



**TrueAllele<sup>®</sup> VUler<sup>™</sup>**  
**Getting Started**



*Cybergentics*

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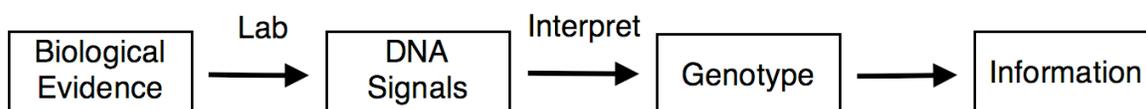
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# 1 Overview

The Getting Started Manual covers installing and upgrading the TrueAllele® Casework 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.

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## 1.1 DNA Interpretation Process



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

The DNA interpretation process can be 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 Cybergentics for learning about the objective computer interpretation of quantitative DNA evidence. Here is a guide to

getting started. The essential information is provided in these manuals. Additional publications and presentations are available on the Cybergenetics website.

### **Newsletters**

The best place to begin is with Cybergenetics DNA Investigator™ newsletters, located at <http://www.cybgen.com/information/newsletters.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 match 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 the 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.

### **Course Lectures**

Course material (videos, slides, transcripts, etc.) is 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.

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

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## 2 Hardware Requirements

The minimum system requirements for the VUIer™ software are:

**OS:** Windows XP or Mac OS X 10.6 or higher

**CPU:** Pentium 4 processor

**RAM:** 1024 MB RAM

**Storage:** 1GB of free hard drive space

**Display:** Screen resolution of 1024x768 (higher resolutions recommended)

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## 3 Software Installation

This chapter walks through the TrueAllele Casework 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. Optionally, the VUIer documentation can also be installed. Cybergenetics supplies each part of the package for the complete installation of all parts. Installation instructions for a PC are found in the **Appendix ▶ PC Installation**.

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### 3.1 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 the VUIer software, but the program must be preinstalled for proper operation.

A user begins by expanding the zip file “MCR\_Engine.pkg.zip”, which makes the package file “MCR\_Engine\_Installer\_v716.pkg” available. The user then double clicks on the package file to begin the installation process.

On the introduction screen (Figure 2), selecting 'Continue' advances to the next screen.

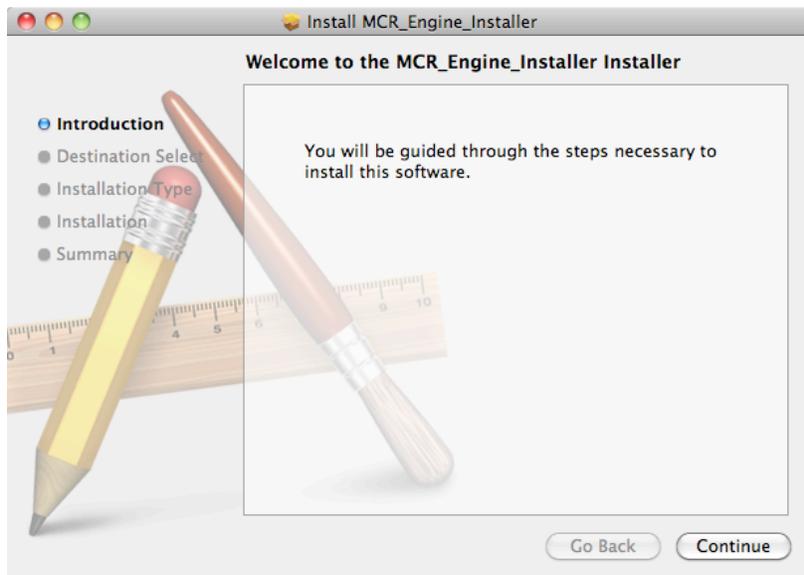


Figure 2. Introduction Screen.

Next, the user must select a destination to install the software in the *Destination Select* window (Figure 3). Most likely, this will be for all users of the computer.

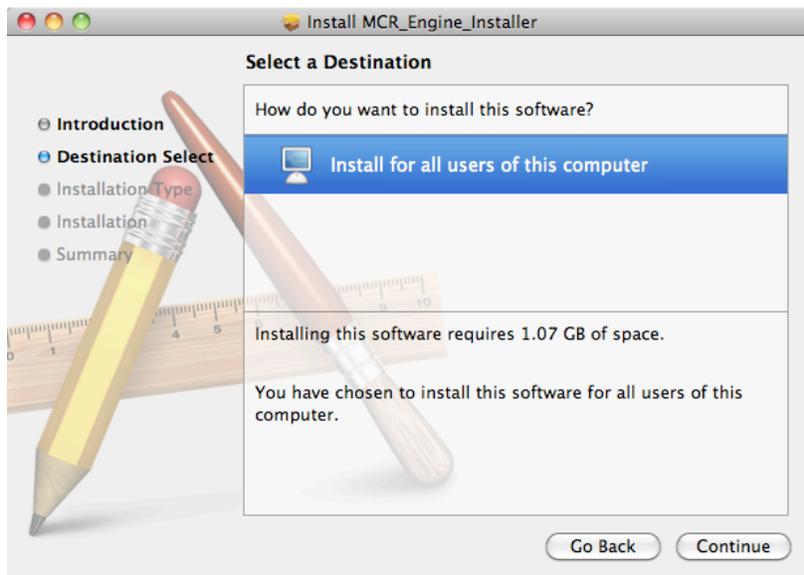


Figure 3. Destination Select Screen

In the *Installation Type* window (Figure 4), the user selects 'Install' to begin the installation process. When prompted, the administrator user name and password is entered.

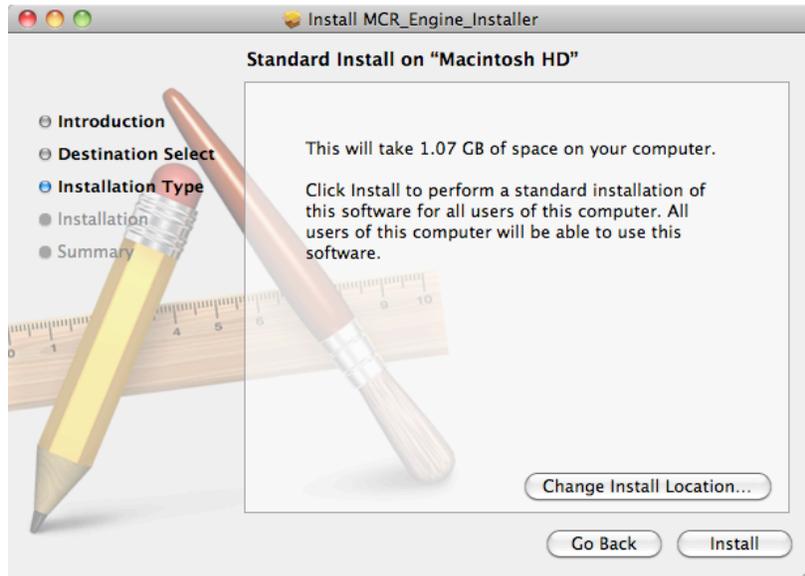


Figure 4. *Standard Install.*

Once installation is complete, selecting 'Close' exits the installer (Figure 5).

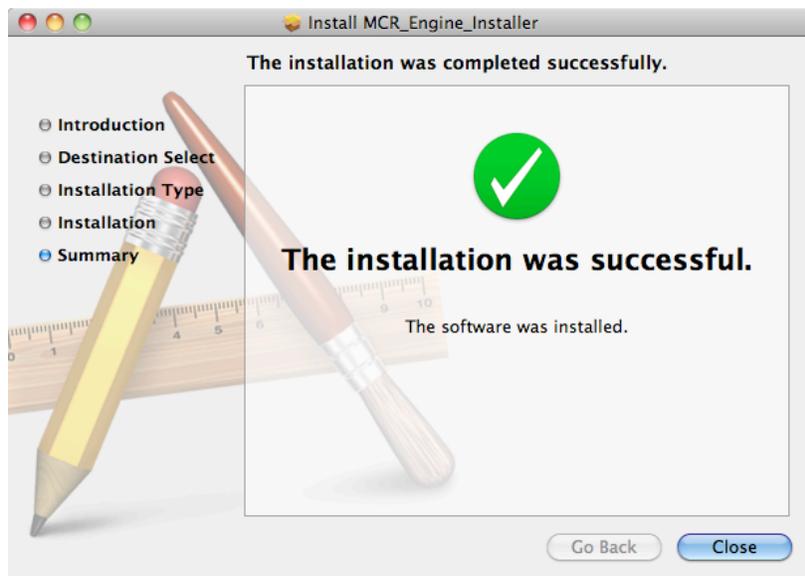


Figure 5. *Installation complete.*

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## 3.2 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 Analysis is already installed on a Viewstation, the user should remove this application and corresponding ‘trueallele’ folder before upgrading the program, saving any customized files elsewhere, if necessary.

### Program Installation

The user starts by expanding on the zip file “Analyze.pkg.zip”, which makes the package file “Analysis.pkg” available. The user then double clicks on the package file to begin the installation process.

On the introduction screen (Figure 6), selecting ‘Continue’ advances to the next screen.

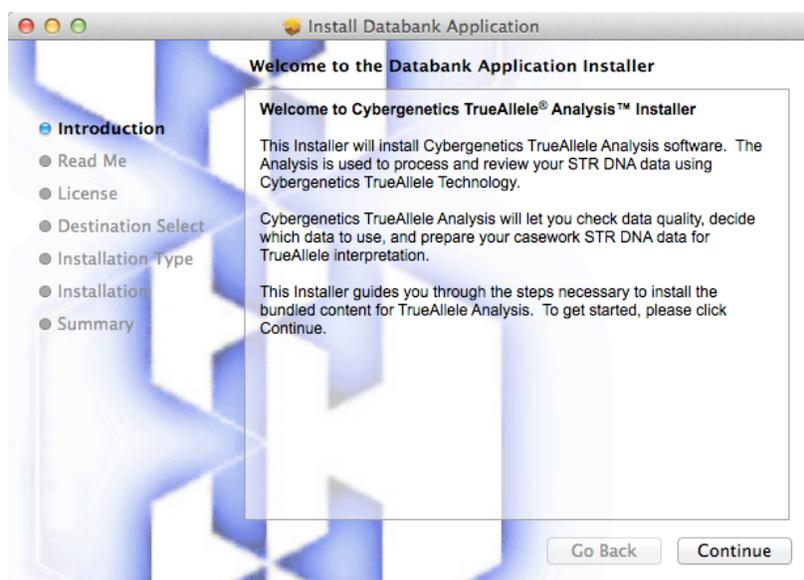


Figure 6. Introduction Screen.

The next screen contains a Read Me file for review (Figure 7). After reading the file, the user selects 'Continue' to advance to the next screen.

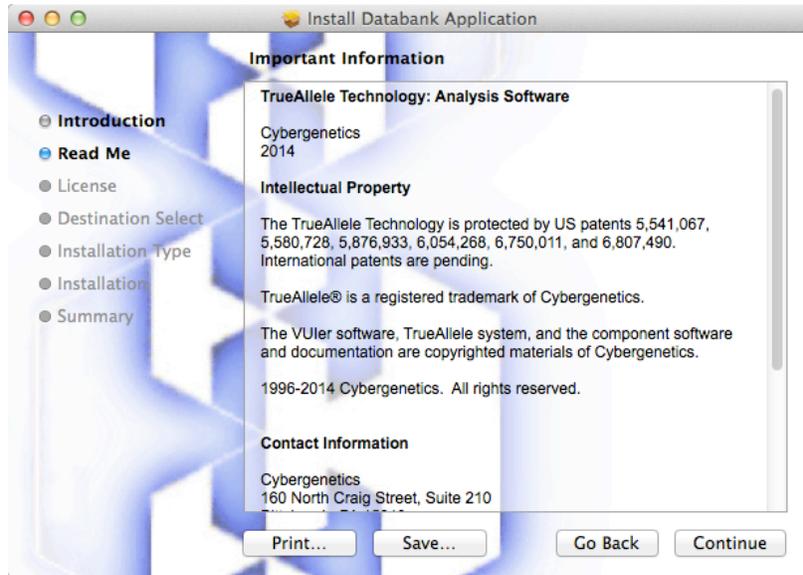


Figure 7. Read Me.

Next is the license agreement (Figure 8). After selecting 'Continue', a prompt appears to confirm agreement with the license. The user proceeds by selecting 'Agree'.

