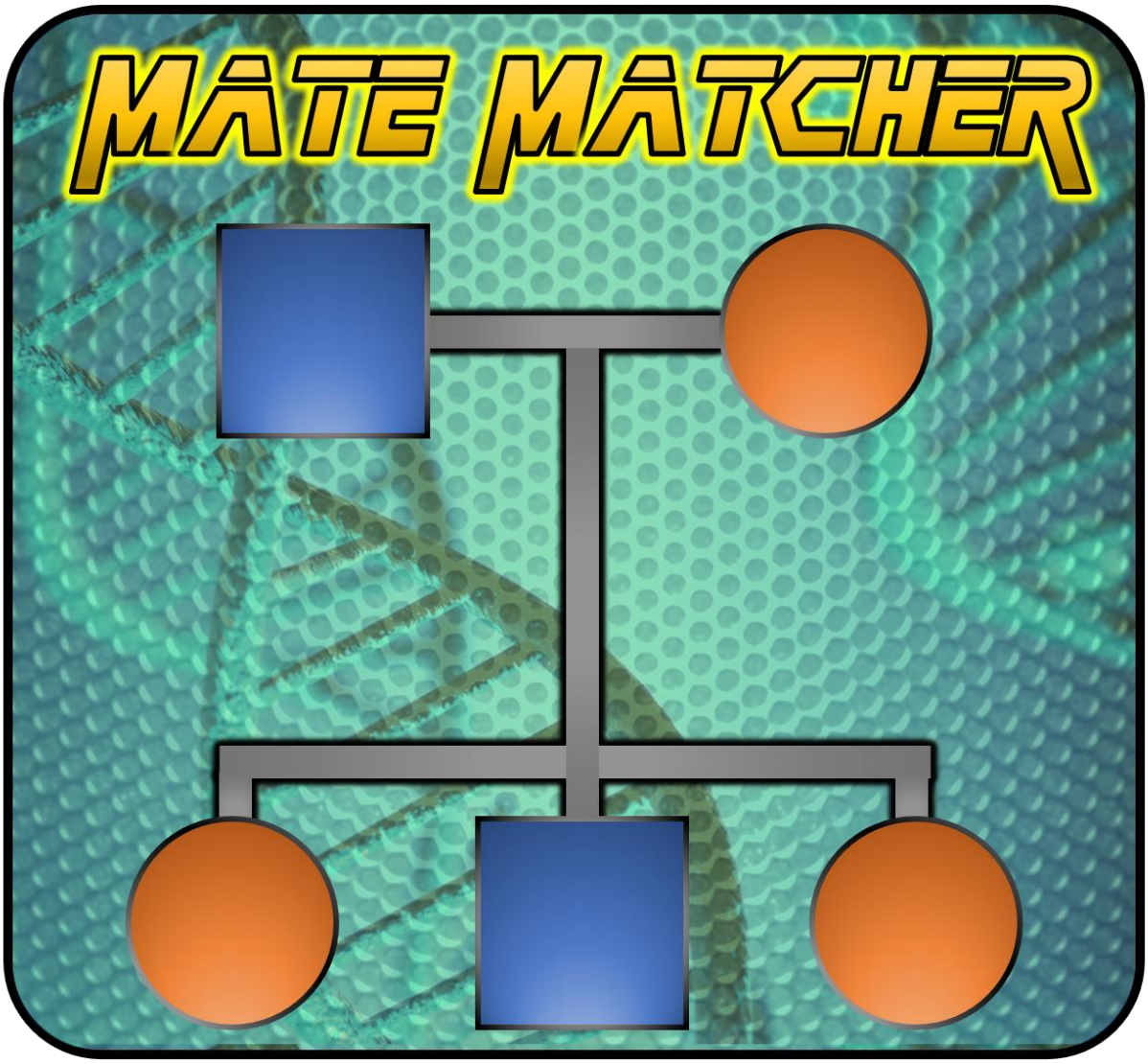


# Mate Matcher

## Mating Optimization Software

## User Guide

## Version 1.0  March 26th, 2019

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# Introduction

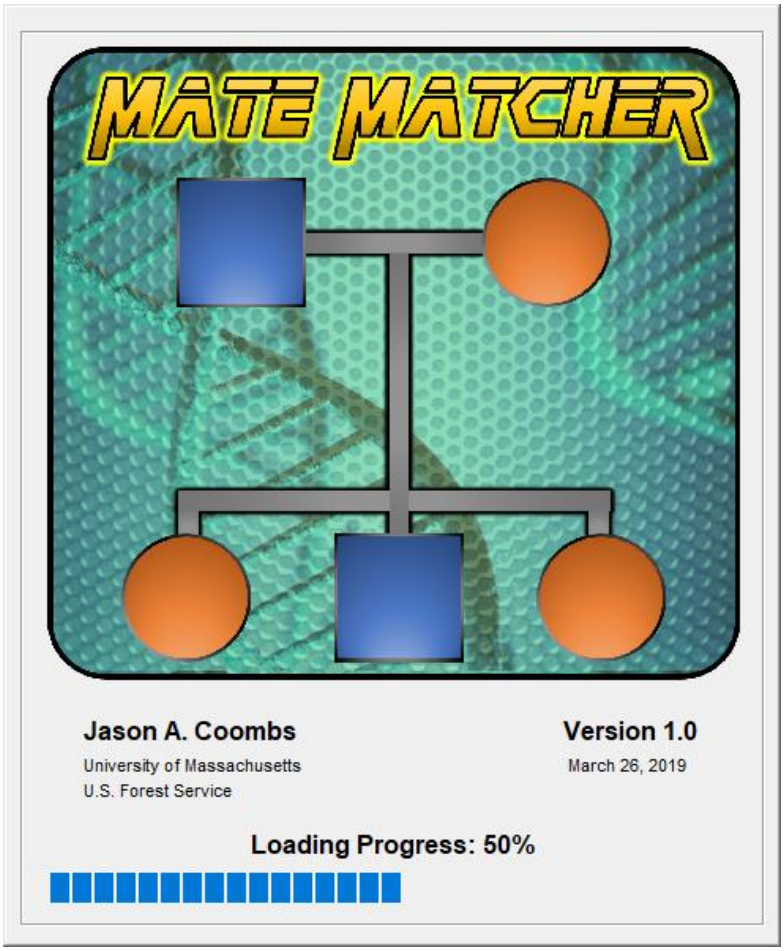
Mate Matcher is a software program used for real-time pairing of mating individuals through optimization of all possible pairings for minimization of genetic relatedness.

# Installation

To install Mate Matcher save the executable, MSCOMM32.OCX, and MSVBVM50.DLL files are saved to the same folder. In some instances, the OCX and DLL files may need to be added to the computer's registry. The following links provide instructions to do so: MSCOMM32.OCX and MSVBVM50.DLL.

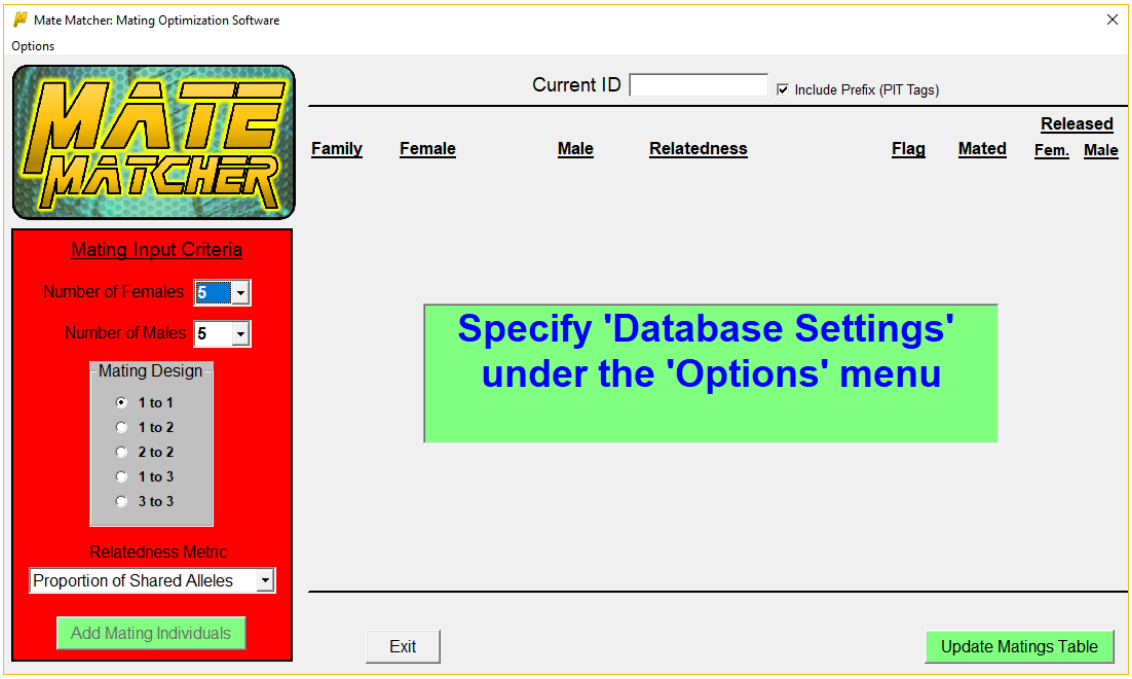
# Start-up

On start-up, Mate Matcher will preload all of the possible mating combinations in order to increase performance during real-time mating optimization. This process takes approximately 30 seconds to complete, and a progress bar on the splash page will inform you of the status.

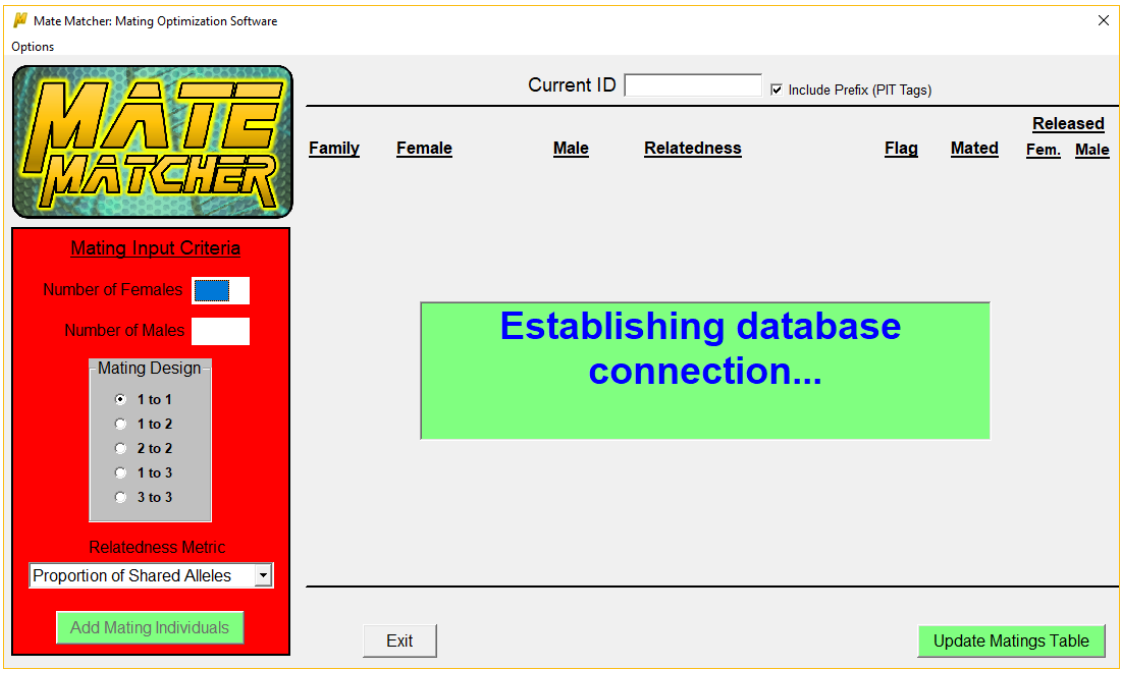


# Main Form Part I

Upon completion of the mating combination loadings, the main form will open. Hovering the cursor over an item will usually show descriptive text about that item. If this is the first time that Mate Matcher has been used, you will be prompted to specify database settings.



