



# TrueAllele<sup>®</sup> VUler<sup>™</sup>

Getting Started



## **TrueAllele® VUIer™: Getting Started**

The TrueAllele® Technology is protected by United States patent 10,489,233.

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# 1 Overview

This manual describes installing and upgrading the TrueAllele® Visual User Interface (VUIer™) software, and provides information about network and backup systems. The basics of starting the program, connecting to a database, and a glossary of common terms are also available in this manual.

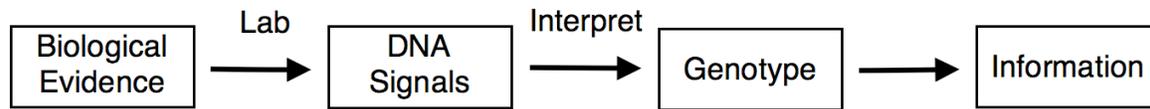
The first two sections of this overview discuss the basics of the DNA interpretation process and where additional educational material is found. This information is useful for understanding how TrueAllele works.

The VUIer section gives information about the software options available for use with TrueAllele. VUIer allows the analyst to interact with the TrueAllele server.

The System Requirements section gives the recommended system requirements for optimal use of the TrueAllele VUIer software. Minimum system requirements are also supplied.

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## 1.1 DNA Interpretation Process



**Figure 1.** *DNA Interpretation Process*

The DNA interpretation process is broken down into two transformations (Figure 1). The goal of each transformation is to preserve as much identification information as possible. In the first step, a laboratory transforms the biological evidence samples into DNA signals. The second transformation involves the interpretation of the DNA signals into genotypes. The TrueAllele Casework software handles this step by quantitatively interpreting DNA signals using probabilistic genotype modeling. Mathematical formulas communicate the genotypes as identification information.

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## 1.2 Background Information

There is a wealth of material available from Cybergenetics for learning about the objective computer interpretation of quantitative DNA evidence. Essential information is provided in this and other supporting manuals. Additional publications and presentations are available on the Cybergenetics website at [www.cybgen.com/information](http://www.cybgen.com/information).

### Newsletters

The best place to begin is with Cybergenetics DNA newsletters, located at <https://www.cybgen.com/news/newsletters/page.shtml>. These short articles are written for the nonscientist. These newsletters introduce TrueAllele Casework and show the system's use in court, different validation studies, and comparisons with human review.

## Publications

An introduction to a DNA likelihood ratio match statistic is found in this short expository article, located at <http://www.cybgen.com/go/ISHI2010>.

The operation and significance of the TrueAllele system are described in this peer-reviewed, scientific validation paper located at <http://www.cybgen.com/go/JFS2011>. It is recommended to read this long article over three separate sessions:

1. *Introduction, Materials and Methods.* These sections teach the underlying principles of probabilistic genotyping and DNA identification information. They also explain how to rigorously assess the reliability of any DNA interpretation method.
2. *Case Example.* A DNA mixture from a real case was analyzed both by man and machine. The computer's match score was a billion times greater. Ten different reasons, explored at ten different genetic loci, are examined to explain how computers can preserve the match information that humans discard.
3. *Results and Discussion.* Computer and human review that were conducted on the same sixteen DNA mixture casework items are compared. The results show TrueAllele computer's reliability and show that the computer is typically a million times more informative than human. The computer simply makes better use of the DNA data.

In addition, Cybergenetics researchers have written many other scientific and peer-reviewed publications about TrueAllele evidence interpretation and how it fully preserves DNA identification information, located at <http://www.cybgen.com/information/publication/page.shtml>.

## Course Lectures

Course materials (videos, slides, transcripts, etc.) are provided about quantitative DNA mixture interpretation, located at <http://www.cybgen.com/information/courses/page.shtml>. The six 20 minute lectures on "DNA Identification for Scientists: Basics & Methods" are the starting point for students desiring a real understanding of scientific DNA interpretation.

## Additional References

After this basic introduction, there are scientific presentations about TrueAllele's methods and results available for review, located at <http://www.cybgen.com/information/presentations/page.shtml>. These short, narrated PowerPoint movies provide a living history of the TrueAllele technology and its applications as presented at scientific meetings.

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## 1.3 Visual User Interface (VUIer)

An analyst installs the TrueAllele VUIer software on their Macintosh or Windows computer to interact with a TrueAllele server. This software allows the analyst to upload data and requests and download the results that are stored on the TrueAllele server. Depending on the needs of the analyst, there are three VUIer versions available: Full, Cloud, and Read-only.

### Full

This VUIer version is available to interact with the laboratory's in-house TrueAllele server. The analyst first analyzes their data in the *Analyze* module, uploads their data in the *Data* module, asks interpretation questions in the *Request* module, and reviews results in the *Review* and *Report* modules. A *Tools* module is available for administrative purposes. Many different interfaces and features are present that allow the analyst to view their data and separated genotypes in detail, ultimately for

reporting purposes. The accompanying user manuals describe the features of this VUler version.

## **Cloud**

This VUler version is available to interact with the TrueAllele Cloud database servers. It lets the analyst upload data for processing on the TrueAllele Cloud server in the *Upload* module. After TrueAllele processing is complete, the analyst downloads interpretation results in the *Download* module.

## **Read-only**

This read-only version of the TrueAllele VUler software is available for reviewing TrueAllele results. This version enables the *Download* module allowing an analyst to download and review TrueAllele interpretation results. The Read-only version is useful for administrative or court related purposes.

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## **1.4 System Requirements**

For best performance, the recommended system requirements for the TrueAllele Visual User Interface (VUler) software are:

For Macintosh computers:

**OS:** Mac OS X 10.14.6 or higher

**CPU:** Intel x86-64 processor or later

**RAM:** 8 GB RAM (4 GB RAM minimum)

**Storage:** 3.4 GB of free hard drive space (5-8 GB for installation)

**Display:** Screen resolution of 1920 x 1080 (Minimum resolution: 1024 x 768)

**Graphics:** Hardware accelerated graphics card supporting OpenGL 3.3 with 1 GB GPU memory is recommended

For Windows computers:

**OS:** Windows 7 or later

**CPU:** Intel or AMD x86-64 or later

**RAM:** 8 GB RAM (4 GB RAM minimum)

**Storage:** 3.5 GB of free hard drive space (5-8 GB for installation)

**Display:** Screen resolution of 1920 x 1080 (Minimum resolution: 1024 x 768)

**Graphics:** Hardware accelerated graphics card supporting OpenGL 3.3 with 1 GB GPU memory is recommended

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## 2 Software Installation (Macintosh)

This section walks through the TrueAllele VUIer installation for a Macintosh computer. A complete TrueAllele Casework installation package includes the MCR Engine, the Analyze module of the VUIer software, and the VUIer software itself. Cybergenetics supplies each part of the package for the complete installation of all parts. Installation instructions for a Windows computer are found in **Section 3**.

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### 2.1 MCR Engine

The MCR Engine is an underlying program that powers the graphics and statistical calculations of the VUIer software. The MCR engine is never independently started when operating VUIer, but the program must be preinstalled for proper operation.

An analyst begins by expanding the zip file

“MATLAB\_Runtime\_R2020b\_Update\_6\_maci64.dmg.zip”, which makes the installer file “MATLAB\_Runtime\_R2020b\_Update\_6\_maci64.dmg” available. The analyst then double clicks that file to begin the installation process. This step may take several minutes.

On the introduction screen (Figure 2), selecting ‘Next’ advances to the next screen.

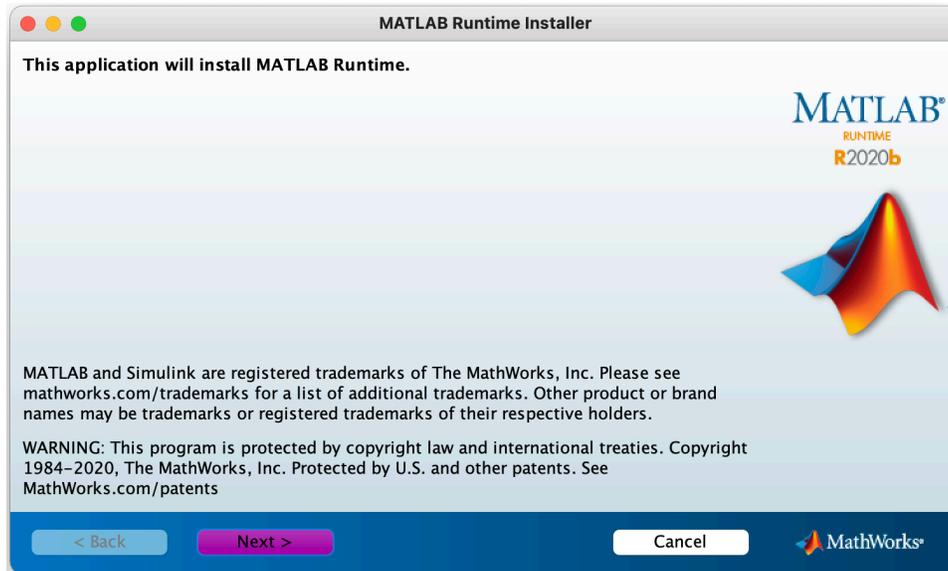


Figure 2. Introduction Screen.

The next screen contains a License Agreement file for review (Figure 3). After reading the file, the analyst selects 'Next to advance to the next screen.

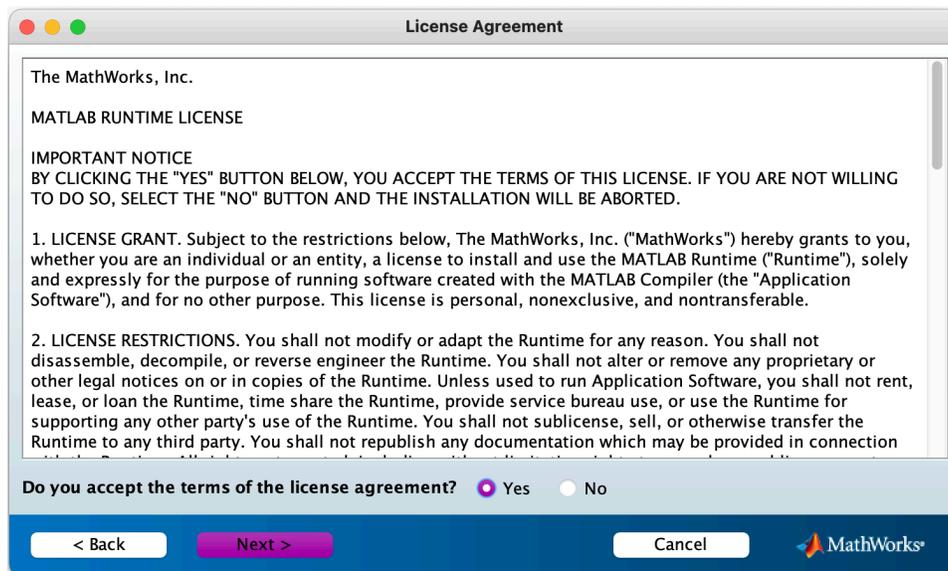


Figure 3. License Agreement.

