](#)

| Person | Sex | Father | Mother | Founder |
|--------|-----|--------|--------|---------|
| Victim | M | UK1 | UK2 | No |
| Ref | M | UK1 | UK2 | No |
| UK1 | M | Victim | Victim | Yes |
| UK2 | F | Victim | Victim | Yes |

[Save](#)

[Cancel](#)

4. Press the **Save** button.

Add information on a relationship

Relationship

Family tree

```
graph TD; UK1[UK1] --- Ref[Ref]; UK1 --- Victim[Victim]; UK2[UK2] --- Ref; UK2 --- Victim;
```

Set a family tree

[Add a person](#)[Delete a person](#)[View family tree](#)

| Person | Sex | Father | Mother | Founder |
|--------|-----|--------|--------|---------|
| Victim | M | UK1 | UK2 | No |
| Ref | M | UK1 | UK2 | No |
| UK1 | M | Victim | Victim | Yes |
| UK2 | F | Victim | Victim | Yes |

SaveCancel



Note

Information on the biological sex, IBD probabilities, paternal lineage, and maternal lineage in the new relationship is automatically determined based on your-defined family tree.

4.2.3 Delete

You can delete a defined relationship from the **Delete** button.

In the pop-up window, select a relationship from the defined relationships. Press the **Save** button to delete the selected relationship.

The screenshot shows the RelSearch version 0.21.0 interface. The main menu bar includes Load, Result, Project, Database, Settings, Example files, and Manual. A sub-menu 'Relationship' is open, showing options like Edit, Add, Delete, Reset, and Family tree. The 'Delete' button is highlighted. A modal dialog box titled 'Delete information on a relationship' is displayed. It contains a dropdown menu labeled 'Select a relationship' with 'Father_Son' selected. At the bottom right of the dialog are 'Save' and 'Cancel' buttons. Below the dialog is a table listing various relationships with columns for gender (M/F), counts (0/1), and lineage (Maternal lineage: Yes/No). The table shows the following data:

| Relationship | M | F | 0 | 1 | 0 | No | Maternal lineage |
|-----------------|---|---|------|-----|------|-----|------------------|
| Father_Daughter | M | F | 0 | 1 | 0 | No | No |
| Mother_Son | F | M | 0 | 1 | 0 | No | Yes |
| Mother_Daughter | F | F | 0 | 1 | 0 | No | Yes |
| Son_Father | M | M | 0 | 1 | 0 | Yes | No |
| Son_Mother | M | F | 0 | 1 | 0 | No | Yes |
| Daughter_Father | F | M | 0 | 1 | 0 | No | No |
| Daughter_Mother | F | F | 0 | 1 | 0 | No | Yes |
| Brother_Brother | M | M | 0.25 | 0.5 | 0.25 | Yes | Yes |
| Brother_Sister | M | F | 0.25 | 0.5 | 0.25 | No | Yes |

At the bottom of the table, it says 'Showing 1 to 10 of 44 entries'. To the right, there are navigation buttons for Previous, Next, and page numbers 1, 2, 3, 4, 5.

4.2.4 Reset

If you want to return to default settings, press the **Reset** button. In the pop-up window, press the **Restore default** button.

The screenshot shows the RelSearch software interface. A modal dialog box titled "Reset information on the relationship" is open in the center. It contains the instruction "Click Restore default to remove all changes." Below this is a table of relationships with columns for gender (M/F), values (0, 0.25, 0.5), and lineage (Yes/No). At the bottom of the dialog are "Restore default" and "Cancel" buttons. The main interface shows a "Relationships" table with 44 entries, a sidebar with buttons for Edit, Add, Delete, Reset, and Family tree, and a top navigation bar with RelSearch version 0.21.0 and various project and database options.

| Relationship | M | F | 0 | 1 | 0 | Yes | No |
|-----------------|---|---|------|-----|------|-----|-----|
| Father_Son | M | M | 0 | 1 | 0 | Yes | No |
| Father_Daughter | M | F | 0 | 1 | 0 | No | No |
| Mother_Son | F | M | 0 | 1 | 0 | No | Yes |
| Mother_Daughter | F | F | 0 | 1 | 0 | No | Yes |
| Son_Father | M | M | 0 | 1 | 0 | Yes | No |
| Son_Mother | M | F | 0 | 1 | 0 | No | Yes |
| Daughter_Father | F | M | 0 | 1 | 0 | No | No |
| Daughter_Mother | F | F | 0 | 1 | 0 | No | Yes |
| Brother_Brother | M | M | 0.25 | 0.5 | 0.25 | Yes | Yes |
| Brother_Sister | M | F | 0.25 | 0.5 | 0.25 | No | Yes |

4.2.5 Family tree

You can check the family tree of each defined relationship. Select a row from the relationship table and press the **Family tree** button.

RelSearch ver. 0.21.0 Load Result Project Database Settings Example files Manual

Relationships

| Relationship | Sex (Victim) | Sex (Reference) | Pr (IBD = 2) | Pr (IBD = 1) | Pr (IBD = 0) | Paternal lineage | Maternal lineage |
|-----------------|--------------|-----------------|--------------|--------------|--------------|------------------|------------------|
| Father_Son | M | M | 0 | 1 | 0 | Yes | No |
| Father_Daughter | M | F | 0 | 1 | 0 | No | No |
| Mother_Son | F | M | 0 | 1 | 0 | No | Yes |
| Mother_Daughter | F | F | 0 | 1 | 0 | No | Yes |
| Son_Father | M | M | 0 | 1 | 0 | Yes | No |
| Son_Mother | M | F | 0 | 1 | 0 | No | Yes |
| Daughter_Father | F | M | 0 | 1 | 0 | No | No |
| Daughter_Mother | F | F | 0 | 1 | 0 | No | Yes |
| Brother_Brother | M | M | 0.25 | 0.5 | 0.25 | Yes | Yes |
| Brother_Sister | M | F | 0.25 | 0.5 | 0.25 | No | Yes |

Show 10 entries Search: _____

Showing 1 to 10 of 44 entries Previous 1 2 3 4 5 Next

Then, the family tree will be displayed.