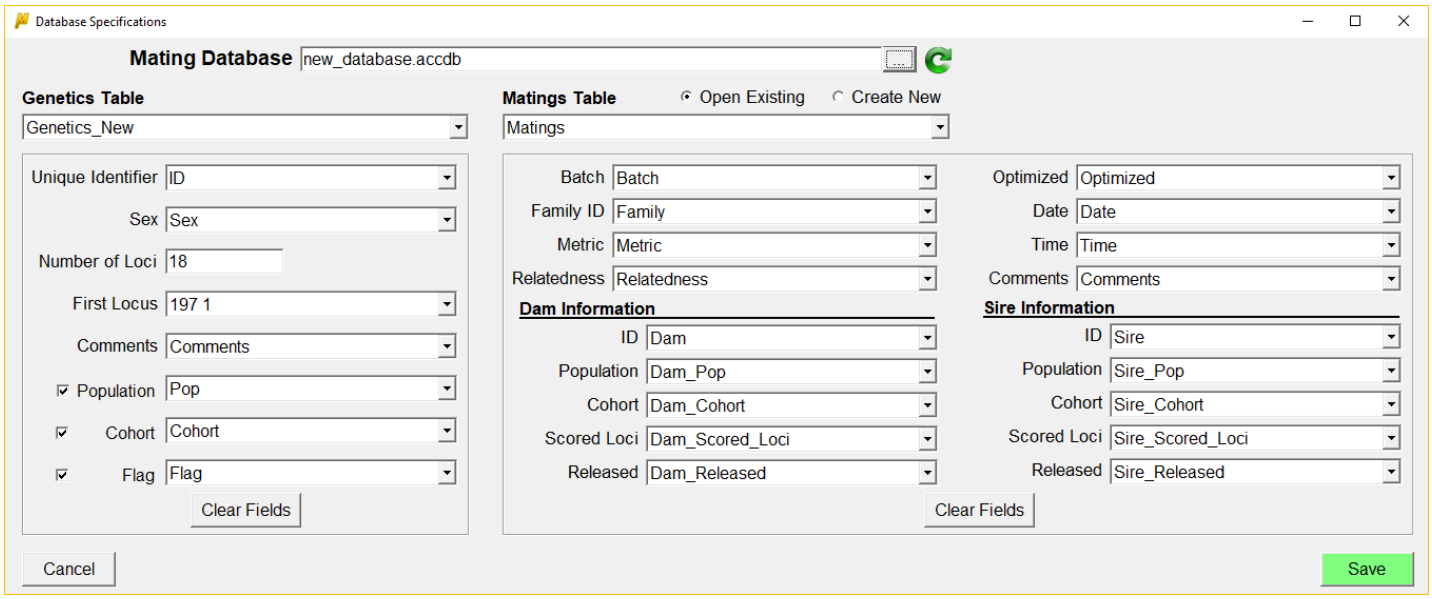

On subsequent opening of Mate Matcher, attempts will be made to connect to the previously used database.




# Database Specifications

Open the database specifications window by clicking ‘Options’ on the top menu of the main form and selecting ‘Database Settings’. On your initial usage of Mate Matcher, you will be required to do the following:

1. Select a mating database
2. Select the table in the database that contains genotypes of individuals to be used for mating (genetics table)
3. Map columns in the genetics table to their associated field
    a. Unique Identifier, Sex, Number of Loci, First Locus, and Comments are required
    b. Population, Cohort, and Flag are optional and will only be used when checked
4. Select the table in the database where the mating pairs will be recorded
    a. The user can either select an existing table or create a new table
        i. An existing table requires the mapping of all fields to columns in the table
            1. If a field does not currently exist in the table it will need to be added
            2. See the below table for required data types of each field
        ii. A new table requires the user to enter in a table name
            1. All fields are auto populated with column headings
5. Click ‘Save’ button to store the database settings




## Genetics Table

| Field | Description |
|---|---|
| Unique Identifier | The unique identifier of the individual |
| Sex | The gender of the individual (e.g. M, F, U) |
| Number of Loci | The number of loci comprising the genotypes of all individuals |
| First Locus | The column corresponding to the first locus reading from left to right in the table |
| Comments | Any comments about the individual, included when adding new individuals to the table |
| Population | The population of the individual |
| Cohort | The cohort of the individual |
| Flag | Warning flags about the individual that will be displayed if used for mating |

## Matings Table

| Field | Allowed Data Type | Description |
|---|---|---|
| Batch | Long, Single, Double, Decimal | Auto assigned unique identifier of mating pairs matched under the same optimization |
| Family ID | Text | User supplied identifier of the mating pair |
| Metric | Text | The relatedness metric used for optimization |
| Relatedness | Single, Double, Decimal | The relatedness value of the mating pair |
| Optimized | Text | Whether the mating pairs were matched using relatedness optimization; can be yes, no, or reoptimized |
| Date | Date/Time | The date the mating pair reproduced |
| Time | Date/Time | The time the mating pair reproduced |
| Comments | Text | Notes regarding the mating pair, specifically any mating flags violated |
| ID | Text | The identifier of the dam/sire |

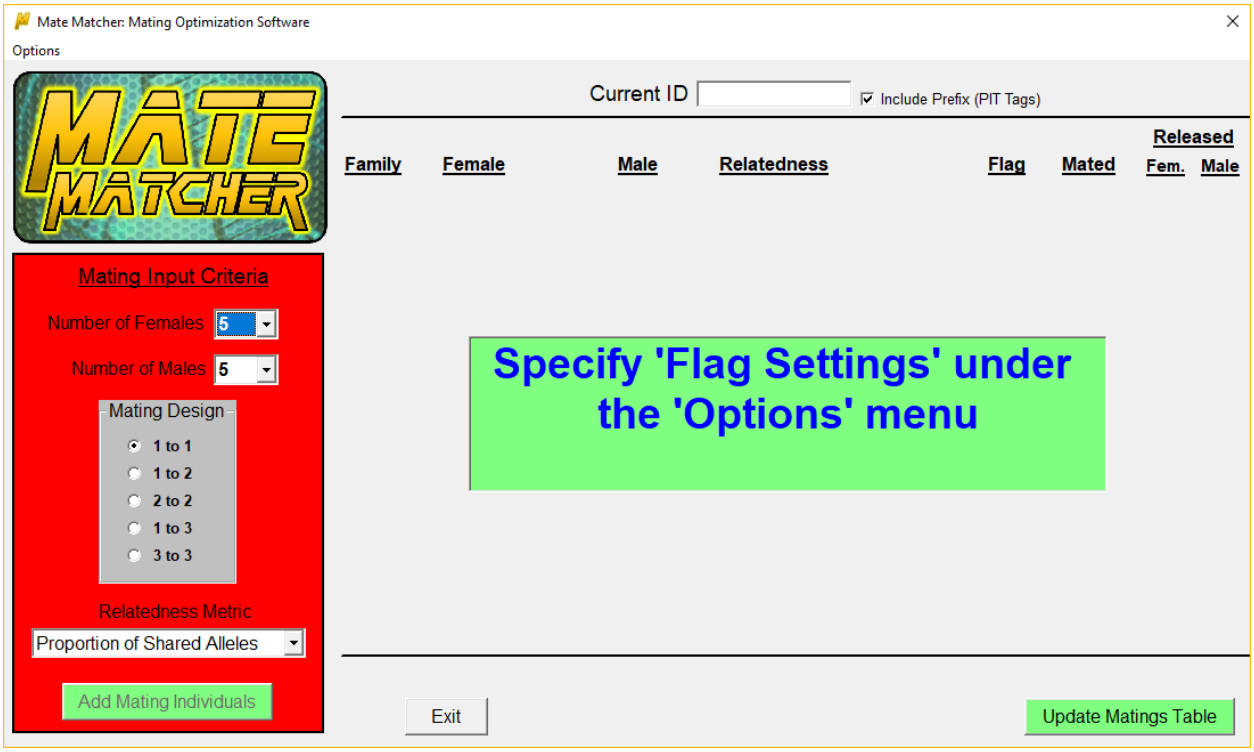
| | | |
|---|---|---|
| Population | Text | The population of the dam/sire |
| Cohort | Long, Single, Double, Decimal | The cohort of the dam/sire |
| Scored Loci | Long, Single, Double, Decimal | The number of loci scored for the dam/sire genotype |
| Released | Yes/No | Whether the dam/sire was released into the wild after mating |

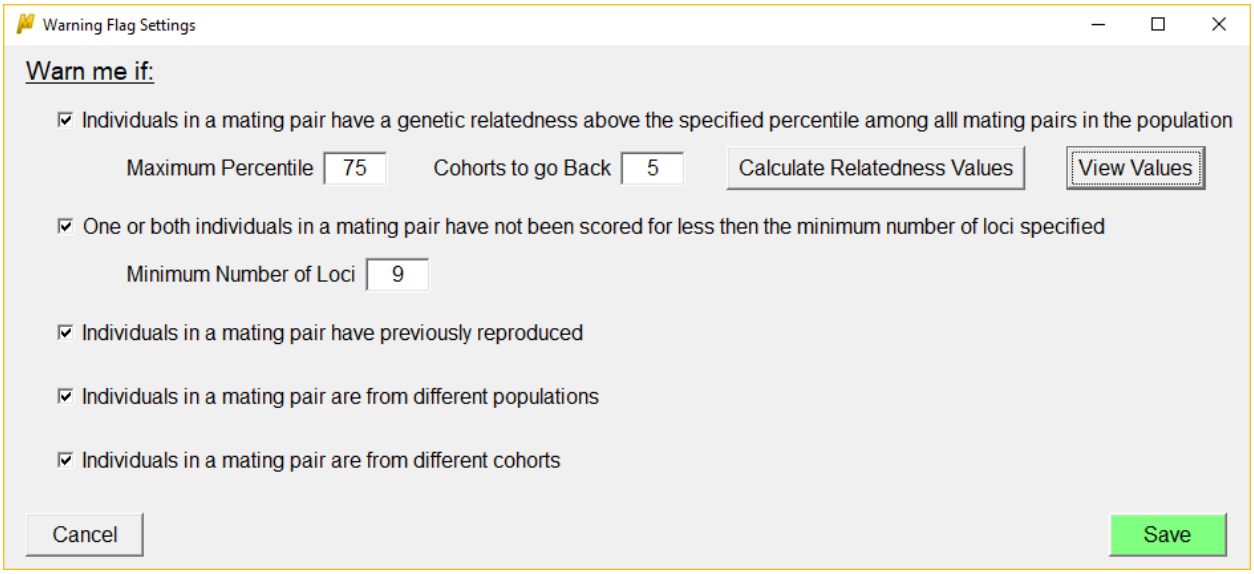
# Warning Flag Settings

Open the warning flag settings window by clicking 'Options' on the top menu of the main form and selecting 'Warning Flag Settings'. These settings provide options for raising warning flags if mating pairs meet flag specifications. Any raised flags will appear on the main form after mating pairs have been assigned.