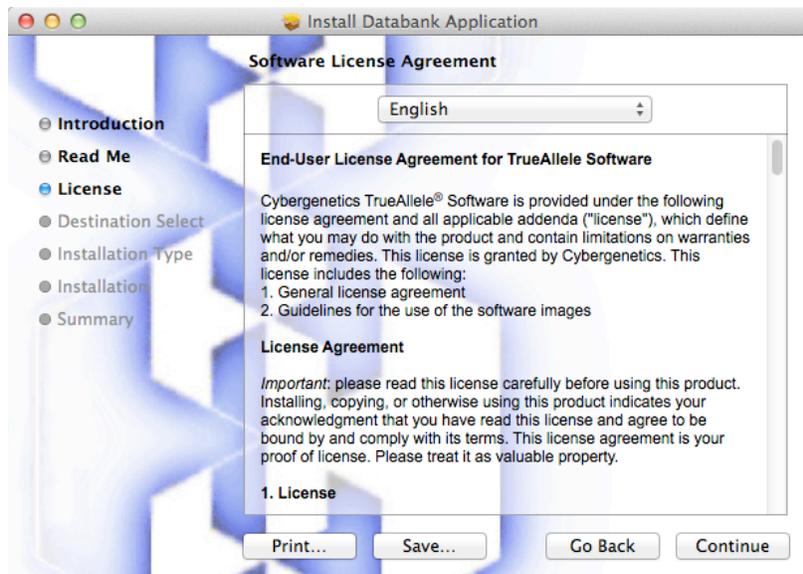
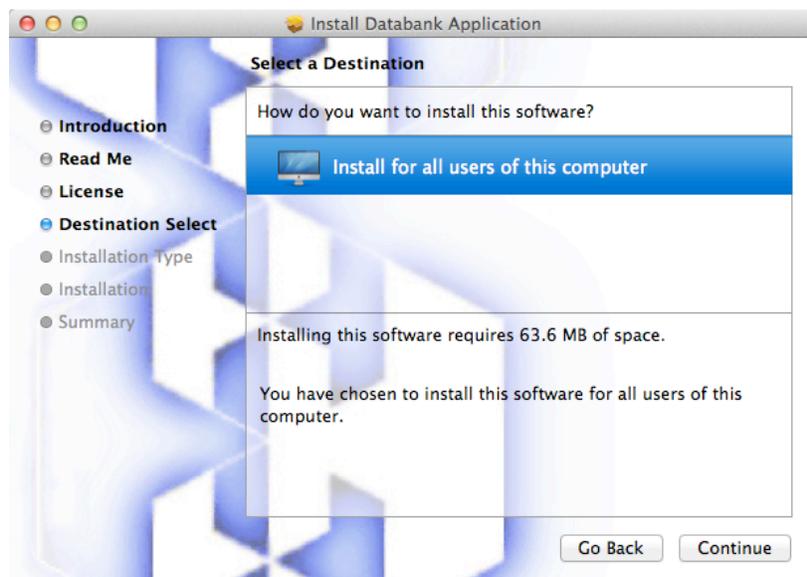


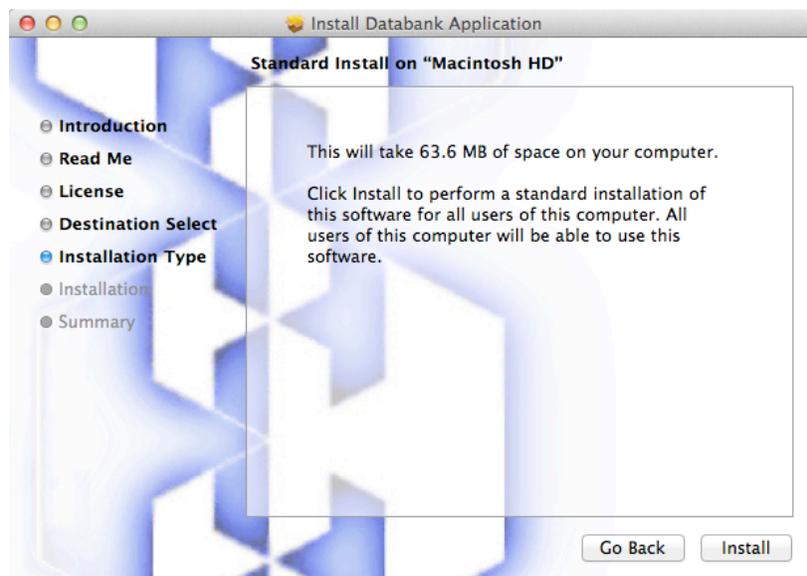
Figure 8. License Agreement.

If prompted, the user selects a destination to install the software in the *Destination Select* window (Figure 9). Most likely this will be for all users of the computer.



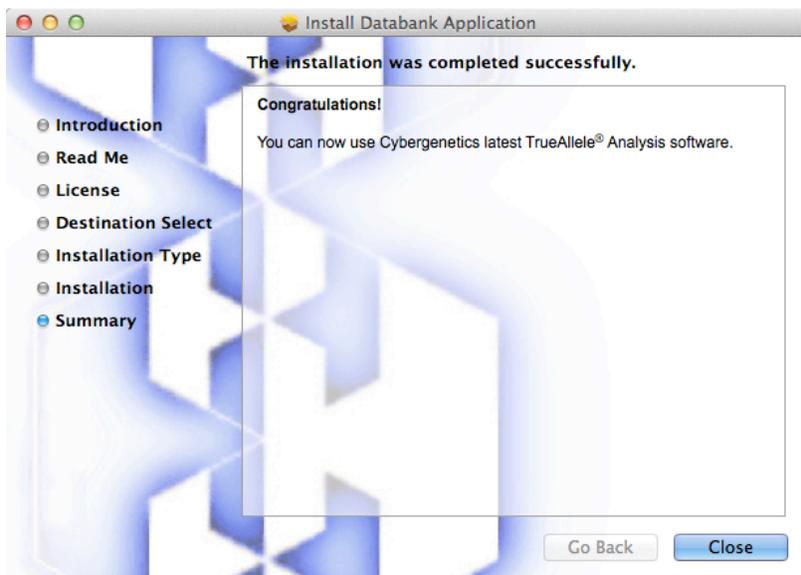
**Figure 9.** *Destination Select Screen.*

A standard install is automatically available. The user 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, and data can now be processed in the Analyze Module.

### **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.

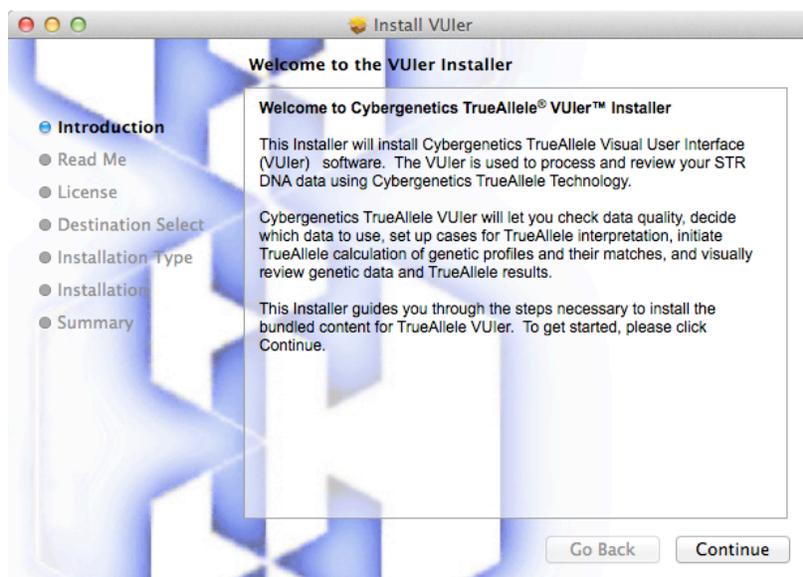
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### 3.3 VUler

The VUler software allows the user to upload and ask questions of the case data and then review and report the answers produced by the genetic calculator.

The user starts by expanding the zip file “VUler.pkg.zip”, which makes the package file “VUler.pkg” available. The user then double clicks on the package file 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 user selects 'Continue' to advance to the next screen.

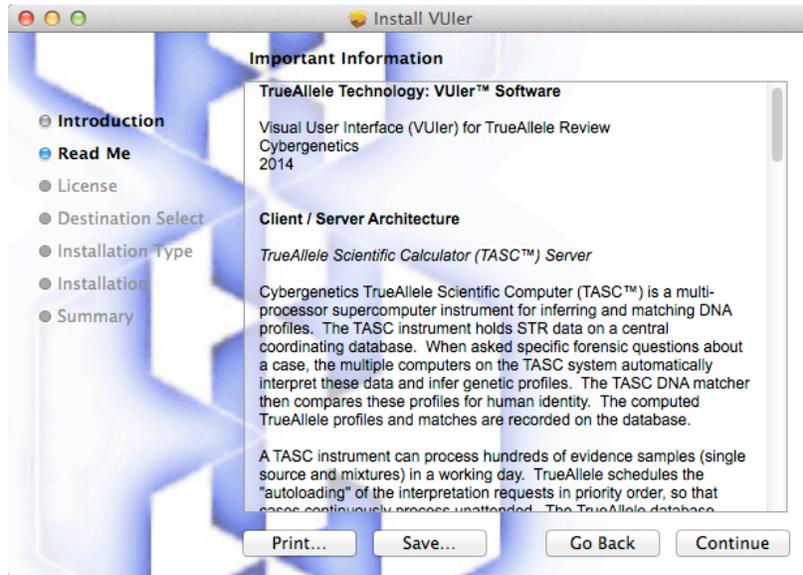


Figure 13. Read Me.

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

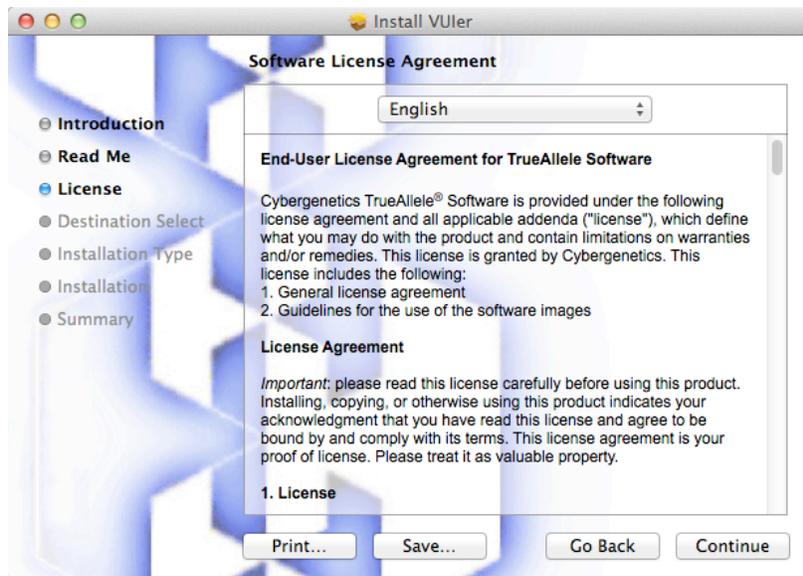
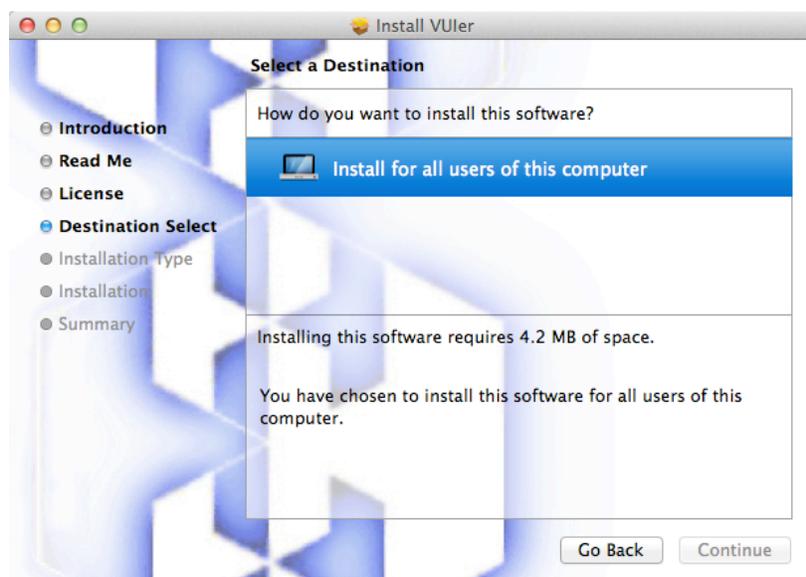


Figure 14. License Agreement.

