TrueAllele® VUIer™

Getting Started

Cybergenetics

TrueAllele® VUIer™: Getting Started

The TrueAllele® Technology is protected by United States patents 5,541,067, 5,580,728, 5,876,933, 6,054,268, 6,750,011, 6,807,490, 8,898,021, 9,708,642 and by European patent 1,229,135.

Document prepared on November 29, 2017 for VUIer™ software release 2017.

Cybergenetics
info@cybgen.com
www.cybgen.com
160 North Craig Street
Suite 210
Pittsburgh, PA 15213

Table of Contents

1 Overview

The Getting Started Manual covers installing and upgrading the TrueAllele® Casework server and 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 Visual User Interface (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.

1.1 DNA Interpretation Process

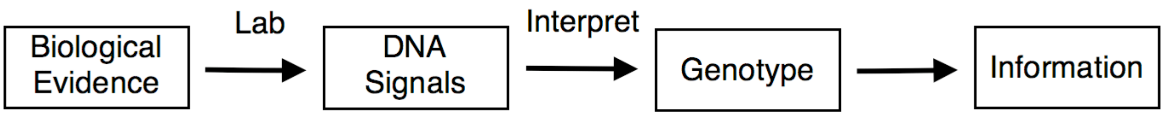


Figure 1. *DNA Interpretation Process*

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.

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.

Newsletters

The best place to begin is with Cybergenetics DNA Investigator™ 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.

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.

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.

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 VUIer version.

Cloud

This VUIer 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 VUIer 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.

1.4 System Requirements

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

For Macintosh computers:
OS: Mac OS X 10.9.5 or higher
CPU: Intel Core 2 or later
RAM: 1 GB RAM
Storage: 1 GB of free hard drive space
Display: Screen resolution of 1920 x 1080 (Minimum resolution: 1024 x 768)
Graphics: Hardware accelerated graphics card supporting OpenGL 3.3 with 1GB GPU memory recommended

For Windows computers:

OS: Windows 7 or later

CPU: Intel Pentium 4 processor or later

RAM: 1 GB RAM

Storage: 1 GB of free hard drive space

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

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

2 Software Installation (Macintosh)

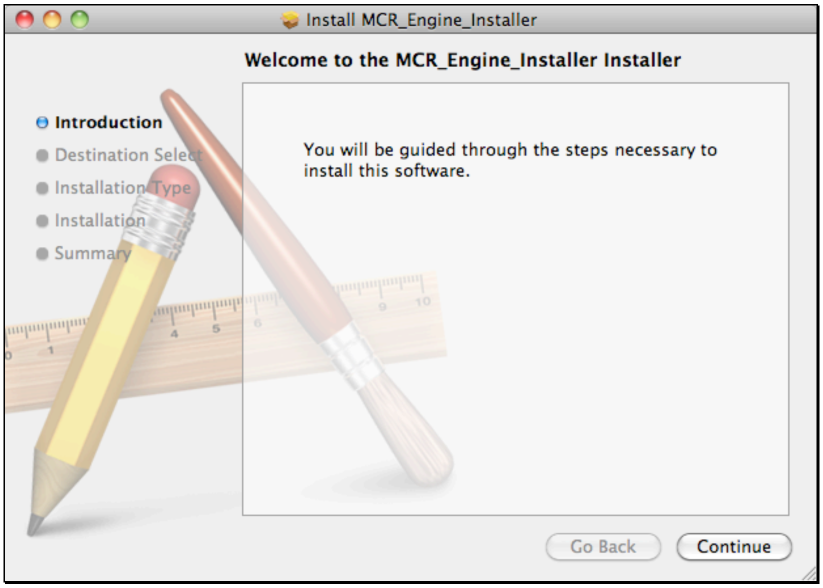
This section walks through the TrueAllele VUIer installation for a Macintosh computer. A complete TrueAllele Casework installation package includes the MCR Engine, the Analyze module of the VUIer software, and the VUIer software itself. Cybergenetics supplies each part of the package for the complete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

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 “MCR_Engine_Installer_v85.pkg.zip”, which makes the package file “MCR_Engine_Installer_v85.pkg” available. The analyst then control clicks on the package file and selects Open to begin the installation process.

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

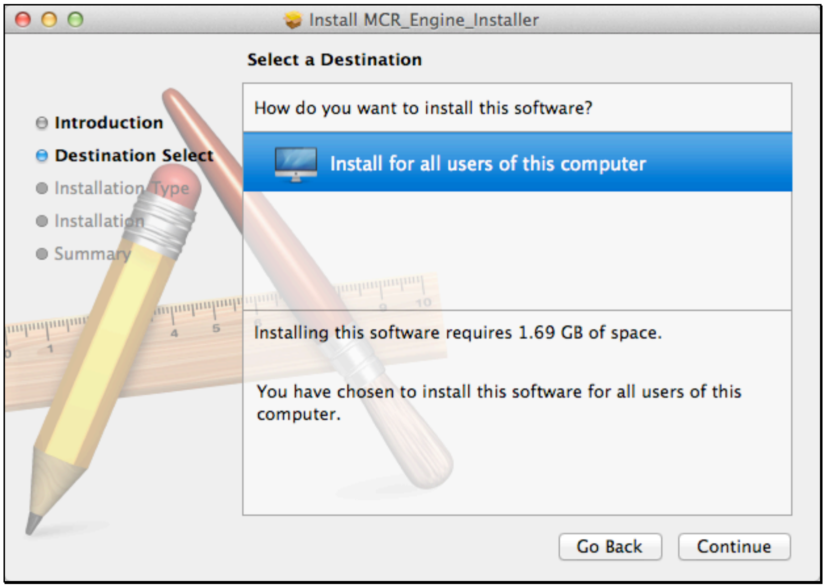

Install MCR_Engine_Installer

Welcome to the MCR_Engine_Installer Installer

You will be guided through the steps necessary to install this software.

Figure 2. *Introduction Screen.*

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


Install MCR_Engine_Installer

Select a Destination

How do you want to install this software?

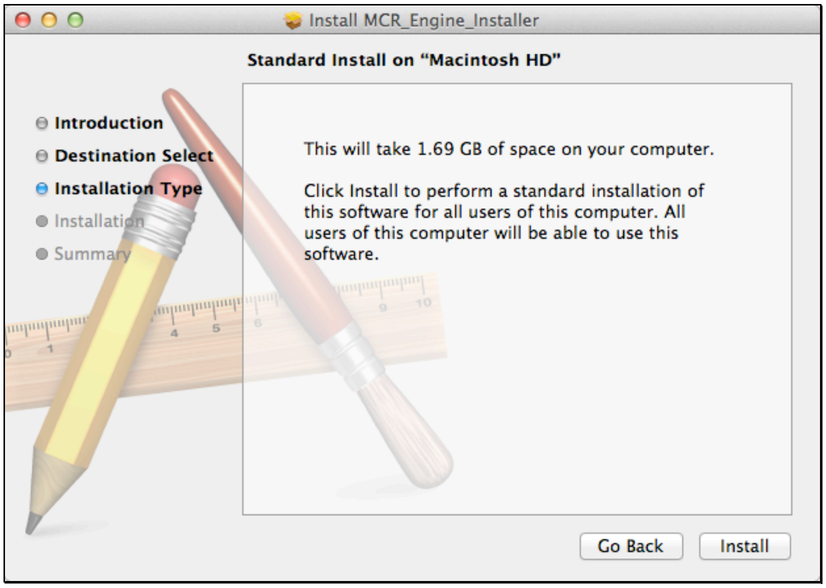
Install for all users of this computer

Installing this software requires 1.69 GB of space.