Available flags include:

- A mating pair has a genetic relatedness value greater than the specified maximum
    - To use this flag pairwise relatedness values must be calculated first
        - Calculations are performed separately for each population
        - Only individuals present in the specified 'Cohorts to go Back' are included
        - The pairwise relatedness value corresponding to the specified maximum percentile can be viewed by clicking on 'View Values'
- One or both mating individuals has allelic information present at less than the specified minimum number of loci
- Individuals in a mating pair have previously reproduced
- Individuals in a mating pair are from different populations
- Individuals in a mating pair are from different cohorts



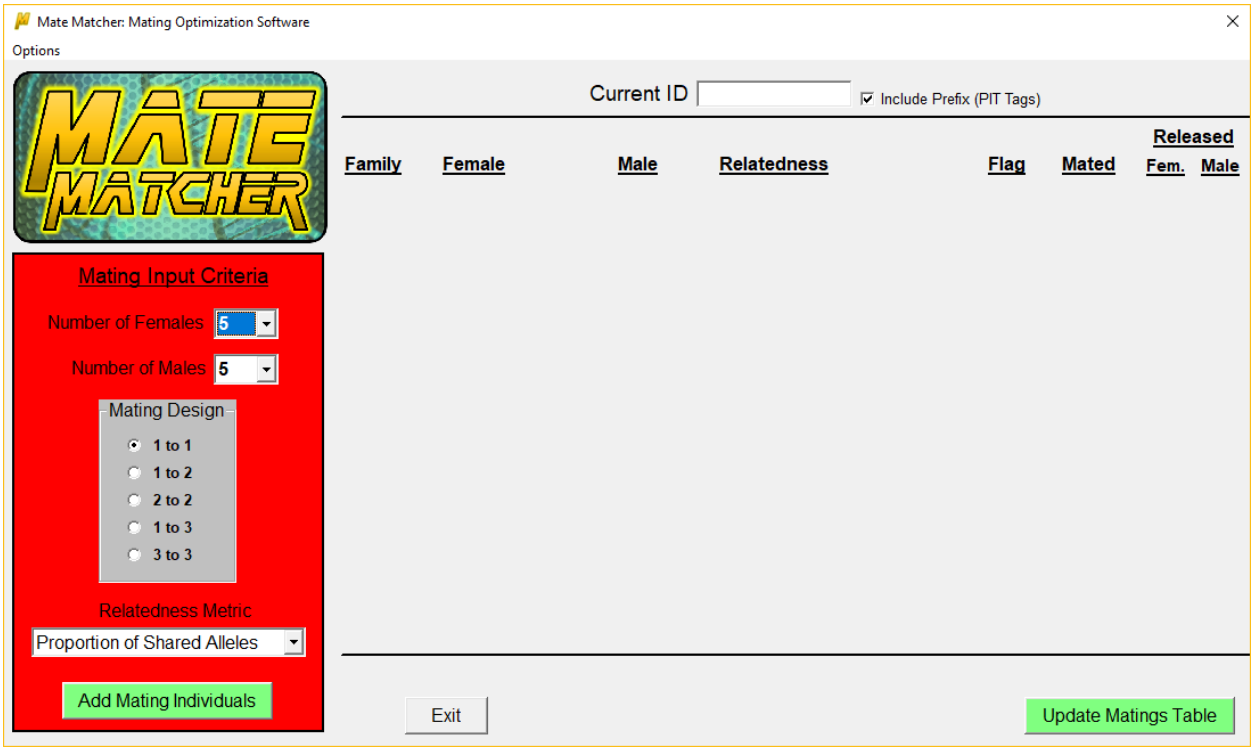

# Mating Design

Mate Matcher allows for five mating designs:

- 1 to 1 (1 Female mated with 1 Male)
- 1 to 2 (1 Female mated with 2 Males
- 2 to 2 (2 Females each mated with 2 Males)
- 1 to 3 (1 Female mated with 3 Males)

- 3 to 3 (3 Females each mated with 3 Males)

The number of females and males that can be optimized at one time (batch) is dependent upon the mating design, but the upper limit is 10 of each sex. Users are allowed to specify a greater number of males than females to attempt to reduce pairwise relatedness through optimization.



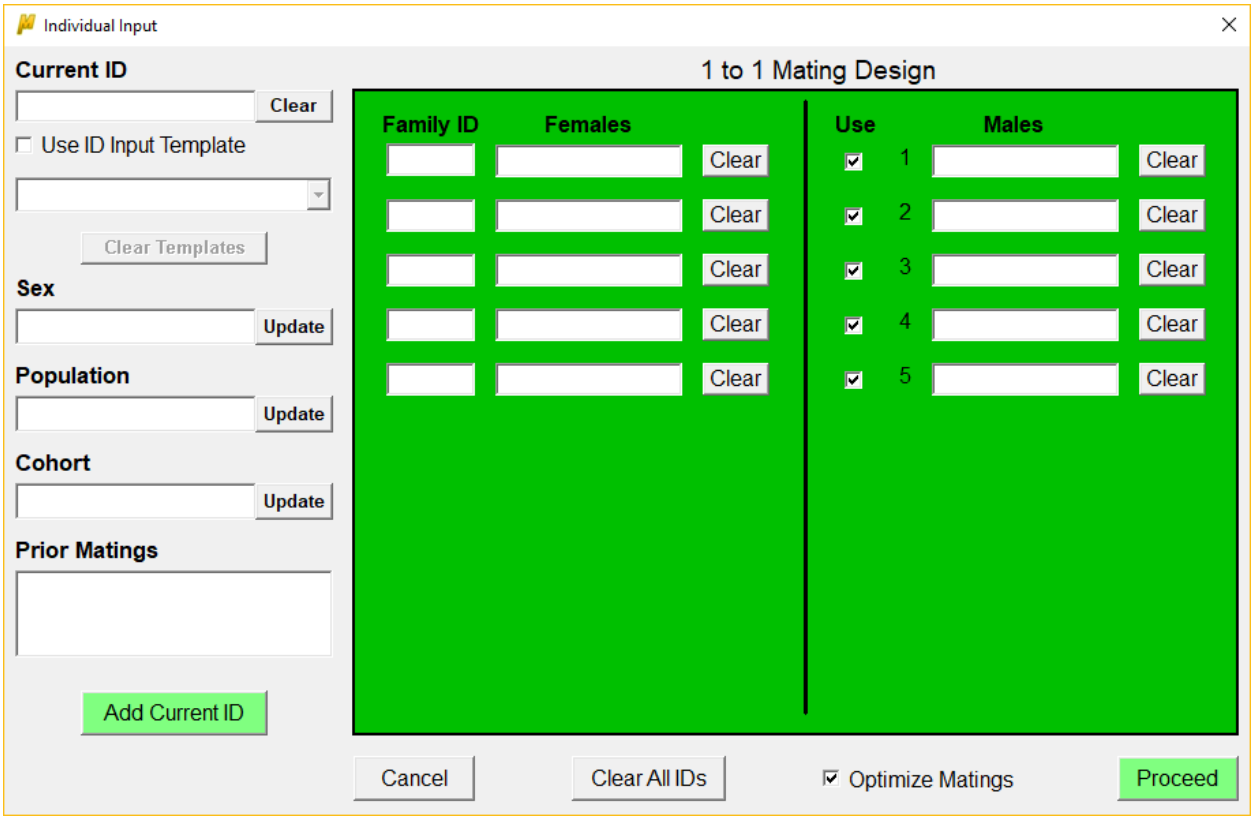

# Relatedness Metric

The relatedness metric is the value that is optimized when matching mating pairs. For now, the sole option is the Proportion of Shared Alleles which is the count of identical alleles shared between two individuals divided by 2 * number of loci with allelic information present. Therefore, it is assumed that the lower the shared proportion the less likely these two individuals are to share common ancestry.

Additional relatedness measures can be incorporated in the future if demand is present.

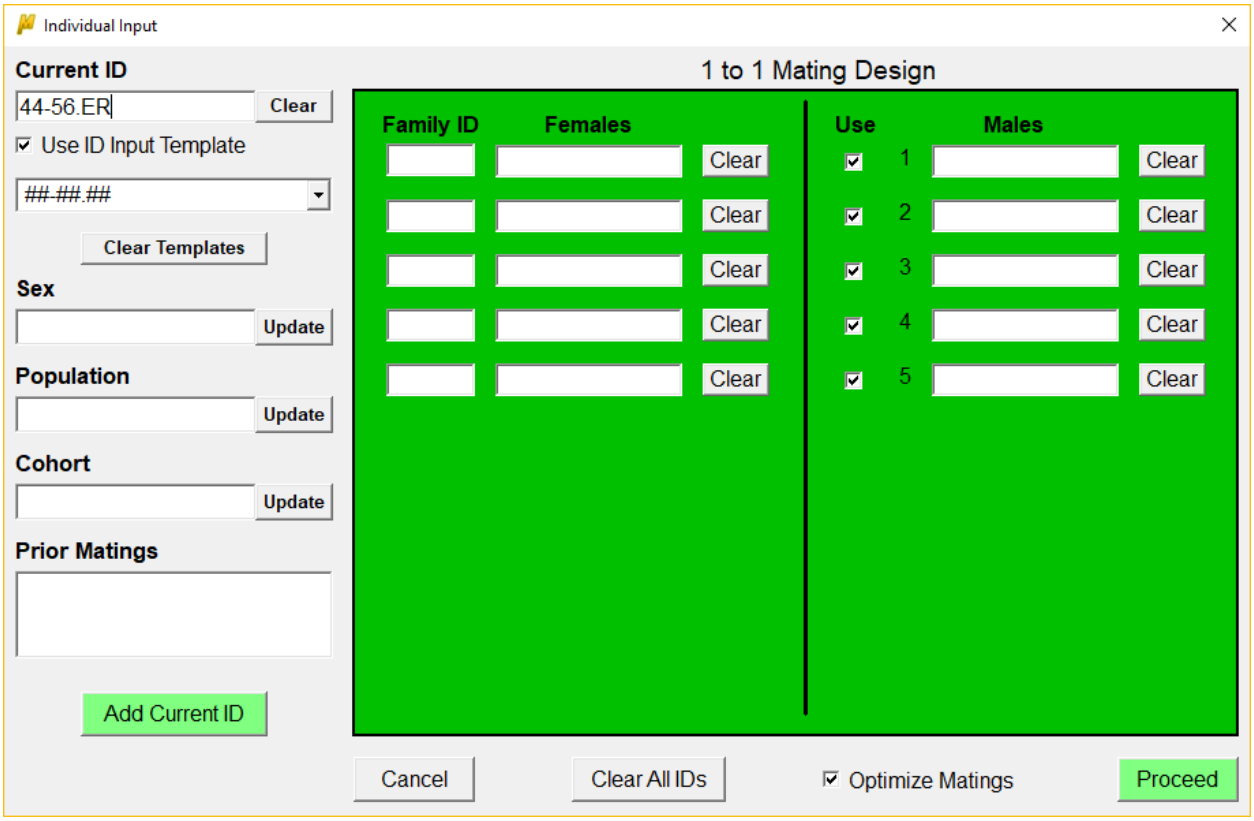
# Individual Input Form

To add individuals for mating optimization, click on the ‘Add Mating Individuals’ button on the main form which opens the individual input window. The number of slots for each sex is dependent upon the mating design and number of females and males specified on the main form.