RelSearch ver. 0.21.0 Load Result Project Database Settings Example files Manual

Relationship: Father_Son

Relationships

| Relationship | Sex (Victim) | Sex (Reference) | Pr (IBD = 2) | Pr (IBD = 1) | Pr (IBD = 0) | Paternal lineage | Maternal lineage |
|-----------------|--------------|-----------------|--------------|--------------|--------------|------------------|------------------|
| Father_Son | M | M | 0 | 1 | 0 | Yes | No |
| Father_Daughter | M | F | 0 | 1 | 0 | No | No |
| Mother_Son | F | M | 0 | 1 | 0 | No | Yes |
| Mother_Daughter | F | F | 0 | 1 | 0 | No | Yes |
| Son_Father | M | M | 0 | 1 | 0 | Yes | No |
| Son_Mother | M | F | 0 | 1 | 0 | No | Yes |
| Daughter_Father | F | M | 0 | 1 | 0 | No | No |
| Daughter_Mother | F | F | 0 | 1 | 0 | No | Yes |
| Brother_Brother | M | M | 0.25 | 0.5 | 0.25 | Yes | Yes |
| Brother_Sister | M | F | 0.25 | 0.5 | 0.25 | No | Yes |

Victim --- UK1

Ref

Close

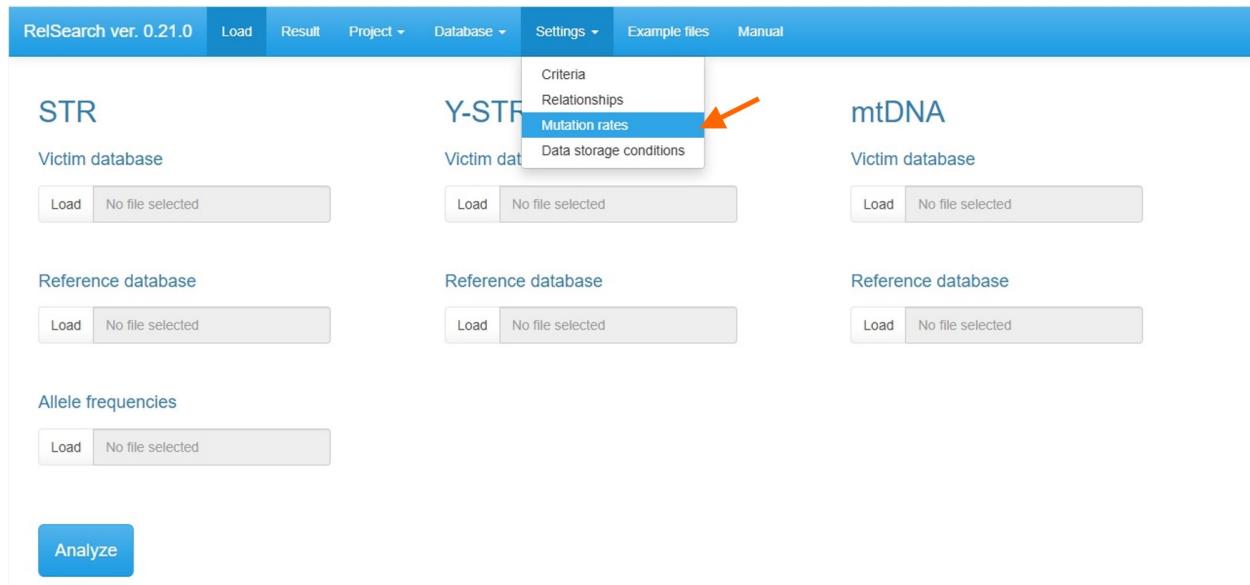
Show 10 entries Search: _____

Showing 1 to 10 of 44 entries Previous 1 2 3 4 5 Next

4.3 Mutation rate

Mutation rates of each autosomal STR marker need to be set to calculate the likelihood ratio (LR) for parent-child relationship. The default mutation rates considering the difference between paternal and maternal and mutational steps (-1, +1, -2, and +2) are reported by Morimoto et al [2].

To set mutation rates, select **Setting ▶ Mutation rates**.



Then the setting window for mutation rates will open automatically.

| Mutation rates | | | | | | | | | | |
|--|------------------|------------------|-----------------|------------------|------------------|------------------|------------------|-----------------|------------------|------------------|
| <input type="button" value="Edit"/> <input type="button" value="Add"/> <input type="button" value="Delete"/> <input type="button" value="Reset"/> Show: <select>50</select> entries Search: <input type="text"/> | | | | | | | | | | |
| Locus | Paternal -2 step | Paternal -1 step | Paternal 0 step | Paternal +1 step | Paternal +2 step | Maternal -2 step | Maternal -1 step | Maternal 0 step | Maternal +1 step | Maternal +2 step |
| D3S1358 | 0.000037 | 0.001423565 | 0.997353441 | 0.001148329 | 0.0000377 | 0 | 0.0001927 | 0.99969733 | 0.0000756 | 0.0000344 |
| VWA | 0.000146413 | 0.002718279 | 0.994905627 | 0.002200527 | 0.0000292 | 0 | 0.000125004 | 0.999377764 | 0.000444731 | 0.0000525 |
| D16S539 | 0.0000841 | 0.00093427 | 0.997628583 | 0.001353042 | 0 | 0 | 0.000484253 | 0.999411835 | 0.000103912 | 0 |
| CSF1PO | 0 | 0.002042983 | 0.996111065 | 0.001845931 | 0 | 0 | 0.000212751 | 0.99940775 | 0.0003795 | 0 |
| TPOX | 0 | 0.000115566 | 0.999697045 | 0.000187388 | 0 | 0 | 0.0000751 | 0.999848984 | 0.0000761 | 0 |
| D8S1179 | 0.0000482 | 0.001301255 | 0.997430135 | 0.001196466 | 0.0000239 | 0 | 0.000133755 | 0.999702176 | 0.000141848 | 0.0000222 |
| D2S111 | 0.000037 | 0.000867972 | 0.998012667 | 0.001082339 | 0 | 0.000036 | 0.000107823 | 0.999727236 | 0.000128943 | 0 |
| D16S51 | 0.000014735 | 0.000942863 | 0.997459246 | 0.001420767 | 0.00000298 | 0.0000213 | 0.000117496 | 0.999364128 | 0.000475501 | 0.0000215 |
| D2S441 | 0.00000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 | 0.00000871 |
| D19S433 | 0 | 0.000958424 | 0.998425005 | 0.000452336 | 0.000164235 | 0 | 0.000504888 | 0.99943539 | 0.0000597 | 0 |
| TH01 | 0 | 0.0000448 | 0.999895495 | 0.0000597 | 0 | 0.000017 | 0.0000546 | 0.999920126 | 0.00000829 | 0 |
| FGA | 0.000277755 | 0.001497345 | 0.995437569 | 0.002707954 | 0.0000794 | 0 | 0.000348321 | 0.999356247 | 0.000293432 | 0 |
| D22S1045 | 0.00000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 | 0.00000871 |
| D5S818 | 0 | 0.001420549 | 0.9968405 | 0.001198 | 0.000540952 | 0 | 0.000258823 | 0.999462401 | 0.000278776 | 0 |
| D13S317 | 0 | 0.001369203 | 0.997193828 | 0.001397392 | 0.0000396 | 0.0000333 | 0.0000708 | 0.999657082 | 0.000238821 | 0 |
| D7S820 | 0 | 0.001302502 | 0.997627141 | 0.000870357 | 0 | 0 | 0.0000622 | 0.999813227 | 0.000124612 | 0 |
| SE33 | 0.00000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 | 0.00000871 |
| D10S1248 | 0.00000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 | 0.00000871 |
| n16S539 | 0.00000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 | 0.00000871 |

4.3.1 Edit

You can edit the mutation rates from the **Edit** button.