You have chosen to install this software for all users of this computer.

Figure 3. *Destination Select Screen*

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

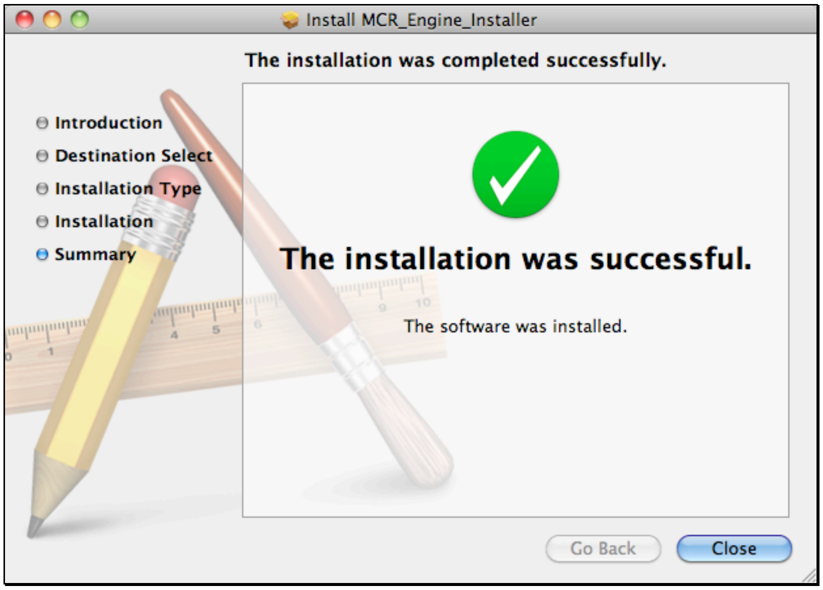


This will take 1.69 GB of space on your computer.

Click Install to perform a standard installation of this software for all users of this computer. All users of this computer will be able to use this software.

Figure 4. *Standard Install.*

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



The installation was completed successfully.

The installation was successful.

The software was installed.

Figure 5. *Installation complete.*

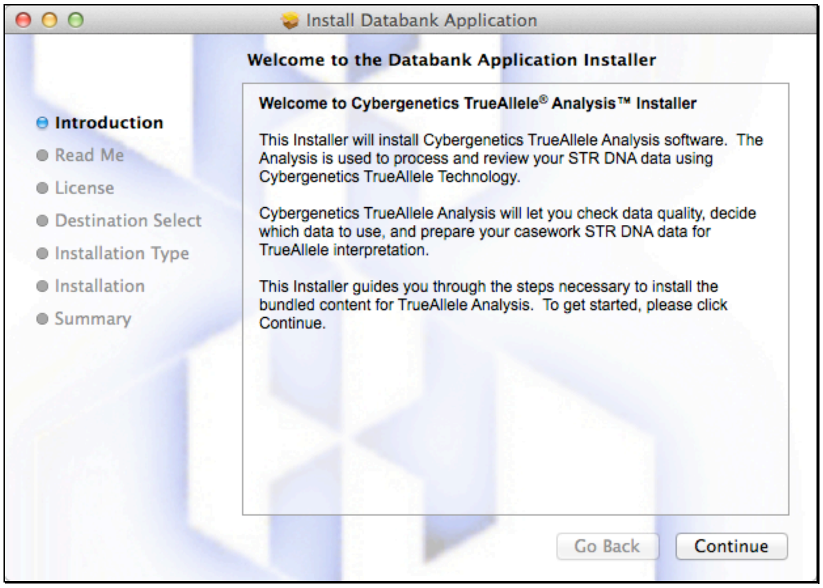
2.2 Analyze

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 6), selecting 'Continue' advances to the next screen.



Welcome to the Databank Application Installer

Welcome to Cybergenetics TrueAllele® Analysis™ Installer

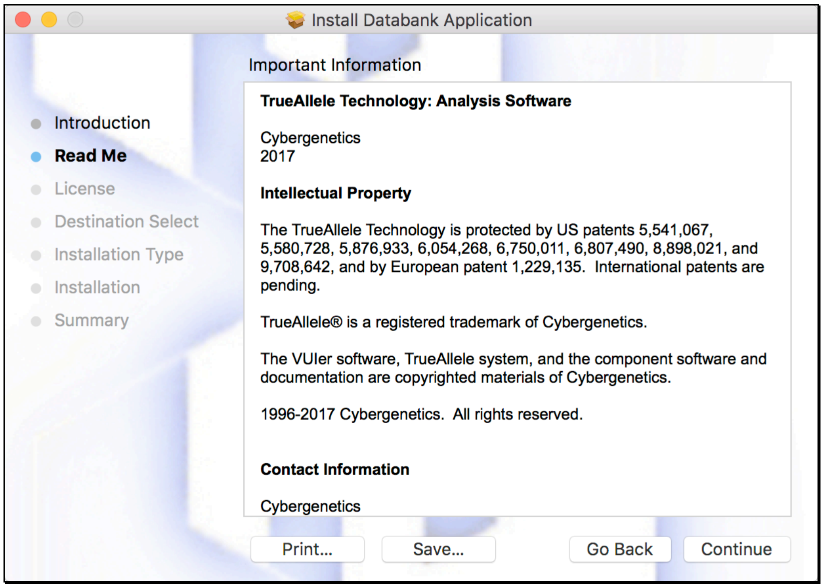
This Installer will install Cybergenetics TrueAllele Analysis software. The Analysis is used to process and review your STR DNA data using Cybergenetics TrueAllele Technology.

Cybergenetics TrueAllele Analysis will let you check data quality, decide which data to use, and prepare your casework STR DNA data for TrueAllele interpretation.

This Installer guides you through the steps necessary to install the bundled content for TrueAllele Analysis. To get started, please click Continue.

Figure 6. *Introduction Screen.*

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



Important Information

TrueAllele Technology: Analysis Software

Cybergenetics
2017

Intellectual Property

The TrueAllele Technology is protected by US patents 5,541,067, 5,580,728, 5,876,933, 6,054,268, 6,750,011, 6,807,490, 8,898,021, and 9,708,642, and by European patent 1,229,135. International patents are pending.

TrueAllele® is a registered trademark of Cybergenetics.

The VUIer software, TrueAllele system, and the component software and documentation are copyrighted materials of Cybergenetics.

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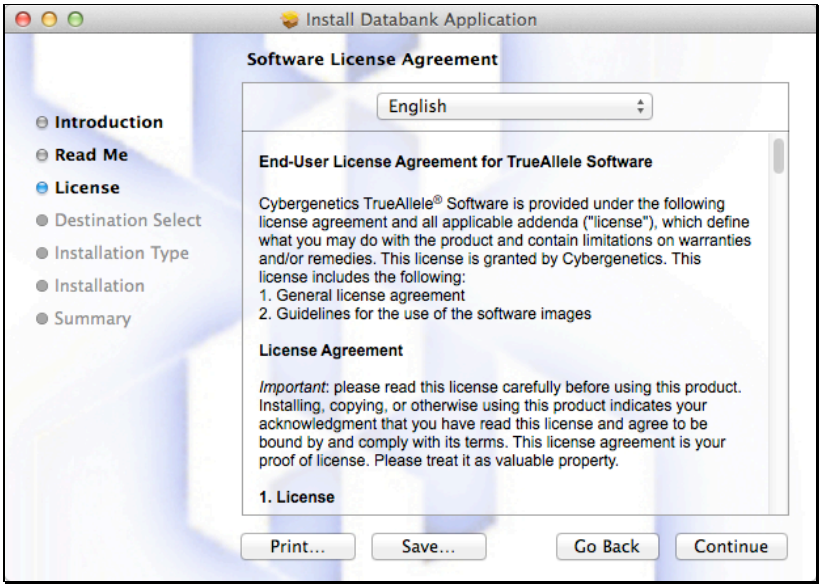
Contact Information

Cybergenetics

Figure 7. *Read Me*.

