

Mate Matcher

Mating Optimization Software

User Guide

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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 MSVBVM60.DLL files all 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 [MSVBVM60.DLL](#).

For both installs, admin rights will be needed.

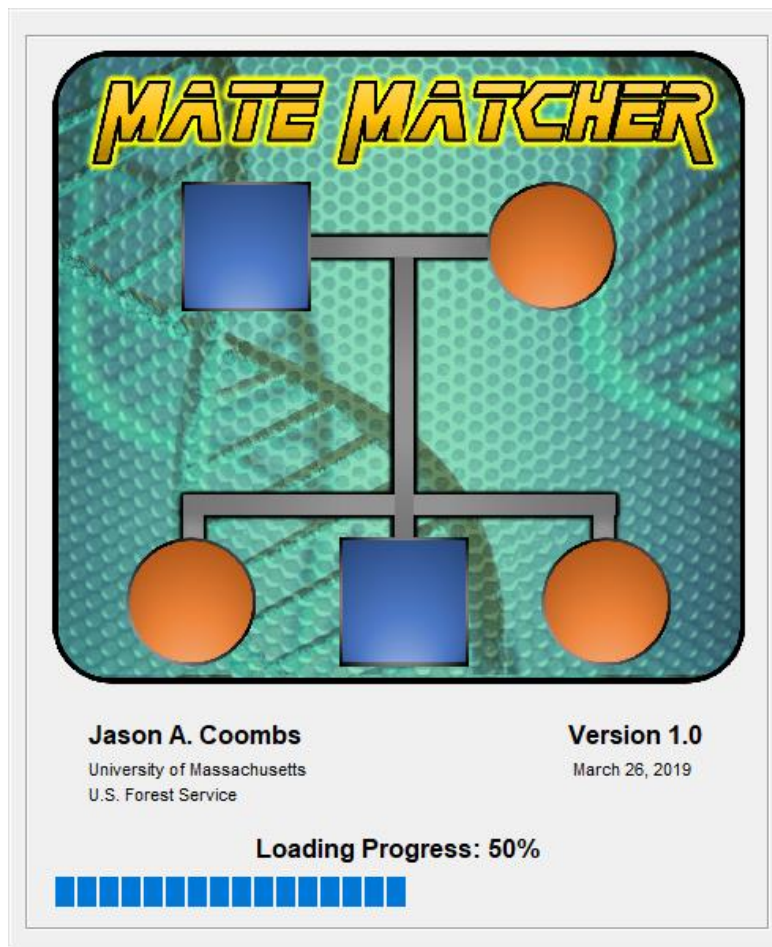
For the MSCOMM32.OCX install:

- Download all files in the github repository by clicking on the green 'Code' button and then clicking 'Download ZIP'.
- Unzip the downloaded file.
- Move the MSCOMM32.OCX file to the C:\Windows\SysWOW64 folder.
- Open the command prompt as an administrator. NOTE: May need to go to the C:\Windows\System32 folder and right-click on the cmd.exe file and select 'Run as administrator'.
- At the command prompt, enter 'cd C:\WindowsSysWOW64' to change to that directory.
- At the prompt, run the following commands:
 - regsvr32 /u C:\WINDOWS\SysWOW64\MSCOMM32.OCX
 - regsvr32 /i C:\WINDOWS\SysWOW64\MSCOMM32.OCX
 - regsvr32 C:\WINDOWS\SysWOW64\MSCOMM32.OCX
- Open Registry Editor as an administrator. NOTE: May need to go to the C:\Windows folder and right-click on the regedit.exe file and select 'Run as administrator'.
- In Registry Editor, click 'File' on the top menu, then click 'Import' and open the 'Regedit_MSCOMM32.reg' file found in the unzipped folder from the initial step.

For the MSVBVM60.DLL, simply double click on the downloaded VB6.0-KB290887-X86.exe file to run the install.