In the pop-up window, select a locus and change the mutation rates. Press the **Save** button to reflect the changes.

The screenshot shows the RelSearch software interface with the 'Edit a mutation rate' dialog box open. The dialog box has a title 'Edit a mutation rate' and a sub-section 'Mutation rate'. On the left, there is a sidebar with buttons for 'Edit', 'Add', 'Delete', and 'Reset'. A dropdown menu 'Select a locus' is set to 'D3S1358'. The main area contains two columns of mutation rate fields for 'Paternal' and 'Maternal' steps across three levels: -2 step, -1 step, +1 step, and +2 step. The 'Edit' button is highlighted in the sidebar. Below the dialog box, a table of mutation rates for various loci is visible.

| Locus | Paternal -2 step | Maternal -2 step | Paternal -1 step | Maternal -1 step | Paternal +1 step | Maternal +1 step | Paternal +2 step | Maternal +2 step | |
|----------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------|
| D19S433 | 0 | 0.000958424 | 0.998425005 | 0.000452336 | 0.000164235 | 0 | 0.000504888 | 0.99943539 | 0.0000597 |
| TH01 | 0 | 0.0000448 | 0.999895495 | 0.0000597 | 0 | 0.000017 | 0.0000546 | 0.999920126 | 0.00000829 |
| FGA | 0.000277755 | 0.001497345 | 0.995437569 | 0.002707964 | 0.0000794 | 0 | 0.000348321 | 0.999358247 | 0.000293432 |
| D22S1045 | 0.0000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 |

4.3.2 Add

You can add a locus from the **Add** button.

In the pop-up window, enter a locus name and enter the mutation rates. Press the **Save** button to add the locus.

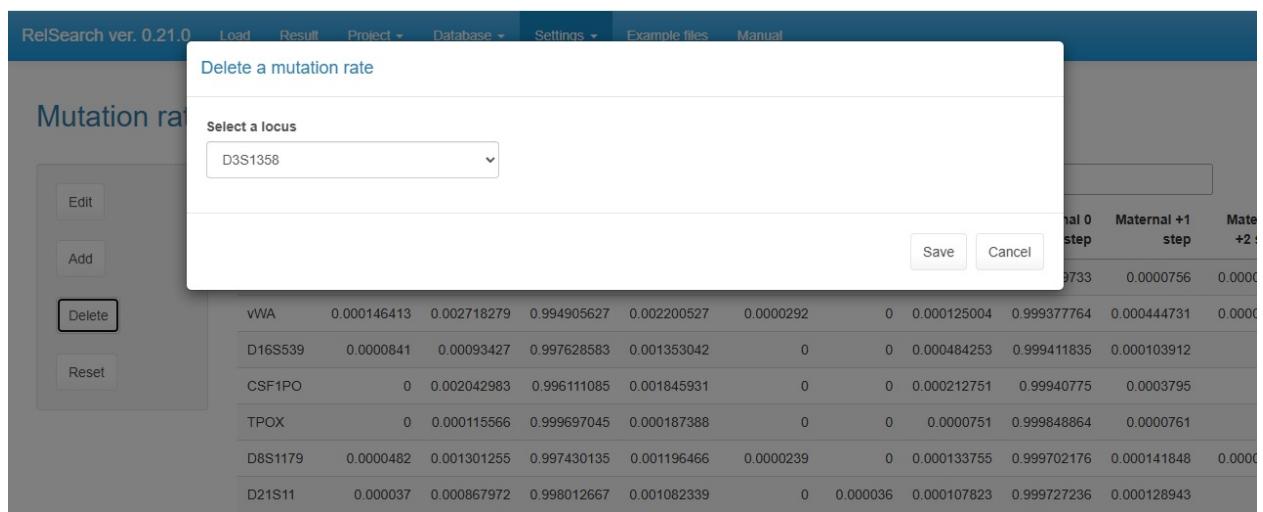
The screenshot shows the RelSearch software interface. At the top, there is a navigation bar with tabs: RelSearch ver. 0.21.0, Load, Result, Project, Database, Settings, Example files, and Manual. Below the navigation bar, there is a sidebar titled "Mutation rates" with buttons for Edit, Add, Delete, and Reset. A modal dialog box titled "Add a mutation rate" is open in the center. This dialog box contains fields for "Locus name" and "Mutation rates" for various steps: Paternal -2 step, Maternal -2 step, Paternal -1 step, Maternal -1 step, Paternal +1 step, Maternal +1 step, and Paternal +2 step. At the bottom of the dialog box are "Save" and "Cancel" buttons. In the background, a table of mutation rates for different loci (D19S433, TH01, FGA, D22S1045) is visible.

| Locus | Paternal -2 step | Maternal -2 step | Paternal -1 step | Maternal -1 step | Paternal +1 step | Maternal +1 step | Paternal +2 step | Maternal +2 step | |
|----------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------|
| D19S433 | 0 | 0.000958424 | 0.998425005 | 0.000452336 | 0.000164235 | 0 | 0.000504888 | 0.99943539 | 0.0000597 |
| TH01 | 0 | 0.0000448 | 0.999895495 | 0.0000597 | 0 | 0.000017 | 0.0000546 | 0.999920126 | 0.00000829 |
| FGA | 0.000277755 | 0.001497345 | 0.995437569 | 0.002707964 | 0.0000794 | 0 | 0.000348321 | 0.999358247 | 0.000293432 |
| D22S1045 | 0.0000544 | 0.001166981 | 0.997463648 | 0.001250749 | 0.0000642 | 0.0000149 | 0.000270098 | 0.999494265 | 0.000212047 |

4.3.3 Delete

You can delete a locus from the **Delete** button.

In the pop-up window, select a locus. Press the **Save** button to delete the selected locus.



4.3.4 Reset

If you want to return to default settings, press the **Reset** button. In the pop-up window, press the **Restore default** button.