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



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End-User License Agreement for TrueAllele Software

Cybergenetics TrueAllele® Software is provided under the following license agreement and all applicable addenda ("license"), which define what you may do with the product and contain limitations on warranties and/or remedies. This license is granted by Cybergenetics. This license includes the following:
1. General license agreement
2. Guidelines for the use of the software images

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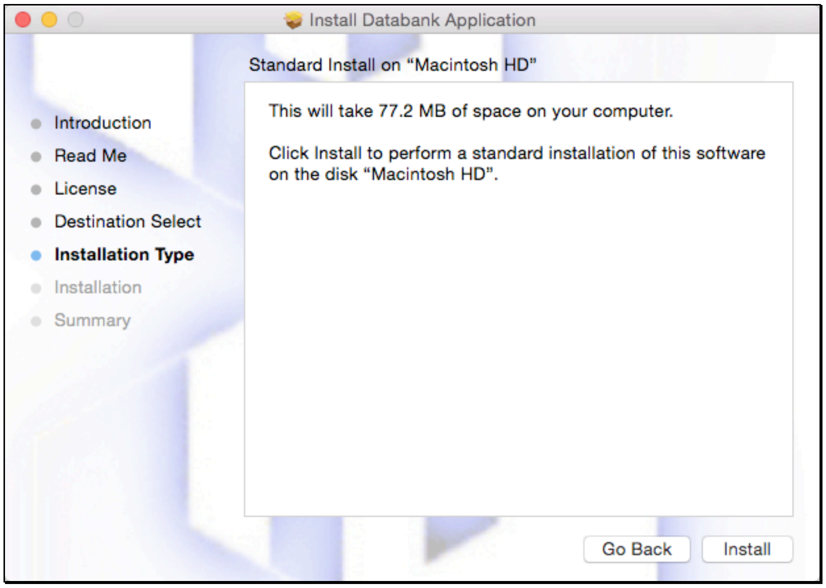
1. License

Figure 8. *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. The analyst begins installation by selecting 'Install' (Figure 9). When prompted, the administrator user name and password is entered.



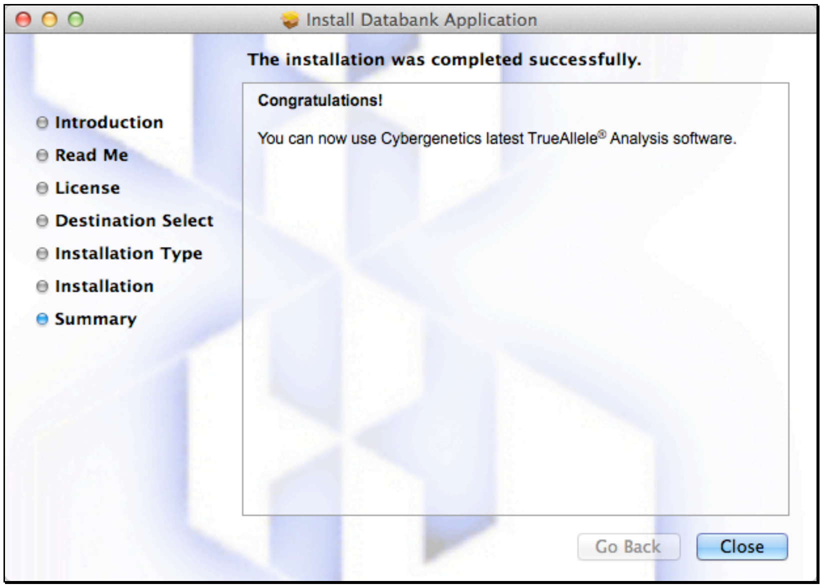
Standard Install on "Macintosh HD"

This will take 77.2 MB of space on your computer.

Click Install to perform a standard installation of this software on the disk "Macintosh HD".

Figure 9. *Standard Install*.

After the installation is complete, selecting 'Close' finishes the process (Figure 10).



The installation was completed successfully.

Congratulations!

You can now use Cybergenetics latest TrueAllele® Analysis software.

Figure 10. *Installation complete*.

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

User Environment

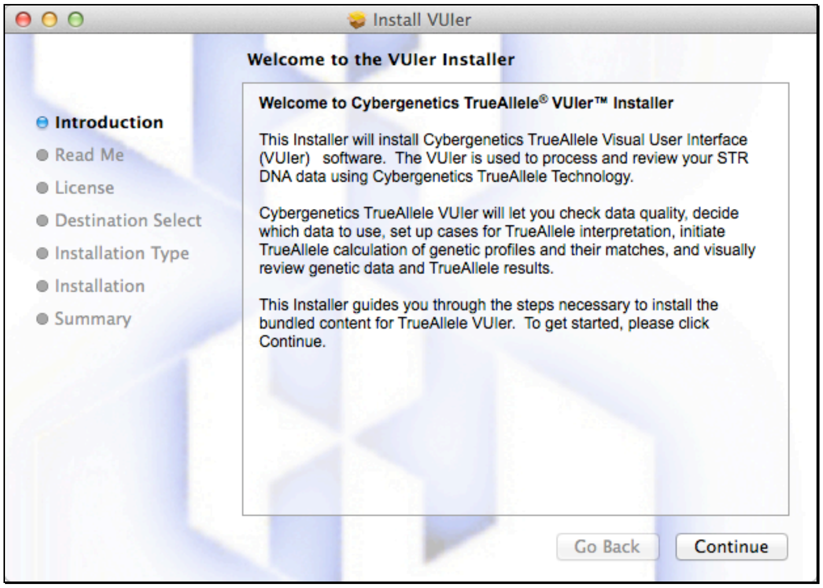
The user environment includes all necessary templates and settings for processing the data in Analyze and is contained in a 'trueallele' folder. After installation, the 'trueallele' folder appears in the Documents folder of the user account. For example, if a user is logged in as 'DNA', the 'trueallele'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

2.3 VUIer

The VUIer software allows the analyst to upload and ask questions of the case data and then review the answers produced by the TrueAllele computer. If VUIer 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 VUIer, if necessary.

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

On the introduction screen (Figure 11), selecting ‘Continue’ advances to the next screen.



Welcome to the VUIer Installer

Welcome to Cybergenetics TrueAllele® VUIer™ Installer

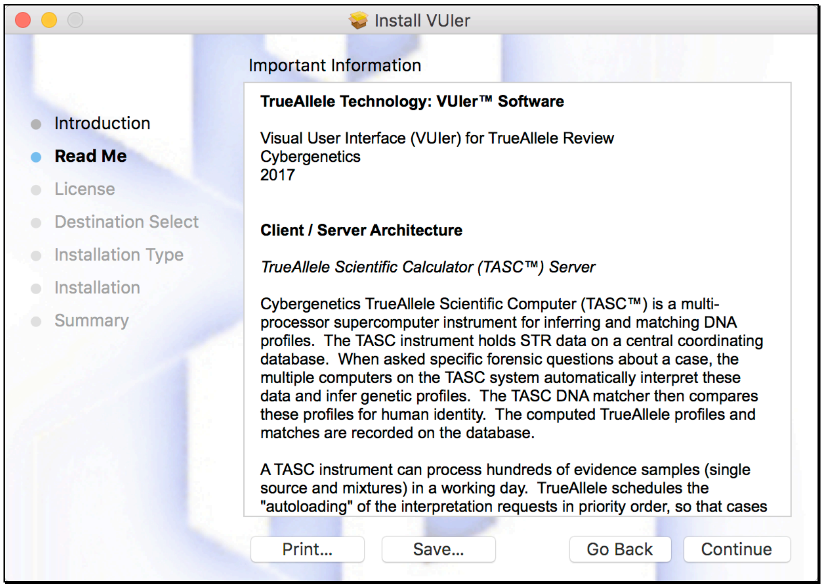
This Installer will install Cybergenetics TrueAllele Visual User Interface (VUIer) software. The VUIer is used to process and review your STR DNA data using Cybergenetics TrueAllele Technology.