Next, the analyst selects a folder to install the software in the *Folder Selection* window (Figure 4). The analyst should ensure that the folder chosen for installation

allows read/write access. If not, the analyst uses the 'Get info' window to set the correct permissions.



Figure 4. Folder Selection Screen

In the *Confirmation* window (Figure 5), the analyst selects 'Install' to begin the installation process. When prompted, the administrator user name and password is entered.

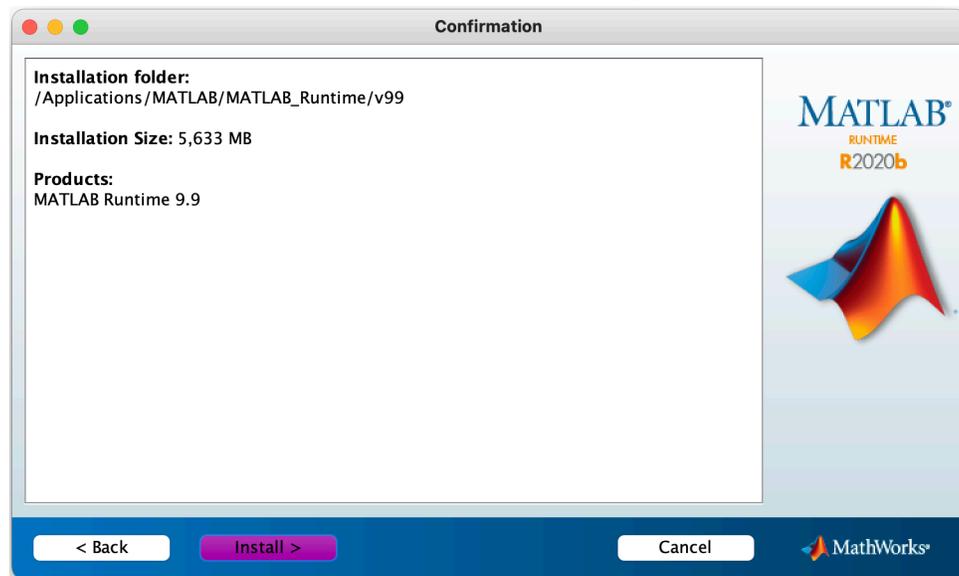
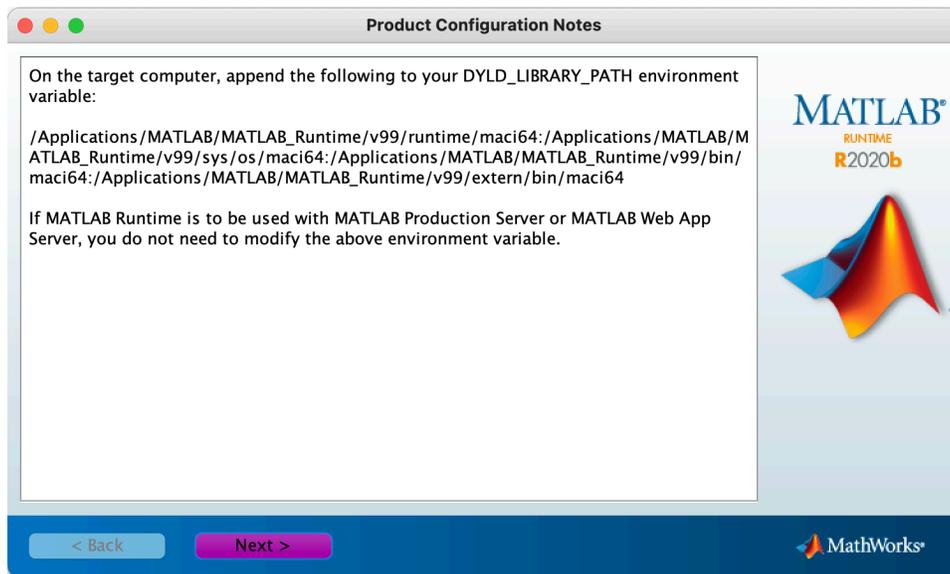


Figure 5. Confirmation Screen.

If the *Product Configuration Notes* screen appears (Figure 6), clicking ‘Next’ will continue installation. Changing the path noted on the screen is not needed to run the VUler software.



**Figure 6.** *Product Configuration Notes.*

Once installation is complete, selecting ‘Finish’ exits the installer (Figure 7).



**Figure 7.** *Installation Complete.*

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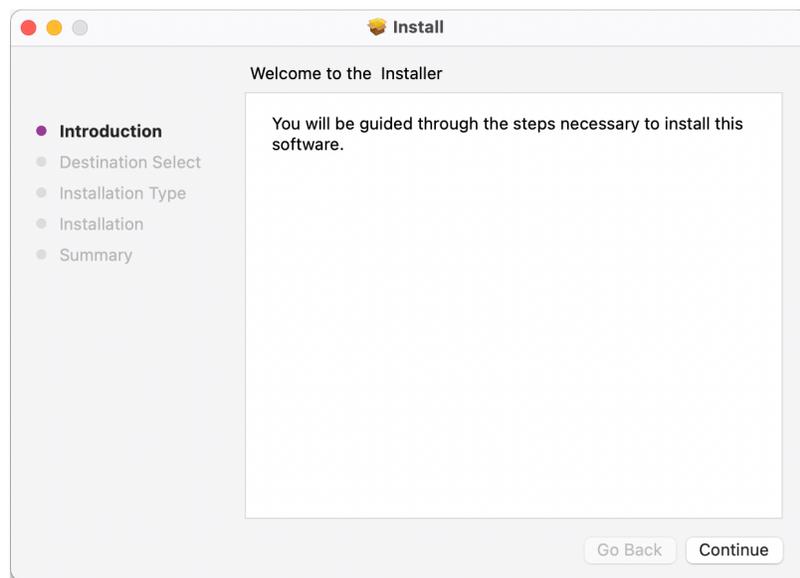
## 2.2 Analyze

The Analyze module transforms the raw sequencer files into quality checked peak data for upload to the TrueAllele Server. Installing the Analyze module installs the program itself and creates the user environment. If Analyze is already installed on a Viewstation, the analyst should remove this application and corresponding 'trueallele' folder (found in Documents) before upgrading the program, saving any customized files elsewhere, if necessary.

### Program Installation

The analyst starts by expanding on the zip file "Analyze.pkg.zip", which makes the package file "Analyze.pkg" available. The analyst then control clicks on the package file and selects Open to begin the installation process.

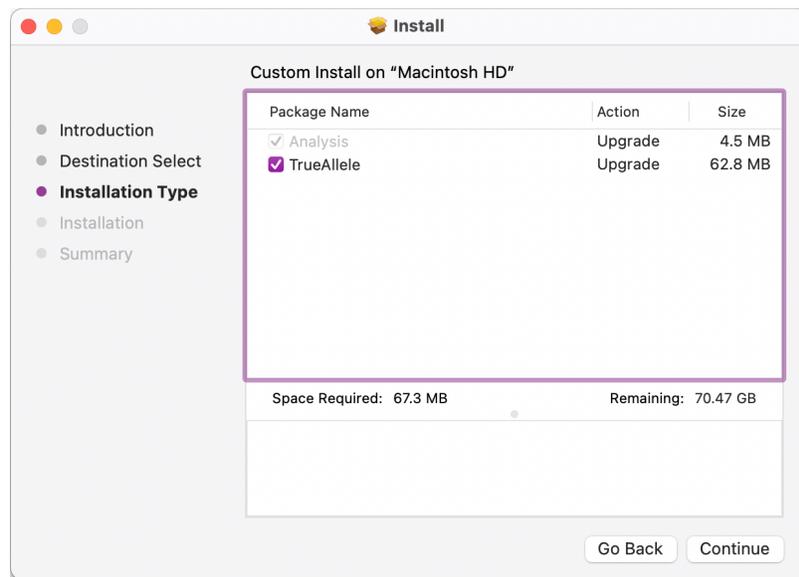
On the introduction screen (Figure 8), selecting 'Continue' advances to the next screen.



**Figure 8.** *Introduction Screen.*

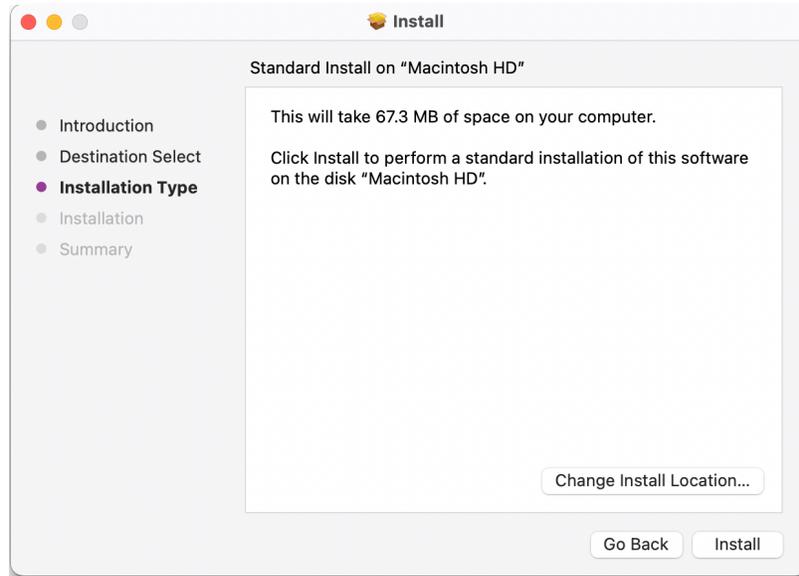
If prompted, the analyst selects a destination to install the software in the *Destination Select* window. Most likely this installation will be for all users of the computer.

A custom install screen may appear (Figure 9). By leaving all boxes checked, the analyst can upgrade the Analyze software and templates. Selecting 'Continue' advances to the next screen.