The screenshot shows the RelSearch version 0.21.0 interface. The main window displays 'Mutation rates' for various loci (D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11) with their respective mutation rates across different steps. A modal dialog box titled 'Reset the mutation rates' is overlaid on the main window. The dialog contains the message 'Click Restore default to remove all changes.' and two buttons: 'Restore default' and 'Cancel'. There is also a 'Search:' input field at the top right of the dialog. The 'Reset' button on the left side of the main window is highlighted with a red box.

| Locus | step | step | step | step | step | -2 step | Maternal -1 step | Maternal 0 step | Maternal +1 step | Mat +2 |
|---------|-------------|-------------|-------------|-------------|-----------|---------|------------------|-----------------|------------------|-------------|
| D3S1358 | 0.000037 | 0.001423565 | 0.997353441 | 0.001148329 | 0.0000377 | 0 | 0.0001927 | 0.99969733 | 0.0000756 | 0.0000 |
| vWA | 0.000146413 | 0.002718279 | 0.994905627 | 0.002200527 | 0.0000292 | 0 | 0.000125004 | 0.999377764 | 0.000444731 | 0.0000 |
| D16S539 | 0.0000841 | 0.00093427 | 0.997628583 | 0.001353042 | | 0 | 0.000484253 | 0.999411835 | 0.000103912 | |
| CSF1PO | 0 | 0.002042983 | 0.996111085 | 0.001845931 | | 0 | 0.000212751 | 0.99940775 | 0.0003795 | |
| TPOX | 0 | 0.000115566 | 0.999697045 | 0.000187388 | | 0 | 0.0000751 | 0.999848864 | 0.0000761 | |
| D8S1179 | 0.0000482 | 0.001301255 | 0.997430135 | 0.001196466 | 0.0000239 | 0 | 0.000133755 | 0.999702176 | 0.000141848 | 0.0000 |
| D21S11 | 0.000037 | 0.000867972 | 0.998012667 | 0.001082339 | | 0 | 0.000036 | 0.000107823 | 0.999727236 | 0.000128943 |

4.4 Data storage conditions

When handling a large number of victim and reference profiles, it may be difficult to store all the results because RelSearch may run out of memory. You can set the data storage conditions.

To set the conditions, select **Setting ▶ Data storage conditions**.

The screenshot shows the RelSearch software interface. At the top, there is a blue header bar with the text "RelSearch ver. 0.21.0", "Load", "Result", "Project", "Database", "Settings", "Example files", and "Manual". Below the header, there are three main sections: STR, Y-STR, and mtDNA. Each section has fields for "Victim database" and "Reference database", each with a "Load" button and a "No file selected" placeholder. An orange arrow points to the "Data storage conditions" option in the "Settings" dropdown menu, which is part of a submenu that also includes "Criteria", "Relationships", and "Mutation rates". At the bottom left, there is a blue "Analyze" button.

Then the setting window for data storage will open automatically.

The screenshot shows the 'Data storage conditions' settings page of RelSearch. At the top, there is a navigation bar with tabs: 'RelSearch ver. 0.21.0', 'Load', 'Result', 'Project ▾', 'Database ▾', 'Settings ▾', 'Example files', and 'Manual'. Below the navigation bar, the title 'Data storage conditions' is displayed. There are two input fields: 'Minimum LR to be stored' (containing the value '1') and 'Maximum number of displayed data' (containing the value '10000'). At the bottom of the page are two buttons: 'Save' and 'Reset'.

- Minimum LR to be stored: The minimum LR to be stored in the project data. If you want to reduce the file size of the project data, the minimum LR should be increased.
- Maximum number of displayed data: The maximum number of data displayed in the Results tab. If this number is set too high, RelSearch may run out of memory.

Press the **Save** button to reflect the changes. Press the **Reset** button if you want to return to default values.

Chapter 5

Result

This section describes the display of results on the Results tab.

5.1 Summary

When the analysis is complete, summary data is automatically displayed. You can change the data displayed using the buttons in the left sidebar. You can also download the displayed data as a .csv file using the **Download** button.

The screenshot shows the RelSearch software interface with the 'Result' tab selected. The top navigation bar includes 'RelSearch ver. 0.21.0', 'Load', 'Result', 'Project', 'Database', 'Settings', 'Example files', and 'Manual'. The 'Result' tab has three sub-options: 'Summary' (selected), 'Selected data in detail', and 'Analysis conditions'. On the left, a sidebar titled 'Display setting' contains buttons for 'Default display' (highlighted in blue), 'Identified' (green), 'Multiple candidates' (blue), 'Inconclusive' (orange), and 'Excluded' (red). It also includes a 'Minimum LR displayed' input field set to '100' and an 'Apply' button. At the bottom of the sidebar is a 'Download' button with a CSV icon. The main area displays a table of 19 entries with columns: Victim, Reference, Family, Assumed relationship, Estimated relationship, LR, Paternal lineage, Maternal lineage, and Group of candidates. The table includes search and filter options at the top. The first few rows of data are:

| Victim | Reference | Family | Assumed relationship | Estimated relationship | LR | Paternal lineage | Maternal lineage | Group of candidates |
|--------|-----------|--------|----------------------|------------------------|---------|------------------|------------------|---------------------|
| V4 | R4 | F4 | Mother_Daughter | Mother_Daughter | 6.33e+9 | All | All | All |
| V2 | R2 | F2 | Father_Daughter | Father_Daughter | 4.50e+8 | All | All | All |
| V3 | R3 | F3 | Mother_Son | Mother_Son | 9.01e+7 | All | All | All |
| V1 | R1 | F1 | Father_Son | Father_Son | 4.12e+6 | Not excluded | Excluded | 1 |
| V19 | R19 | F19 | Father_Daughter | Father_Daughter | 3.93e+6 | Excluded | 1 | 1 |
| V5 | R5 | F5 | Brother_Brother | Brother_Brother | 2.48e+5 | Not excluded | Not excluded | 1 |
| V7 | R7 | F7 | Sister_Brother | Sister_Brother | 5.90e+4 | All | All | All |
| V22 | R22 | F21 | Brother_Sister | Brother_Sister | 1.77e+4 | Excluded | Excluded | 2 |
| V21 | R21 | F20 | Paternal-aunt_Nephew | Paternal-aunt_Nephew | 7.95e+3 | Excluded | Excluded | 2 |
| V21 | R21 | F20 | Sister_Brother | Sister_Brother | 3.11e+3 | Excluded | Excluded | 2 |

At the bottom of the main area, it says 'Showing 1 to 10 of 19 entries' and has navigation buttons for 'Previous', page numbers '1', '2', and 'Next'.

Default display

Default display depends on whether the input data includes autosomal STR data or not.

- If the input data includes autosomal STR data, the data that satisfies the criterion of the 'Minimum LR to support the assumed relationship' (see section [Setting](#)) is displayed.
- If the input data is composed of only Y-STR and/or mtDNA data, data that is not excluded from paternal or maternal lineages (see section [Setting](#)) is displayed.
- If the number of data that satisfies the above conditions is more than the upper limit (i.e., the maximum number of displayed data explained in section [Data storage conditions](#)), the number of data displayed is the upper limit.

Identified

If the data supports that a victim (or a reference) has the assumed relationship with only one reference (or victim), the victim-reference pair is classified as "Identified". The LR must be greater than 'Minimum LR to support the assumed relationship' (see section [Criteria](#)) for classification as "Identified". In addition, if the assumed relationship is paternal or maternal lineage, the paternal or maternal lineage criteria (see section [Criteria](#)) must be also satisfied.