Cybergenetics TrueAllele VUIer will let you check data quality, decide which data to use, set up cases for TrueAllele interpretation, initiate TrueAllele calculation of genetic profiles and their matches, and visually review genetic data and TrueAllele results.

This Installer guides you through the steps necessary to install the bundled content for TrueAllele VUIer. To get started, please click Continue.

Figure 11. *Introduction Screen.*

The next screen contains a Read Me file for review (Figure 12). After reading the file, the analyst selects ‘Continue’ to advance to the next screen.



Important Information

TrueAllele Technology: VUIer™ Software

Visual User Interface (VUIer) for TrueAllele Review
Cybergenetics
2017

Client / Server Architecture

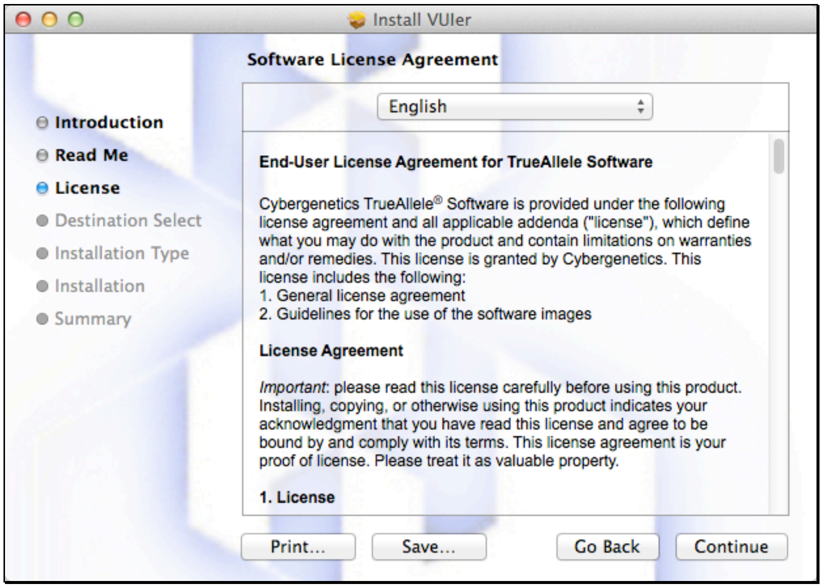
TrueAllele Scientific Calculator (TASC™) Server

Cybergenetics TrueAllele Scientific Computer (TASC™) is a multi-processor supercomputer instrument for inferring and matching DNA profiles. The TASC instrument holds STR data on a central coordinating database. When asked specific forensic questions about a case, the multiple computers on the TASC system automatically interpret these data and infer genetic profiles. The TASC DNA matcher then compares these profiles for human identity. The computed TrueAllele profiles and matches are recorded on the database.

A TASC instrument can process hundreds of evidence samples (single source and mixtures) in a working day. TrueAllele schedules the "autoloading" of the interpretation requests in priority order, so that cases

Figure 12. *Read Me*.

Next is the license agreement (Figure 13). After selecting ‘Continue’, a prompt appears to confirm agreement with the license. The analyst proceeds by selecting ‘Agree’.



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1. General license agreement
2. Guidelines for the use of the software images

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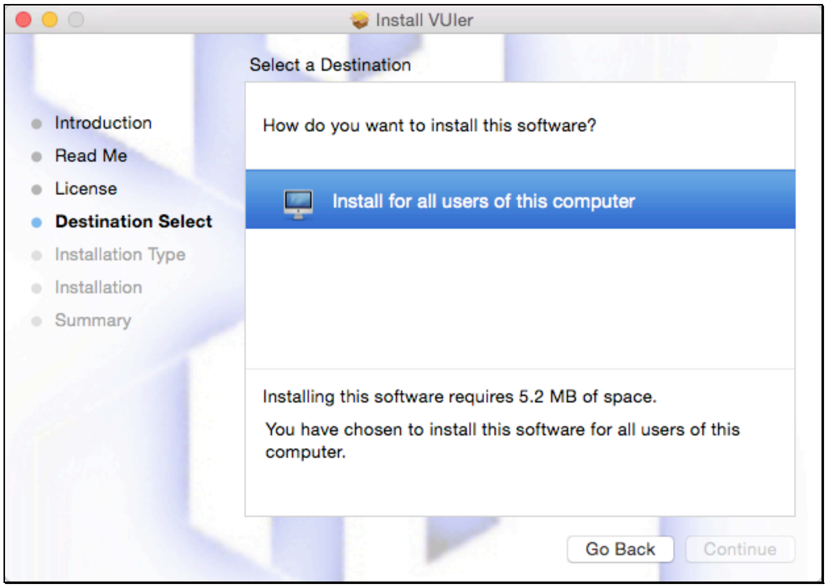
1. License

Figure 13. *License Agreement*.

If prompted, the analyst selects a destination to install the software in the *Destination Select* window (Figure 14). Most likely this installation will be for all users of the computer.



Select a Destination

How do you want to install this software?

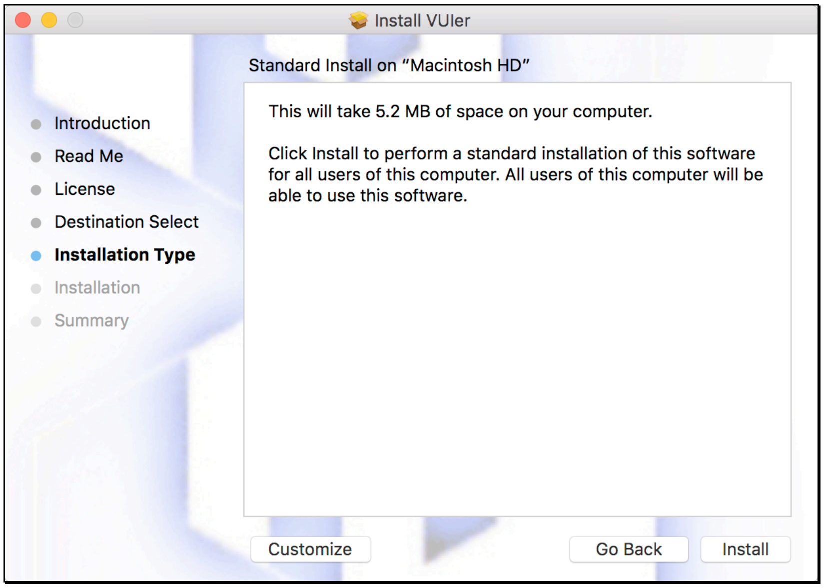
Install for all users of this computer

Installing this software requires 5.2 MB of space.

You have chosen to install this software for all users of this computer.