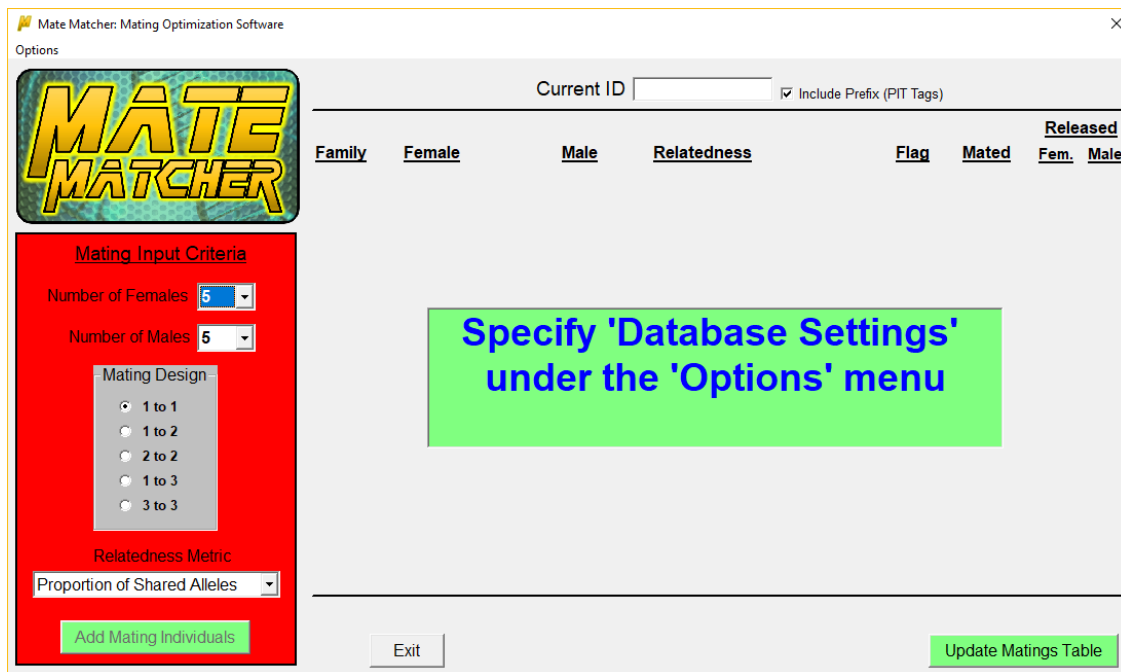
Start-up

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.

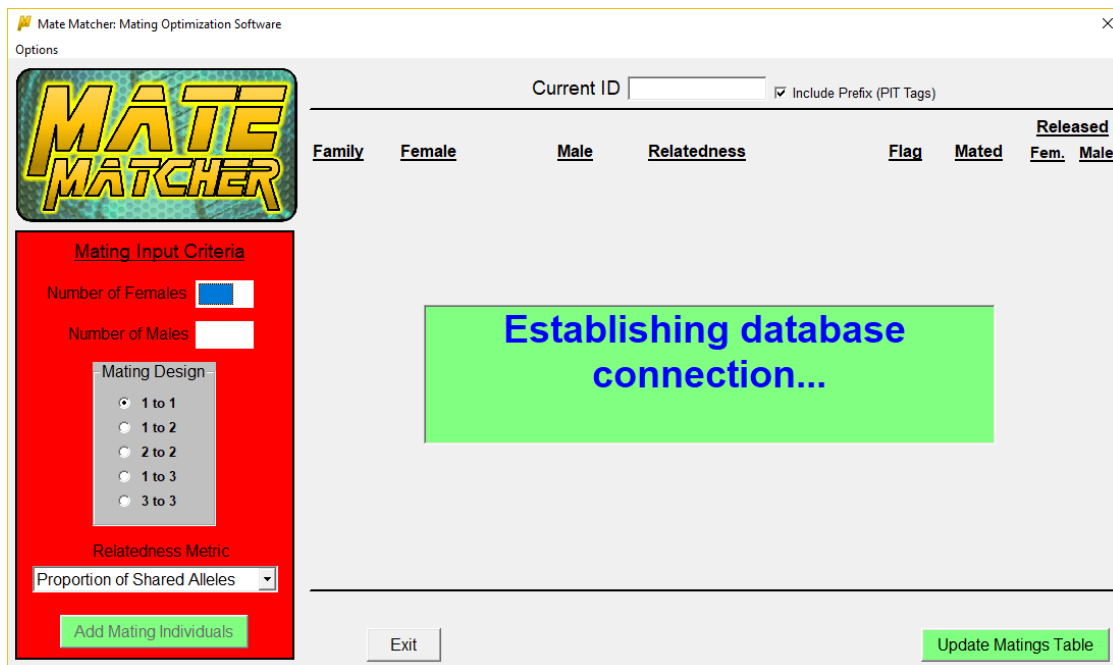


Main Form Part I

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
 - a. Must be a Microsoft Access database (either .mdb or .accdb extensions will work)
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
 - i. There must be two fields for each locus (diploid, 2 alleles)
 - ii. All allelic fields must be contiguous in the table (2 x number of loci)
 - b. Population, Cohort, and Flag are optional and will only be used when checked
 - i. Cohort must be a field with numeric data type
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

The screenshot shows the 'Database Specifications' window with the 'Mating Database' set to 'MaineBroodstock.mdb'. The 'Genetics Table' is set to 'Genetics_2'. The 'Matings Table' is set to 'matings_table_test'. The 'Genetics Table' section includes fields for Unique Identifier (PIT), Sex (Gender), Number of Loci (18), First Locus (197 1), Comments (Comments), and checkboxes for Population (Drainage), Cohort (Year), and Flag (Flag). The 'Matings Table' section includes fields for Batch (Batch), Family ID (Family), Metric (Metric), Relatedness (Relatedness), Mating Design (Mating Design), Optimized (Optimized), Date (Date), Time (Time), and Comments (Comments). The 'Dam Information' section includes fields for ID (Dam), Population (Dam_Pop), Cohort (Dam_Cohort), Scored Loci (Dam_Scored_Loci), and Released (Dam_Released). The 'Sire Information' section includes fields for ID (Sire), Population (Sire_Pop), Cohort (Sire_Cohort), Scored Loci (Sire_Scored_Loci), and Released (Sire_Released). There are 'Clear Fields' buttons for both the Dam and Sire information sections. The window has 'Cancel' and 'Save' buttons at the bottom.