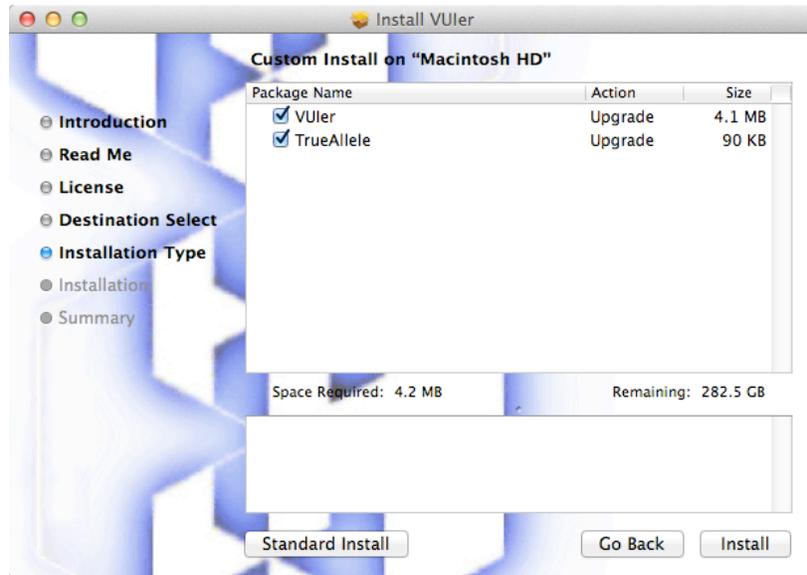
If prompted, the user selects a destination to install the software in the *Destination Select* window (Figure 15). Most likely this will be for all users of the computer.



**Figure 15.** *Destination Select Screen*

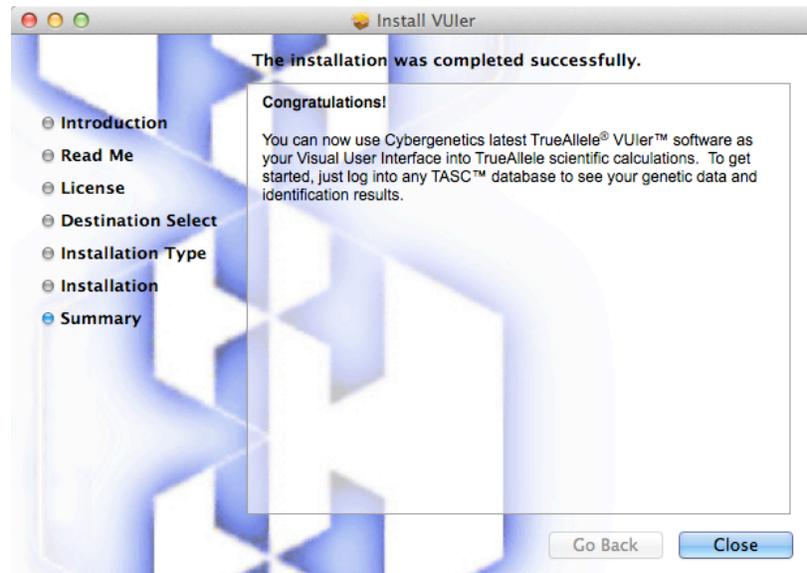
A standard install is automatically available. The user begins the installation by selecting 'Install'. When prompted, the administrator user name and password is entered.

A custom installation can be performed anytime that the VUIer software is installed on a computer. In the *Installation Type* window, selecting 'Customize' brings up the Custom Install options (Figure 16). The user is able to deselect any of the items that they do not wish to install when installing/upgrading VUIer. This action will affect the installation of some required user files.



**Figure 16.** Custom Install.

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



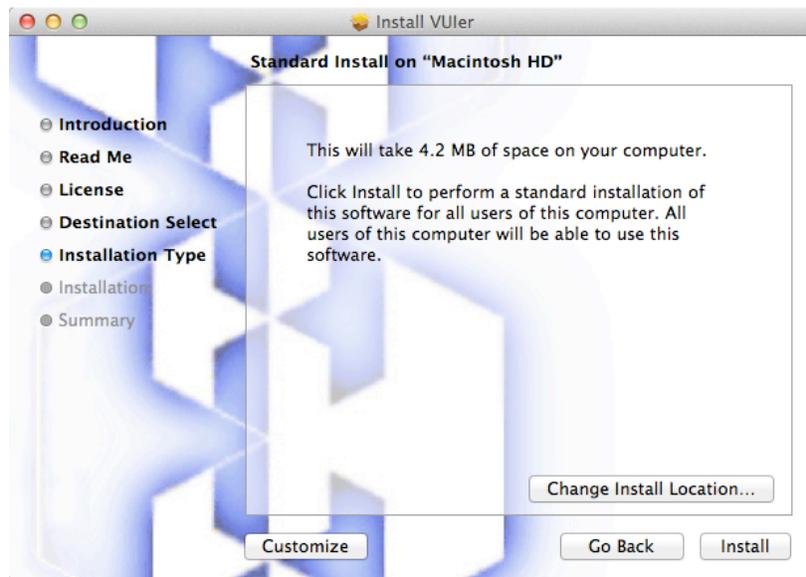
**Figure 17.** Installation complete.

---

## 3.4 Update

The same process is followed when updating the VUIer software as described in section 3.3. However, the user can save any customized preference files (such as the report.txt file) elsewhere on the computer before updating VUIer.

In the *Installation Type* window (Figure 18), the user selects 'Install'. When prompted, the administrator user name and password is entered.



**Figure 18.** *Standard Install.*

After the installation is complete, selecting 'Close' finishes the process. The VUIer software is now updated and available for use. The user can then replace any of the preference files with their customized ones.

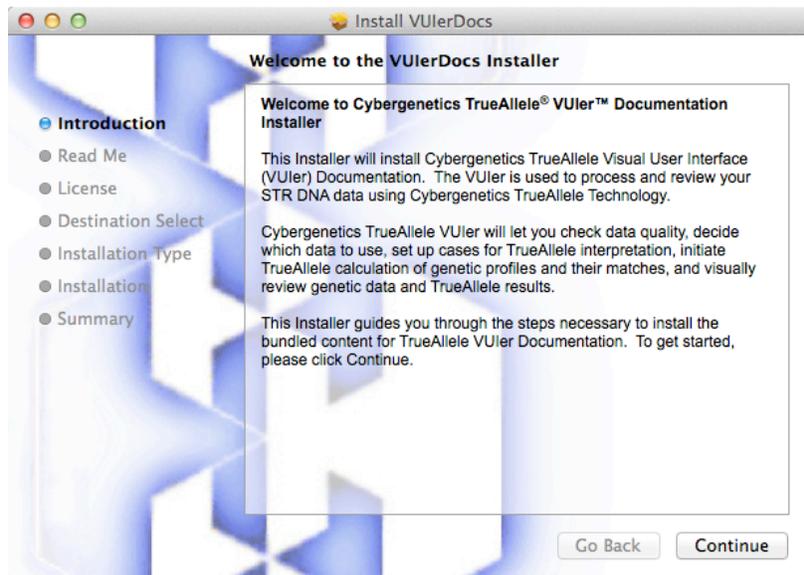
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## 3.5 Documentation

If desired, the user can install the VUIer documentation to be accessed from the Help menu of any module in the VUIer software. This documentation includes the Workflow manual, the Getting Started manual, the various module manuals, and a Tutorial manual as well as Database and Kinship application notes.

The user starts by expanding the zip file “VUIer\_Documentation.pkg.zip”, which makes the package file “VUIer\_Documentation.pkg” available. The user then double clicks on the package file to begin installation.

On the introduction screen (Figure 19), selecting ‘Continue’ advances to the next screen.



**Figure 19.** *Introduction Screen.*

The next screen contains a Read Me file for review (Figure 20). After reading the file, the user selects 'Continue' to advance to the next screen.

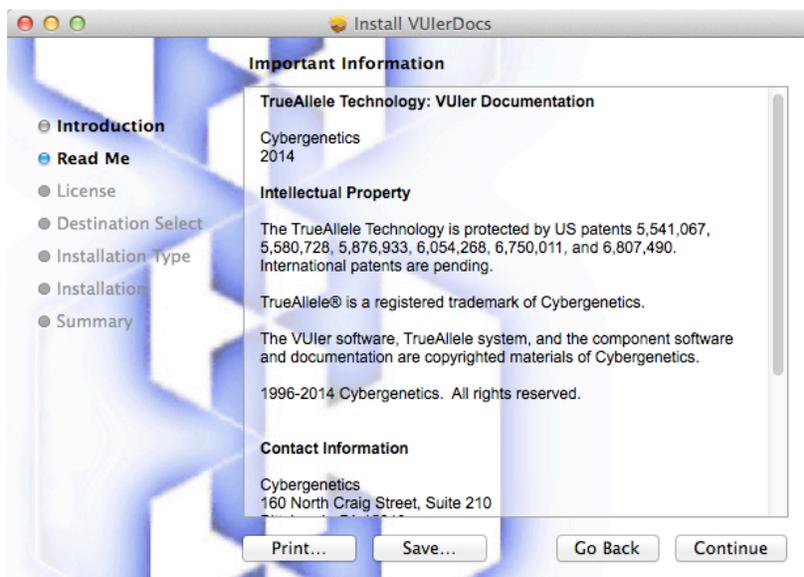


Figure 20. Read Me.

Next is the license agreement (Figure 21). After selecting 'Continue', a prompt appears to confirm agreement with the license. The user proceeds by selecting 'Agree'.

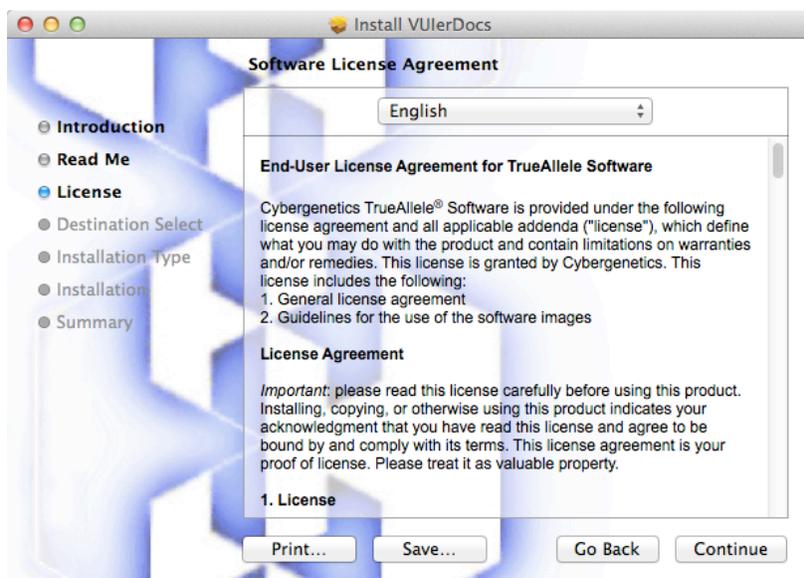


Figure 21. License Agreement.

If prompted, the user selects a destination to install the documentation in the *Destination Select* window (Figure 22). The documentation can only be installed for the current user account.

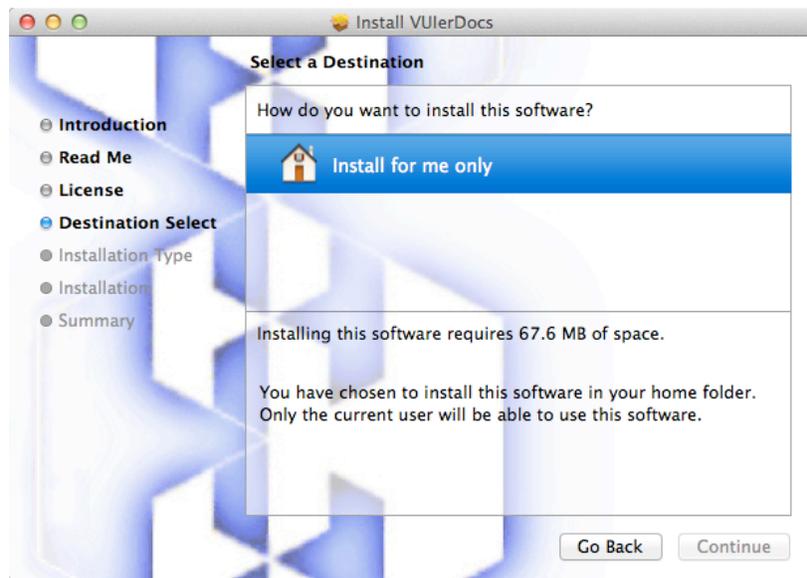


Figure 22. *Destination Select* Screen

The user begins the installation by selecting 'Install' (Figure 23). When prompted, the administrator user name and password is entered.