Multiple candidates

If the data supports that a victim (or a reference) has the assumed relationship with multiple references (or victims), the victim-reference pair is classified as "Multiple candidates". The LR must be greater than 'Minimum LR to support the assumed relationship' (see section [Criteria](#)) for classification as "Multiple candidates". In addition, if the assumed relationship is paternal or maternal lineage, the paternal or maternal lineage criteria (see section [Criteria](#)) must be also satisfied.

Inconclusive

The victim-reference pair is classified as "Inconclusive" if the pair is not classified in any of the other categories. The "Inconclusive" category includes the following data.

- The LR is between 'Maximum LR to exclude the assumed relationship' and 'Minimum LR to support the assumed relationship' (see section [Criteria](#)).
- The data does not meet the Y-STR Usage Criteria when the victim-reference pair is not excluded from the paternal lineage (see section [Criteria](#)).
- The data does not meet the mtDNA Usage Criteria when the victim-reference pair is not excluded from the maternal lineage (see section [Criteria](#)).
- Autosomal STR data is not available.

Excluded

The victim-reference pair is excluded from the assumed relationship according to the following conditions:

- The LR is less than 'Maximum LR to exclude the assumed relationship' (see section [Criteria](#)).
- The paternal or maternal lineage criteria (see section [Criteria](#)) is not satisfied when the assumed relationship is paternal or maternal lineage.

Minimum LR displayed

You can change the minimum LR displayed. After setting the value, press the **Apply** button. Please note that the amount of data stored in the project data is limited according to the data storage conditions (see [Data storage conditions](#)). For example, even if you set the minimum LR displayed to less than 1, you cannot check the data with $LR < 1$ as long as the minimum LR to be stored in the project data is set to 1.

5.2 Selected data in detail

The detailed data of a selected victim-reference pair is displayed in **Selected data in detail** tab.

1. Select a row in the summary table.

RelSearch ver. 0.21.0 Load Result Project Database Settings Example files Manual

Result

Summary Selected data in detail Analysis conditions

Display setting

Show 10 entries

Victim Reference Family Assumed relationship Estimated relationship LR Paternal lineage Maternal lineage Group of candidates

| Victim | Reference | Family | Assumed relationship | Estimated relationship | LR | Paternal lineage | Maternal lineage | Group of candidates |
|--------|-----------|--------|----------------------|------------------------|---------|------------------|------------------|---------------------|
| All | All | All | All | All | All | All | All | All |
| V4 | R4 | F4 | Mother_Daughter | Mother_Daughter | 6.33e+9 | Not excluded | | |
| V2 | R2 | F2 | Father_Daughter | Father_Daughter | 4.50e+8 | Excluded | | |
| V3 | R3 | F3 | Mother_Son | Mother_Son | 9.01e+7 | Not excluded | | |
| V1 | R1 | F1 | Father_Son | Father_Son | 4.12e+6 | Not excluded | Excluded | |
| V19 | R19 | F19 | Father_Daughter | Father_Daughter | 3.93e+6 | Excluded | 1 | |
| V5 | R5 | F5 | Brother_Brother | Brother_Brother | 2.48e+5 | Not excluded | Not excluded | |
| V7 | R7 | F7 | Sister_Brother | Sister_Brother | 5.90e+4 | Not excluded | | |
| V22 | R22 | F21 | Brother_Sister | Brother_Sister | 1.77e+4 | Excluded | | |
| V21 | R21 | F20 | Paternal-aunt_Nephew | Paternal-aunt_Nephew | 7.95e+3 | Excluded | 2 | |
| V21 | R21 | F20 | Sister_Brother | Sister_Brother | 3.11e+3 | Excluded | | |

Search:

Download

Showing 1 to 10 of 19 entries

Previous 1 2 Next

2. Go to **Selected data in detail** tab.

RelSearch ver. 0.21.0 Load Result Project Database Settings Example files Manual

Result

Summary Selected data in detail Analysis conditions

Display setting

Show 10 entries

Victim Reference Family Assumed relationship Estimated relationship LR Paternal lineage Maternal lineage Group of candidates

| Victim | Reference | Family | Assumed relationship | Estimated relationship | LR | Paternal lineage | Maternal lineage | Group of candidates |
|--------|-----------|--------|----------------------|------------------------|---------|------------------|------------------|---------------------|
| All | All | All | All | All | All | All | All | All |
| V4 | R4 | F4 | Mother_Daughter | Mother_Daughter | 6.33e+9 | Not excluded | | |
| V2 | R2 | F2 | Father_Daughter | Father_Daughter | 4.50e+8 | Excluded | | |
| V3 | R3 | F3 | Mother_Son | Mother_Son | 9.01e+7 | Not excluded | | |
| V1 | R1 | F1 | Father_Son | Father_Son | 4.12e+6 | Not excluded | Excluded | |
| V19 | R19 | F19 | Father_Daughter | Father_Daughter | 3.93e+6 | Excluded | 1 | |
| V5 | R5 | F5 | Brother_Brother | Brother_Brother | 2.48e+5 | Not excluded | Not excluded | |
| V7 | R7 | F7 | Sister_Brother | Sister_Brother | 5.90e+4 | Not excluded | | |
| V22 | R22 | F21 | Brother_Sister | Brother_Sister | 1.77e+4 | Excluded | | |
| V21 | R21 | F20 | Paternal-aunt_Nephew | Paternal-aunt_Nephew | 7.95e+3 | Excluded | 2 | |
| V21 | R21 | F20 | Sister_Brother | Sister_Brother | 3.11e+3 | Excluded | | |

Search:

Download

Showing 1 to 10 of 19 entries

Previous 1 2 Next

In **Selected data in detail** tab, you can review and download the analyzed STR, Y-STR, and mtDNA data for the selected victim-reference pair. You can check all members of the family to which the selected reference belongs.