Genetics Table

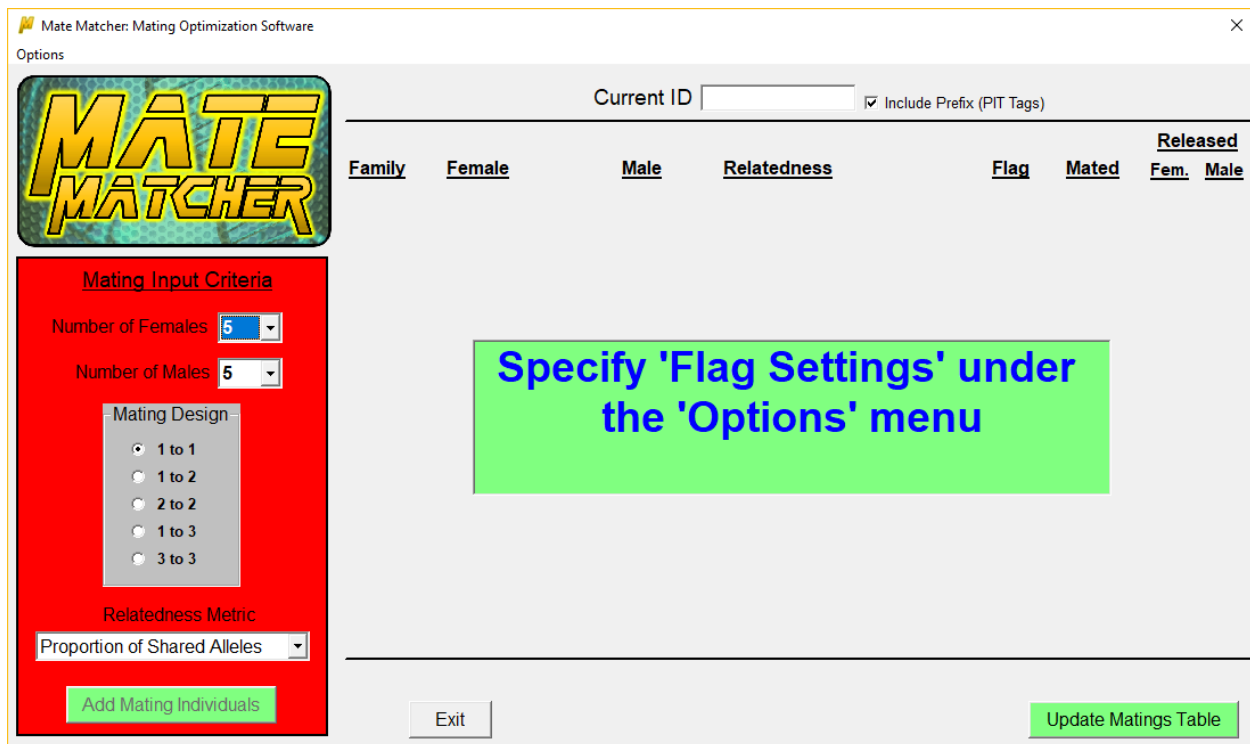
Field	Description
Unique Identifier	The unique identifier of the individual
Sex	The gender of the individual (e.g. M, F, U)
Number of Loci	The number of loci comprising the genotypes of all individuals
First Locus	The column corresponding to the first locus reading from left to right in the table
Comments	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, NOTE: Must be a numeric field
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
Mating Design	Text	The mating design used when optimizing mating pairs
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