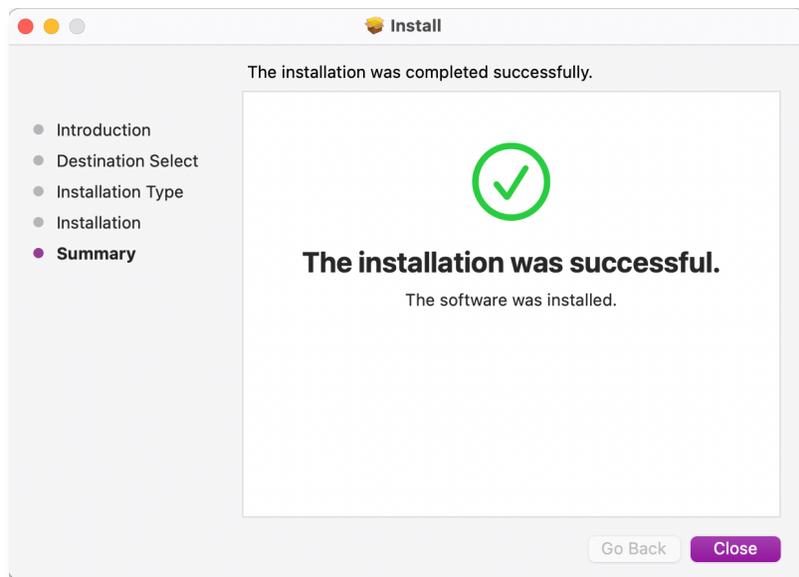
**Figure 9.** *Custom Install.*

A standard install is automatically available. The analyst begins installation by selecting 'Install' (Figure 10). When prompted, the administrator user name and password is entered.



**Figure 10.** *Standard Install.*

After the installation is complete, selecting 'Close' finishes the process (Figure 11).



**Figure 11.** *Installation complete.*

This completes the installation of the Analyze module. The analyst's data can now be processed.

## User Environment

The user environment includes all necessary templates and settings for processing the data in Analyze and is contained in a 'trueallele' folder. After installation, the 'trueallele' folder appears in the Documents folder of the user account. For example, if a user is logged in as 'DNA', the 'trueallele' folder will be created in DNA's documents folder.

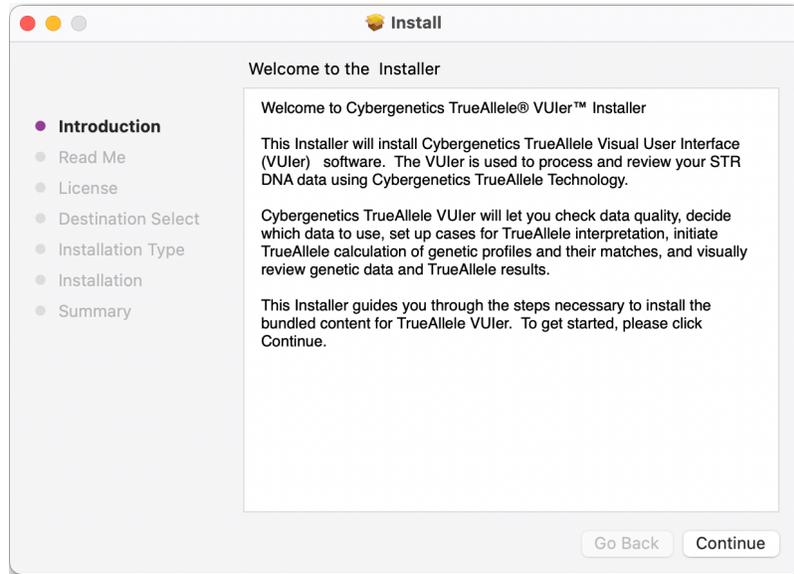
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## 2.3 VUler

The VUler software allows the analyst to upload and ask questions of the case data and then review the answers produced by the TrueAllele computer. If VUler is already installed on a Viewstation, the analyst should remove this application and save any customized preference files (such as the connect.txt or report.txt files) elsewhere on the computer before updating VUler, if necessary.

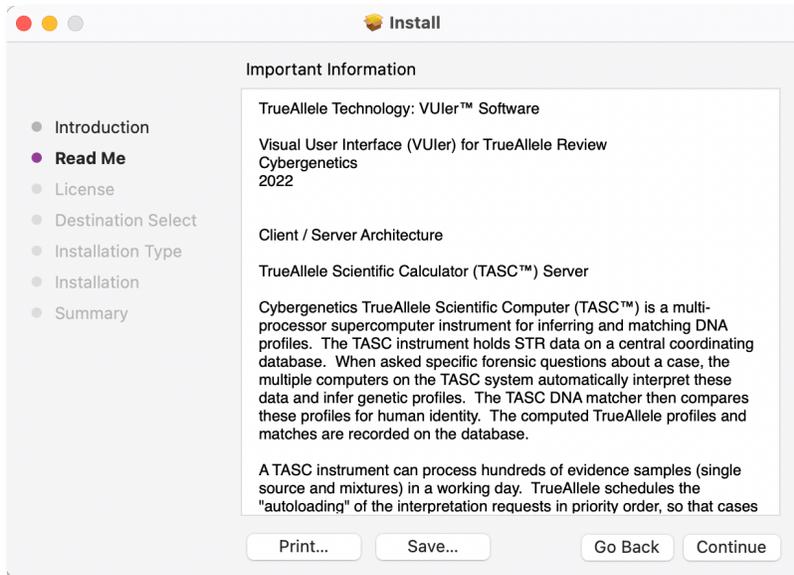
The analyst starts by expanding the zip file "VUler.pkg.zip", which makes the package file "VUler.pkg" available. The analyst then control clicks on the package file and selects open to begin installation.

On the introduction screen (Figure 12), selecting 'Continue' advances to the next screen.



**Figure 12.** *Introduction Screen.*

The next screen contains a Read Me file for review (Figure 13). After reading the file, the analyst selects 'Continue' to advance to the next screen.



**Figure 13.** *Read Me.*

Next is the license agreement (Figure 14). After selecting 'Continue', a prompt appears to confirm agreement with the license (Figure 15). The analyst proceeds by selecting 'Agree'.

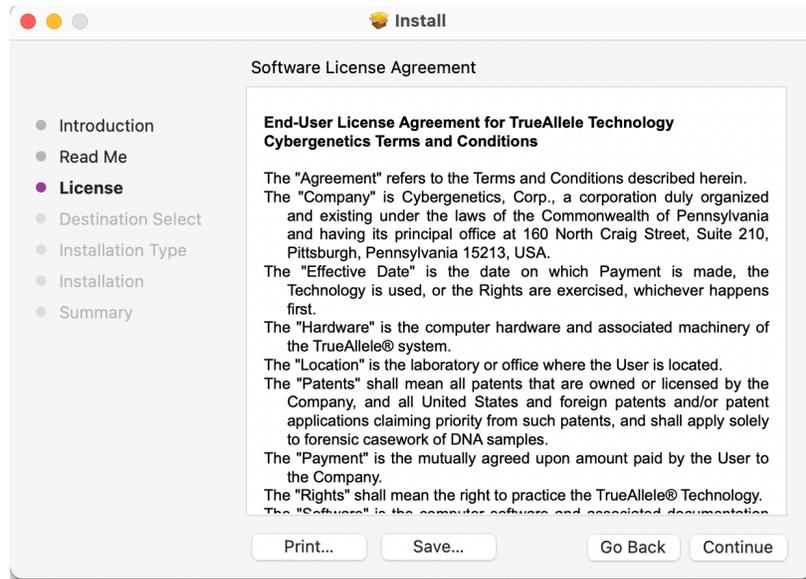


Figure 14. License Agreement.

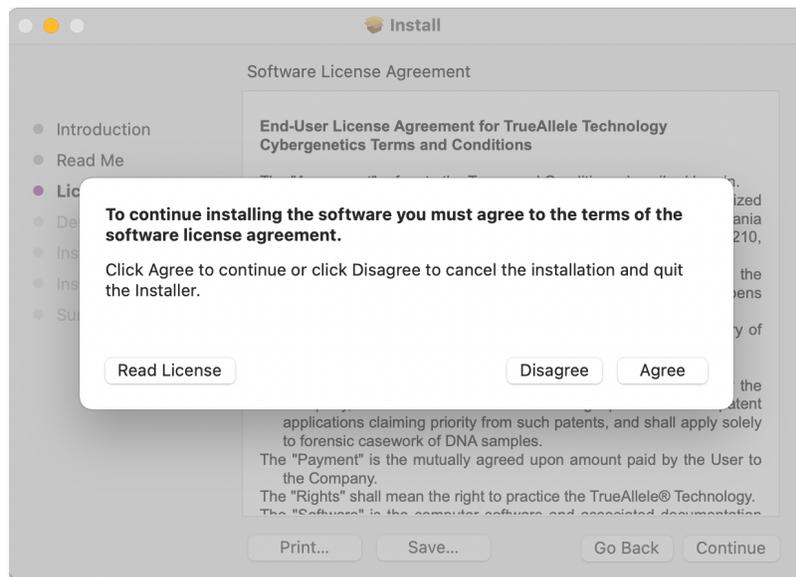
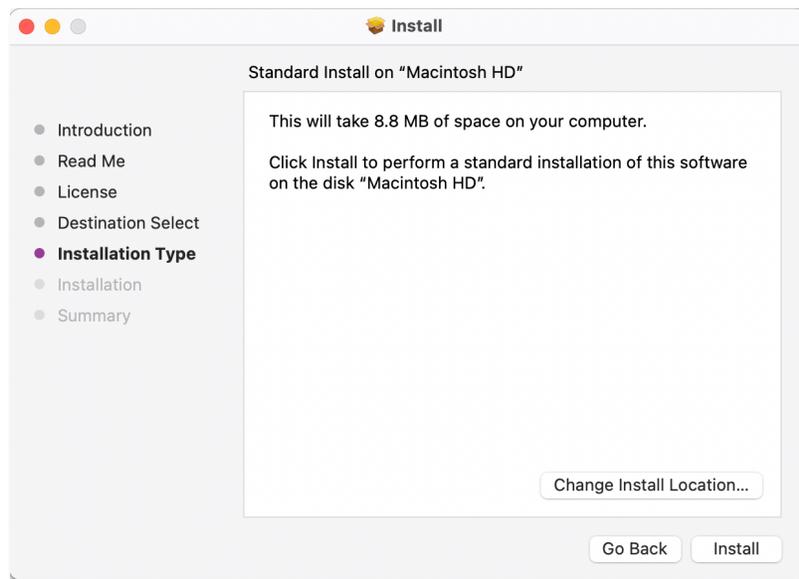


Figure 15. License Agreement.