Figure 14. *Destination Select Screen*

A standard install is automatically available (Figure 15). The analyst begins the installation by selecting ‘Install’. When prompted, the administrator user name and password is entered.



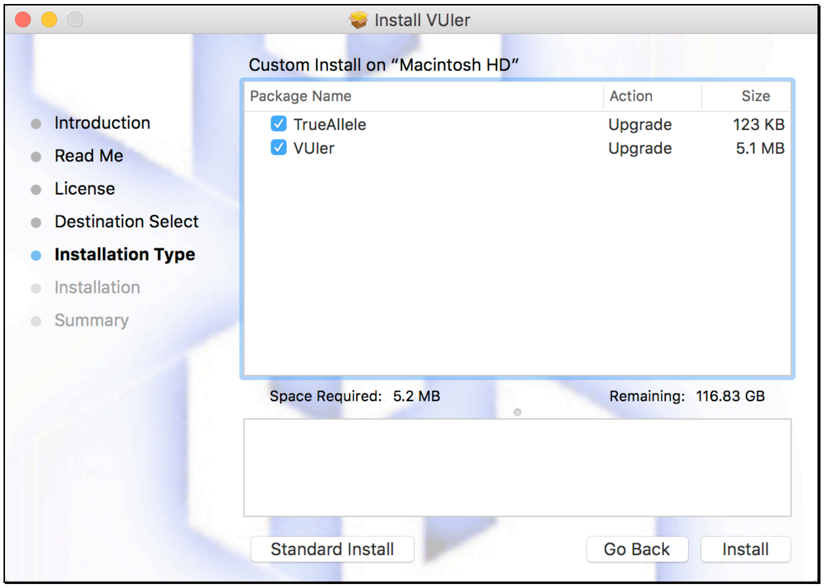
Standard Install on "Macintosh HD"

This will take 5.2 MB of space on your computer.

Click Install to perform a standard installation of this software for all users of this computer. All users of this computer will be able to use this software.

Figure 15. *Standard Install*.

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 analyst is able to deselect any of the items that they do note wish to install when installing/upgrading VUIer. This action will affect the installation of some required user files.



Custom Install on "Macintosh HD"

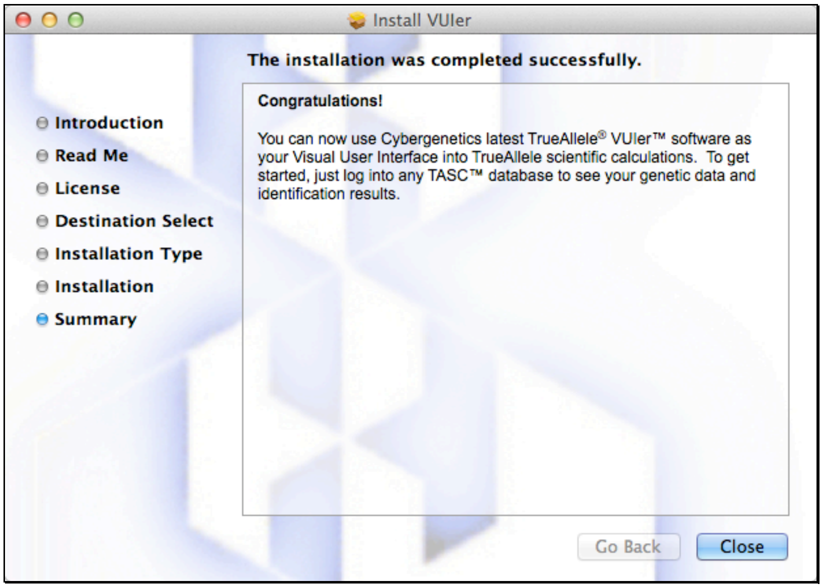
Package Name	Action	Size
☑ TrueAllele	Upgrade	123 KB
☑ VUIer	Upgrade	5.1 MB

Space Required: 5.2 MB

Remaining: 116.83 GB

Figure 16. *Custom Install*.

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



The installation was completed successfully.

Congratulations!

You can now use Cybergenetics latest TrueAllele® VUIer™ software as your Visual User Interface into TrueAllele scientific calculations. To get started, just log into any TASC™ database to see your genetic data and identification results.

Figure 17. *Installation complete*.

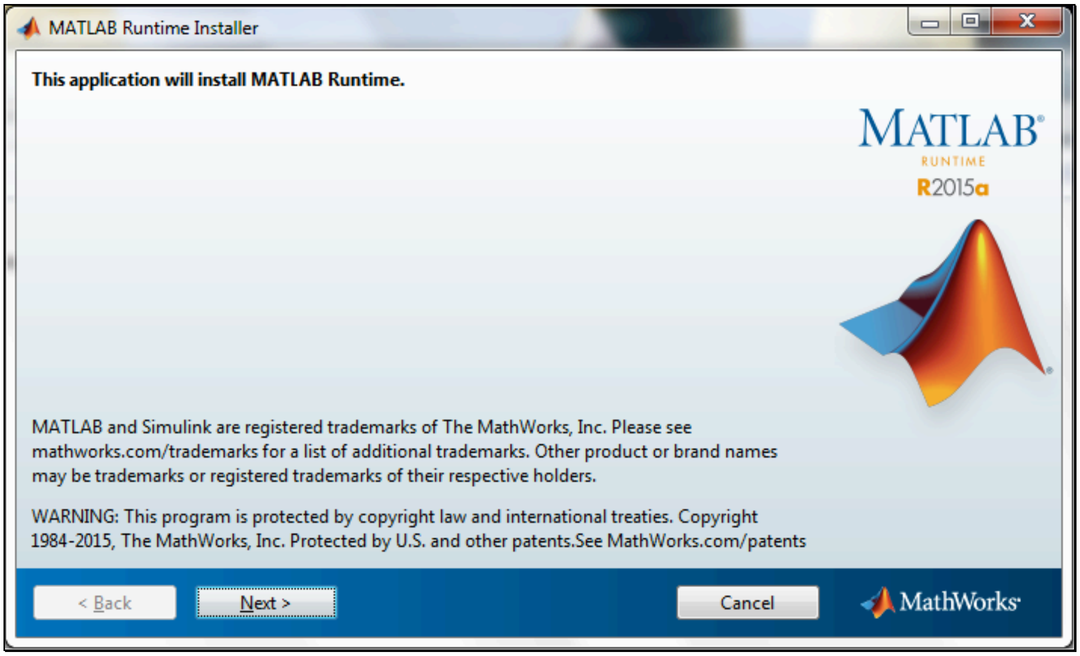
3 Installation (Windows)

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.

3.1 MCR Engine

An analyst begins by expanding the zip file “MCR_Engine_Installer_v85.exe.zip”, which makes the executable file “MCR_Engine_Installer_v85.exe” available. The analyst then double clicks on the executable file to begin the installation process.

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



This application will install MATLAB Runtime.