STR tab

| | Summary | Selected data in detail | Analysis conditions | | | | |
|-----------------------------------|-----------------|--|---|---|---|--|---|
| | STR | Y-STR | mtDNA | | | | |
| | Locus | Victim profile | Reference profile | Likelihood (related) | Likelihood (unrelated) | LR | |
| Selected victim | V5 | | | | | | |
| Selected reference | R5 | D3S1358 WVA D16S539 CSF1PO TP0X D8S1179 D21S11 D18S51 D2S441 D19S433 TH01 FGA | 15, 17 16, 18 9, 12 10, 10 11, 11 13, 13 29, 30 11, 19 11, 14 14, 15.2 6, 9 22, 24 | 15, 17 14, 19 9, 13 12, 12 10, 11 11, 13 30, 31.2 11, 19 10, 11 13, 15.2 6, 6 22, 24 | 0.0704 0.000584 0.00369 0.00206 0.00290 0.00330 0.00473 0.000951 0.00767 0.00700 0.0118 0.0219 | 0.0257 0.00234 0.00615 0.00823 0.00304 0.00243 0.00766 1.33e-7 0.0125 0.00521 0.00851 0.00382 | 2.74 0.250 0.599 0.250 0.951 1.36 0.617 714 0.614 1.34 1.38 5.72 |
| Estimated relationship | Brother_Brother | | | | | | |
| Paternal lineage | Not excluded | | | | | | |
| Maternal lineage | Not excluded | | | | | | |
| All family members | R6 | D18S51 D2S441 D19S433 TH01 D7S820 SE33 D10S1248 D15S1656 D12S391 D2S1338 | 11, 19 11, 14 14, 15.2 6, 9 10, 11 19, 26.2 14, 15 14, 15 18, 19 21, 23 | 11, 19 10, 11 13, 15.2 8, 9 10, 11 19, 26.2 13, 15 12, 14 18, 24 23, 23 | 0.00156 0.0249 0.0619 0.00359 0.0138 0.000475 0.00118 0.000170 | 0.00624 0.00466 0.0213 0.000150 0.0171 0.000275 0.00159 0.0000837 | 0.250 5.35 2.90 23.9 0.806 1.73 0.744 2.04 |
| | | Total | | 1.06e-50 | 4.27e-56 | 2.48e+5 | |
| Download (STR) | | | | | | | |
| Download (Y-STR) | | | | | | | |
| Download (mtDNA) | | | | | | | |

Y-STR tab

Selected victim
V5
STR Y-STR mtDNA

| Locus | Victim profile | Reference profile | Ignored locus | Mismatched locus | Mutational step |
|----------|----------------|-------------------|---------------|------------------|-----------------|
| DYS576 | 20 | 20 | 0 | 0 | 0 |
| DYS389I | 13 | 13 | 0 | 0 | 0 |
| DYS635 | 21 | 21 | 0 | 0 | 0 |
| DYS389II | 29 | 29 | 0 | 0 | 0 |
| DYS627 | 19 | 20 | 0 | 1 | 1 |
| DYS460 | 10 | 10 | 0 | 0 | 0 |
| DYS458 | 19 | 19 | 0 | 0 | 0 |
| DYS19 | 15 | 15 | 0 | 0 | 0 |
| GATA_H4 | 12 | 12 | 0 | 0 | 0 |
| DYS448 | 18 | 18 | 0 | 0 | 0 |
| DYS391 | 8 | 8 | 0 | 0 | 0 |
| DYS456 | 15 | 15 | 0 | 0 | 0 |
| DYS390 | 22 | 22 | 0 | 0 | 0 |
| DYS438 | 13 | 13 | 0 | 0 | 0 |
| DYS392 | 13 | 13 | 0 | 0 | 0 |
| DYS518 | 42 | 42 | 0 | 0 | 0 |
| DYS570 | 17 | 17 | 0 | 0 | 0 |
| DYS437 | 13 | 13 | 0 | 0 | 0 |
| DYS385 | 10,17 | 10,17 | 0 | 0 | 0 |
| DYS449 | 30 | 30 | 0 | 0 | 0 |
| DYS393 | 14 | 14 | 0 | 0 | 0 |
| DYS439 | 12 | 12 | 0 | 0 | 0 |
| DYS481 | 21 | 21 | 0 | 0 | 0 |
| DYF387S1 | 37 | 37 | 0 | 0 | 0 |
| DYS533 | 11 | 11 | 0 | 0 | 0 |
| Total | | | 0 | 1 | 1 |

[Download \(STR\)](#)
[Download \(Y-STR\)](#)
[Download \(mtDNA\)](#)

mtDNA tab

RelSearch ver. 0.21.0 Load Result Project ▾ Database ▾ Settings ▾ Example files Manual

Result

Summary Selected data in detail Analysis conditions

Selected victim
V6

Selected reference
R6

Estimated relationship
Brother_Brother

Paternal lineage
Not excluded

Maternal lineage
Not excluded

All family members
R6

STR Y-STR mtDNA

| Number of mismatches | Shared range | Shared length (bp) | |
|----------------------|--------------------|---------------------|----------|
| 0 | 73-340 16024-16365 | 610 | |
| Victim profile | Reference profile | Out of shared range | Mismatch |
| 73G | 73G | | |
| 152C | 152C | | |
| 263G | 263G | | |
| 16071T | 16071T | | |
| 16093C | 16093C | | |
| 16109G | 16109G | | |
| 16129A | 16129A | | |
| 16223T | 16223T | | |
| 16249C | 16249C | | |
| 16362C | 16362C | | |

Download (STR) Download (Y-STR) Download (mtDNA)

5.3 Analysis conditions

You can review the following analysis conditions in **Analysis conditions** tab.

- **Database:** Input .csv file names of each database are displayed.
- **Allele probability:** Unobserved alleles in the population database are displayed, if any. You can download the allele probabilities that are estimated based on Dirichlet distribution.
- **Criteria:** The user-defined criteria to determine whether each victim-reference pair has an assumed relationship or not (see section [Setting](#)) is displayed.
- **Assumed relationship:** Information on the user-defined relationships (see section [Setting](#)) is displayed.
- **Mutation rate:** The user-defined mutation rates (see section [Setting](#)) are displayed.
- **Data storage conditions:** The user-defined conditions for data storage (see section [Setting](#)) is displayed.