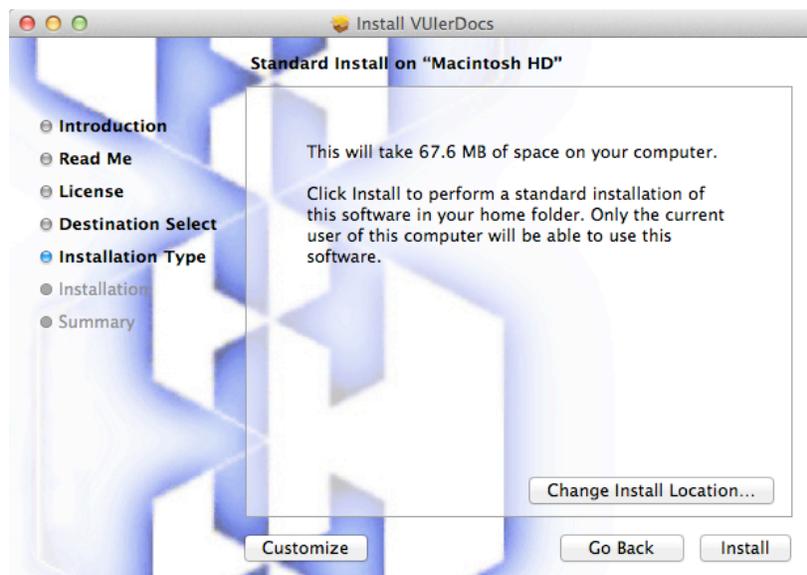
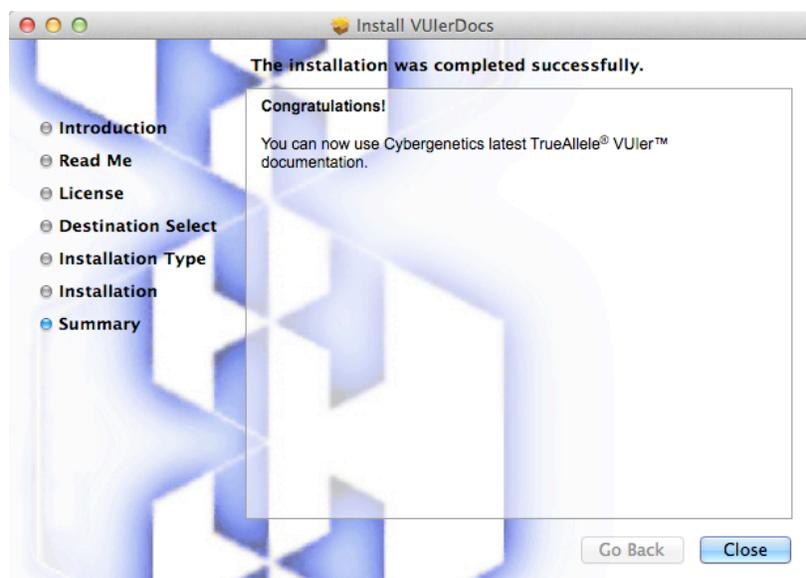


Figure 23. *Standard Install*.

After the installation is complete, selecting 'Close' finishes the process (Figure 24). The VUIer documentation is now installed in the Documents/trueallele/docs folder and is available from the Help menu in the VUIer modules. Note: the documentation will be opened with the default PDF reader on the computer. A PDF reader must be installed in order to view the documentation. Also, after an Analyze update, the documentation will need to be reinstalled.



**Figure 24.** *Installation complete.*

---

## 4 Software Function

Now the typical method of opening the VUler program is reviewed. An alternative method for starting the program is covered in the **Appendix ► Diagnostic Support**.

---

### 4.1 Starting the VUler program

The user starts the VUler program by clicking on its icon (Figure 25) in the Dock on a Macintosh (typically located at the bottom of the screen) or from the Desktop shortcut or Programs Files folder on a PC. On some computers, the Dock may automatically hide, but placing the mouse cursor at the bottom of the screen will make it appear.



**Figure 25.** *VUler icon.*

If the VUler icon is not already in the Dock, it can be placed there in a few simple steps. First, the user selects the Finder icon (Figure 26) in the dock.



**Figure 26.** *Finder icon.*

This selection opens the Finder window, displaying the computer's folders and files. From the left side bar, the user selects Applications. In the Applications folder, the user locates the VUIer icon, then clicks and drags the icon down to the Dock. This will place VUIer in the Dock.

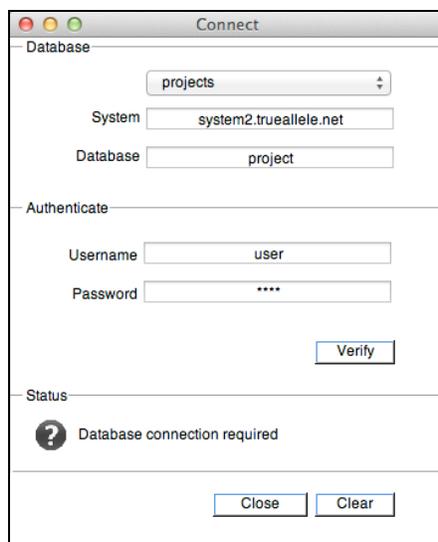
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## 4.2 Connecting to a Database

In the VUIer program, the *Connect* window allows a user to connect to a database or to switch to a different database at any time during the TrueAllele process. The user can open the *Connect* window by selecting the **Database ► Connect** menu option in any VUIer Module.

### Connect window

To connect, a user selects the desired database from the dropdown menu (this action fills in the *System* field as well). The user then enters a username and password under the *Authenticate* heading and clicks 'Verify'. A blue check mark is present when the connection is verified. The *Connect* window (Figure 27) will automatically close when the connection is verified indicating that the process is complete.



**Figure 27.** *The Connect window.*

## Clearing Information

To clear all of the information entered in the *Connect* window fields, the user 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 user should first check that the information was entered correctly.

---

## 4.3 Closing the VUler Program

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

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

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

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

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## 5 Network Setup

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### 5.1 Adding Server to Client Network

Before using TrueAllele, the server must be set up. The following section addresses the steps to set up the server and network. If additional help is needed, Cybergenetics should be contacted for support.

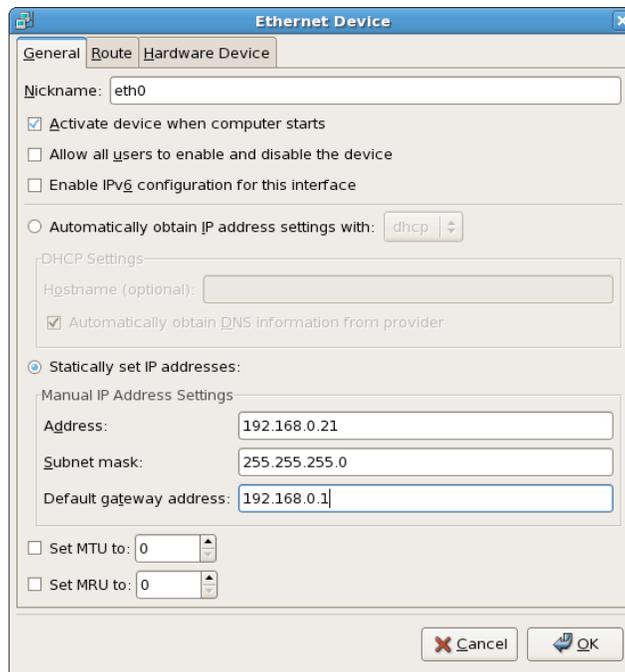
To add the server to the network:

Unpack server then locate network and power.

- Plug Ethernet cord in **Ethernet port #1**.

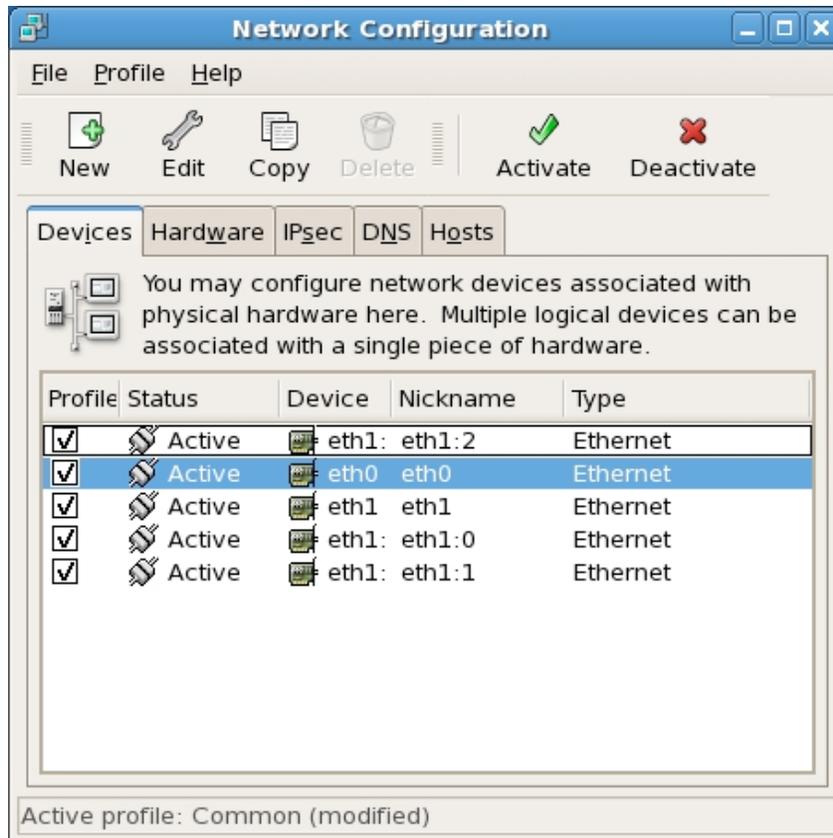
Log in with root password.

- Type 'startx' to bring up the graphical user interface.
- The Star icon  is the Network dialog and is found in the top menu bar or under the System ► Administration ► Network menu.
- Select eth0 by double clicking it from the dialog that opens (Figure 28).
- Type IP address, subnet mask and gateway (if necessary) into Ethernet Device dialog that opens. Click OK after all information is entered.



**Figure 28.** *The Ethernet Device dialog.*

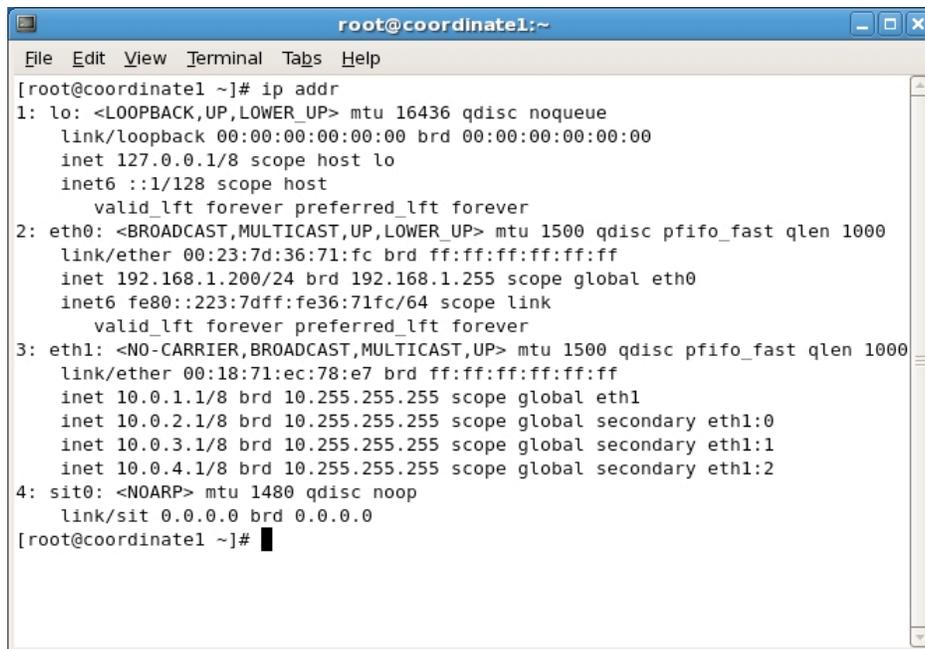
Next, the Network Configuration window opens. Select eth0 from the list and click the Deactivate button to refresh network (Figure 29). If prompted, save changes. Click the Activate button to bring the network back up with the new settings applied.



**Figure 29.** *The Network Configuration window.*

If you need to restart the network manually you can do so from the Terminal. To restart the Network: In Terminal, type “service network restart” and then press Enter.