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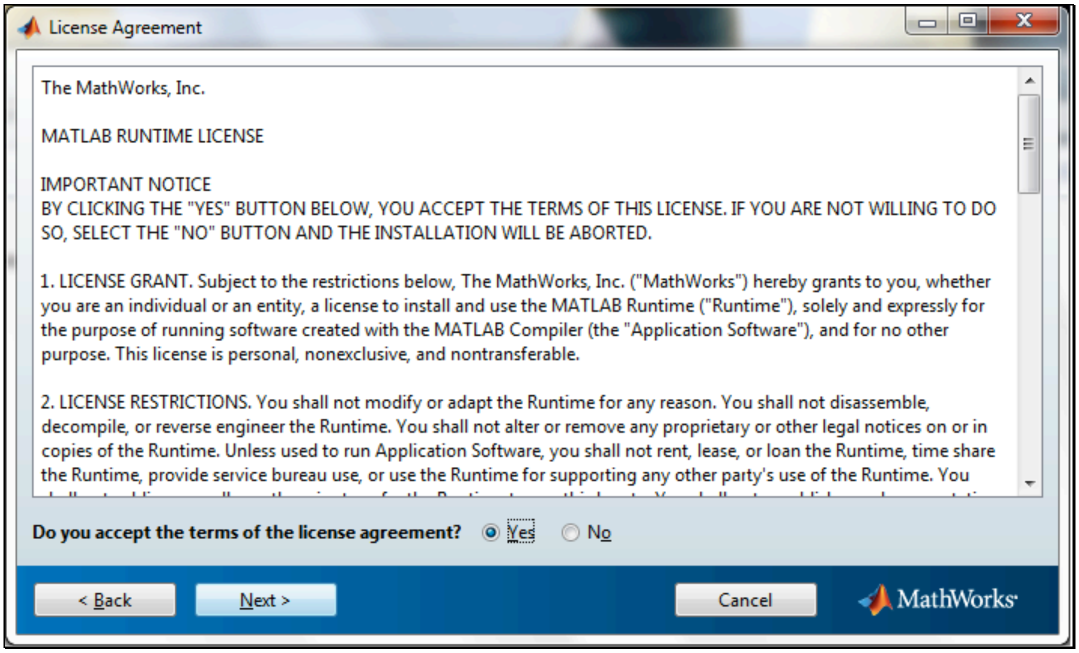
Figure 18. *Introduction Screen.*

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.



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MATLAB RUNTIME LICENSE

IMPORTANT NOTICE
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1. LICENSE GRANT. Subject to the restrictions below, The MathWorks, Inc. ("MathWorks") hereby grants to you, whether you are an individual or an entity, a license to install and use the MATLAB Runtime ("Runtime"), solely and expressly for the purpose of running software created with the MATLAB Compiler (the "Application Software"), and for no other purpose. This license is personal, nonexclusive, and nontransferable.

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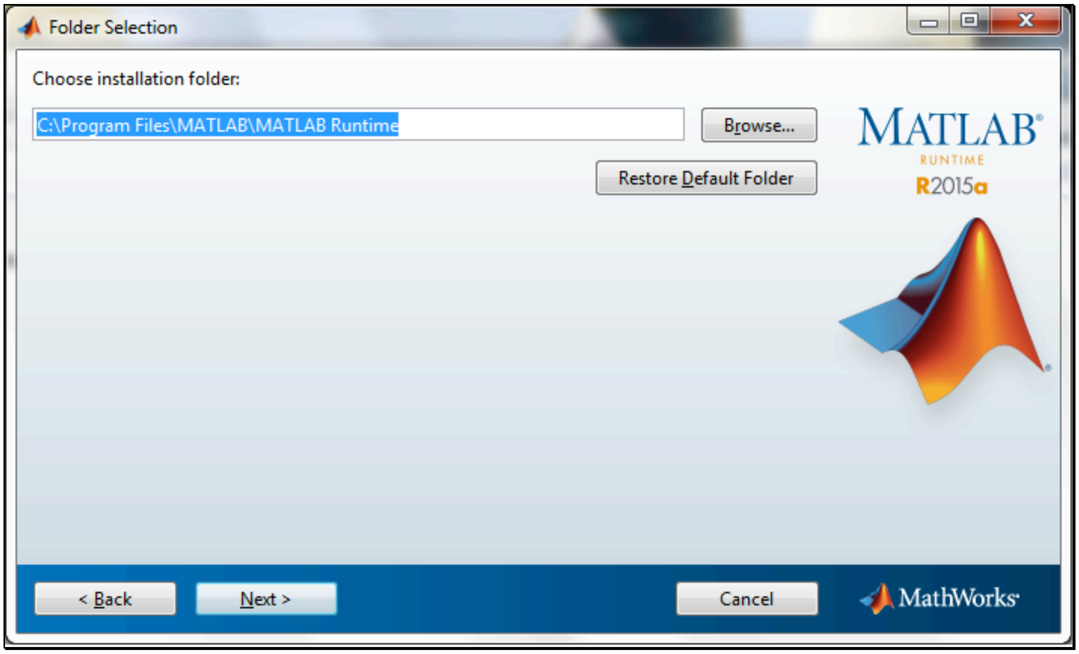
Do you accept the terms of the license agreement? ● Yes ○ No

Figure 19. *License Agreement.*

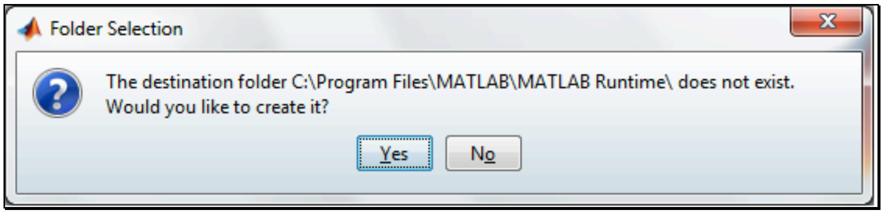
Next, the analyst clicks ‘Next’ in the *Folder Selection* screen to install the software in the default destination folder (Figure 20).



Choose installation folder: C:\Program Files\MATLAB\MATLAB Runtime

Figure 20. *Folder Selection Screen.*

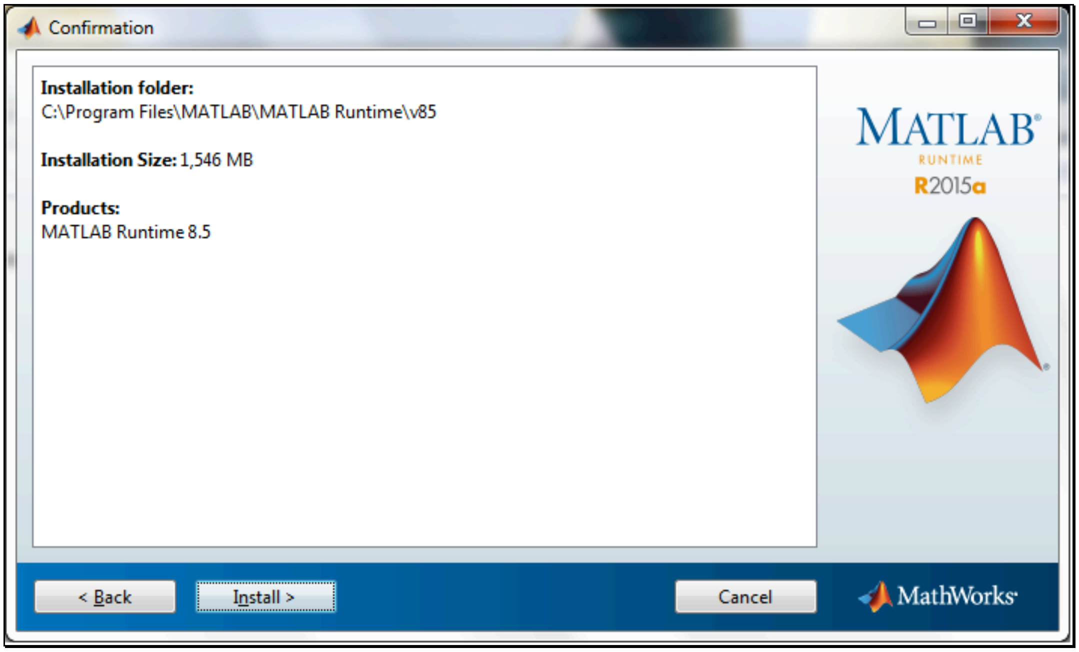
If prompted, the analyst confirms the creation of the destination folder by selecting ‘Yes’ (Figure 21).