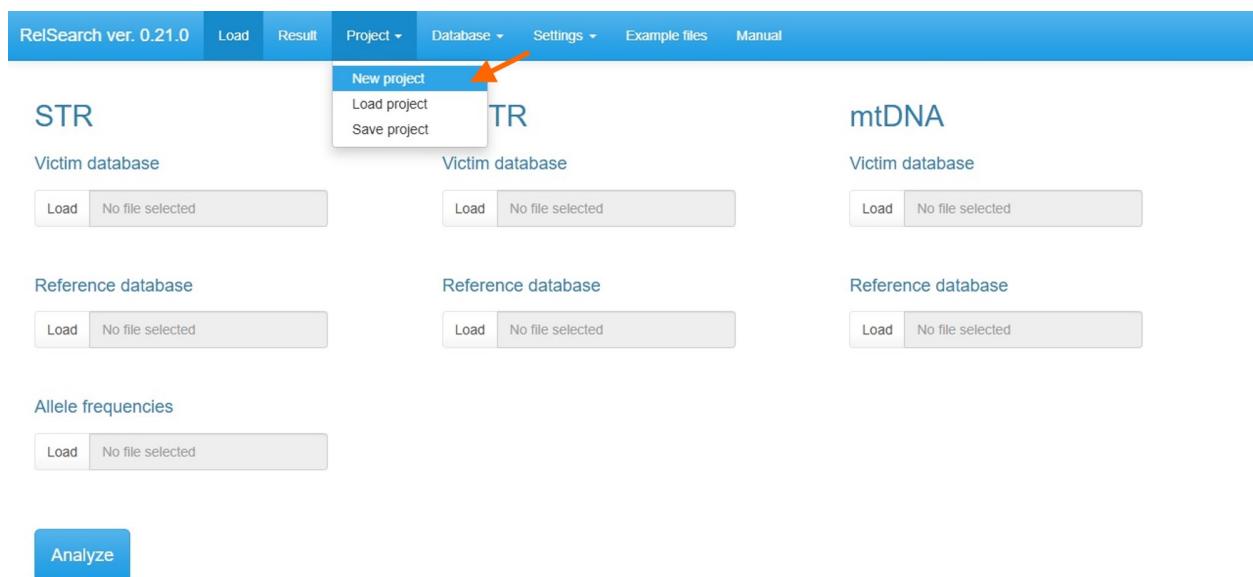
Chapter 6

Other functions

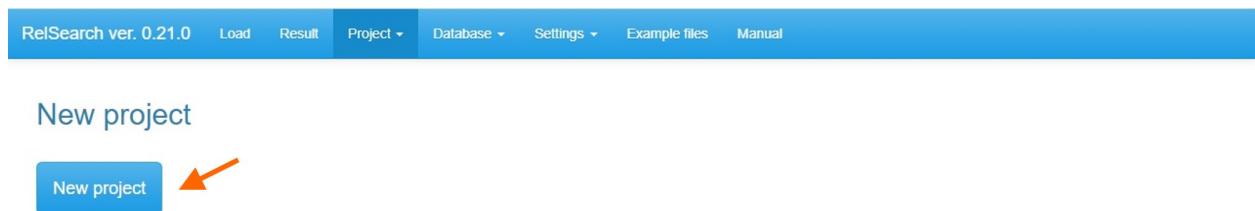
6.1 Project

6.1.1 New project

To start a new project, go to **Project ▶ New project**.



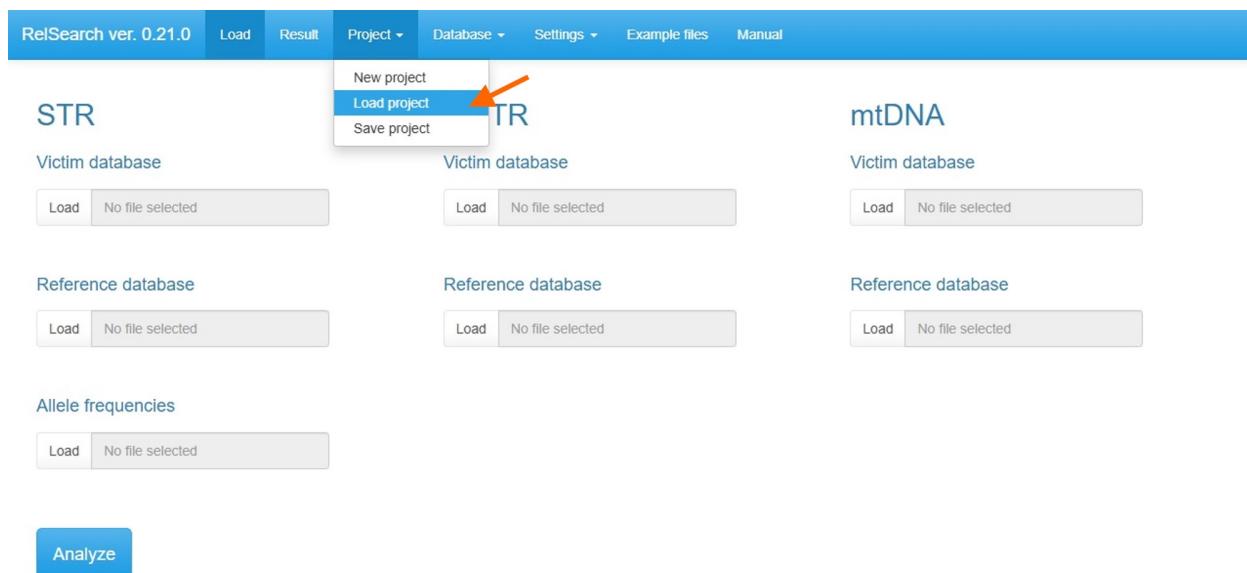
Press the **New project** button.



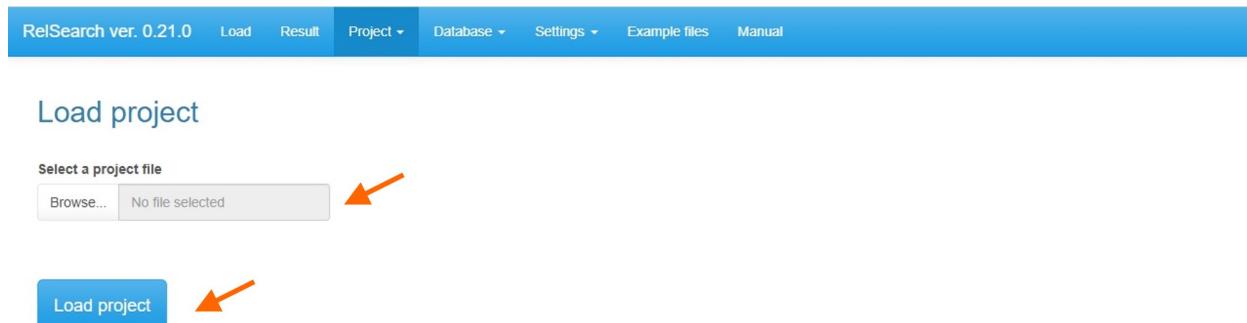
Important: The current project should be saved before starting a new project because the current project will be deleted.

6.1.2 Load project

To load a previous project, go to **Project ▶ Load project**.