In Terminal, type “ip addr” to check that the ip address is correct (under eth0 entry, inet line) (Figure 30).



```
root@coordinate1:~  
File Edit View Terminal Tabs Help  
[root@coordinate1 ~]# ip addr  
1: lo: <LOOPBACK,UP,LOWER_UP> mtu 16436 qdisc noqueue  
   link/loopback 00:00:00:00:00:00 brd 00:00:00:00:00:00  
   inet 127.0.0.1/8 scope host lo  
   inet6 ::1/128 scope host  
       valid_lft forever preferred_lft forever  
2: eth0: <BROADCAST,MULTICAST,UP,LOWER_UP> mtu 1500 qdisc pfifo_fast qlen 1000  
   link/ether 00:23:7d:36:71:fc brd ff:ff:ff:ff:ff:ff  
   inet 192.168.1.200/24 brd 192.168.1.255 scope global eth0  
   inet6 fe80::223:7dff:fe36:71fc/64 scope link  
       valid_lft forever preferred_lft forever  
3: eth1: <NO-CARRIER,BROADCAST,MULTICAST,UP> mtu 1500 qdisc pfifo_fast qlen 1000  
   link/ether 00:18:71:ec:78:e7 brd ff:ff:ff:ff:ff:ff  
   inet 10.0.1.1/8 brd 10.255.255.255 scope global eth1  
   inet 10.0.2.1/8 brd 10.255.255.255 scope global secondary eth1:0  
   inet 10.0.3.1/8 brd 10.255.255.255 scope global secondary eth1:1  
   inet 10.0.4.1/8 brd 10.255.255.255 scope global secondary eth1:2  
4: sit0: <NOARP> mtu 1480 qdisc noop  
   link/sit 0.0.0.0 brd 0.0.0.0  
[root@coordinate1 ~]#
```

**Figure 30.** The results of `ip addr`.

You can confirm the server has been correctly setup from the TrueAllele ViewStation.

---

## 5.2 Confirm the Network Connection

The following section outlines the steps for confirming the network connection to the server.

To confirm the network connection:

Open the VUIer and select the Request Module.

- In the menu bar, select Database ► Connect.
- Select 'general use' from the drop-down menu.
- In the URL enter the server IP address.
- Enter general TrueAllele World account information.
- Press the Verify button.
- Blue check means that the network is up and running.

If there is a red X, the VUIer is unable to reach the server.

---

## 5.3 Update the Connect File

After the server is running, the connect file can be edited in order to have the software auto-complete the connection information.

To update the connect file:

Connect File:

- Open the Tools module.
- From the Tools menu select 'VUIer Preferences'.
- From the drop-down menu in the dialog select Connect.
- Edit the connect file by replacing (insert server IP) with the server's IP address.
- Save the file as text.

---

## 6 Backup Setup

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### 6.1 Overview

The TrueAllele Server performs automated daily backups of each of the TrueAllele Worlds on the server. These backup files contain a complete copy of all requests and data that are present on that World.

The backup files are stored on the server in the `/backup/download` directory. This folder is accessible via the root account and can be copied to other media to provide off-machine backup.

---

### 6.2 Copying to Physical Media

The following section outlines the steps to backup the server onto physical media. Physical media includes CDs, external hard drives, etc.

*Note: This assumes that the system has not yet been logged in and the process is starting from the log in window.*

To save backups to physical media:

At the login prompt, log in as the root user. Once you are logged in as root, type 'startx' to start the GUI.

To navigate to the `/backup` directory, select the Computer icon on the desktop. This will open a Linux file explorer window. Select Filesystem to open a window showing

the top-level / directory. Select backup to enter the backup directory and see the /download directory. The /download directory contains all of the backup files.

When you insert optical media (DVD or CD), a new icon will appear on the desktop called Blank DVD+R Disc. (The exact name will vary based on the media used). Simply click and drag the /download directory to the media. Select the media icon to open a CD/DVD Creator. All files that will be burned to the media will be displayed in this window. Select the 'Write to Disc' button in the top right to begin the writing process.

For external hard drives or thumb drives, simply plug the drive into the server. A new icon for the hard drive will appear on the desktop. You can simply drag the /download directory to that icon to move files to the hard drive.

---

## 6.3 Copying Files via the Network

To aid the transfer of files between the server and another computer, an FTP client can be used. Cybergenetics recommends using WinSCP for Windows or Cyberduck for Macintosh. These programs provide a visual interface for moving files over a network via SFTP. The steps to perform this task are outlined in the following section.

*Note: The following instructions are for using Cyberduck on a Mac ViewStation. The steps for using WinSCP on a PC are similar.*

To transfer files between the server and another computer:

Start Cyberduck, and select the Open Connection button in the menu bar (Figure 31). This will open a New Connection dialog.



**Figure 31.** *The Open Connection icon.*

Fill out the New Connection dialog with the following parameters (Figure 32):

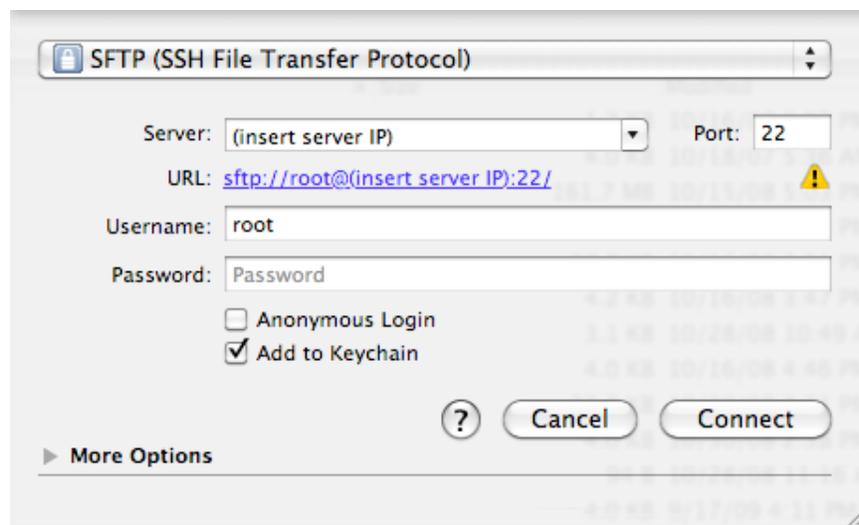
Username: root

Password: *root password (this information is specific to the server)*

Server: *server IP address (this information is specific to the server)*

File protocol: SFTP

Port number: 22

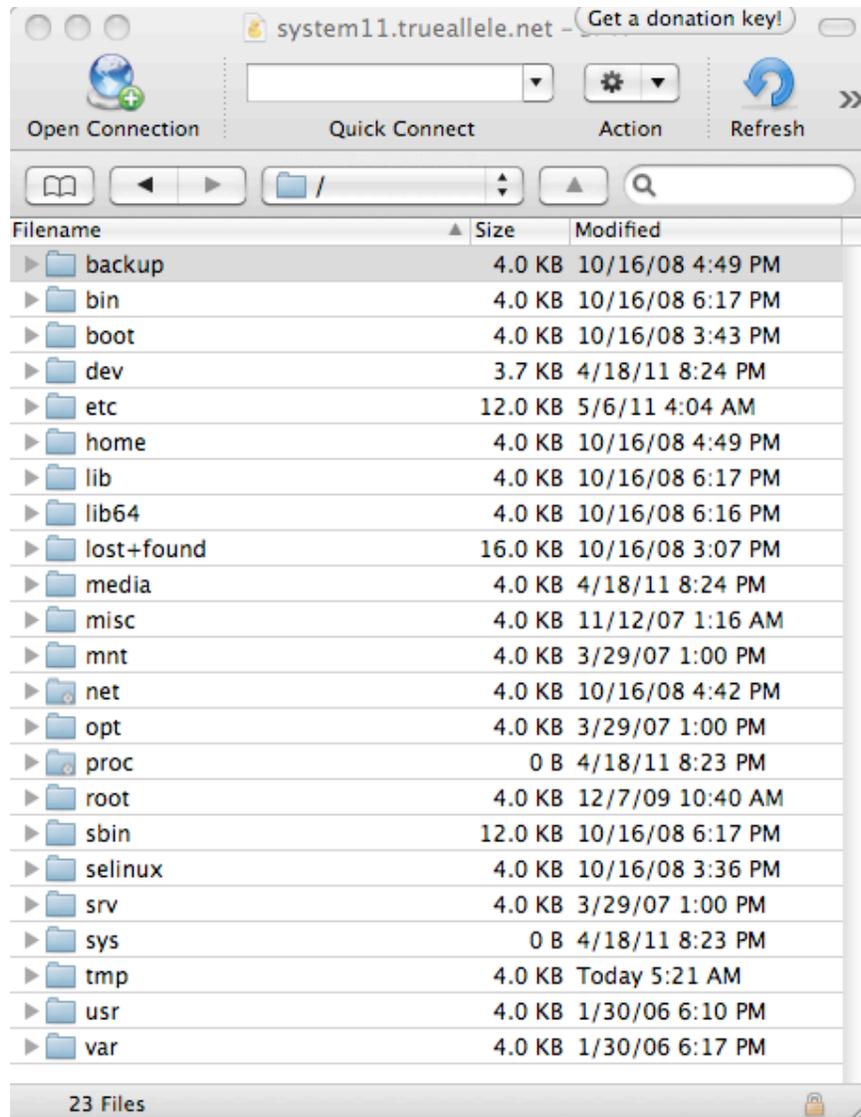


**Figure 32.** *The New Connection dialog.*

After establishing a secure FTP connection, you will be presented with a file explorer interface. This interface will let you drag files and folders to the remote computer.

Select the directory drop-down from the menu bar and select the top-level directory `/`. The main finder window (Figure 33) will now display all the directories under the top-level including `/backup`. Select `/backup`, and you will see the `/download` directo-

ry. Simply drag and drop the /download directory onto the Mac Desktop to begin copying the complete backup information.



**Figure 33.** The main Finder window displaying /.

Once the files have finished moving, you can store the backup on other media. The iMac ViewStation supports burning to a DVD or moving the files to an external hard drive.

---

## 7 Appendix

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

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### 7.1 PC Installation

The steps for installing the MCR Engine, Analysis Module, and VUIer software on both a 32-bit and 64-bit Windows PC are found in this Appendix. The user should note that before updating any of the programs, the customized user directories and preferences can be saved elsewhere on the computer in order to preserve and reinstate them after an update.

#### **MCR Engine**

A user begins by expanding the zip file “MCR\_Engine\_64bit.exe.zip” (or “MCR\_Engine\_32bit.exe.zip”), which makes the executable file “MCR\_Engine\_64bit.exe” (or “MCR\_Engine\_32bit.exe”) available. The user then double clicks on the execute file to begin the installation process.

On the introduction screen (Figure 34), selecting 'Next' advances to the next screen.



Figure 34. Introduction Screen.

Next, the user must select a destination folder in which to install the software in the *Folder Selection* screen (Figure 35).