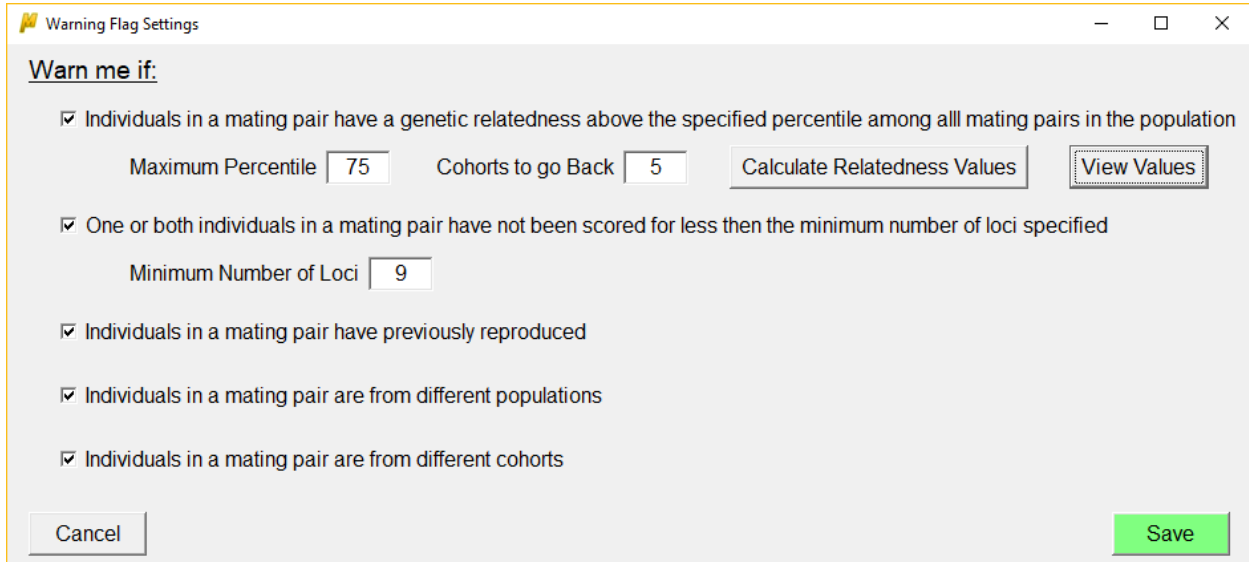
Open the warning flag settings window by clicking 'Options' on the top menu of the main form and selecting 'Warning Flag Settings'. These settings provide options for raising warning flags if mating pairs meet flag specifications. Any raised flags will appear on the main form after mating pairs have 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 (if population is specified)
 - Only individuals present in the specified 'Cohorts to go Back' are included
 - **NOTE:**
 - Depending on the number of individuals the time to calculate these values can reach upward of an hour
 - A large number of individuals (~10,000-15,000) may result in a memory shortage error
 - In these instances, you may need to limit the number of cohorts to go back
 - Once calculations have been completed, the pairwise relatedness value corresponding to the specified maximum percentile can be viewed by clicking on the 'View Values' button
- One or both mating individuals has allelic information present at less than the specified minimum number of loci
 - Unscored alleles should be represented by an empty (null) cell
 - An allele with a 0 value will be considered to be scored by Mate Matcher
- 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



Warning Flag Settings

Warn me if:

- ☒ Individuals in a mating pair have a genetic relatedness above the specified percentile among all mating pairs in the population

Maximum Percentile
 Cohorts to go Back
Calculate Relatedness Values
View Values
- ☒ One or both individuals in a mating pair have not been scored for less than the minimum number of loci 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

Cancel Save

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 $2 * \text{number of loci with allelic information present}$. 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 Input

×

Current ID

Clear

☒ Use ID Input Template

▼

Clear Templates

Sex

Update

Population

Update

Cohort

Update

Prior Matings

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use	Males	
<input type="text"/>	<input type="text"/>	Clear	<input checked="" type="checkbox"/>	1	<input type="text"/> Clear
<input type="text"/>	<input type="text"/>	Clear	<input checked="" type="checkbox"/>	2	<input type="text"/> Clear
<input type="text"/>	<input type="text"/>	Clear	<input checked="" type="checkbox"/>	3	<input type="text"/> Clear
<input type="text"/>	<input type="text"/>	Clear	<input checked="" type="checkbox"/>	4	<input type="text"/> Clear
<input type="text"/>	<input type="text"/>	Clear	<input checked="" type="checkbox"/>	5	<input type="text"/> Clear

Clear All

Cancel

☒ Use Family ID Prefix

Clear

☒ Optimize Matings

Proceed

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 already present. If a template is used, you will only be asked once the entered ID matches the template. To create 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 ##.##

Individual Input

Current ID

3DD.003BD41044

Clear

☒ Use ID Input Template

###.#####

▼

Clear Templates

Sex

Female

Update

Population

Gill

Update

Cohort

2019

Update

Prior Matings

04/01/2019 3DD.003BB4AE4B

04/01/2019 3DD.003BB4AE4B

04/01/2019 3DD.003BB4AE4B

▲

▼

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use	Males	
		Clear	<input checked="" type="checkbox"/>	1	Clear
		Clear	<input checked="" type="checkbox"/>	2	Clear
		Clear	<input checked="" type="checkbox"/>	3	Clear
		Clear	<input checked="" type="checkbox"/>	4	Clear
		Clear	<input checked="" type="checkbox"/>	5	Clear

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

▼

Clear

☒ Optimize Matings

Proceed

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 checked on the database settings form), and cohort (if checked on the database settings form) information will be queried from the genetics table, and the individual's 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