Individual identifiers can be added by either scanning in a PIT tag, copying and pasting, or typing in directly. When typing, it is recommended that you use an ID input template otherwise you will be asked after each keystroke if you want to add the current ID to the genetics table if it isn't present already. If a template is used, you will only be asked once the entered ID matches the template. To enter a template, check the 'Use ID Input Template' box, click in the dropdown box beneath it, and type the template. The rules for entering a template are:

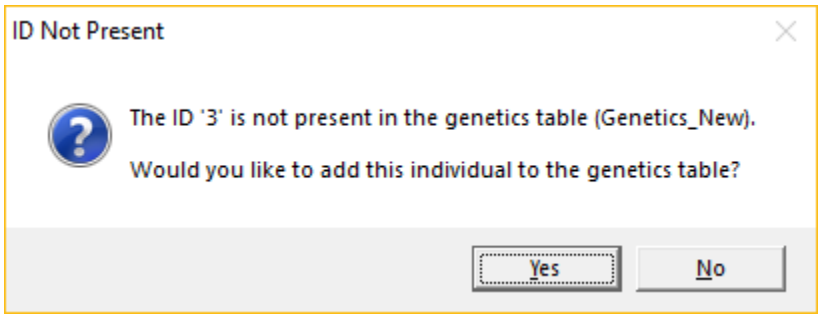
- Numbers and letters are represented by the # symbol
    - To add a template for a 5 digit alphanumeric ID you would enter #####
- Symbols are represented by the symbol itself
    - To add a period as the third character in the above template example you would enter ##.##



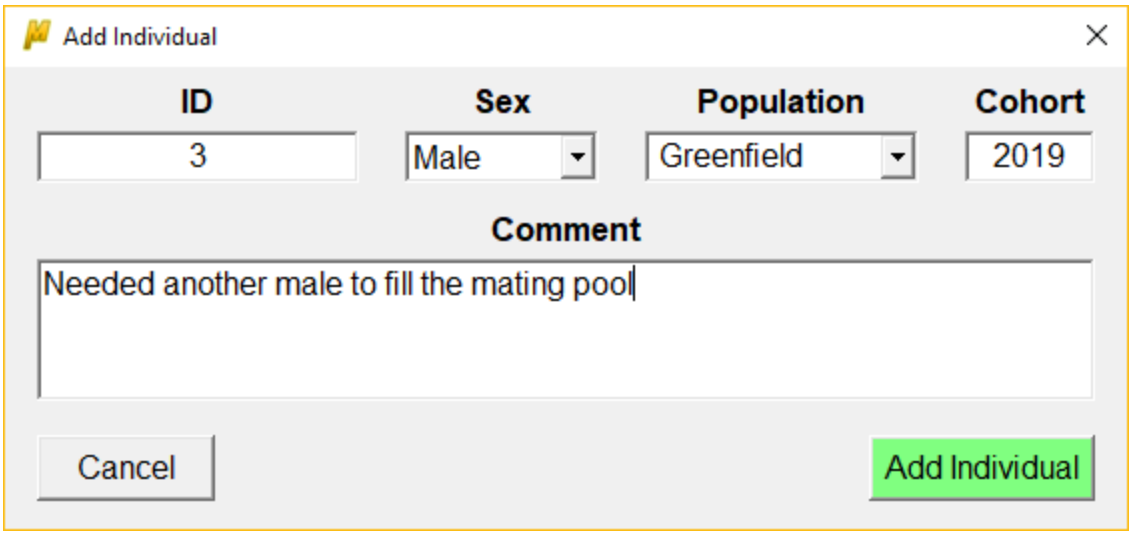

Once your template is matched (if you are using a template) or a character is typed (if you are not using a template), a query is performed on the genetics table to see if that ID is present.

If the ID is present, the sex, population (if specified), and cohort (if specified) information will be queried from the genetics table, and the individuals involvement in any prior matings will be queried from the matings table.

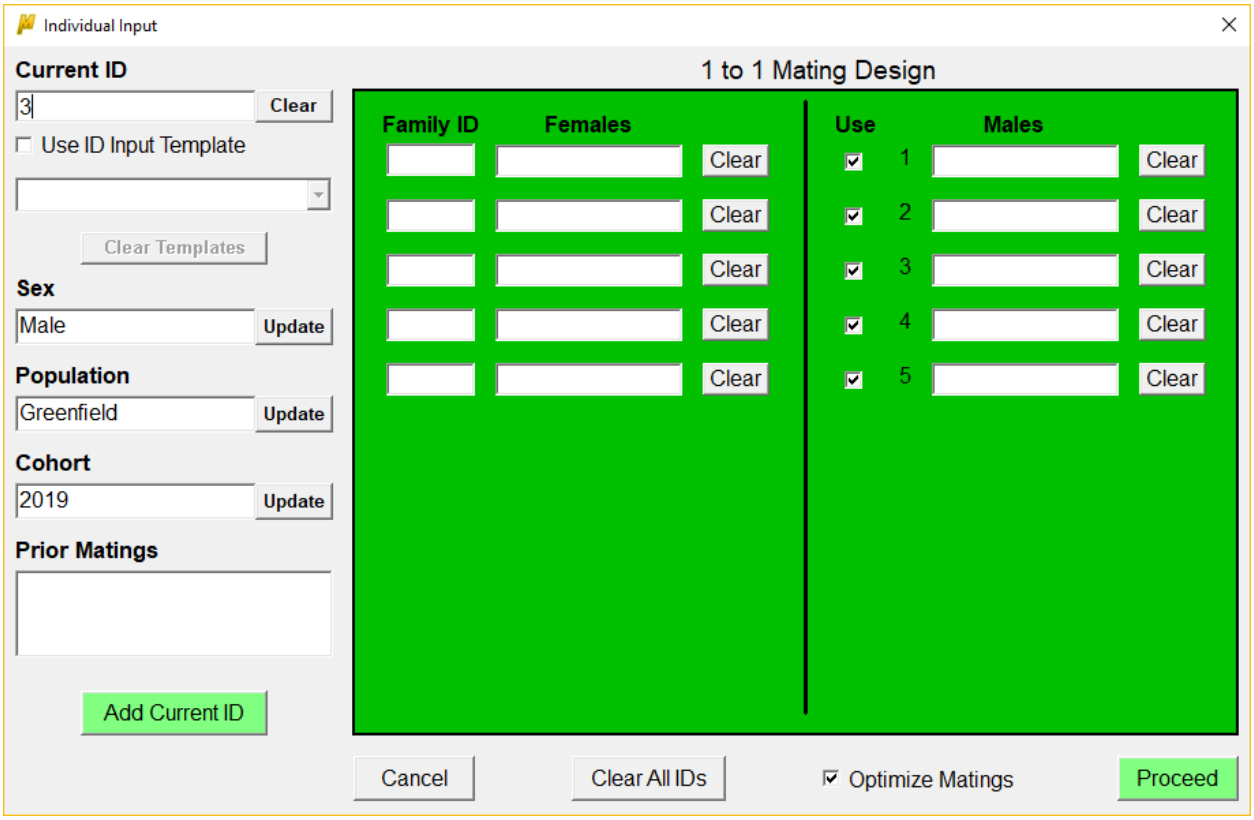
If the ID is not present, the user will be asked if they would like to add it to the genetics table



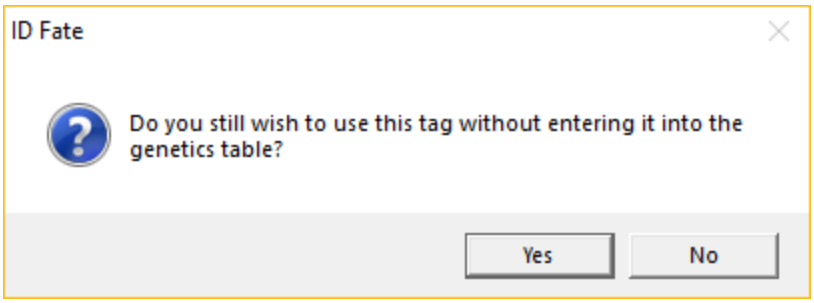

If Yes is selected, the user will be required to supply additional information. Sex information is always required, while population and cohort information is dependent upon whether these optional fields were checked for the genetics table on the database settings form.



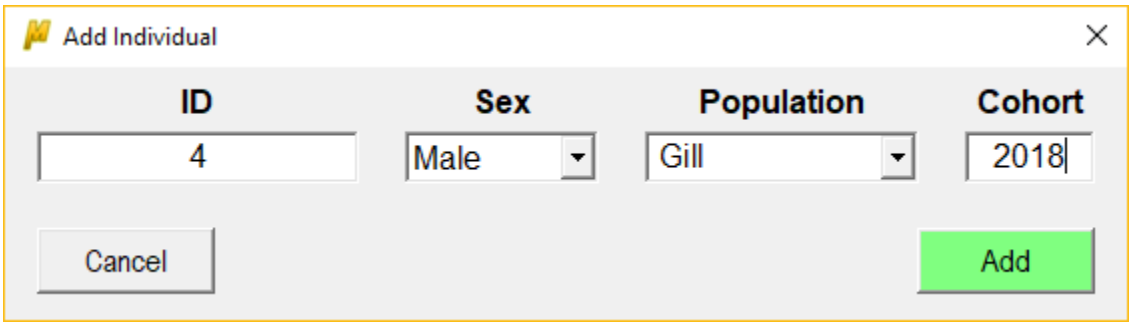

Adding the individual populations the information into the fields on the input form and enables the use of this individual for mating optimization.