The destination folder C:\Program Files\MATLAB\MATLAB Runtime\ does not exist. Would you like to create it?

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.



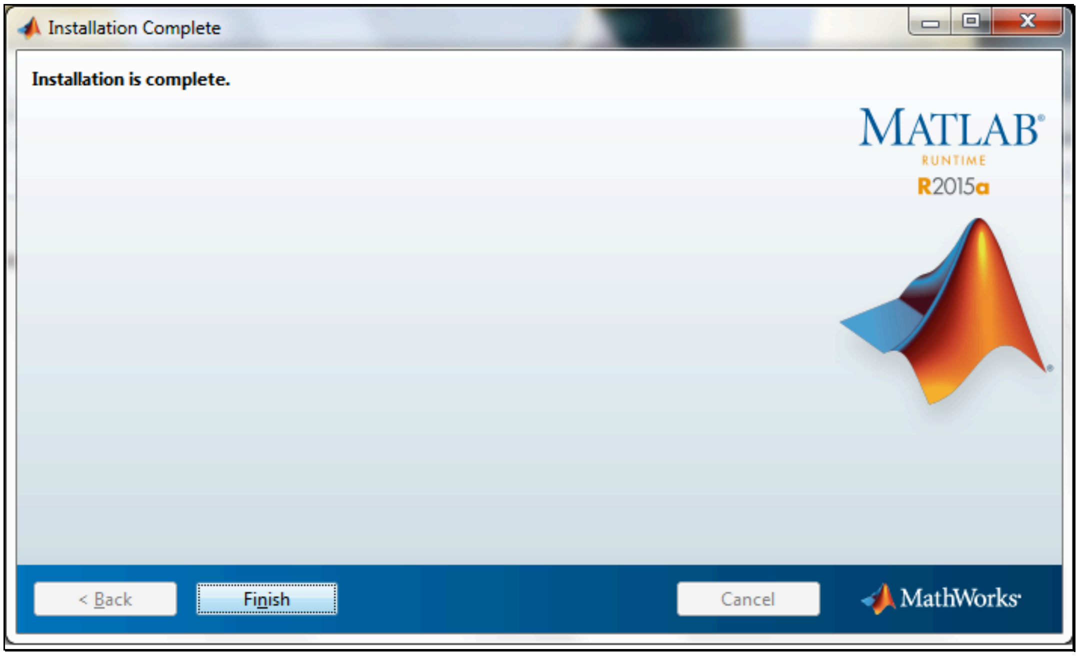
Installation folder:
C:\Program Files\MATLAB\MATLAB Runtime\v85

Installation Size: 1,546 MB

Products:
MATLAB Runtime 8.5

Figure 22. *Confirmation Window.*

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



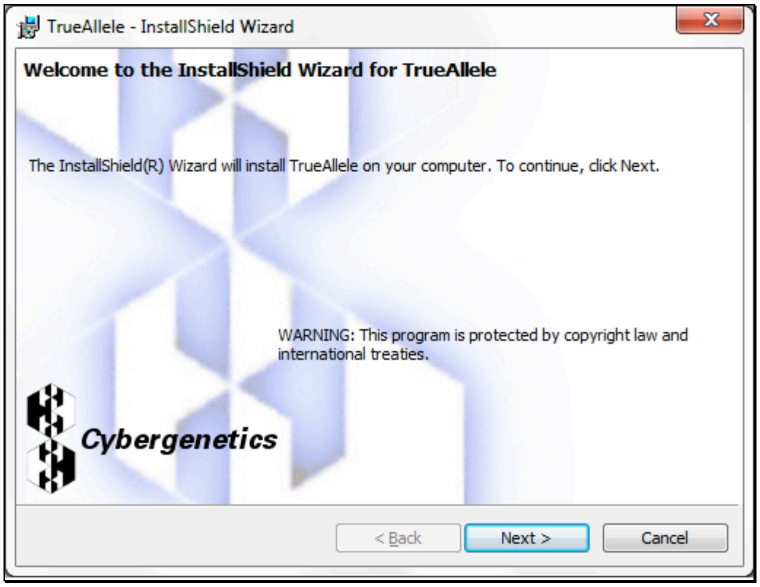
Installation is complete.

Figure 23. *Installation Complete Screen.*

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.



TrueAllele - InstallShield Wizard

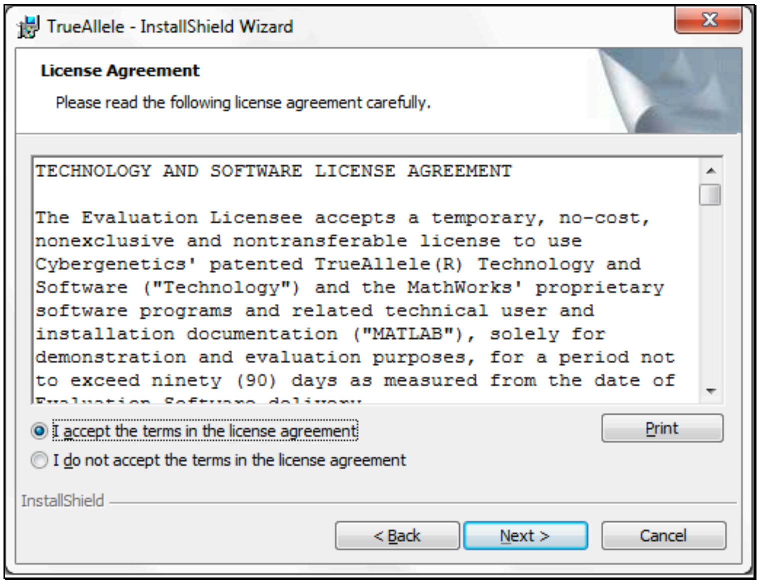
Welcome to the InstallShield Wizard for TrueAllele

The InstallShield(R) Wizard will install TrueAllele on your computer. To continue, click Next.

WARNING: This program is protected by copyright law and international treaties.

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.



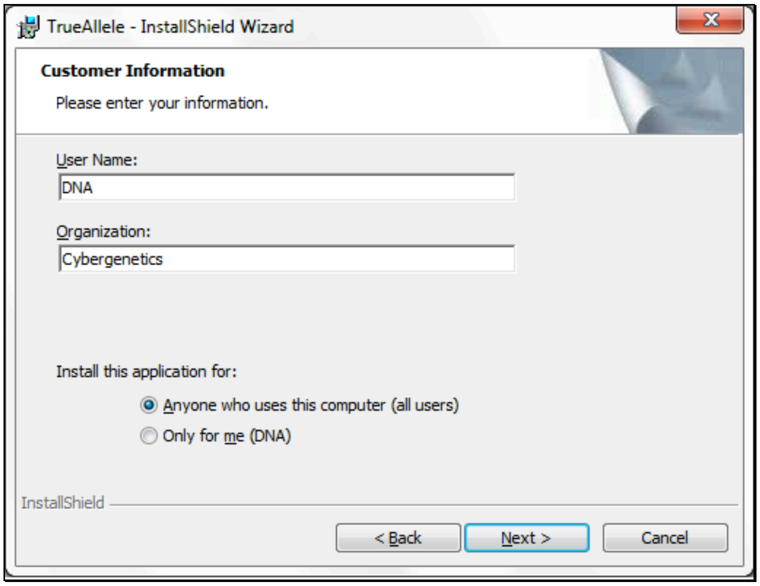
```
TECHNOLOGY AND SOFTWARE LICENSE AGREEMENT

The Evaluation Licensee accepts a temporary, no-cost,
nonexclusive and nontransferable license to use
Cybergenetics' patented TrueAllele(R) Technology and
Software ("Technology") and the MathWorks' proprietary
software programs and related technical user and
installation documentation ("MATLAB"), solely for
demonstration and evaluation purposes, for a period not
to exceed ninety (90) days as measured from the date of
```

● I accept the terms in the license agreement

○ I do not accept the terms in the license agreement

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.