ID Not Present

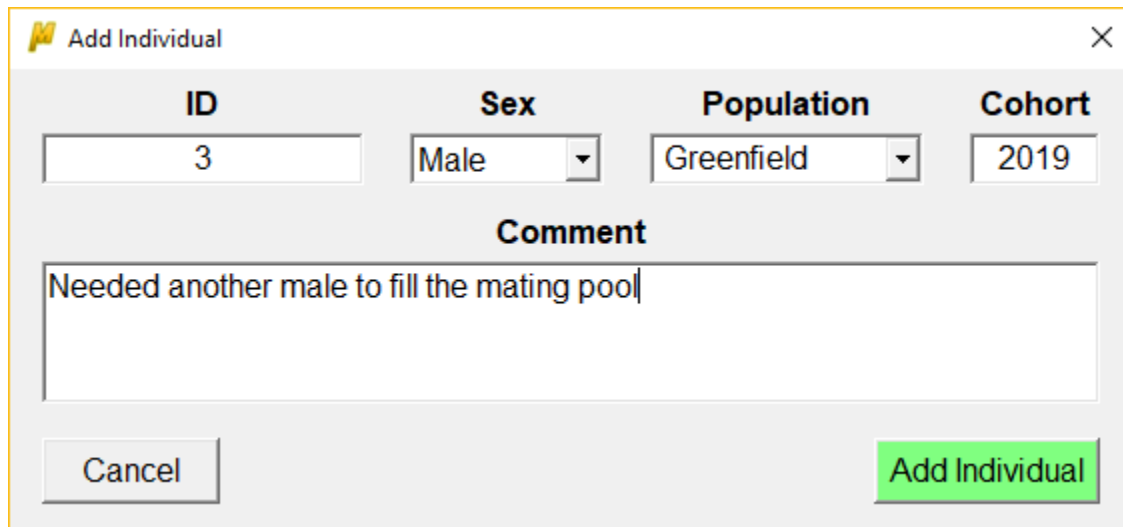
?

The ID '3' is not present in the genetics table (Genetics_New).
 Would you like to add this individual to the genetics table?

Yes

No

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.



Add Individual

ID	Sex	Population	Cohort
3	Male	Greenfield	2019

Comment

Needed another male to fill the mating pool

Cancel Add Individual

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

Individual Input

Current ID

3

Clear

☐ Use ID Input Template

###.#####

Clear Templates

Sex

Male

Update

Population

Greenfield

Update

Cohort

2019

Update

Prior Matings

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use		Males	
		Clear	<input checked="" type="checkbox"/>	1		Clear
		Clear	<input checked="" type="checkbox"/>	2		Clear
		Clear	<input checked="" type="checkbox"/>	3		Clear
		Clear	<input checked="" type="checkbox"/>	4		Clear
		Clear	<input checked="" type="checkbox"/>	5		Clear

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

Clear

☒ Optimize Matings

Proceed

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.

ID Fate

?

Do you still wish to use this tag without entering it into the genetics table?

Yes

No

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 conditions specified under the 'Warning Flags Settings' if it ends up being used in a mating pair.

Add Individual

ID

4

Sex

Male

Population

Gill

Cohort

2018

Cancel

Add

Individual Input

Current ID

4

Clear

☐ Use ID Input Template

####.#####

Clear Templates

Sex

Male

Update

Population

Gill

Update

Cohort

2018

Update

Prior Matings

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use		Males	
		Clear	<input checked="" type="checkbox"/>	1		Clear
		Clear	<input checked="" type="checkbox"/>	2		Clear
		Clear	<input checked="" type="checkbox"/>	3		Clear
		Clear	<input checked="" type="checkbox"/>	4		Clear
		Clear	<input checked="" type="checkbox"/>	5		Clear

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

Clear

☒ Optimize Matings

Proceed

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

Enter Different Individual

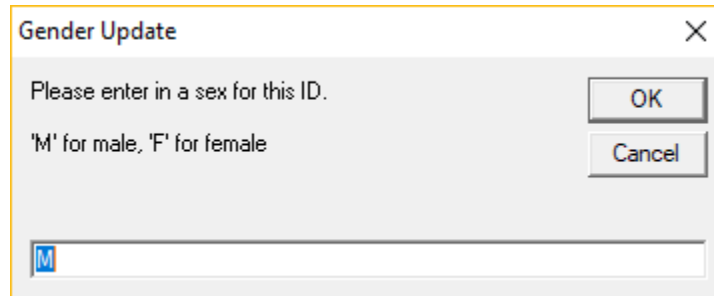
×

Please enter another ID.