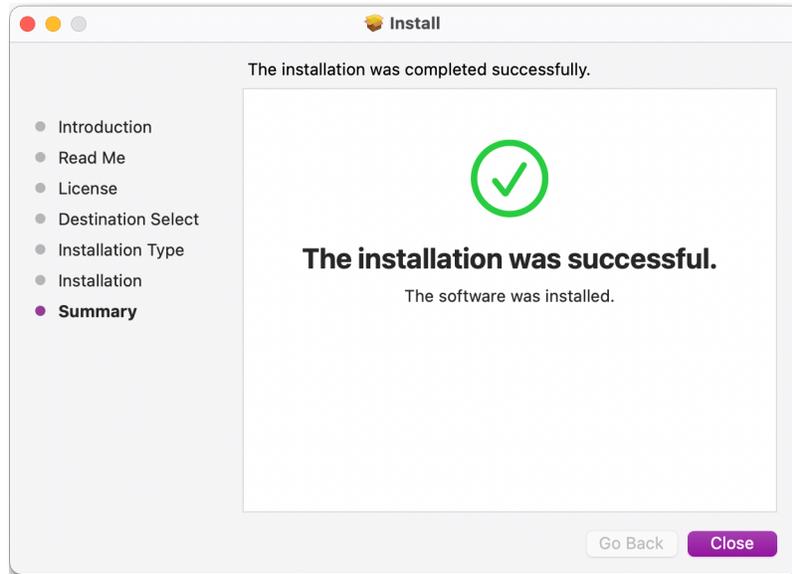
If prompted, the analyst selects a destination to install the software in the *Destination Select* window. Most likely this installation will be for all users of the computer.

A standard install is automatically available (Figure 16). The analyst begins the installation by selecting 'Install'. When prompted, the administrator user name and password is entered.



**Figure 16.** *Standard Install.*

After the installation is complete, selecting 'Close' finishes the process (Figure 17). The VUIer software is now installed and available for use.



**Figure 17.** *Installation complete.*

Once VUler has been installed, the analyst uses the icon in the Applications folder to start the program. This icon can be added to the Dock, as desired.

The user account must allow permissions to read/write to the /Library/TrueAllele folder to start the software. The analyst uses the 'Get info' window to set the correct folder permissions.

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## 3 Installation (Windows)

The steps for installing the MCR Engine, Analyze, and VUIer software on a 64-bit Windows computer are found in this section. As with a Macintosh, the MCR engine must be installed first to allow the VUIer software to be used. Also, the analyst should note that before updating any of the programs, the customized user directories and preferences could be saved elsewhere on the computer in order to preserve and reinstate them after an update.

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### 3.1 MCR Engine

An analyst begins by expanding the zip file “MATLAB\_Runtime\_R2020b\_Update\_6\_win64.zip”, which makes the folder “MATLAB\_Runtime\_R2020b\_Update\_6\_win64” available. Inside this folder, the analyst then double clicks on the executable file “setup.exe” to begin the installation process.

On the introduction screen (Figure 18), selecting ‘Next’ advances to the next screen.

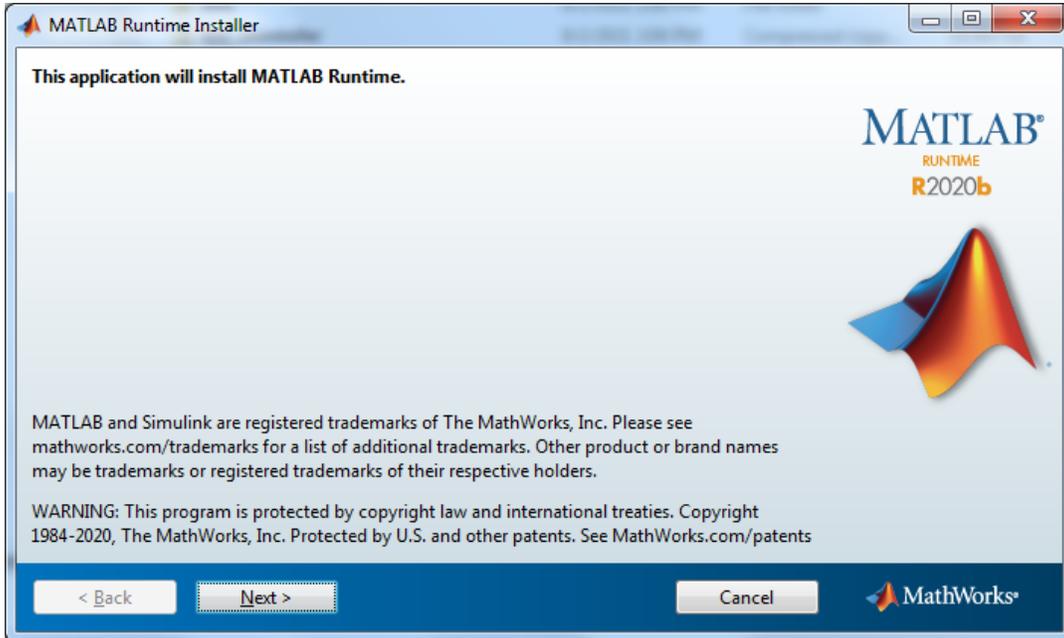


Figure 18. Introduction Screen.

The next screen contains a license agreement for review (Figure 19). After reading and accepting the agreement, the analyst selects 'Next' to advance to the next screen.

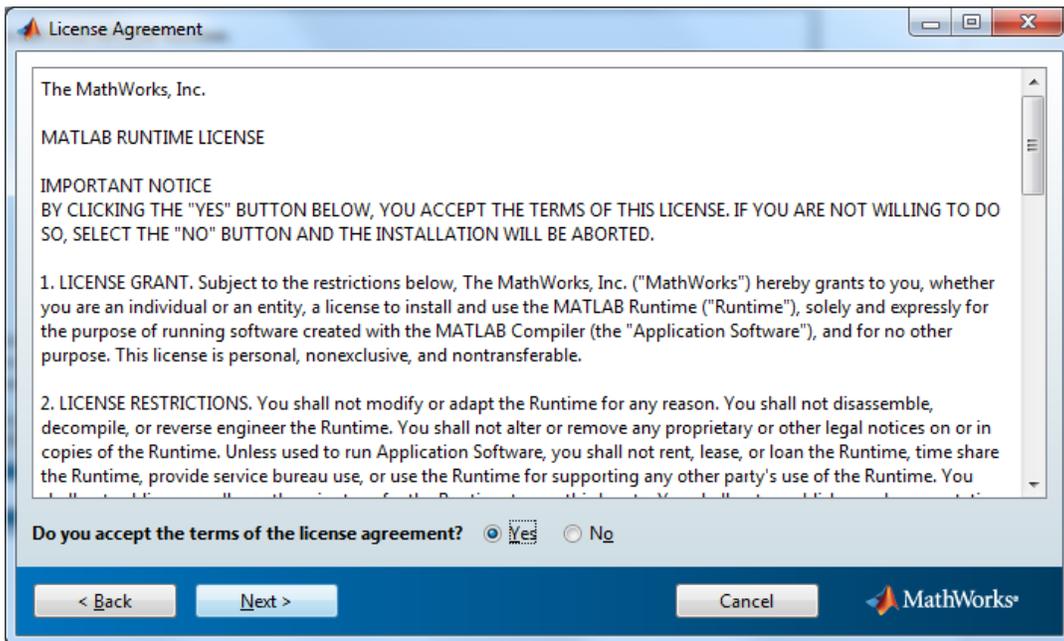
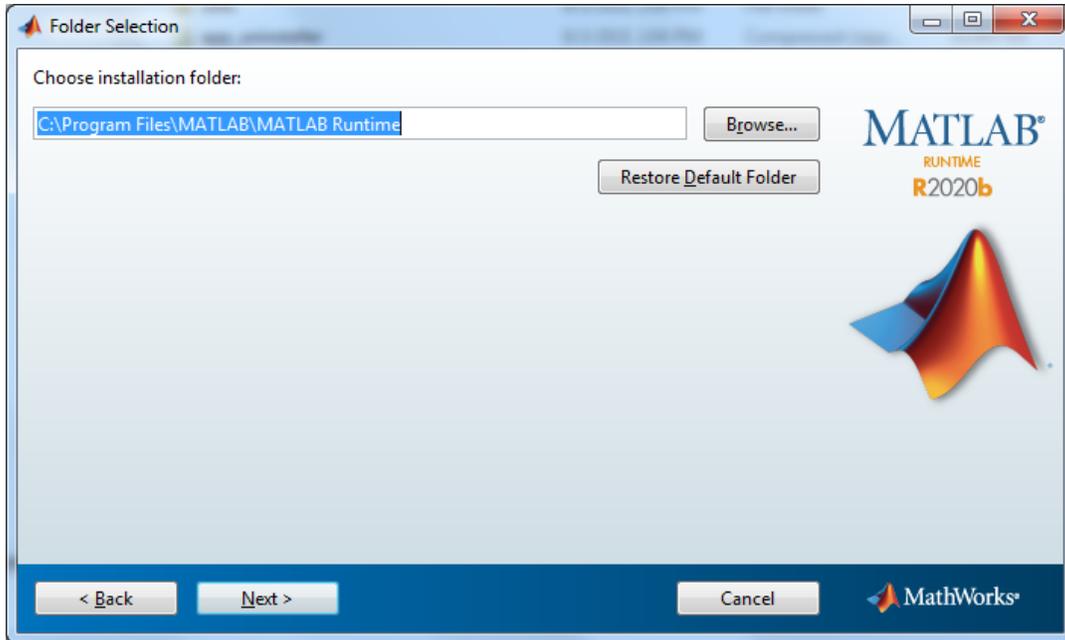


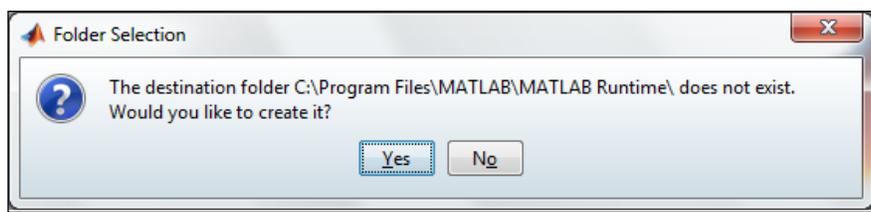
Figure 19. License Agreement.