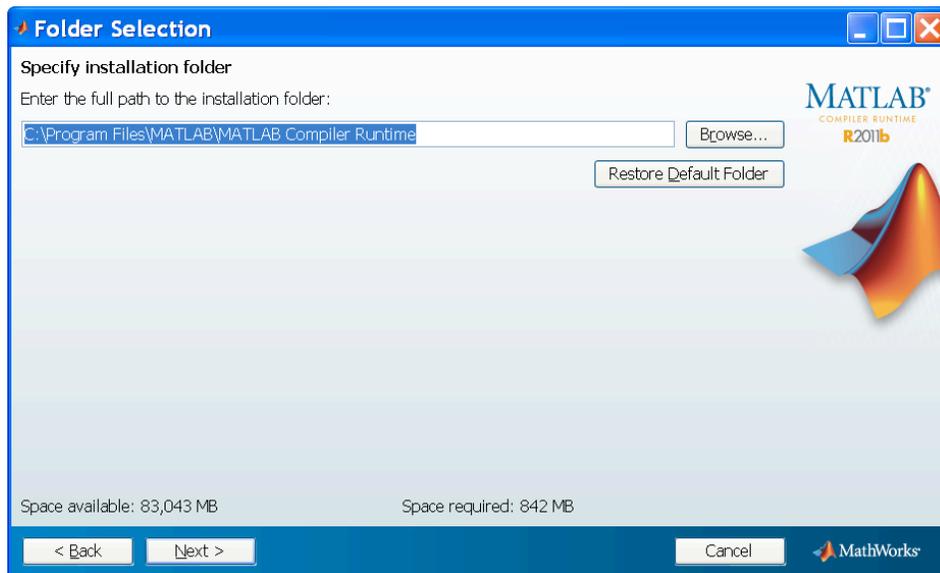
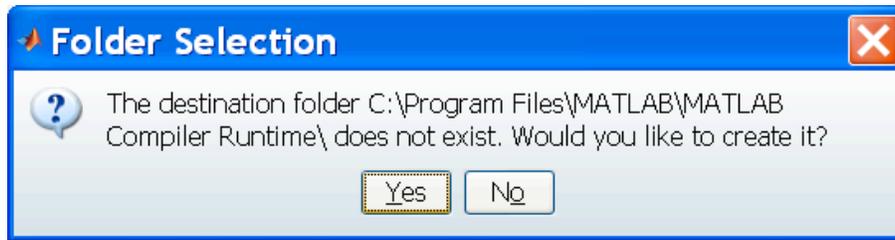


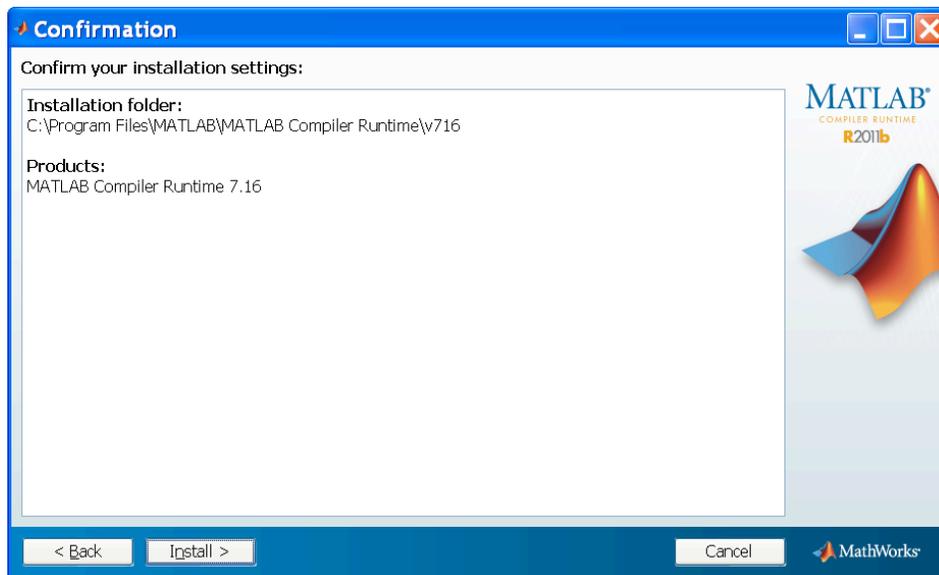
Figure 35. Folder Selection Screen.

After selecting a destination to install the software, the user must confirm the creation of the destination folder by selecting 'Yes' (Figure 36).



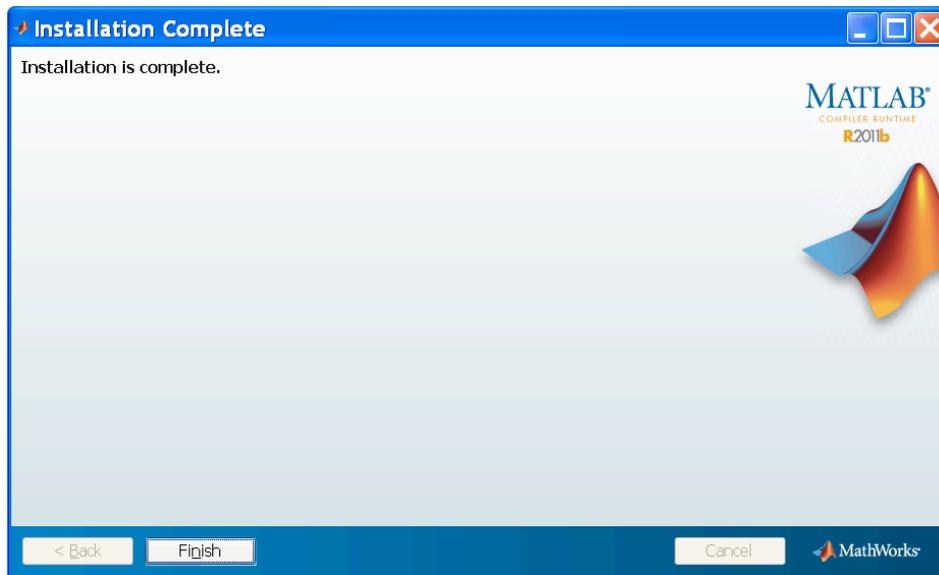
**Figure 36.** Folder Selection Confirmation.

In the *Confirmation* window (Figure 37), the user selects 'Install' to begin the installation process. If prompted, the administrator user name and password is entered.



**Figure 37.** Confirmation Window.

Once installation is complete, selecting 'Finish' exits the installer (Figure 38).



**Figure 38.** *Installation Complete Screen.*

## Analyze

To install the Analyze module on a PC (either 32-bit or 64-bit), expanding on the zip file "Analyze\_64bit.exe.zip" (or "Analyze\_32bit.exe.zip"), which makes the executable file "Analyze\_64bit.exe" (or "Analyze\_32bit.exe") available. The user then double clicks on the execute file to begin the installation process.

On the introduction screen (Figure 39), selecting 'Continue' advances to the next screen.

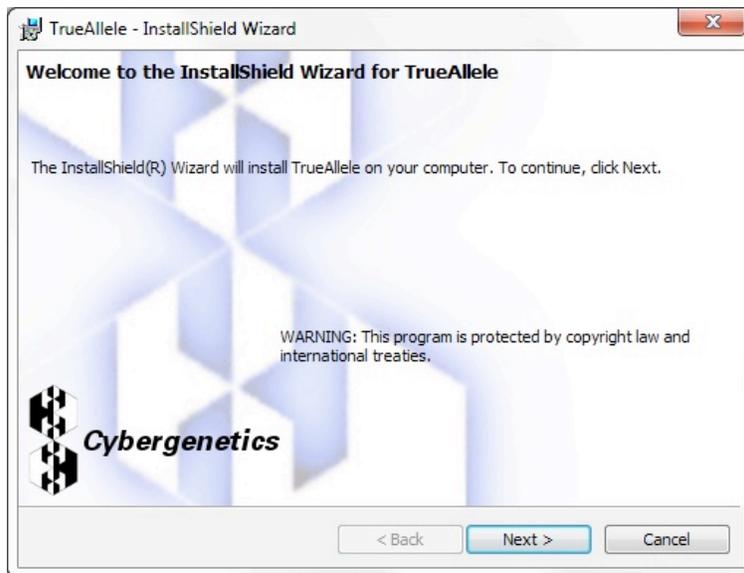


Figure 39. Introduction Screen.

The next screen contains a license agreement for review (Figure 40). After reading and accepting the agreement, the user selects 'Next' to advance to the next screen.

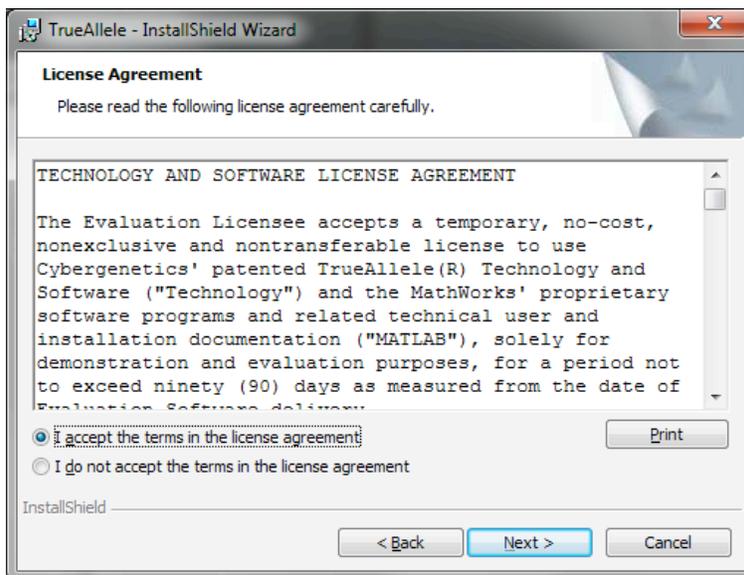
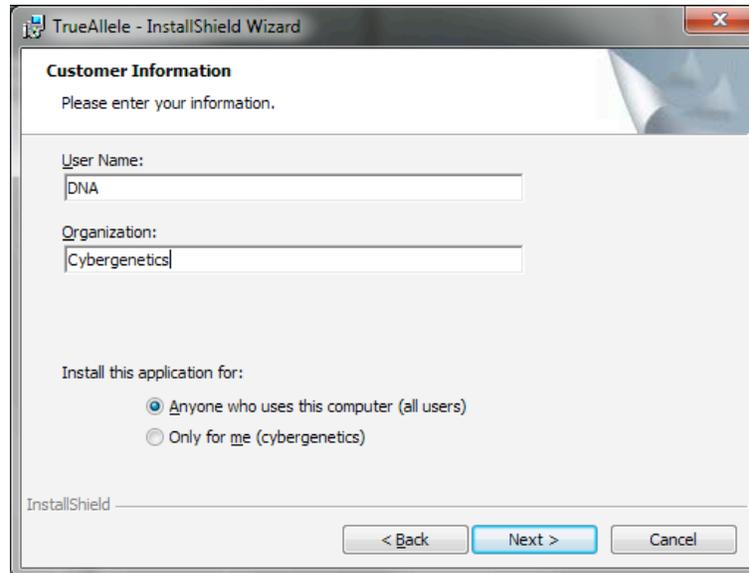


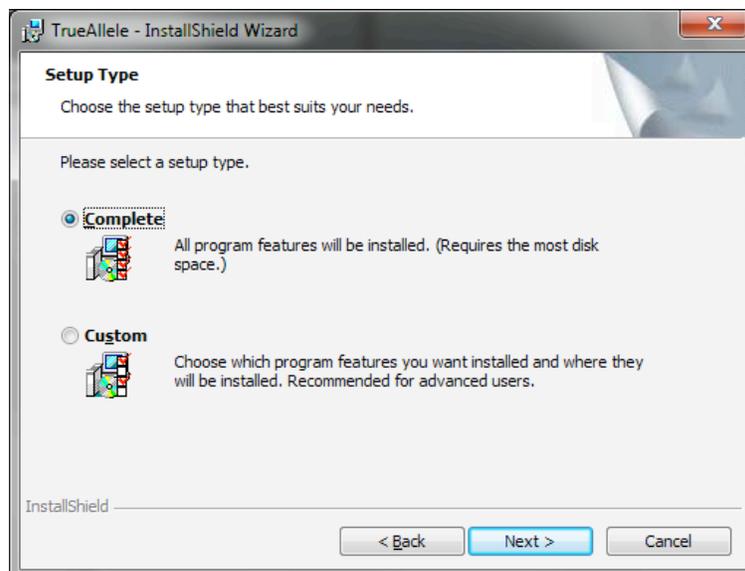
Figure 40. License Agreement.

Next is the customer information screen (Figure 41). After entering the appropriate information and selecting the user(s) to install the application for, the user selects 'Next' to proceed.



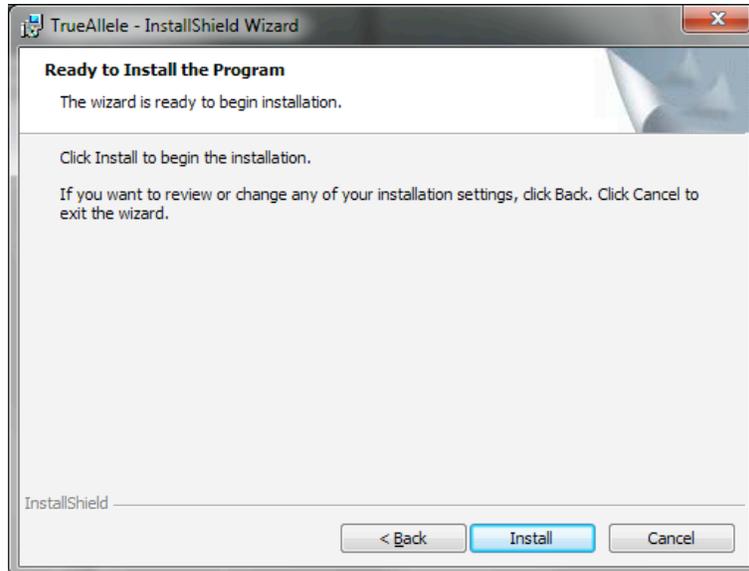
**Figure 41.** Customer Information Screen.

On the next screen, the user chooses the default setup type and clicks 'Next' to continue (Figure 42).