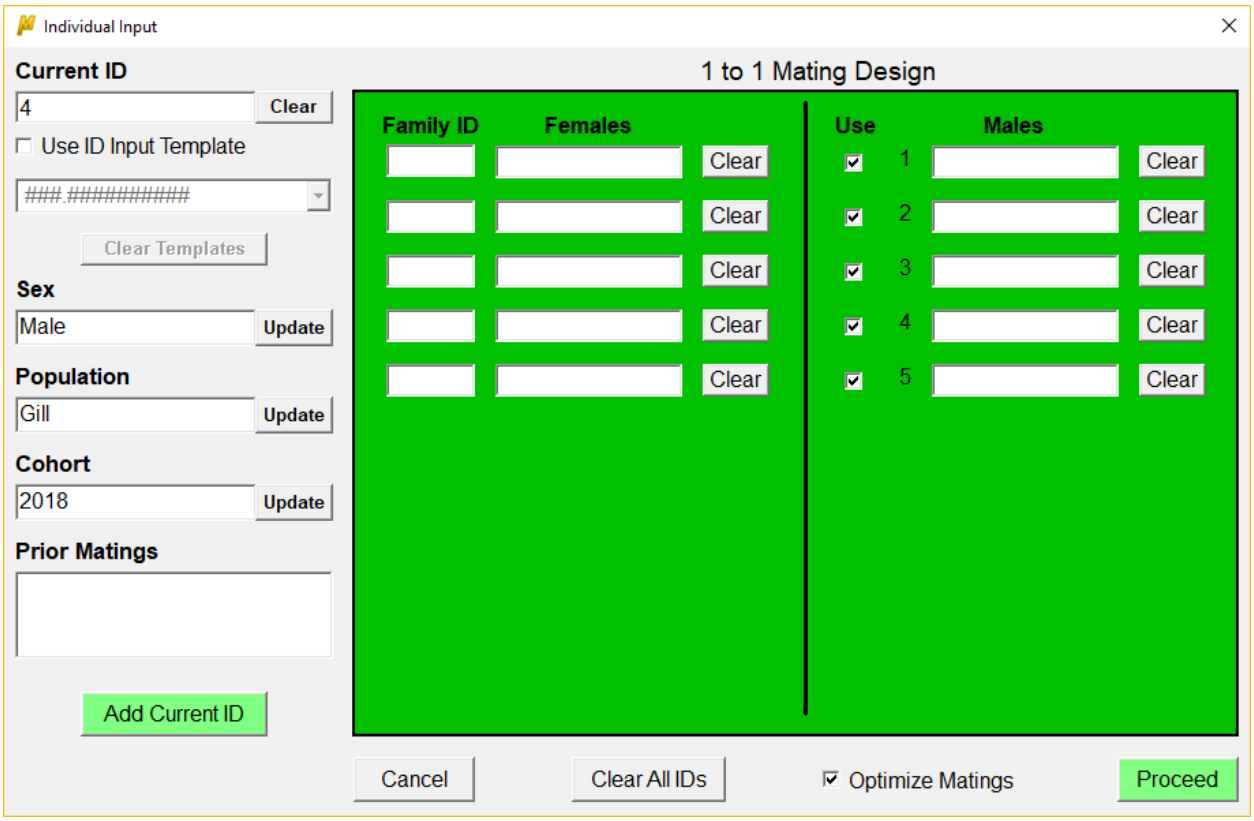



If you choose to not add it to the genetics table you will then be asked if you wish to use the ID without recording it to the genetics table.

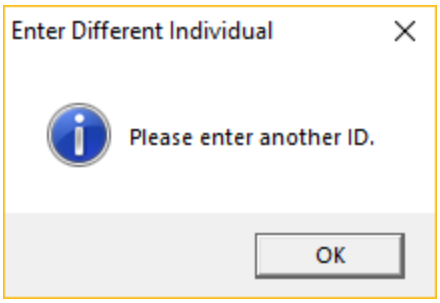



If you choose Yes, then you will be required to enter in information about the individual so that it can be used to evaluate any warning flags if it ends up being used in a mating pair.



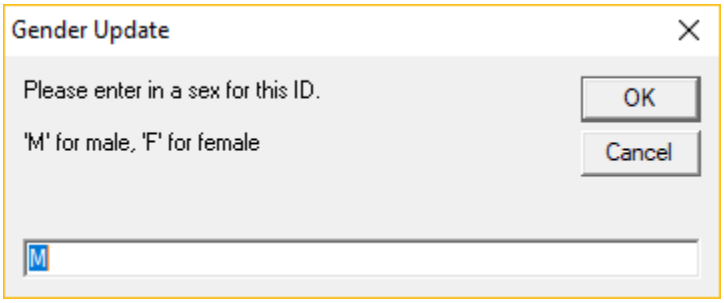



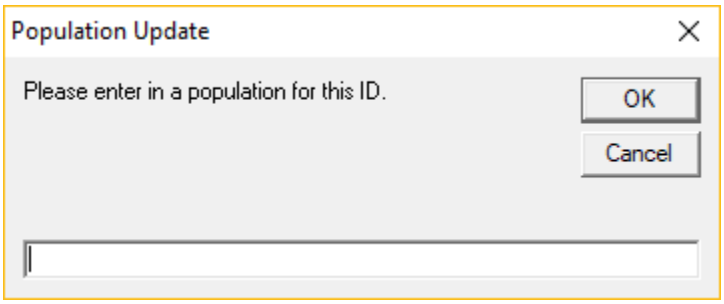

If you choose No, the user will be prompted to enter another ID.

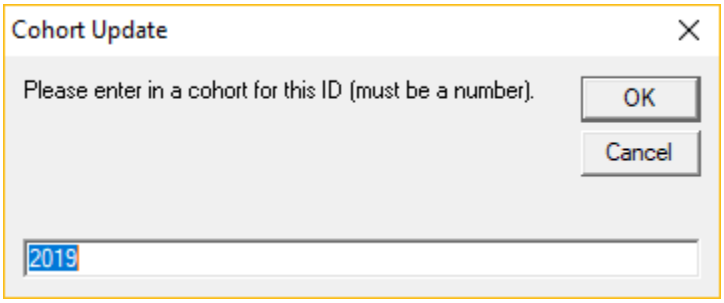



# Updating Individual Information

Once an individual has either been queried or added to the genetics table or used without recording to the genetics table, its information is populated into the sex, population (if specified), and cohort (if specified) fields. To accommodate issues that may arise from incorrect data, these three fields are able to be updated at this stage, with any changes automatically being updated in the genetics table if the individual was already present or just added.