Next, the analyst clicks 'Next' in the *Folder Selection* screen to install the software in the default destination folder (Figure 20).



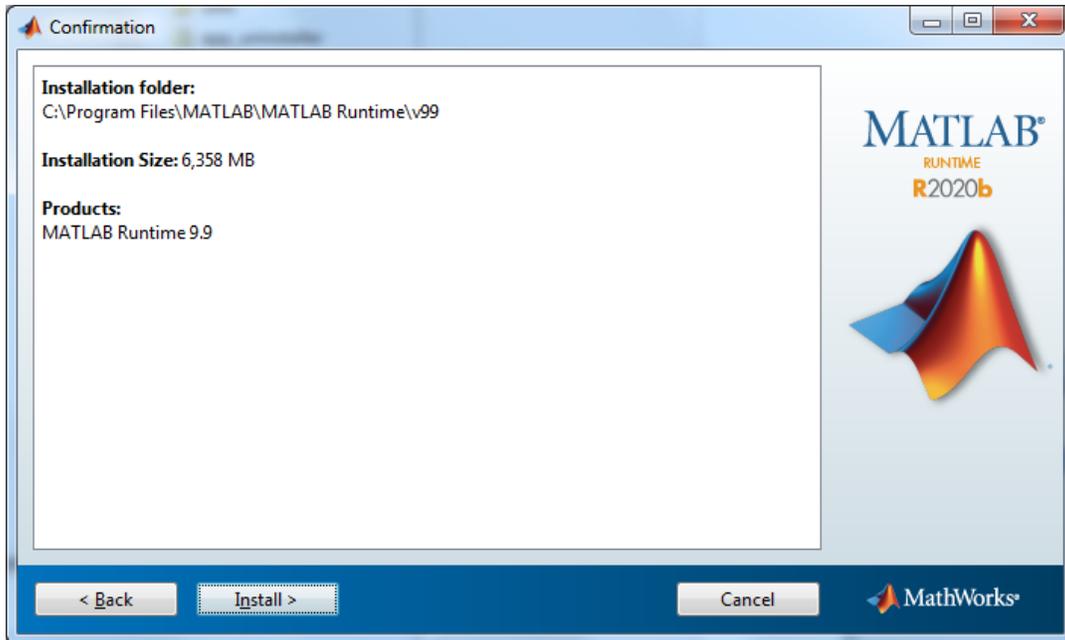
**Figure 20.** *Folder Selection Screen.*

If prompted, the analyst confirms the creation of the destination folder by selecting 'Yes' (Figure 21).



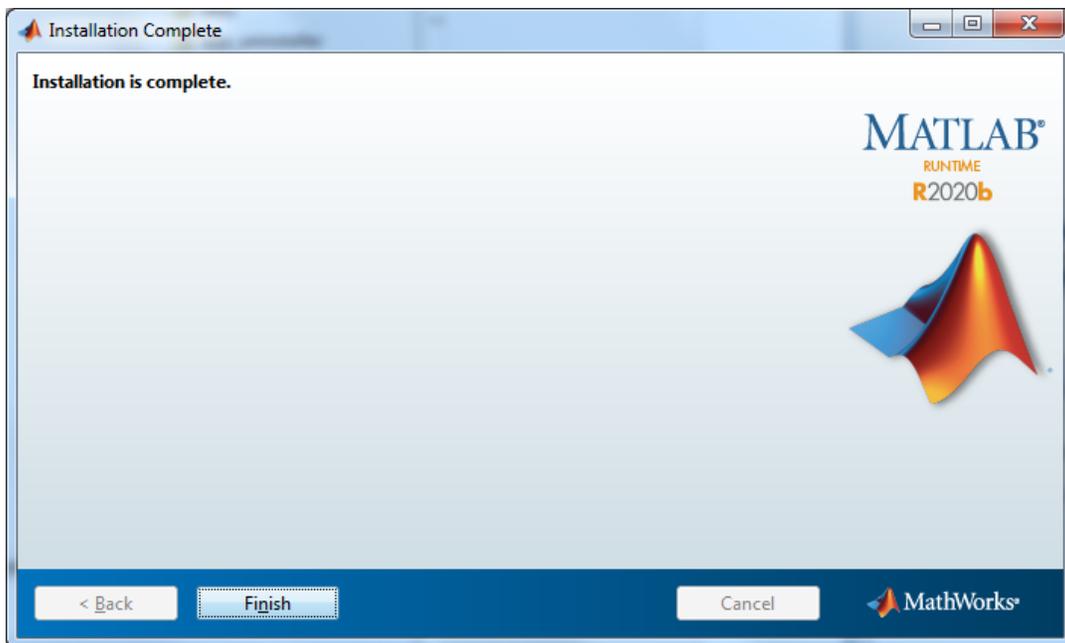
**Figure 21.** *Folder Selection Confirmation.*

In the *Confirmation* window (Figure 22), the analyst selects 'Install' to begin the installation process. If prompted, the administrator user name and password is entered.



**Figure 22.** Confirmation Window.

Once installation is complete, selecting 'Finish' exits the installer (Figure 23).



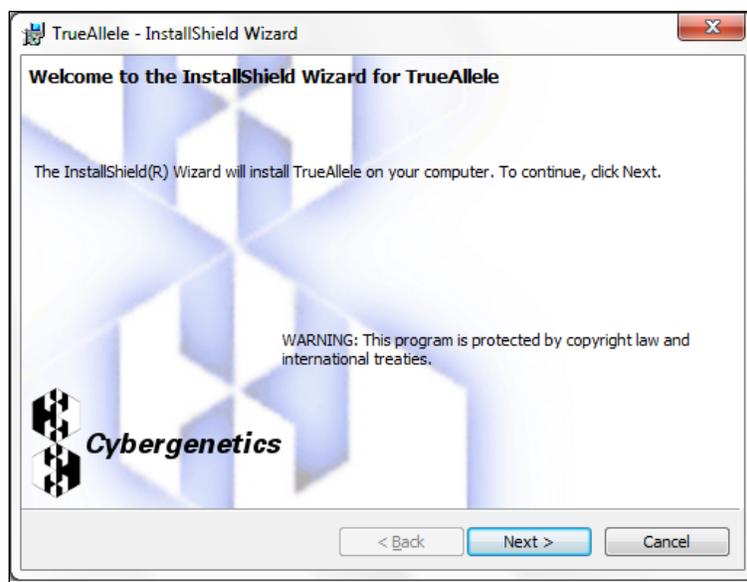
**Figure 23.** Installation Complete Screen.

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## 3.2 Analyze

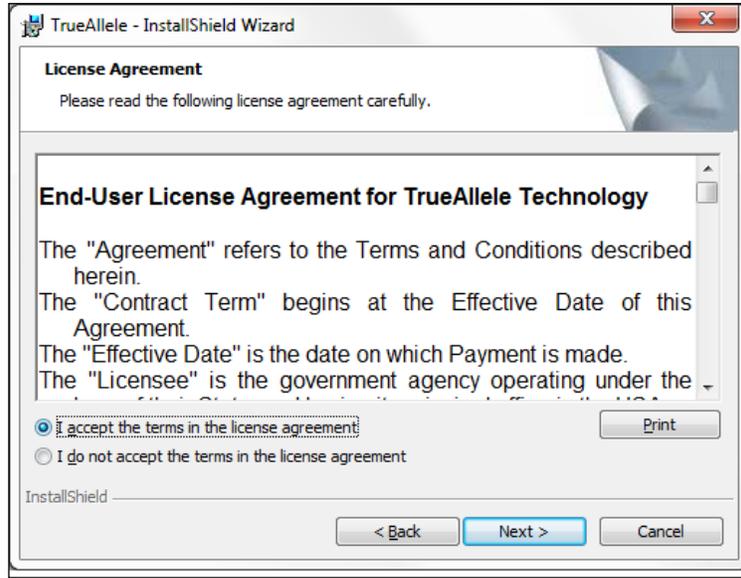
To install the Analyze module on a Windows computer, the analyst starts by expanding the zip file “Analyze\_64bit.exe.zip”, which makes the executable file “Analyze\_64bit.exe” available. The analyst then double clicks on the execute file to begin the installation process.

On the introduction screen (Figure 24), selecting ‘Next’ advances to the next screen.



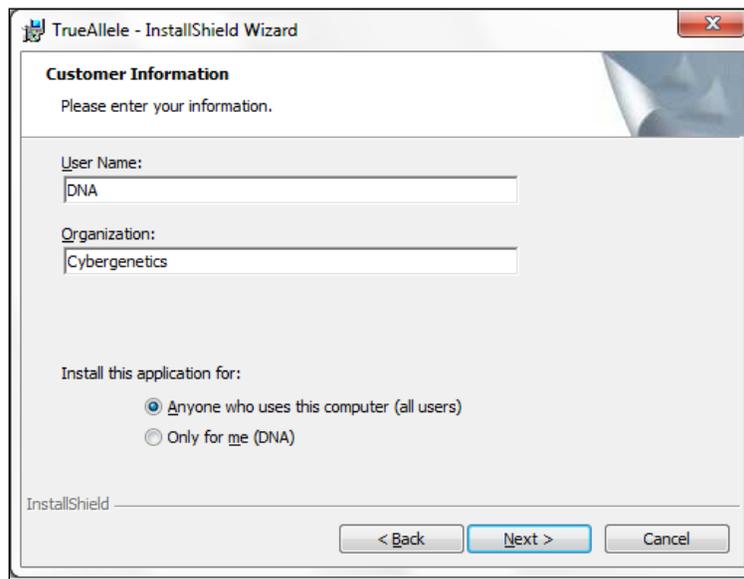
**Figure 24.** *Introduction Screen.*

The next screen contains a license agreement for review (Figure 25). After reading and accepting the agreement, the analyst selects ‘Next’ to advance to the next screen.