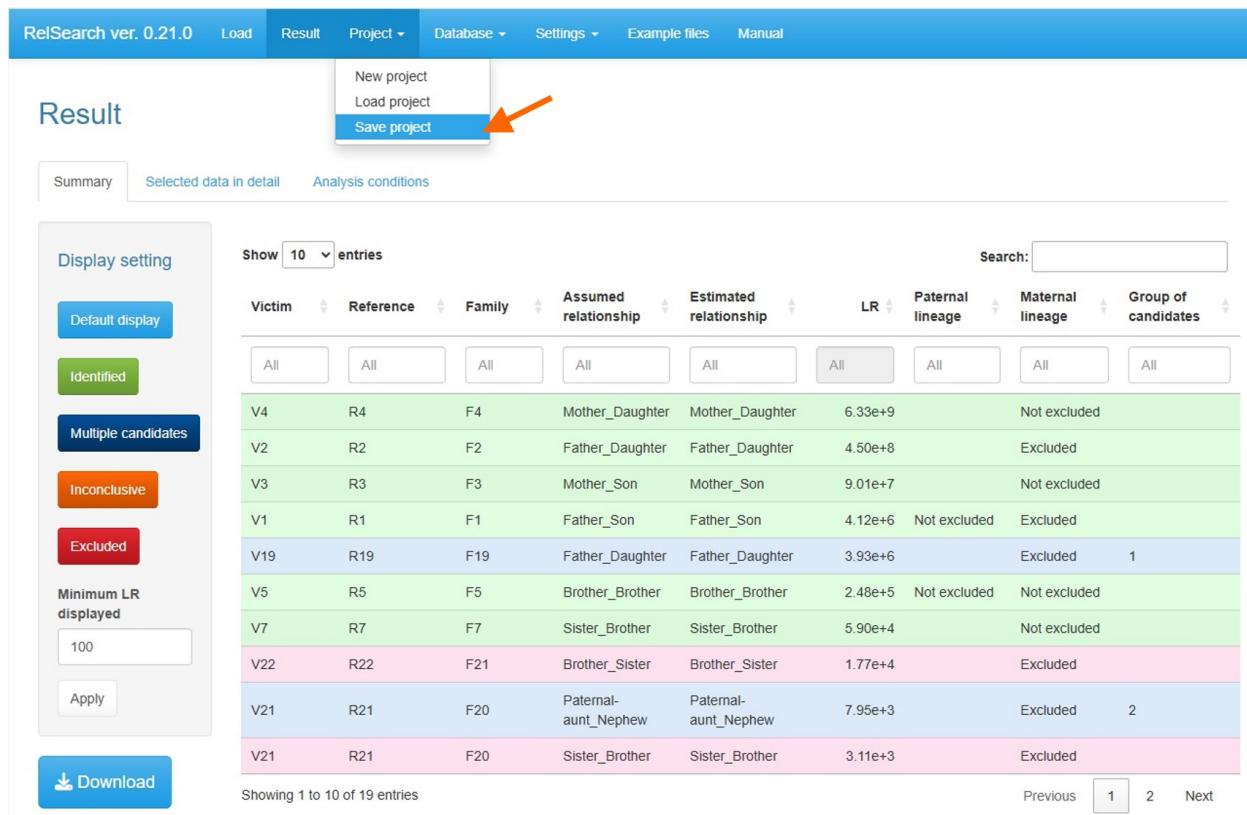
Select a project file from the **Browse...** button and press the **Load project** button.



Important: The current project should be saved before loading another project because the current project will be deleted.

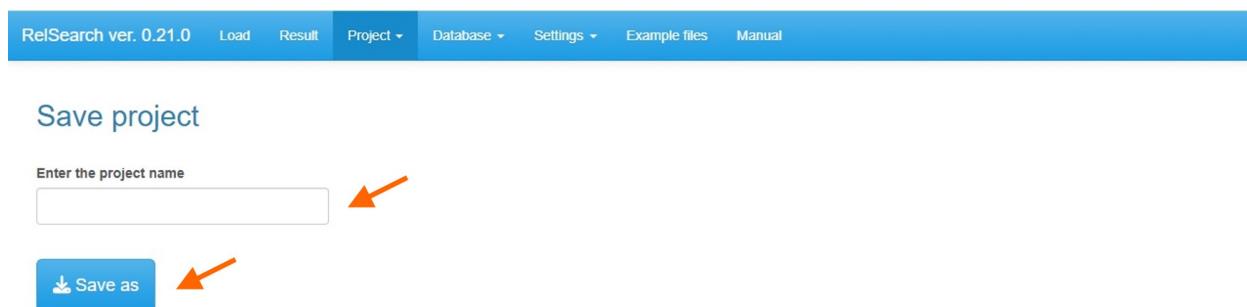
6.1.3 Save project

To save the current project, go to **Project ▶ Save project**.



The screenshot shows the RelSearch software interface. At the top, there is a navigation bar with tabs for 'RelSearch ver. 0.21.0', 'Load', 'Result', 'Project ▾', 'Database ▾', 'Settings ▾', 'Example files', and 'Manual'. The 'Result' tab is active. Below the navigation bar, there is a sub-navigation bar with tabs for 'Summary', 'Selected data in detail', and 'Analysis conditions'. On the left side, there is a sidebar titled 'Display setting' with buttons for 'Default display', 'Identified', 'Multiple candidates' (which is selected), 'Inconclusive', 'Excluded', 'Minimum LR displayed' (set to 100), 'Apply', and a 'Download' button. The main area is titled 'Result' and contains a table of analysis results. The table has columns for Victim, Reference, Family, Assumed relationship, Estimated relationship, LR, Paternal lineage, Maternal lineage, and Group of candidates. The table shows 19 entries, with the first few rows visible. An orange arrow points to the 'Save project' button in the top right corner of the main interface area.

Enter the project name and press the **Save as** button.



The screenshot shows a 'Save project' dialog box. At the top, there is a header 'Save project'. Below the header, there is a text input field labeled 'Enter the project name' with a placeholder 'Project Name'. An orange arrow points to this input field. At the bottom of the dialog box is a blue button labeled 'Save as' with a download icon. Another orange arrow points to this button.

6.2 View database

Each loaded database can be reviewed in **Database** tab.

The screenshot shows the RelSearch software interface. At the top, there is a navigation bar with tabs: RelSearch ver. 0.21.0, Load, Result, Project, Database, Settings, Example files, and Manual. The Database tab is currently selected.

STR

Victim database

- Load str_victim_example.csv
- Upload complete

Reference database

- Load str_reference_example.csv
- Upload complete

Allele frequencies

- Load str_allele-freq_example.csv
- Upload complete

Analyze

mtDNA

Victim database

- Load mt_victim_example.csv
- Upload complete

Reference database

- Load y_reference_example.csv
- Upload complete

Reference database

- Load mt_reference_example.csv
- Upload complete

A red box highlights the "STR" section, specifically the "Allele frequencies" and "Analyze" button area.

6.3 Example files

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

The screenshot shows the RelSearch software interface. At the top, there is a blue header bar with the text "RelSearch ver. 0.21.0" and several menu items: "Load", "Result", "Project", "Database", "Settings", "Example files" (which is highlighted in blue), and "Manual". Below the header, the main area has a title "Example files" in blue. Underneath this title, there is a list of download links, each enclosed in a small button-like box:

- STR victim database
- STR reference database
- Allele frequencies
- Y-STR victim database
- Y-STR reference database
- mtDNA victim database
- mtDNA reference database

Reference

- [1] R.M. Andrews, I. Kubacka, P.F. Chinnery, R.N. Lightowlers, D.M. Turnbull, N. Howell, Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA, *Nature Genetics* 23 (1999) 147.
- [2] C. Morimoto, H. Tsujii, S. Manabe, S. Fujimoto, E. Hirai, Y. Hamano, K. Tamaki, Development of a software for kinship analysis considering linkage and mutation based on a Bayesian network, *Forensic Science International: Genetics* 47 (2020) 102279.