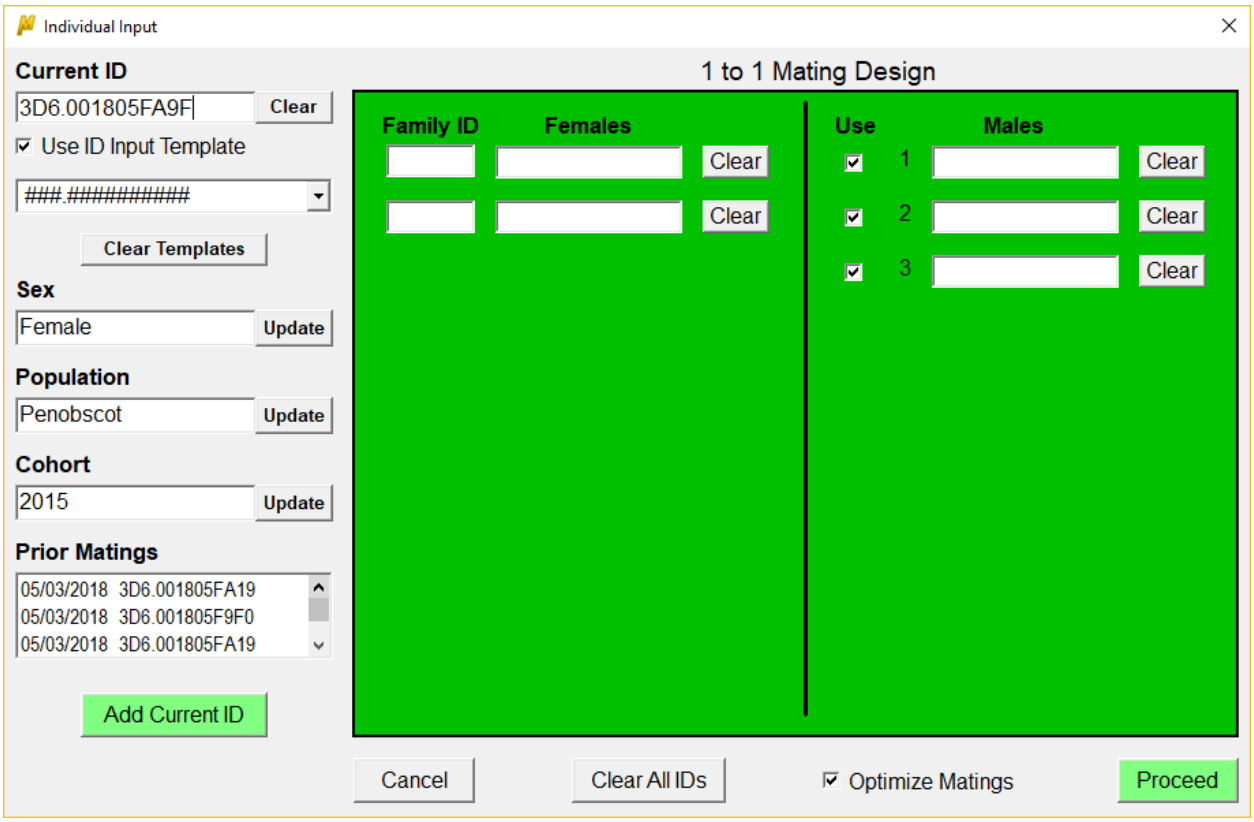


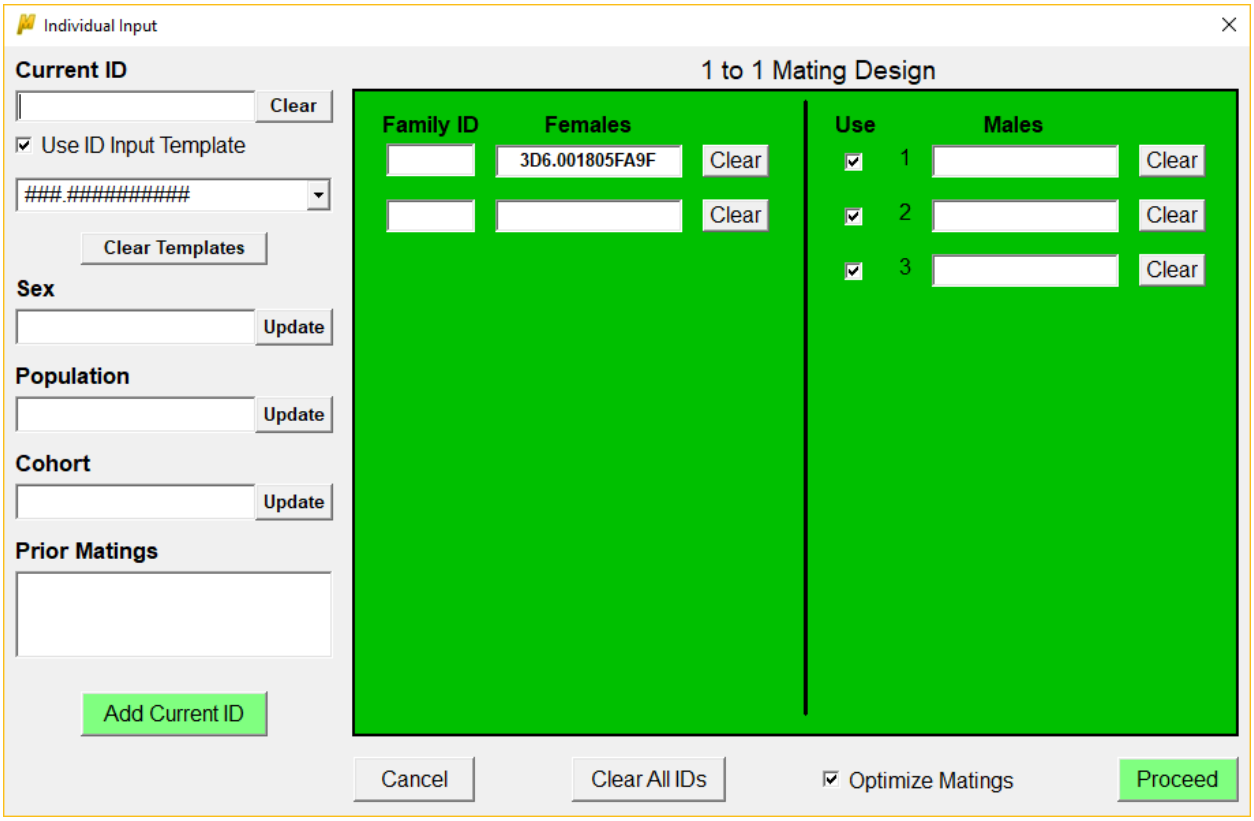



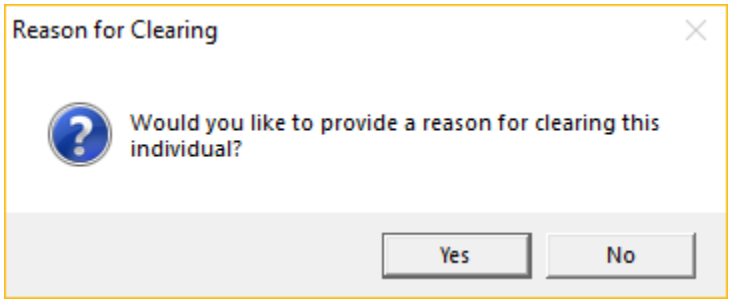
# Creating Mating Pairs

To add individuals to the mating pool, click on the ‘Add Current ID’ button after you have scanned or entered an ID. The individual will automatically be added to the first available slot under the corresponding sex.

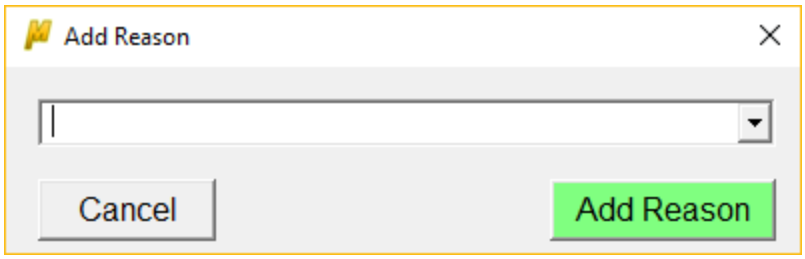




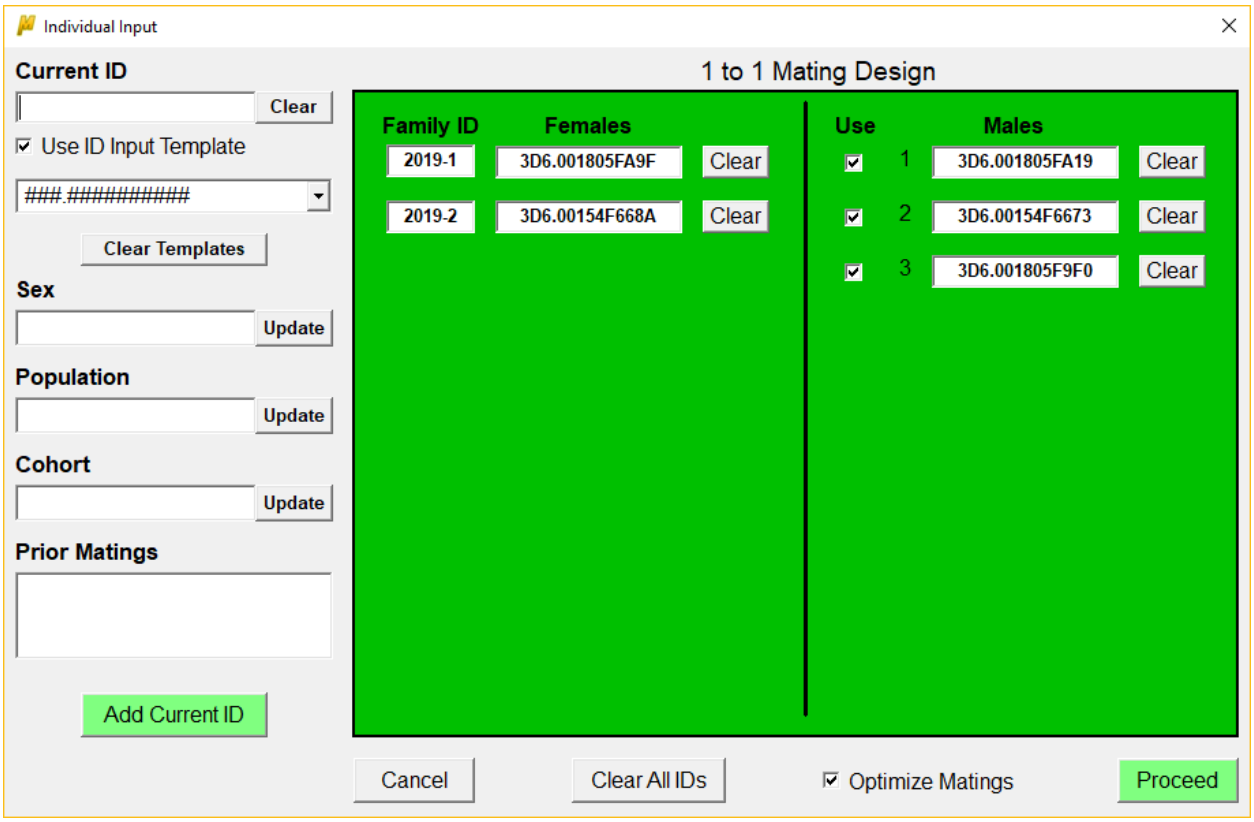

Continue to add individuals until all of the available slots are filled. An added individual can be removed at any time by clicking on the 'Clear' button located to the right of the ID number. If this happens you will be asked if you wish to supply a reason for removing the individual.




If you choose Yes, the user can either select from a list of reasons queried from the genetics table 'Comments' field or type a new one. The reason will then be added to the comments field for the genetics table record of that individual.



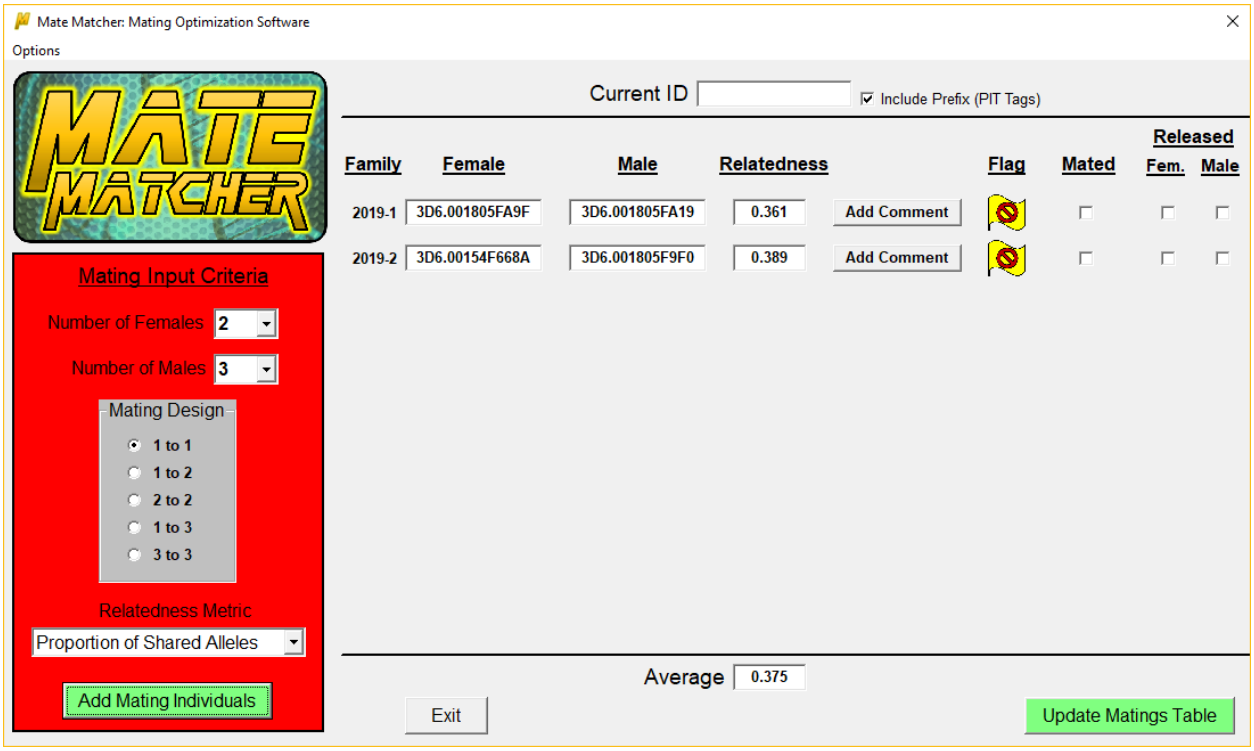

Once all of the mating pool slots have been filled, the user must fill in the Family ID values located to the left of each female before proceeding. The user also has the option to 'Use' male candidates. This option is only viable if there is a surplus of male candidates. To exclude a male from being used uncheck the 'Use' box to the left of its ID slot.