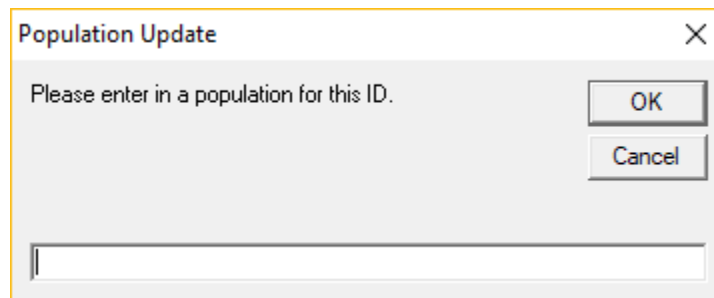
OK

Updating Individual Information

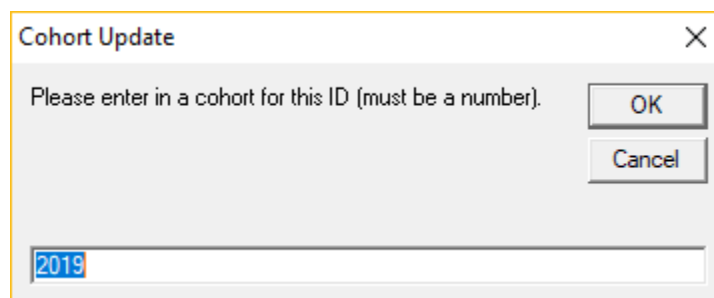
Once an individual has either been queried or added to the genetics table or used without recording to the genetics table, its information is populated into the sex, population (if specified), and cohort (if specified) fields. To accommodate issues that may arise from incorrect data, these three fields 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.



A dialog box titled "Gender Update" with a close button (X) in the top right corner. The text inside says "Please enter in a sex for this ID." followed by "'M' for male, 'F' for female". There are two buttons on the right: "OK" and "Cancel". At the bottom, there is a text input field containing the letter "M".



A dialog box titled "Population Update" with a close button (X) in the top right corner. The text inside says "Please enter in a population for this ID.". There are two buttons on the right: "OK" and "Cancel". At the bottom, there is an empty text input field.



A dialog box titled "Cohort Update" with a close button (X) in the top right corner. The text inside says "Please enter in a cohort for this ID (must be a number).". There are two buttons on the right: "OK" and "Cancel". At the bottom, there is a text input field containing the year "2019".

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.

Individual Input

Current ID

3D6.001805FA9F

Clear

☒ Use ID Input Template

###.#####

▼

Clear Templates

Sex

Female

Update

Population

Penobscot

Update

Cohort

2014

Update

Prior Matings

04/08/2019 3DD.003BB4AE4B

04/08/2019 3D6.001805FA19

04/09/2019 3DD.003BB4AE4B

▲

▼

Add Current ID

1 to 1 Mating Design

Family ID	Females	Use	Males
		<input checked="" type="checkbox"/>	1
		<input checked="" type="checkbox"/>	2
		<input checked="" type="checkbox"/>	3

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

▼

Clear

☒ Optimize Matings

Proceed

Individual Input

Current ID

Clear

☒ Use ID Input Template

###.#####

▼

Clear Templates

Sex

Update

Population

Update

Cohort

Update

Prior Matings

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use		Males	
<input type="text"/>	3D6.001805FA9F	Clear	<input checked="" type="checkbox"/>	1	<input type="text"/>	Clear
<input type="text"/>	<input type="text"/>	Clear	<input checked="" type="checkbox"/>	2	<input type="text"/>	Clear
			<input checked="" type="checkbox"/>	3	<input type="text"/>	Clear

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

▼

Clear

☒ Optimize Matings

Proceed

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.

Reason for Clearing

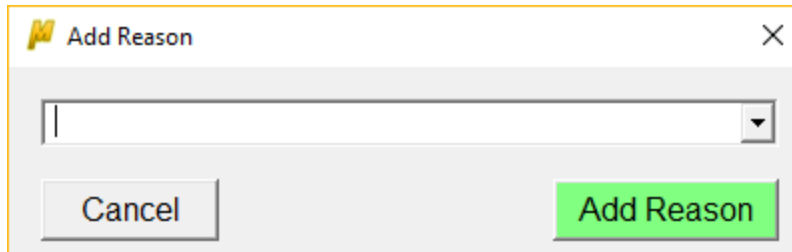
?

Would you like to provide a reason for clearing this individual?

Yes

No

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.

A screenshot of a software dialog box titled "Add Reason". The dialog box has a light gray background and a thin orange border. At the top left is a small yellow icon of a notepad and pencil, followed by the title "Add Reason". At the top right is a close button represented by a black "X". Below the title bar is a large, empty text input field. At the bottom of the dialog box are two buttons: a "Cancel" button on the left and an "Add Reason" button on the right. The "Add Reason" button is highlighted with a green background.

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 of including a prefix that will be added to each family ID. To use a prefix, check the box next to 'Use Family ID Prefix' located at the bottom of the page and enter a prefix into the drop-down box. Prefixes will be saved for future use, and can be cleared at any time by clicking the 'Clear' button located to the right of the drop-down box.

Lastly, the user 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.