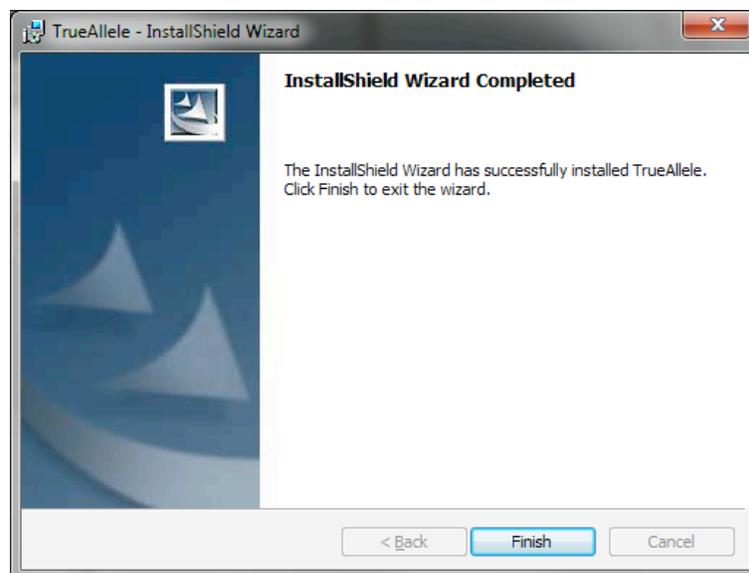
**Figure 42.** Setup Type Window.

On the ready to install screen (Figure 43), the user selects Install to begin the Analyze installation. If prompted, the administrator user name and password is entered.



**Figure 43.** *Ready to Install.*

After the installation is complete, selecting 'Finish' completes the process (Figure 44). This completes the installation of the Analyze Module, and data can now be processed in the Analyze Module.



**Figure 44.** *Installation Complete.*

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

### **VUIer**

The user starts by expanding the zip file "VUIer\_64bit.exe.zip" (or "VUIer\_32bit.exe.zip"), which makes the package file "VUIer\_64bit.exe" (or "VUIer\_32bit.exe") available. The user then double clicks on the executable file to begin installation.

On the introduction screen (Figure 45), selecting 'Next' advances to the next screen.

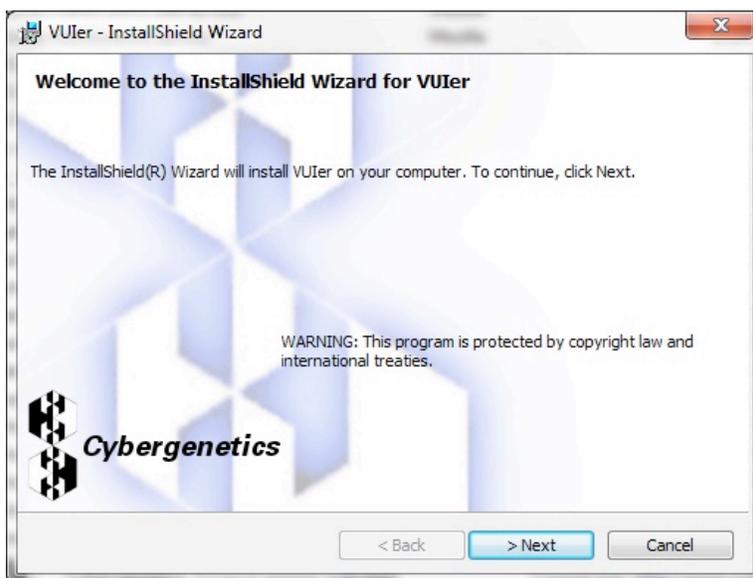


Figure 45. Introduction Screen.

The next screen contains a license agreement for review (Figure 46). After reading and accepting the agreement, the user selects 'Next' to advance to the next screen.

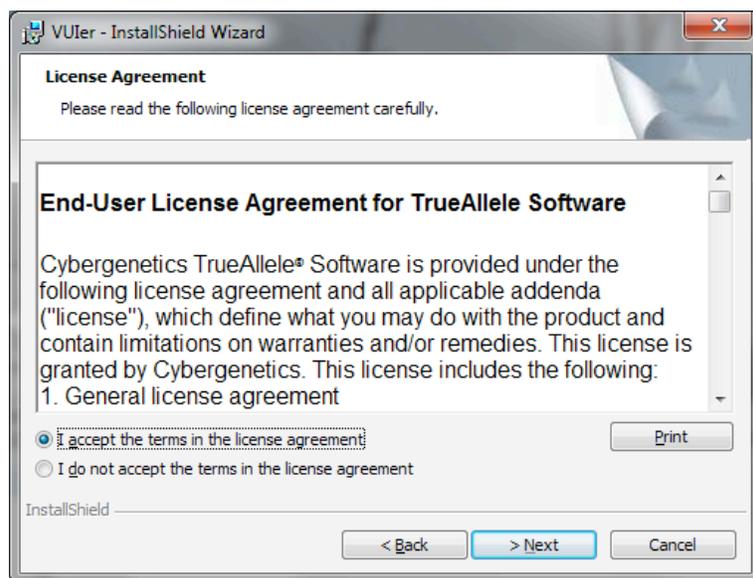
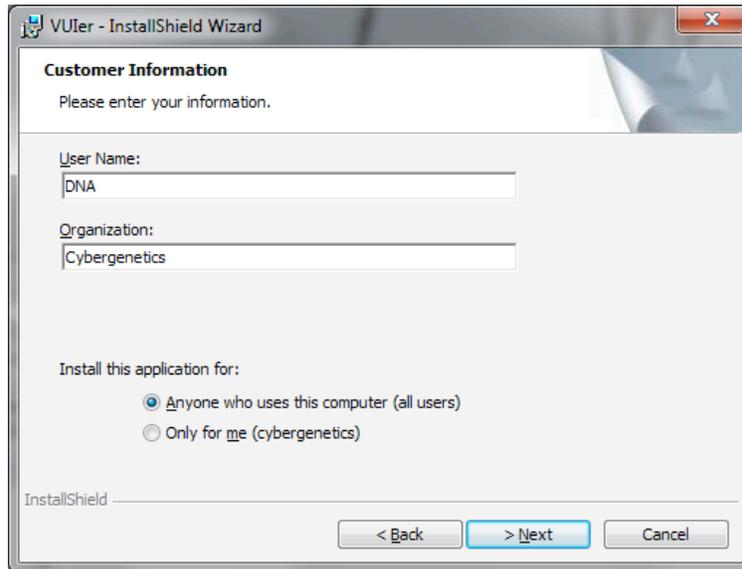


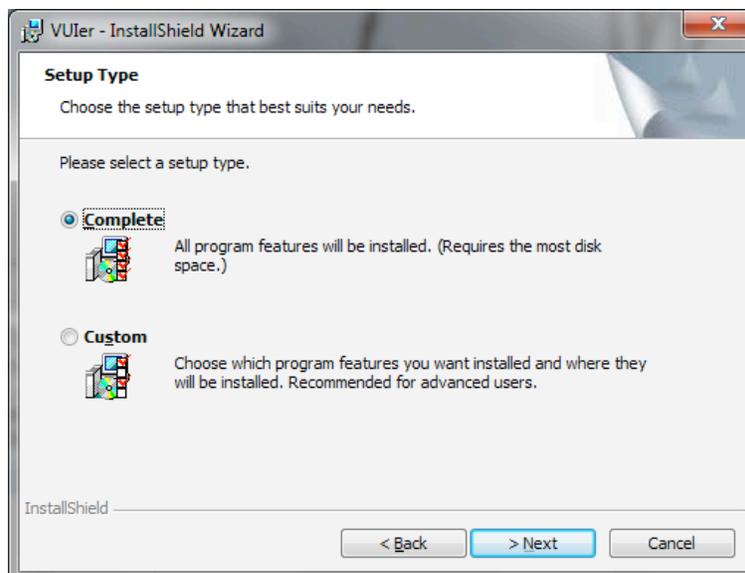
Figure 46. License Agreement.

Next is the customer information screen (Figure 47). After entering the appropriate information and selecting the user(s) to install the application for, the user selects 'Next' to proceed.



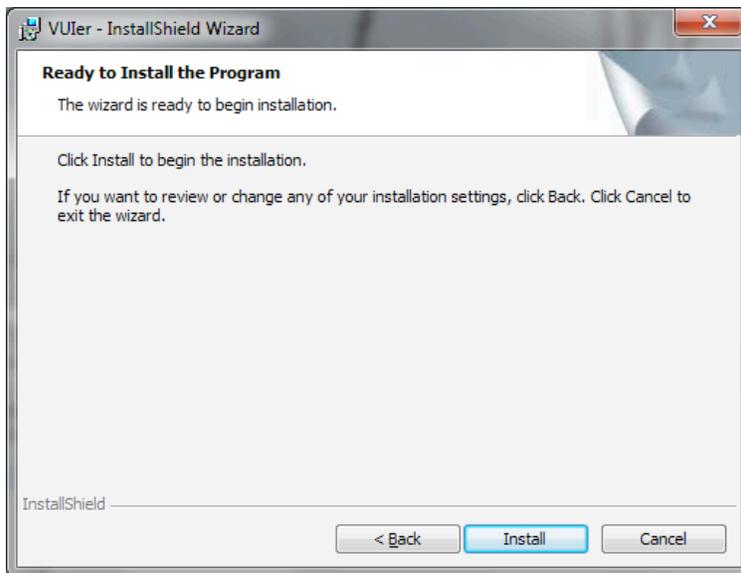
**Figure 47.** *Customer Information Screen.*

On the next screen, the user chooses the default setup type and clicks 'Next' to continue (Figure 48).



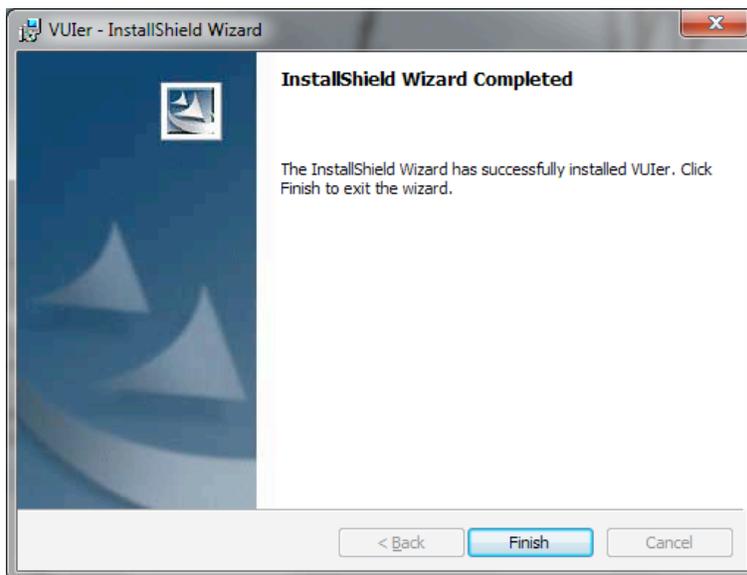
**Figure 48.** *Setup Type Window.*

On the ready to install screen (Figure 49), the user selects Install to begin the VUIer installation. If prompted, the administrator user name and password is entered.



**Figure 49.** *Ready to Install.*

After the installation is complete, selecting 'Finish' completes the process (Figure 50). The VUIer software is now installed and available for use.



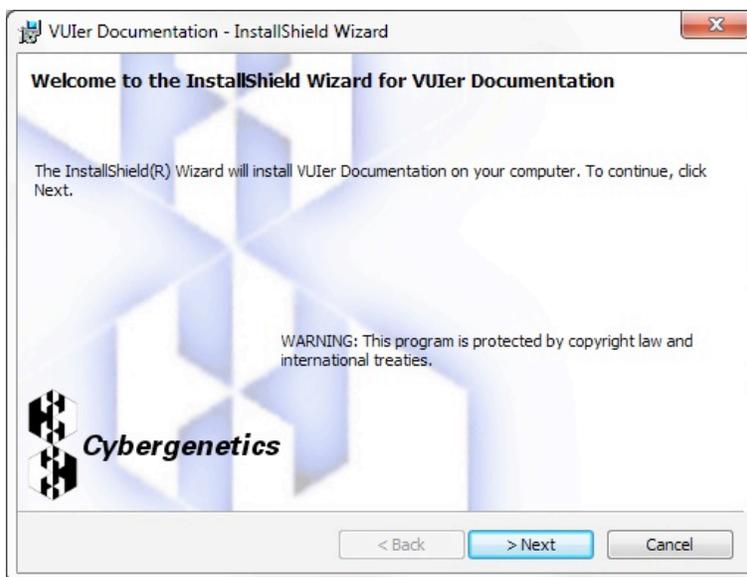
**Figure 50.** *Installation Complete.*

For updating VUIer, the same steps are followed. However, the user can save any customized preference files before updating in order to preserve the customizations. The user is then able to create a VUIer shortcut on the Desktop by right-clicking the program file and selecting **Send to → Desktop (create shortcut)**.