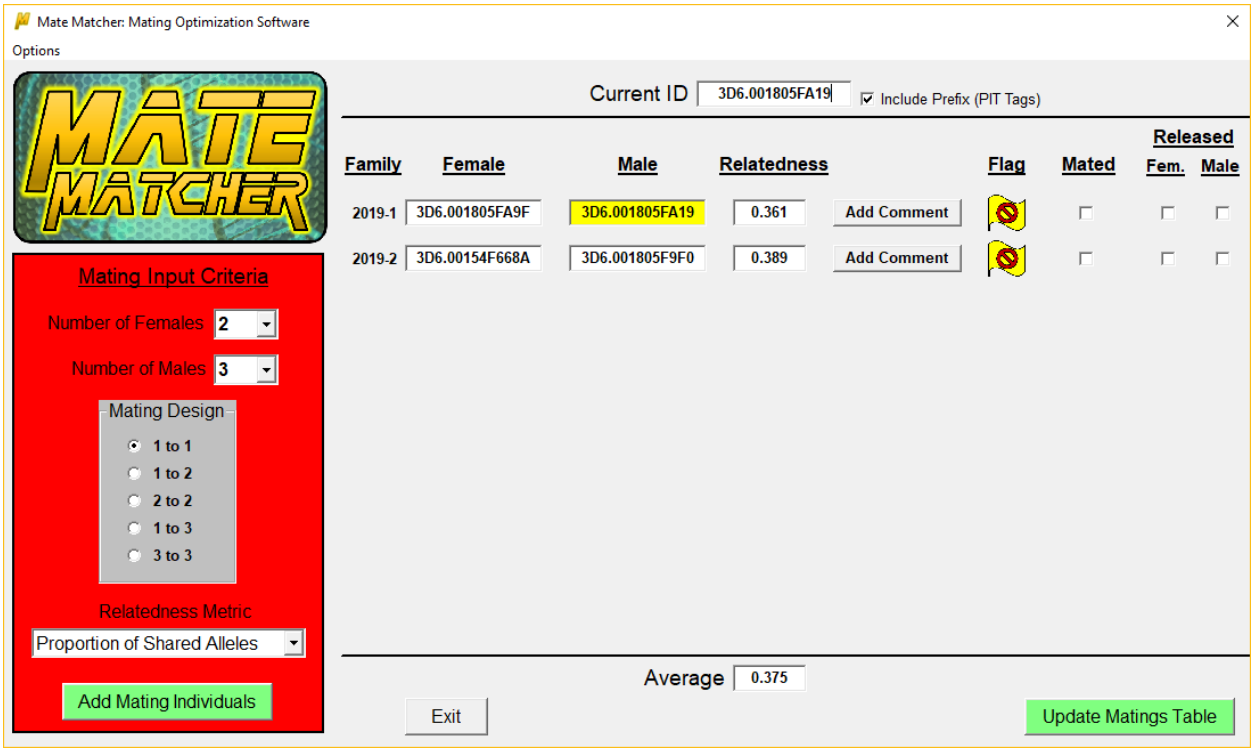

When this is complete, Mate Matcher is ready to create mating pairs. The default is for genetic optimization to be used when creating pairs. However, if the user just wants to use Mate Matcher to record mating pairs and is not interested in optimization or does not have the necessary genetic data to perform optimization, then the 'Optimize Matings' check box at the bottom of the form may be unchecked, in which case mating pairs are matched by the order in which they were entered. Finally, click the 'Proceed' button to create mating pairs.

# Main Form Part II

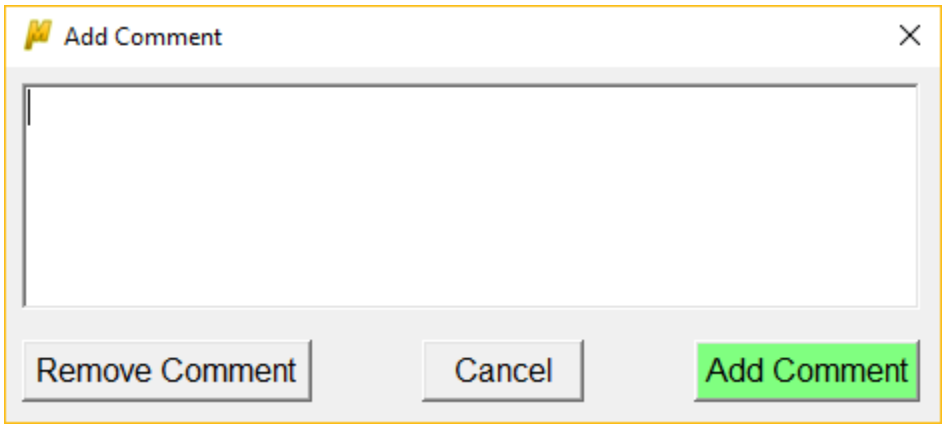
After hitting the ‘Proceed’ button, the matched mating pairs will be listed on the main form.



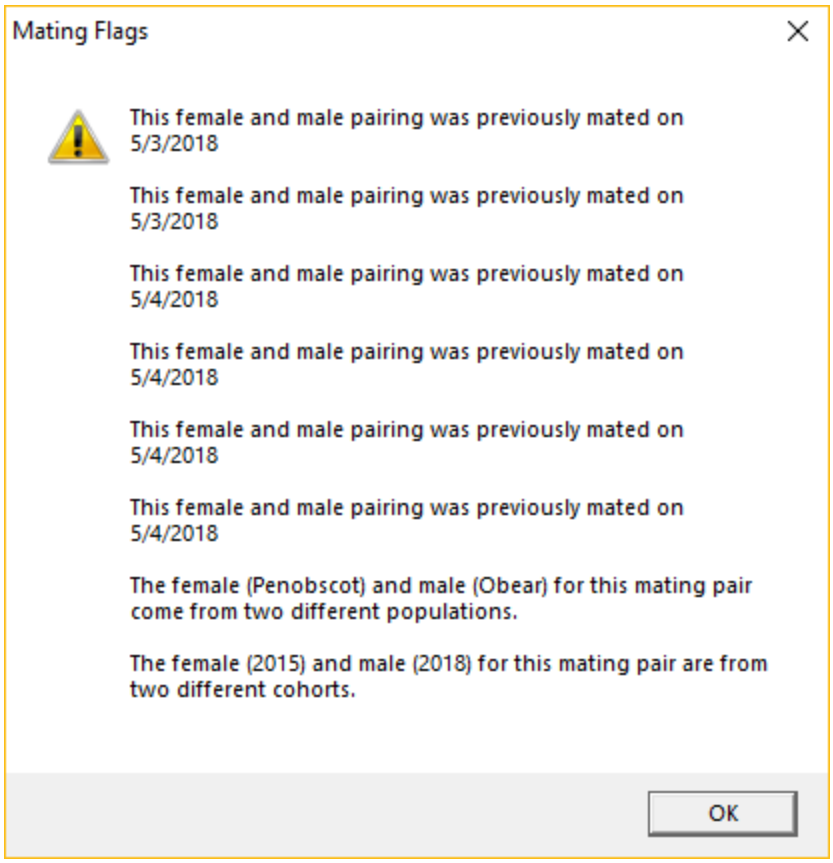

To quickly locate an individual, the user can scan or enter an ID into the ‘Current ID’ text box and the associated tag will by highlighted.



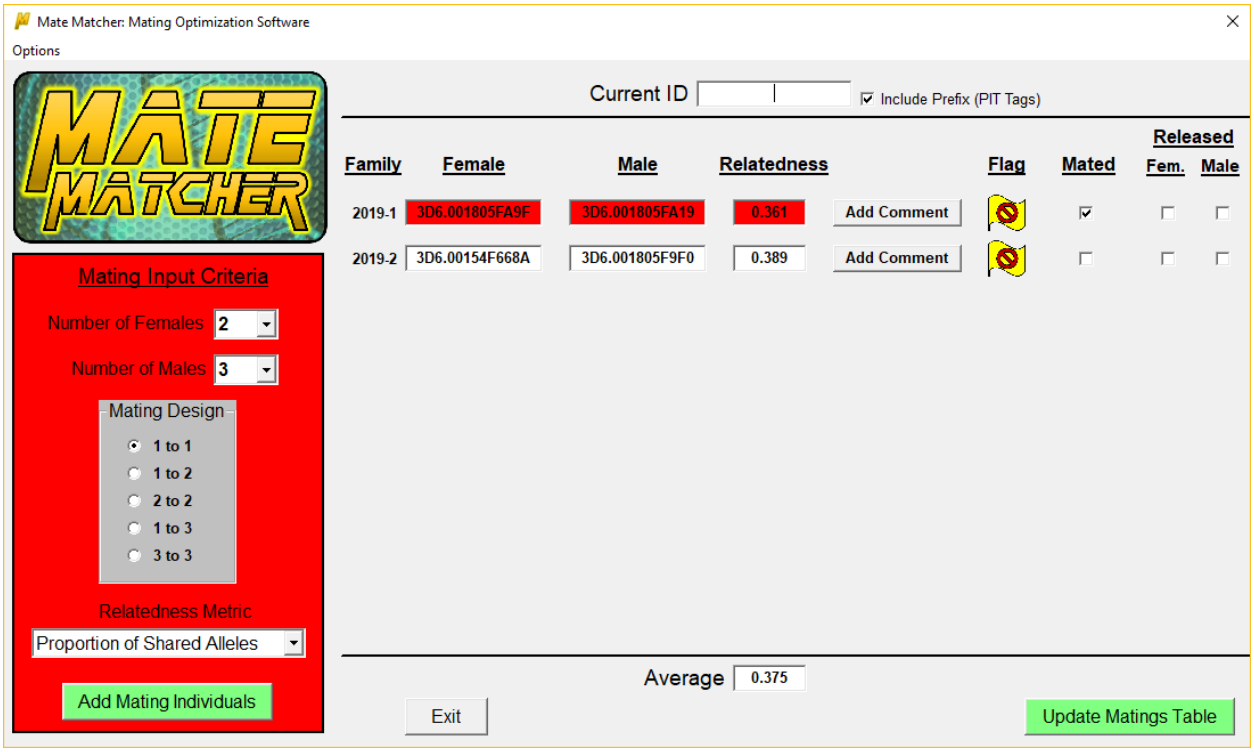

To add any comments about the mating pair, click the 'Add Comment' button and enter the text in the pop-up window.




If any of the warning flag settings specified by the user have been violated than a flag will be displayed for the mating pair under the 'Flag' column. Clicking on the flag will display a list of the violated flags.