Individual Input

Current ID

Clear

☒ Use ID Input Template

###.#####

▼

Clear Templates

Sex

Update

Population

Update

Cohort

Update

Prior Matings

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use		Males	
0001	3D6.001805FA9F	Clear	<input checked="" type="checkbox"/>	1	3D6.001805FA19	Clear
0002	3D6.00154F668A	Clear	<input checked="" type="checkbox"/>	2	3D6.00154F6673	Clear
			<input checked="" type="checkbox"/>	3	3D6.001805F9F0	Clear

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

▼

Clear

☒ Optimize Matings

Proceed


When all settings have been completed, 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.

Mate Matcher: Mating Optimization Software

Options



Mating Input Criteria

Number of Females

Number of Males

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

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		<input type="checkbox"/>	<input type="checkbox"/>
2019-2	3D6.00154F668A	3D6.001805F9F0	0.389	Add Comment		<input type="checkbox"/>	<input type="checkbox"/>


Average

Exit Update Matings Table

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

Mate Matcher: Mating Optimization Software

Options



Mating Input Criteria

Number of Females

Number of Males

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

Current ID

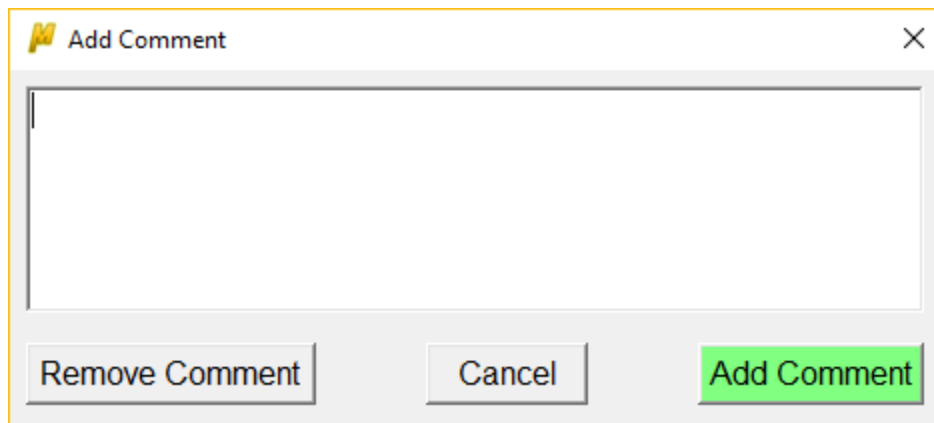
☒ Include Prefix (PIT Tags)

Family	Female	Male	Relatedness	Flag	Mated	Released	
						Fem.	Male
2019-1	3D6.001805FA9F	3D6.001805FA19	0.361	Add Comment		<input type="checkbox"/>	<input type="checkbox"/>
2019-2	3D6.00154F668A	3D6.001805F9F0	0.389	Add Comment		<input type="checkbox"/>	<input type="checkbox"/>

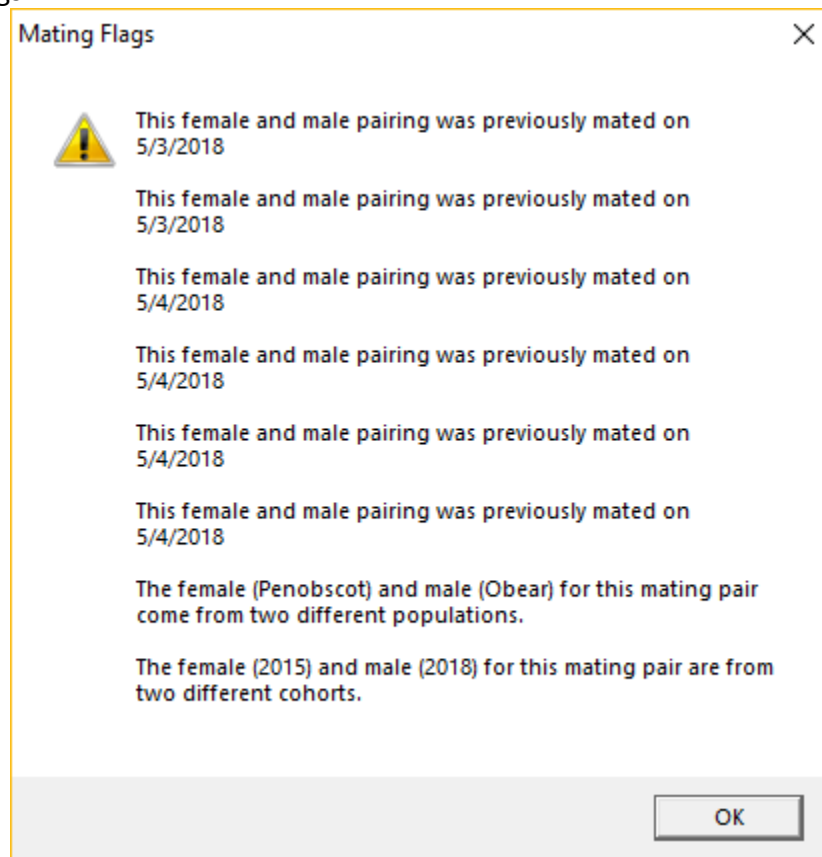
Average

Exit Update Matings Table

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 then 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.