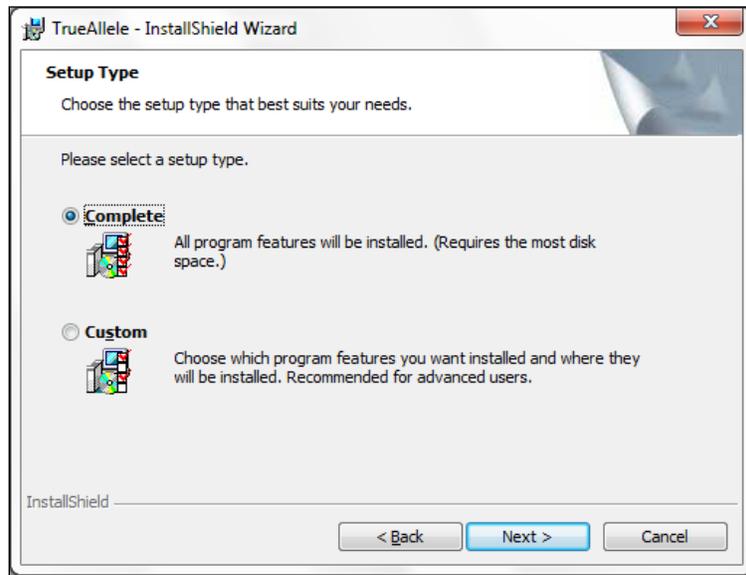
**Figure 25.** License Agreement.

Next is the customer information screen (Figure 26). After entering the appropriate information and selecting the user(s) to install the application for, the analyst selects 'Next' to proceed.



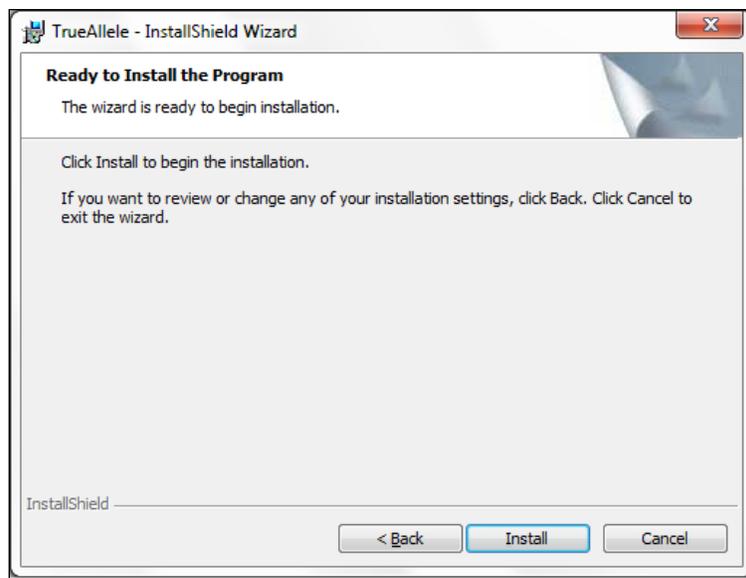
**Figure 26.** Customer Information Screen.

On the next screen, the analyst chooses the default setup type and clicks 'Next' to continue (Figure 27).



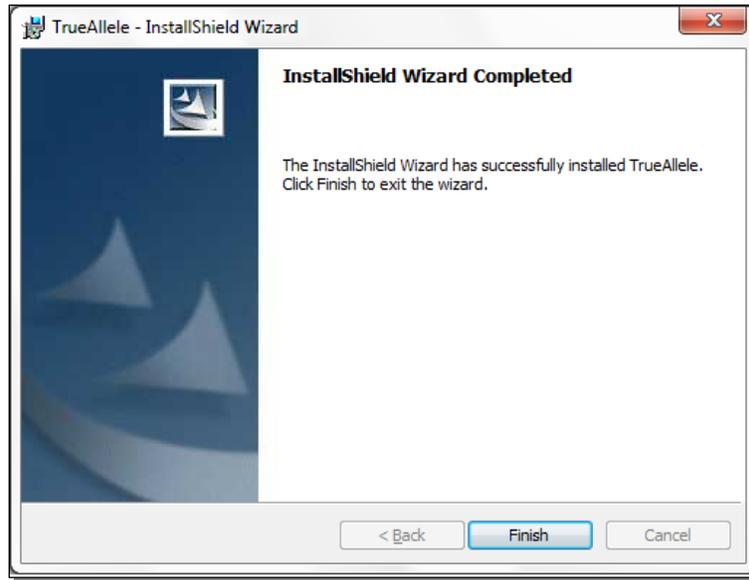
**Figure 27.** Setup Type Window.

On the ready to install screen (Figure 28), the analyst selects 'Install' to begin the Analyze installation. If prompted, the administrator user name and password is entered.



**Figure 28.** Ready to Install.

After the installation is complete, selecting 'Finish' completes the process (Figure 29). This completes the installation of the Analyze module, and data can now be processed in the Analyze module.



**Figure 29.** *Installation Complete.*

If necessary, the analyst should copy the 'trueallele' folder to every user's 'My Documents' directory and add or replace any custom user directories or templates to this 'trueallele' folder.

### **Updating Analyze**

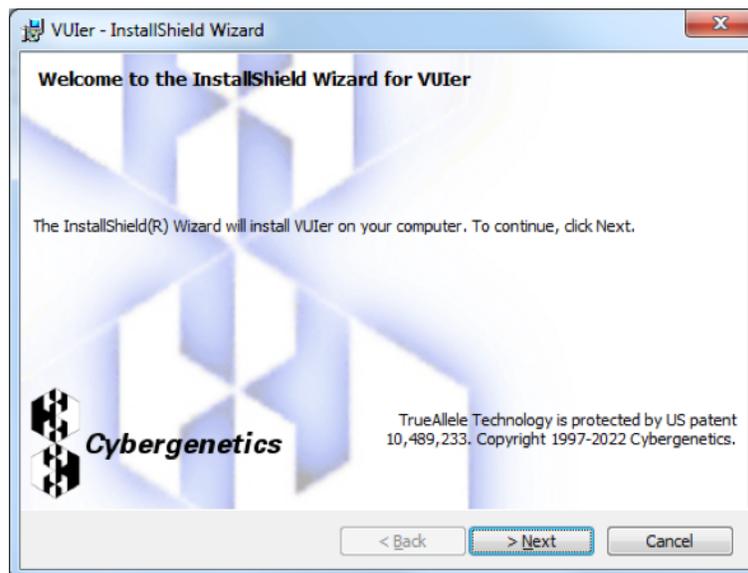
Before updating Analyze, the analyst should first copy any customized files to be kept from the C:/Users/username/My Documents/trueallele/system folder. Then, the analyst should uninstall any older versions of Analyze by using the Add or Remove Programs feature. After removing the software, the analyst should delete the C:/Users/username/My Documents/trueallele directory for every user. Then, Analysis can be updated following the same steps outlined previously.

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### 3.3 VUler Software

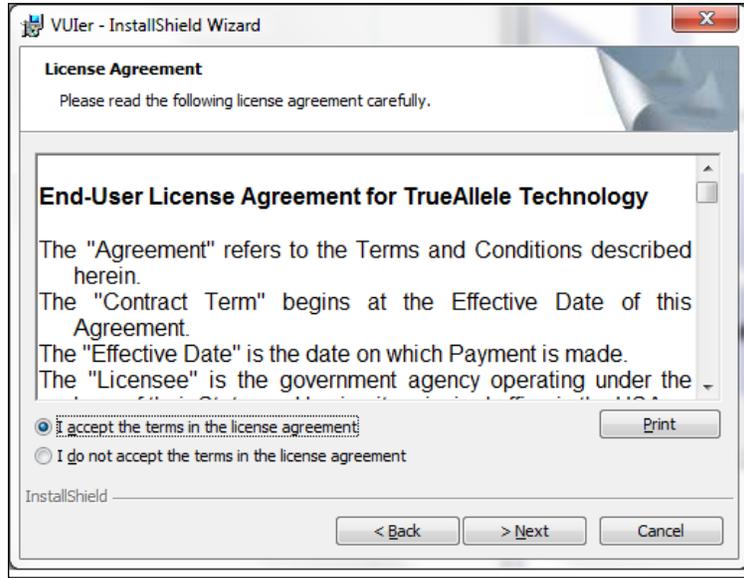
To install the VUler software, the analyst starts by expanding the zip file “VUler\_64bit.exe.zip”, which makes the package file “VUler\_64bit.exe” available. The analyst then double clicks on the executable file to begin installation.

On the introduction screen (Figure 30), selecting ‘Next’ advances to the next screen.



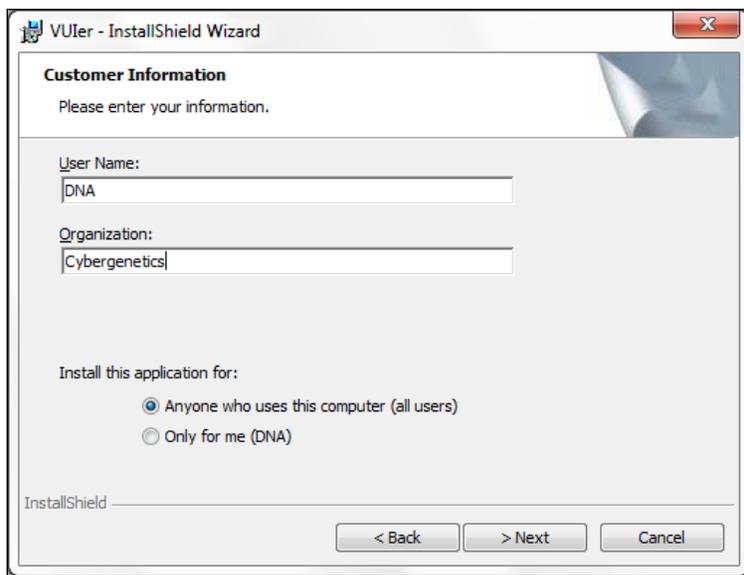
**Figure 30.** *Introduction Screen.*

The next screen contains a license agreement for review (Figure 31). After reading and accepting the agreement, the analyst selects ‘Next’ to advance to the following screen.



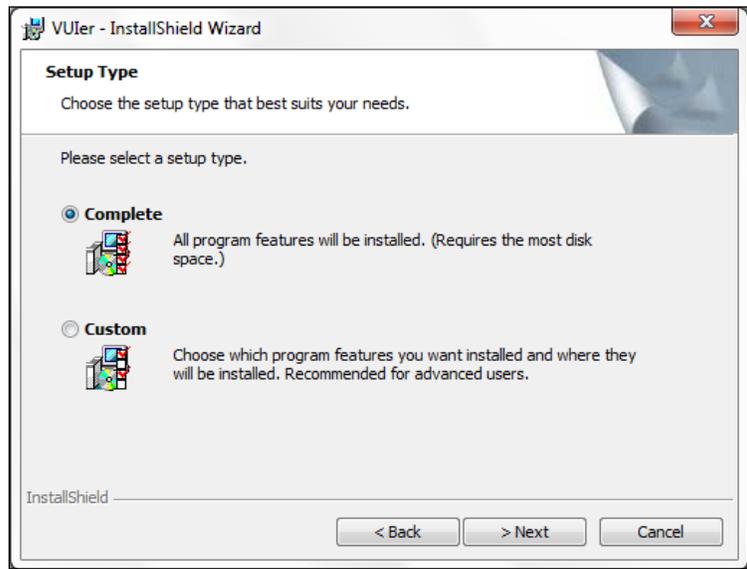
**Figure 31.** License Agreement.