## Documentation

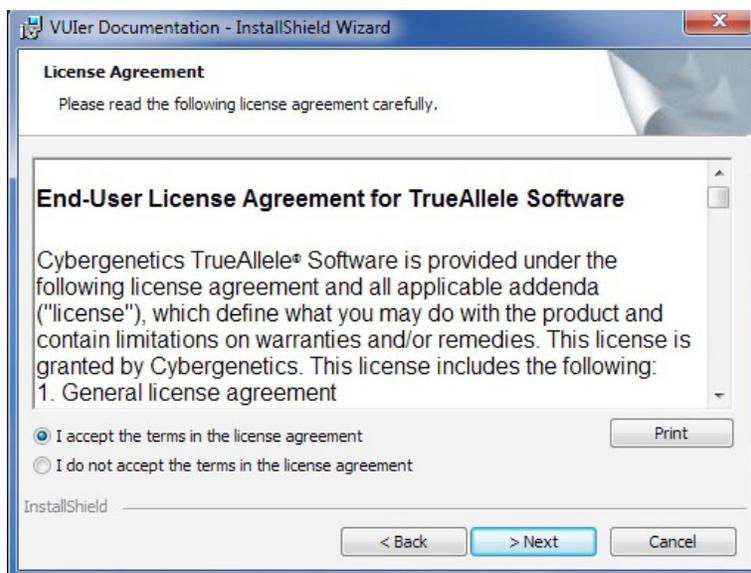
The user starts by expanding the zip file “VUIer\_Documentation.exe.zip”, which makes the package file “VUIer\_Documentation.exe” available. The user then double clicks on the executable file to begin installation.

On the introduction screen (Figure 51), selecting ‘Next’ advances to the next screen.



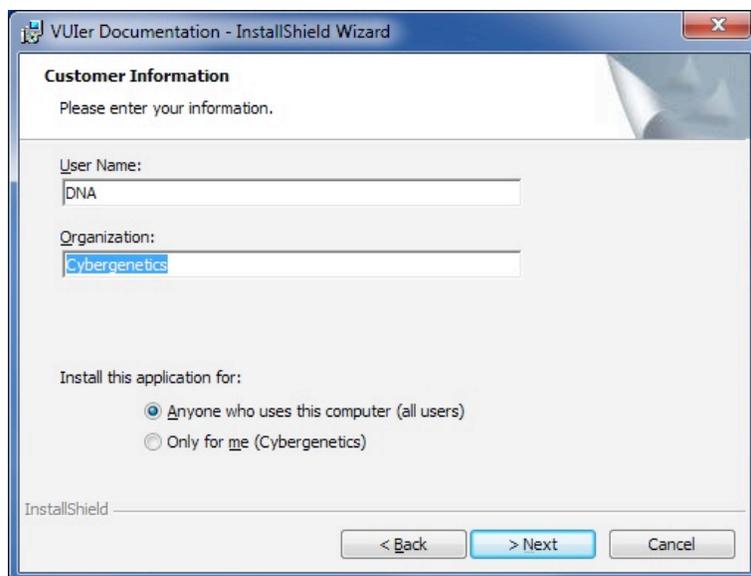
**Figure 51.** *Introduction Screen.*

The next screen contains a license agreement for review (Figure 52). After reading and accepting the agreement, the user selects 'Next' to advance to the next screen.



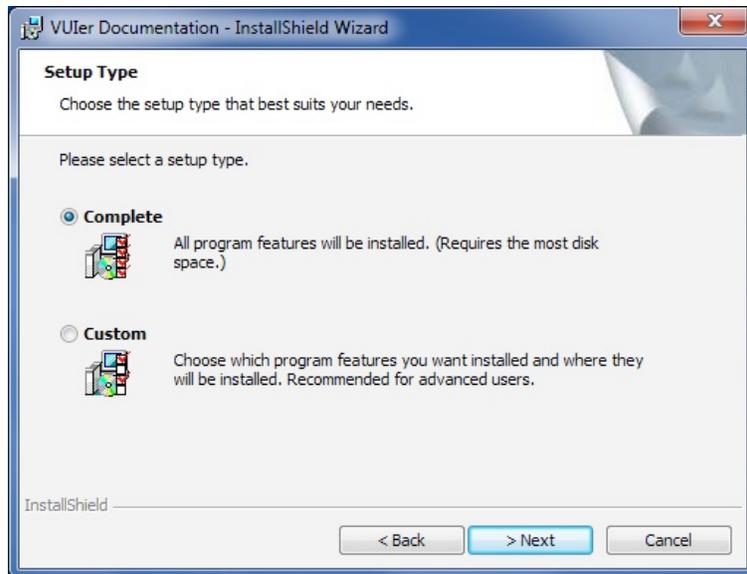
**Figure 52.** License Agreement.

Next is the customer information screen (Figure 53). After entering the appropriate information and selecting the user(s) to install the application for, the user selects 'Next' to proceed.



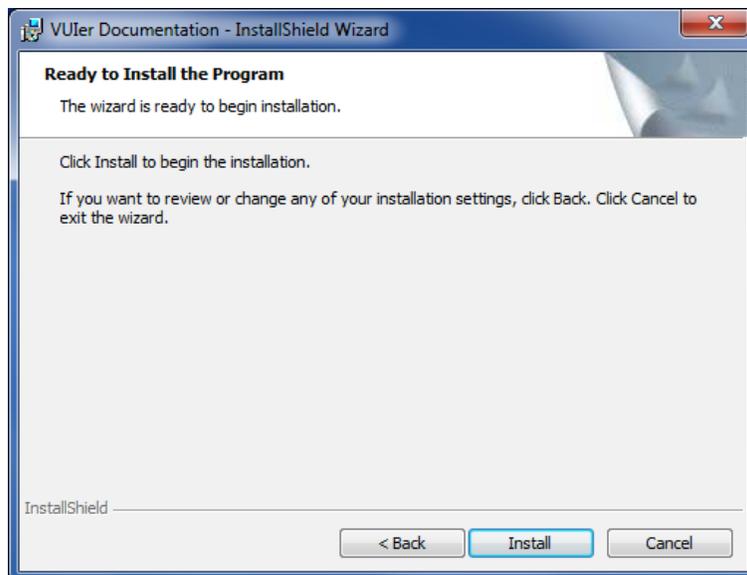
**Figure 53.** Customer Information Screen.

On the next screen, the user chooses the default setup type and clicks 'Next' to continue (Figure 54).



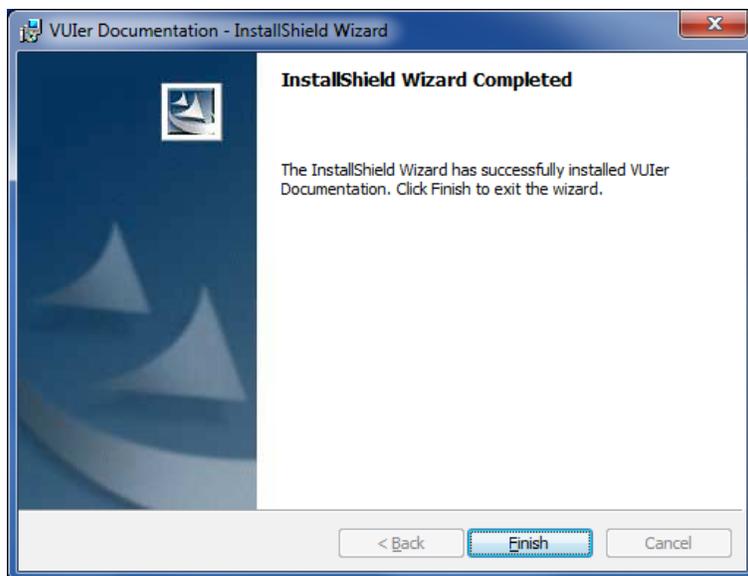
**Figure 54.** Setup Type Window.

On the ready to install screen (Figure 55), the user selects Install to begin the VUIer documentation installation. If prompted, the administrator user name and password is entered.



**Figure 55.** Ready to Install.

After the installation is complete, selecting 'Finish' completes the process (Figure 56). The VUIer documentation is now installed and available from the Help menu in the VUIer modules. Note: the documentation will be opened with the default PDF reader on the computer. A PDF reader must be installed in order to view the documentation. Also, after an Analyze update, the documentation will need to be reinstalled.



**Figure 56.** *Installation Complete.*

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## 7.2 Spinning Wait Cursor



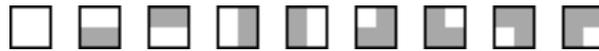
Spinning Wait Cursor

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

---

## 7.3 View Menu

In several modules of the VUIer program, there is a *View Menu*. This menu allows the user to change 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 user to position the interface windows on the screen (Figure 57), 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- on a PC).



**Figure 57.** *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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## 7.4 Diagnostic Support

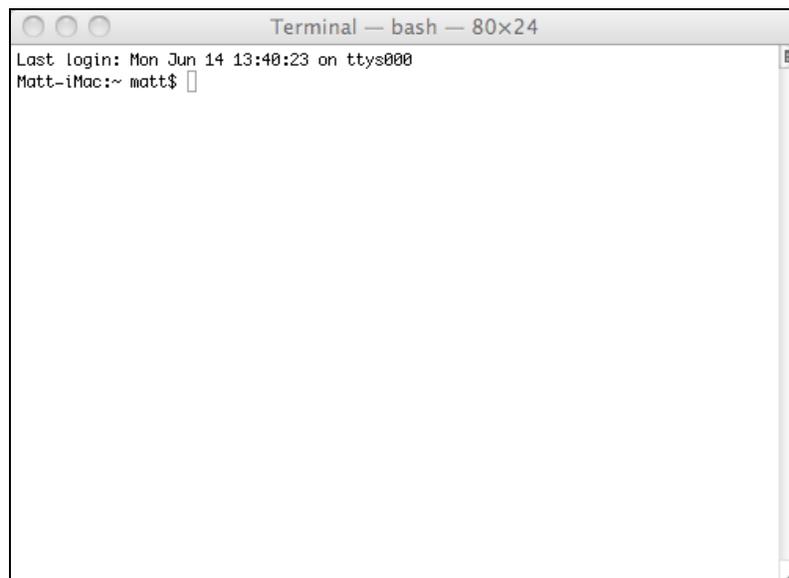
To aid in diagnostic support of the VUIer program, an alternate means of starting the program is available. This method is not routinely used but is available to aid in support calls to Cybergenetics.

First, the user opens a Terminal window by selecting the Terminal icon (Figure 58) from the Dock.



**Figure 58.** *Terminal icon.*

A blank Terminal window opens (Figure 59), displaying the computer's name and a command prompt.

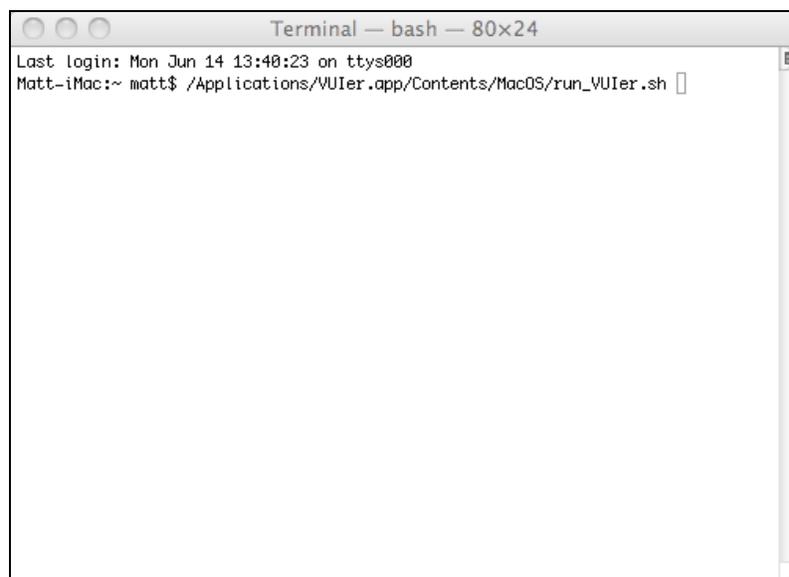


**Figure 59.** A blank Terminal window.

In the Terminal window, the user copy and pastes the path:

```
/Applications/VUIer.app/Contents/MacOS/run_VUIer.sh
```

And then hits the enter key (Figure 60).



**Figure 60.** A Terminal 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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## 7.5 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.