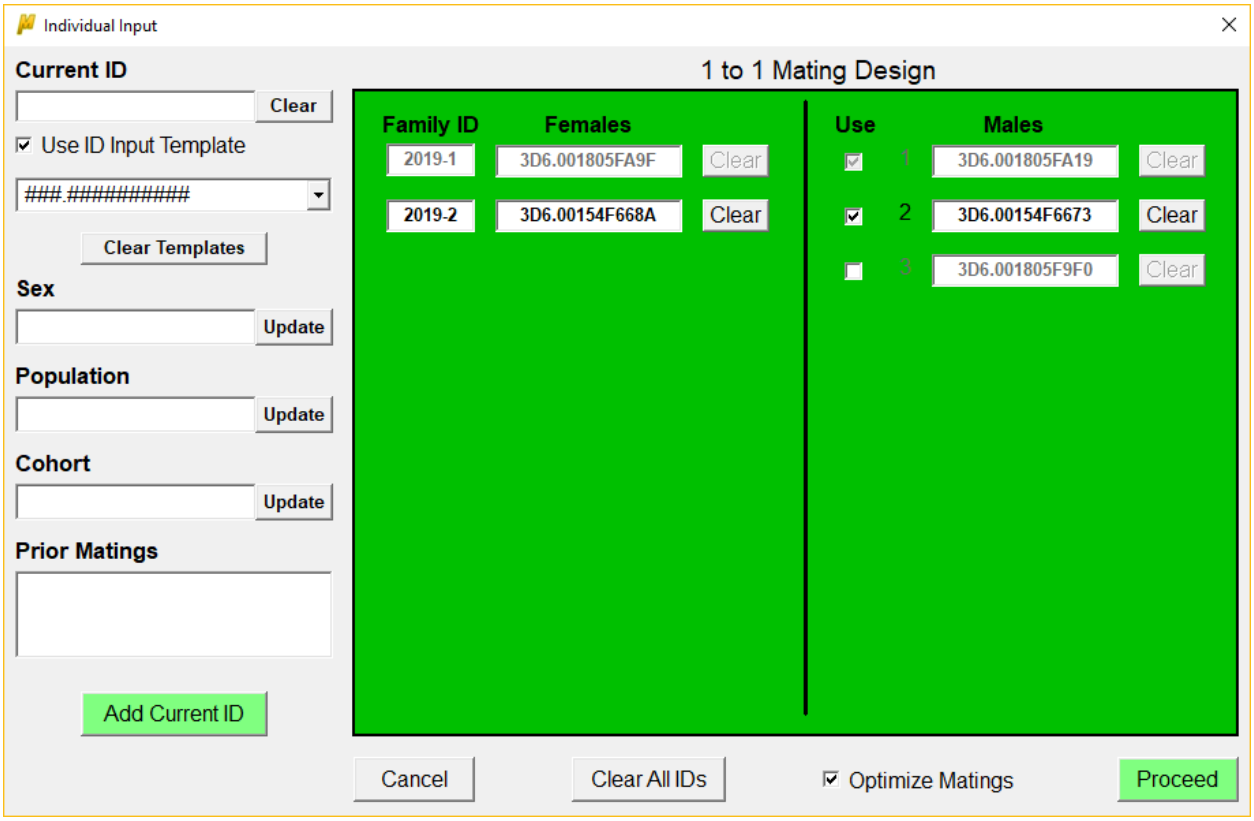

Once a matched pair has been mated, the user should check the associated box under the 'Mated' column. When checked, both the female and male will be highlighted in red to indicate that the mating has been completed.



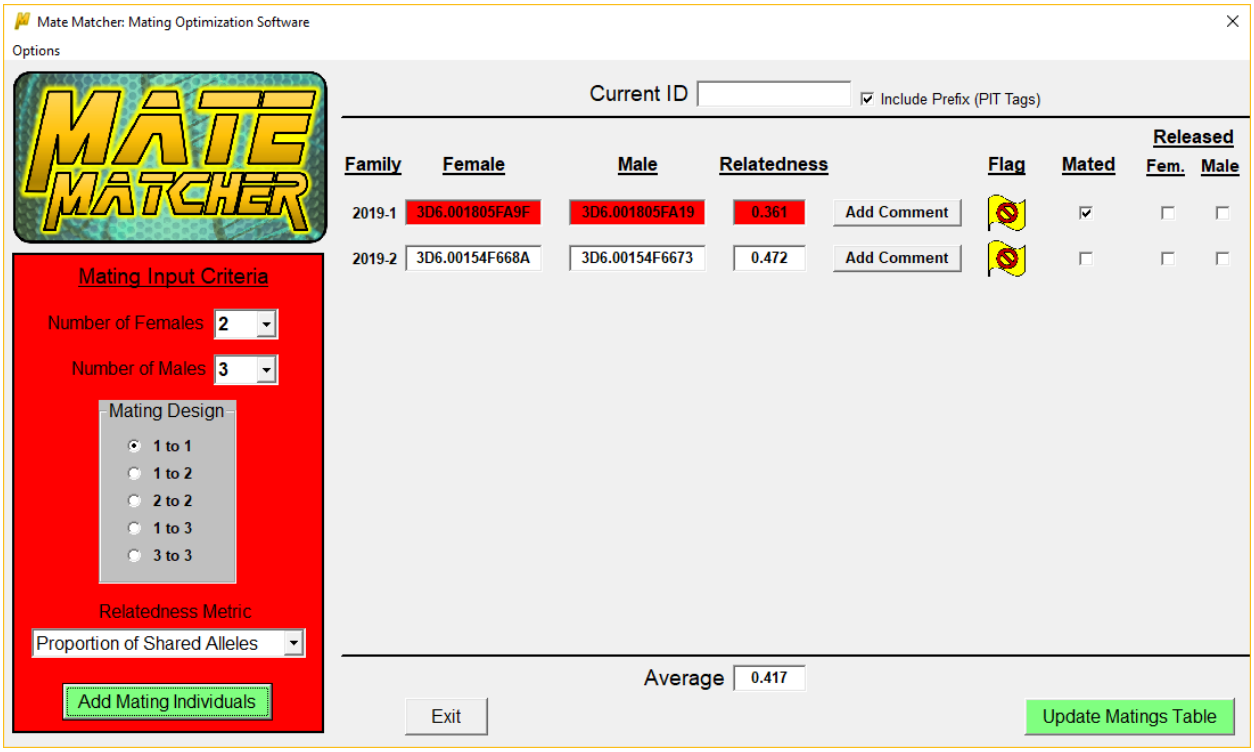

A checked ‘Mated’ box also locks in these individuals and precludes them from being removed if re-optimization becomes necessary.

## Re-optimization

Re-optimization takes place when at least one of the originally optimized mating pairs has been successfully mated, but one or more individuals from the remaining mating pairs needs to be replaced. To re-optimize, the user clicks the ‘Add Mating Individuals’ button to reopen the Individual Input form. Individuals from pairs that are checked as having been mated will be greyed out, disabling the ability to remove them from the parent pool.

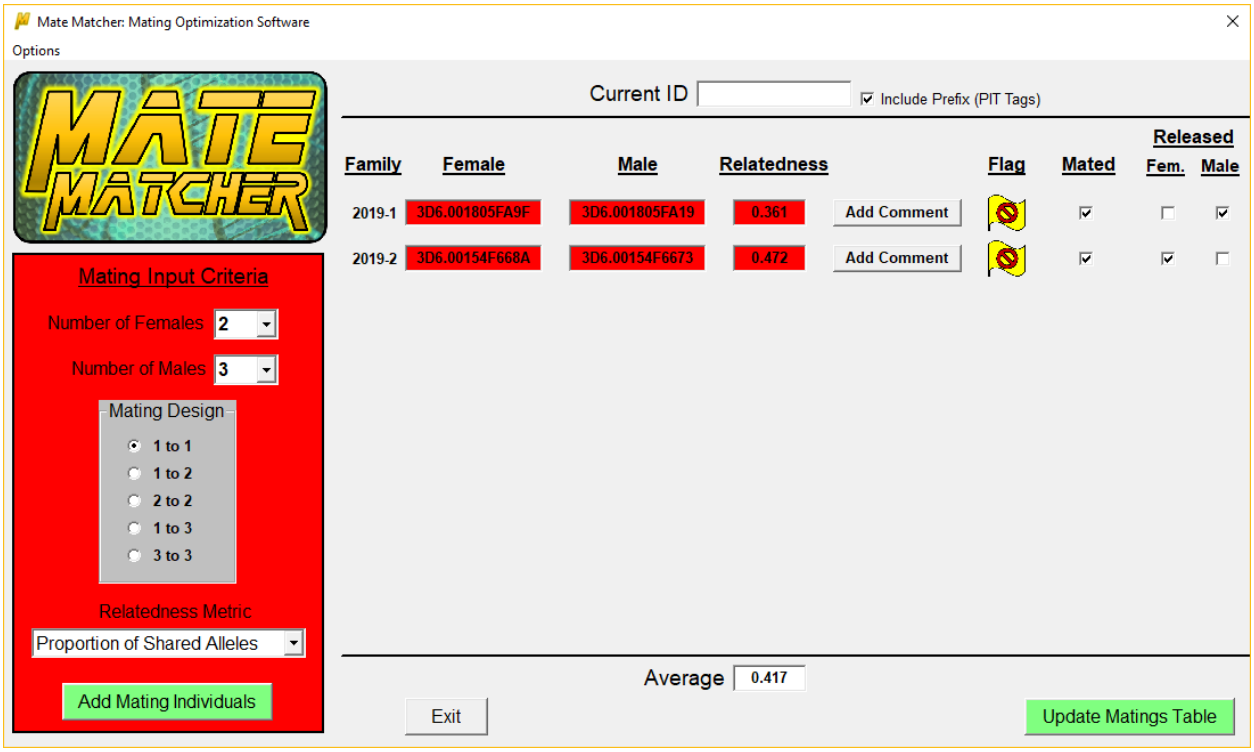


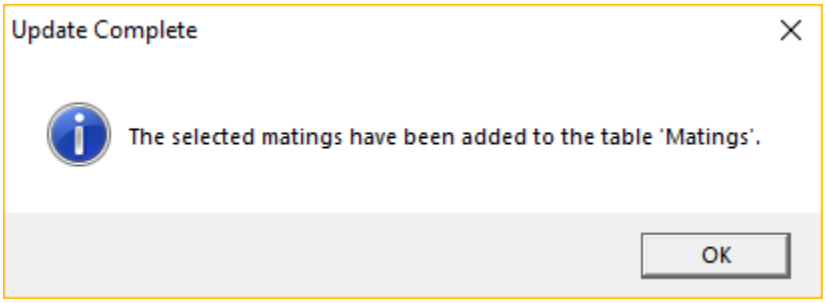

At this point the user can clear and replace any necessary individuals, or if it is a male and there are surplus individuals present in the pool then they have the option of unchecking the 'Use' box for that male. Once this is complete the user would then click on the 'Proceed' button and mating pair matching occurs again for all of the individuals that aren't greyed out.




# Appending Mating Pairs

When all of the matching pairs have been mated, the user can specify if the female, male, or both are going to be released into the wild after mating. Once this is complete, the user needs to record the matings and all of the associated information to the matings table. This is done by clicking on the ‘Update Matings Table’ button. Only mating pairs with the ‘Mated’ box checked will be added to the table. A message will pop-up when the update is complete.


Mate Matcher: Mating Optimization Software
Options
MATE MATCHER
Current ID
Include Prefix (PIT Tags)
Family
Female
Male
Relatedness
Flag
Mated
Released
Fem.
Male
2019-1
3D6.001805FA9F
3D6.001805FA19
0.361
Add Comment
2019-2
3D6.00154F668A
3D6.00154F6673
0.472
Add Comment
Mating Input Criteria
Number of Females
2
Number of Males
3
Mating Design
1 to 1
1 to 2
2 to 2
1 to 3
3 to 3
Relatedness Metric
Proportion of Shared Alleles
Add Mating Individuals
Average
0.417
Exit
Update Matings Table


Update Complete
The selected matings have been added to the table 'Matings'.
OK