Figure 32 shows the customer information screen. After entering the appropriate information and selecting the user(s) to install the application for, the analyst selects 'Next' to proceed.



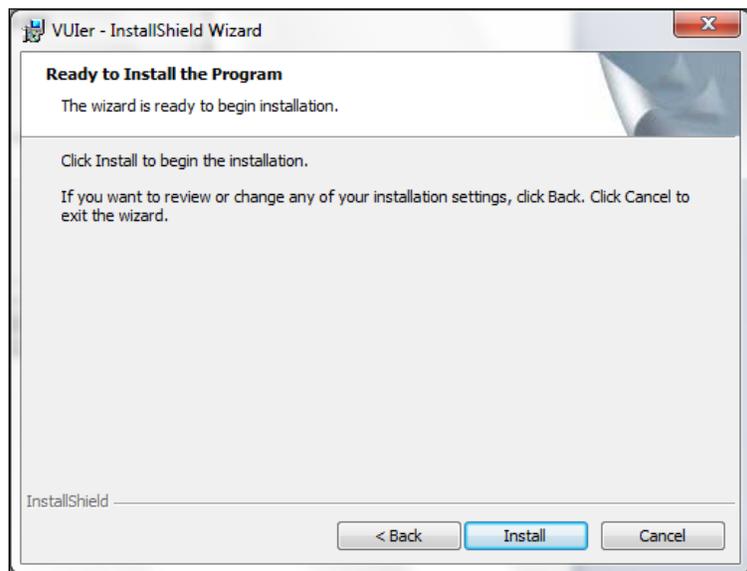
**Figure 32.** Customer Information Screen.

On the next screen, the analyst chooses the default setup type and clicks 'Next' to continue (Figure 33).



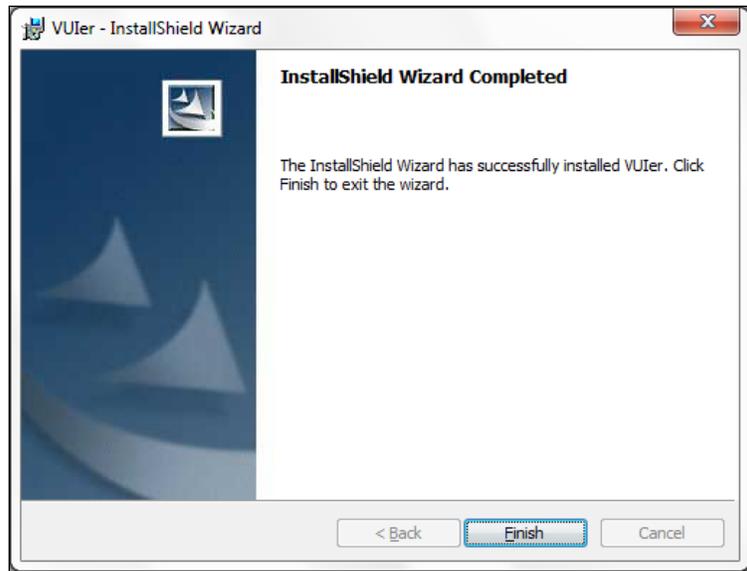
**Figure 33.** Setup Type Window.

On the ready to install screen (Figure 34), the analyst selects 'Install' to begin the VUIer installation. If prompted, the administrator user name and password is entered.



**Figure 34.** Ready to Install.

After the installation is complete, selecting 'Finish' completes the process (Figure 35). The VUIer software is now installed and available for use.



**Figure 35.** *Installation Complete.*

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## 4 Software Function

This section covers the starting the VUler program including information about the license key and *Module Chooser*. The **Appendix ▶ Diagnostic Support** covers an alternative method for starting the program. In addition, this section discusses connecting to a database and closing the VUler program.

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### 4.1 License

After installing VUler, the analyst starts the program by clicking on its icon (Figure 36). The application is located in the Dock or Applications folder on a Macintosh or from the Desktop shortcut or Start Menu on a Windows computer.

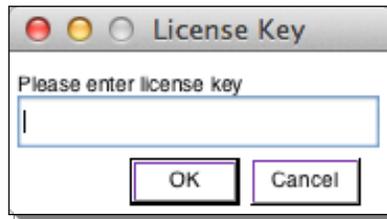


Figure 36. VUler icon.

A valid license key is required to use the VUler software. Cybergeneitics provides this license key. When starting VUler for the first time, a dialog box appears prompting the analyst to enter a license key (Figure 37). This key is only entered the first time the software is started. VUler will open to the *Module Chooser* after a valid license key is entered.

If the software fails to start after entering a valid license key on a Macintosh, the analyst should verify that the /Library/TrueAllele folder allows read/write

permissions. If not, the analyst should enable the permissions for all enclosed files and folders.



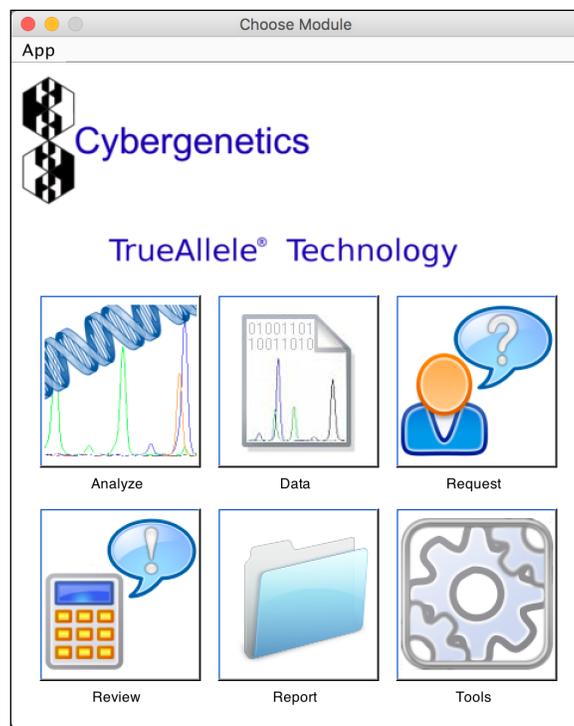
**Figure 37.** License key input dialog box.

---

## 4.2 Module Chooser

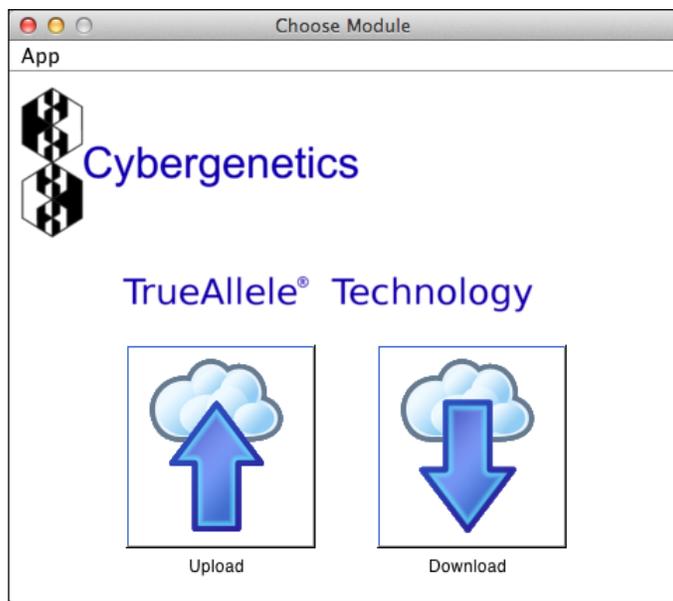
The *Module Chooser* opens after a valid license key is entered. This interface is where the analyst uploads data and downloads results. The interface is different for each of the VUIer versions.

In the Full VUIer version, all modules are available for use (Figure 38).



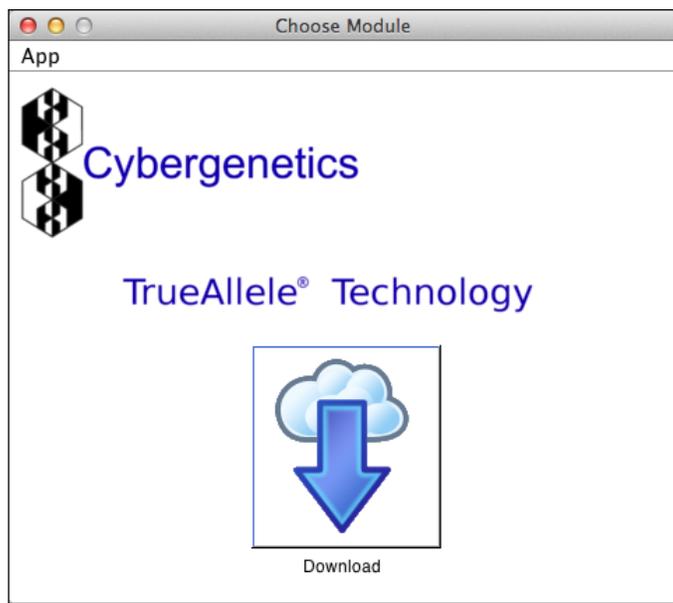
**Figure 38.** Full Module Chooser.

In the VUIer Cloud version, both the *Upload* and *Download* modules are available (Figure 39).



**Figure 39.** *Cloud Module Chooser.*

For the VUIer Read-only version, only the *Download* module is available for reviewing results (Figure 40).



**Figure 40.** *Read-only Module Chooser.*

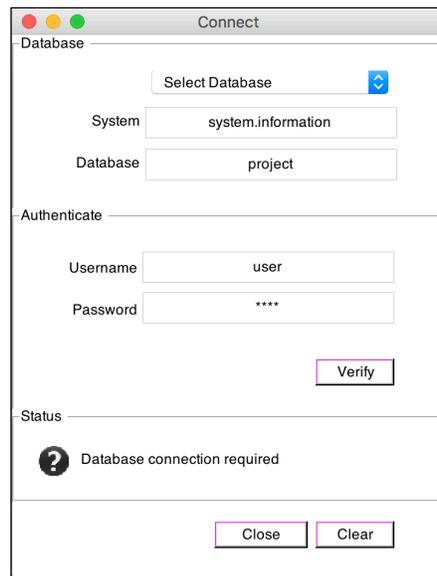
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## 4.3 Connecting to a Database

In the VUIer program, the *Connect* window allows an analyst to connect to a database or to switch to a different database at any time during the TrueAllele process. The analyst opens the *Connect* window by selecting the **Database ▶ Connect** menu option in any VUIer module.