Mate Matcher: Mating Optimization Software

Options



Current ID

☒ Include Prefix (PIT Tags)

Family	Female	Male	Relatedness	Flag	Mated	Released	
						Fem.	Male
2019-1	3D6.001805FA9F	3D6.001805FA19	0.361		<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
2019-2	3D6.00154F668A	3D6.001805F9F0	0.389		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Mating Input Criteria

Number of Females

Number of Males

Mating Design

- ☒ 1 to 1
- ☐ 1 to 2
- ☐ 2 to 2
- ☐ 1 to 3
- ☐ 3 to 3

Relatedness Metric

Average

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.

Individual Input

×

Current ID

Clear

☒ Use ID Input Template

###.#####

▼

Clear Templates

Sex

Update

Population

Update

Cohort

Update

Prior Matings

Add Current ID

1 to 1 Mating Design

Family ID	Females		Use		Males	
0001	3D6.001805FA9F	Clear	<input checked="" type="checkbox"/>	1	3D6.001805FA19	Clear
0002	3D6.00154F668A	Clear	<input checked="" type="checkbox"/>	2	3D6.00154F6673	Clear
			<input type="checkbox"/>	3	3D6.001805F9F0	Clear

Clear All

Cancel

☒ Use Family ID Prefix

PE2019GL

▼

Clear


☒ Optimize Matings

Proceed

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.

Mate Matcher: Mating Optimization Software

Options



Current ID

☒ Include Prefix (PIT Tags)

Family	Female	Male	Relatedness	Flag	Mated	Released	
						Fem.	Male
2019-1	3D6.001805FA9F	3D6.001805FA19	0.361		<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
2019-2	3D6.00154F668A	3D6.00154F6673	0.472		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Mating Input Criteria

Number of Females

Number of Males

Mating Design

- ☒ 1 to 1
- ☐ 1 to 2
- ☐ 2 to 2
- ☐ 1 to 3
- ☐ 3 to 3

Relatedness Metric

Average

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.

Mating pairs matched after the initial optimization (like the second pair in the example above) will be labelled as 'reoptimized' under the optimized column in the matings table, as opposed to 'Yes' (first optimization) or 'No' (optimize matings is unchecked).

A message will pop-up when the update is complete.

Mate Matcher: Mating Optimization Software

Options



Current ID

☒ Include Prefix (PIT Tags)

Family	Female	Male	Relatedness	Add Comment	Flag	Mated	Released	
							Fem.	Male
2019-1	3D6.001805FA9F	3D6.001805FA19	0.361	Add Comment		<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
2019-2	3D6.00154F668A	3D6.00154F6673	0.472	Add Comment		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Mating Input Criteria

Number of Females

Number of Males

Mating Design

- ☒ 1 to 1
- ☐ 1 to 2
- ☐ 2 to 2
- ☐ 1 to 3
- ☐ 3 to 3

Relatedness Metric

Add Mating Individuals

Average

Exit Update Matings Table

Update Complete

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

OK

Recording of Non-optimized Pairs

An additional table is automatically created for recording the mating pairs that would have occurred if no optimization was employed. This is useful for comparison between optimized and non-optimized matings to quantify decreases in mating pair relatedness compared to random.

The default name for this table is 'matings_nonopt'. When the user appends mating pairs to the specified matings table, the 'matings_nonopt' table is also updated. This is done by reading in the female and male pairs as they were added to the input form. In the below example, 3D6.001805FA9F would be paired with 3D6.001805FA19, and 3D6.00154F668A would be paired with 3D6.00154F6673. In the event that a male's 'Use' box is unchecked or the male has already been mated and is thus disabled, the next available male is used instead.

Information added to the 'mating_nonopt' table is the same as that added to the specified matings table with the following exceptions: no comments and no sire/dam release information is recorded.

Individual Input

Current ID

☒ Use ID Input Template

Sex

Population

Cohort

Prior Matings

1 to 1 Mating Design

Family ID	Females		Use		Males	
0001	3D6.001805FA9F	<input type="button" value="Clear"/>	<input checked="" type="checkbox"/>	1	3D6.001805FA19	<input type="button" value="Clear"/>
0002	3D6.00154F668A	<input type="button" value="Clear"/>	<input checked="" type="checkbox"/>	2	3D6.00154F6673	<input type="button" value="Clear"/>
			<input checked="" type="checkbox"/>	3	3D6.001805F9F0	<input type="button" value="Clear"/>

☒ Use Family ID Prefix
 ☒ Optimize Matings