### Connect window

To connect, an analyst selects the desired server *System* from the dropdown menu (this action fills in the *System* field as well). The analyst then enters a username and password under the *Authenticate* heading and clicks 'Verify'. A blue check mark is present when the connection is verified, and the *Connect* window (Figure 41) will automatically close.



The screenshot shows a window titled "Connect" with a standard macOS-style title bar (red, yellow, green buttons). The window is divided into three main sections by horizontal lines:

- Database:** Contains a dropdown menu labeled "Select Database" with a blue arrow icon. Below it are two text input fields: "System" containing "system.information" and "Database" containing "project".
- Authenticate:** Contains two text input fields: "Username" containing "user" and "Password" containing "\*\*\*\*". A "Verify" button is positioned to the right of the password field.
- Status:** Contains a question mark icon in a circle followed by the text "Database connection required".

At the bottom of the window, there are two buttons: "Close" and "Clear".

**Figure 41.** *The Connect window.*

## Clearing Information

To clear all of the information entered in the *Connect* window fields and exit the database, the analyst can use the 'Clear' button at the bottom right of the window. When finished with this process, the 'Close' button will close the window.

## Connection Difficulties

If a red "X" appears with the message "Database Connection Failure" when clicking the 'Verify' button instead of the blue check or the window closing, the connection to the database was not successful.

This message could mean that incorrect user account information was entered. The user name and password are case sensitive, so the analyst should first check that the information was entered correctly.

---

## 4.4 Closing the VUler Program

The TrueAllele Server accepts a limited number of concurrent user connections. An analyst must properly end user sessions so the connection is open for another analyst. There are two main methods of ending a user session.

When finished using the VUler software, the analyst can close the program by selecting **App ▶ Quit**. This will close the program and automatically log out of any current connections.

If an analyst does not want to close the VUler program but wishes to end the current session, the analyst can logout of a TrueAllele World. From within any module, selecting **Database ▶ Logout** will log an analyst out of the current database, making the connection available for other users.

To close a window within a module, the analyst selects **File ▶ Close**. To close a module and go back to the *Module Chooser*, an analyst selects **File ▶ Exit Module**. This selection brings up a dialog box asking an analyst if they wish to exit the particular module and choose a different one. Here an analyst selects “Yes” to exit or “Cancel” to remain in the current module.

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## Appendix

This appendix is designed to provide specific information that may help in using the TrueAllele VUler software. A glossary of common terms is also provided.

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### Spinning Wait Cursor



Spinning Wait Cursor

The spinning wait cursor is equivalent to the hourglass icon on a Windows computer. This icon indicates that TrueAllele is retrieving data from the database. This cursor is only active when it is held over a VUler window. If the mouse is moved off of the window (for example, to the desktop), the cursor will go back to the normal pointer.

---

### View Menu

In several modules of the VUler program, there is a *View Menu*. This menu allows the analyst to change the window sizing options for modules that have more than one interface window open at a time. The *View Menu* includes options for automatically sizing and positioning the interfaces as well as making the interface text larger and smaller. There are also toolbar buttons that allow the analyst to position the interface windows on the screen (Figure 42), where the white portion of the icon indicates where the window will be positioned. In addition, keyboard shortcuts exist for making interface text larger (⌘=) and smaller (⌘-) (ctrl= and ctrl- for Windows).



**Figure 42.** *View Icons.* These icons position the active interface window to the position on the screen denoted by the white part of the square.

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## Diagnostic Support

To aid in diagnostic support of the VUIer program, an alternate means of starting the program is available. This method is not routinely used but is available to aid in support calls to Cybergenetics.

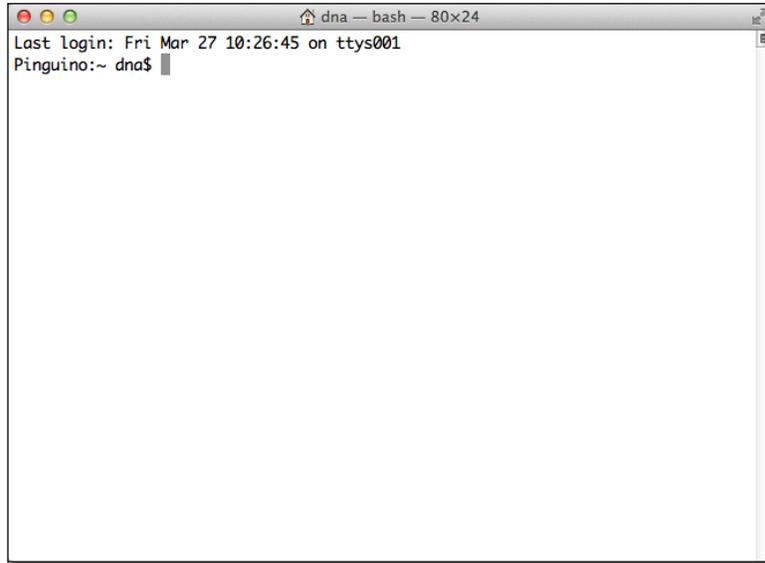
### Macintosh support

On a Macintosh, the analyst opens a Terminal window by selecting the Terminal icon (Figure 43) from the Dock or Applications/Utilities folder.



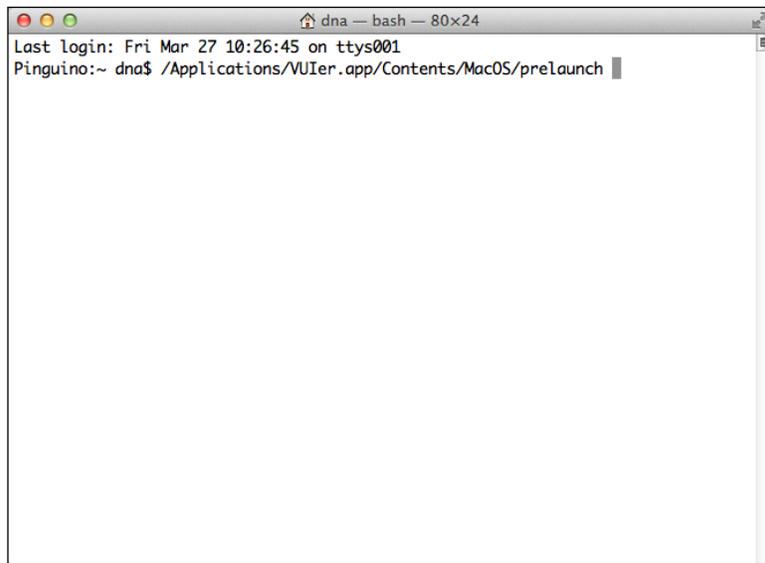
**Figure 43.** *Terminal icon.*

A blank Terminal window opens (Figure 44), displaying the computer's name and a command prompt.



**Figure 44.** A blank Terminal window.

In the Terminal window, the analyst copies and pastes the path:  
`/Applications/VUIer.app/Contents/MacOS/preLaunch`  
And then hits the enter key (Figure 45).



**Figure 45.** A Terminal window with the path filled in.

## Windows support

On a Windows computer, the analyst opens a Command Prompt window by selecting the program from the computer.

A blank Command Prompt window opens (Figure 46), displaying the computer user's name and a command prompt.

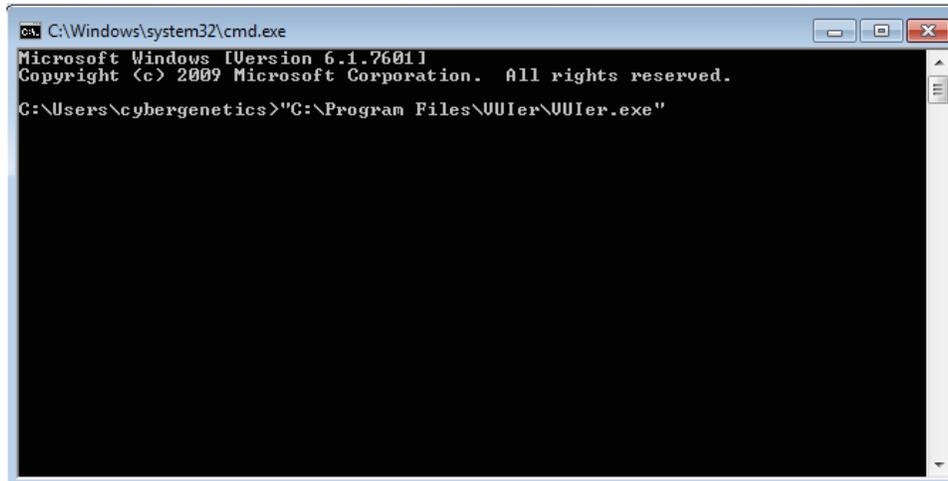


**Figure 46.** A blank Command Prompt window.

In the Terminal window, the analyst copies and pastes the path:

```
C:\Program Files\VUIer\VUIer.exe
```

And then hits the enter key (Figure 47).



**Figure 47.** A Command Prompt window with the path filled in.

By starting the VUIer program this way, diagnostic messages that are displayed during software operation appear in the Terminal window. These messages can be copied and pasted into an email to Cybergenetics if support is required.

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## Glossary

This glossary presents some commonly used terms. The term of interest is italicized.

Evidence *data* comprise STR experiments on a set of samples.

An observed *genotype* is a probability distribution over a set of possible allele pairs at a locus.

The identification *hypothesis* is that a suspect contributed their DNA to an evidence sample.

Identification *information* is the logarithm of the identification LR.

A *likelihood function* determines the fit between data and model. (More formally, it is the probability of the data given a model.)

An identification *likelihood ratio* (LR) is the weight of evidence in favor of an identification hypothesis. The LR can be calculated as a ratio of two match probabilities.

A *Markov chain* is a visual history of the search that the system performs in order to find the best-fit model for the data.

A *match* occurs when two genotypes are equal.

A *match probability* is the probability of a genotype match.

A *mixture* is a DNA sample that contains two or more individual contributors.

A probability *model* is a mathematical formulation that accounts for observed data.

A *validation* study assesses the efficacy and reproducibility of an interpretation method for extracting identification information from DNA data.