User Name: DNA

Organization: Cybergenetics

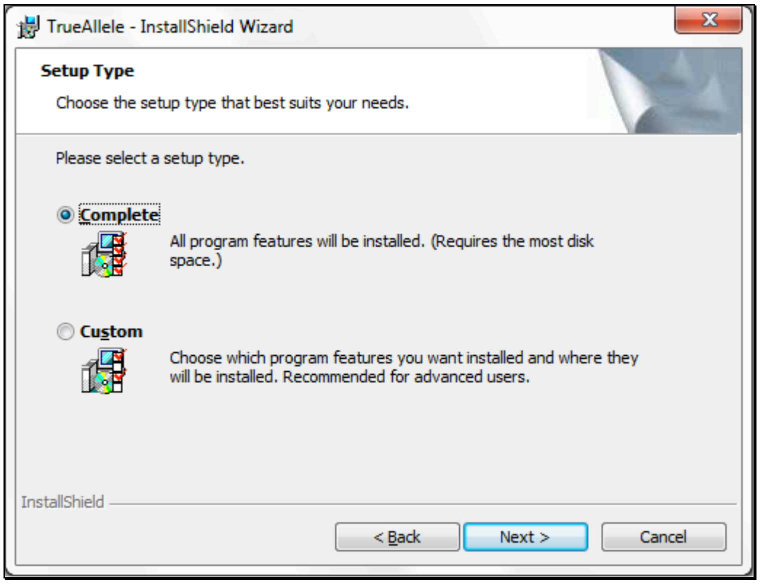
Install this application for:

● Anyone who uses this computer (all users)

○ Only for me (DNA)

Figure 26. *Customer Information Screen.*

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



TrueAllele - InstallShield Wizard

Setup Type

Choose the setup type that best suits your needs.

Please select a setup type.

● **Complete**

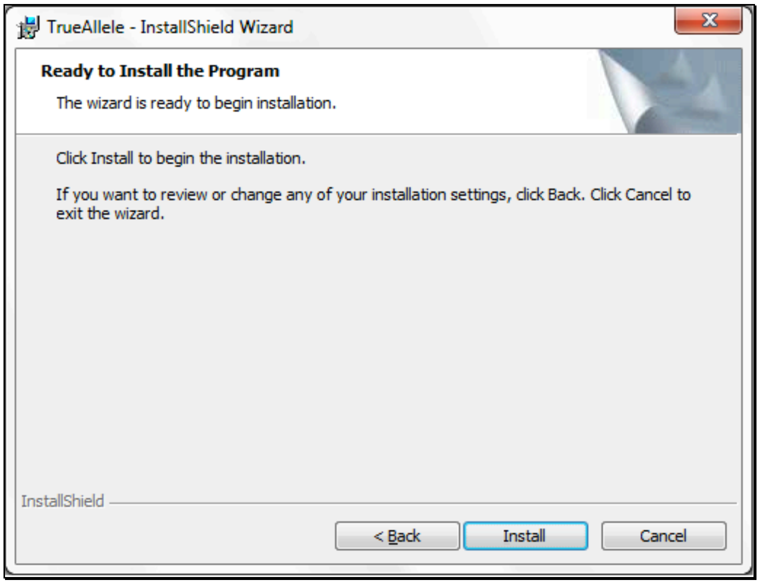
All program features will be installed. (Requires the most disk space.)

○ **Custom**

Choose which program features you want installed and where they will be installed. Recommended for advanced users.

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.



TrueAllele - InstallShield Wizard

Ready to Install the Program

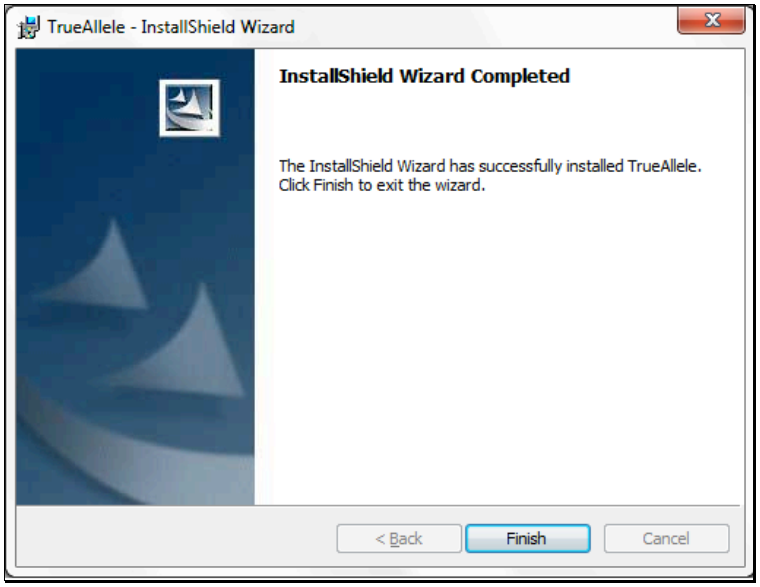
The wizard is ready to begin installation.

Click Install to begin the installation.

If you want to review or change any of your installation settings, click Back. Click Cancel to exit the wizard.

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.



InstallShield Wizard Completed

The InstallShield Wizard has successfully installed TrueAllele.
Click Finish to exit the wizard.

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.

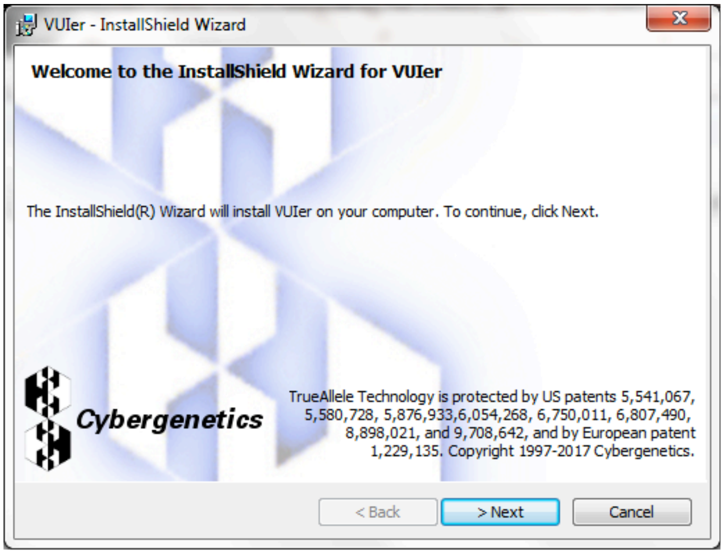
Updating Analyze

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.

3.3 VUIer Software

To install the VUIer software, the analyst starts by expanding the zip file "VUIer_64bit.exe.zip", which makes the package file "VUIer_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.



VUIer - InstallShield Wizard

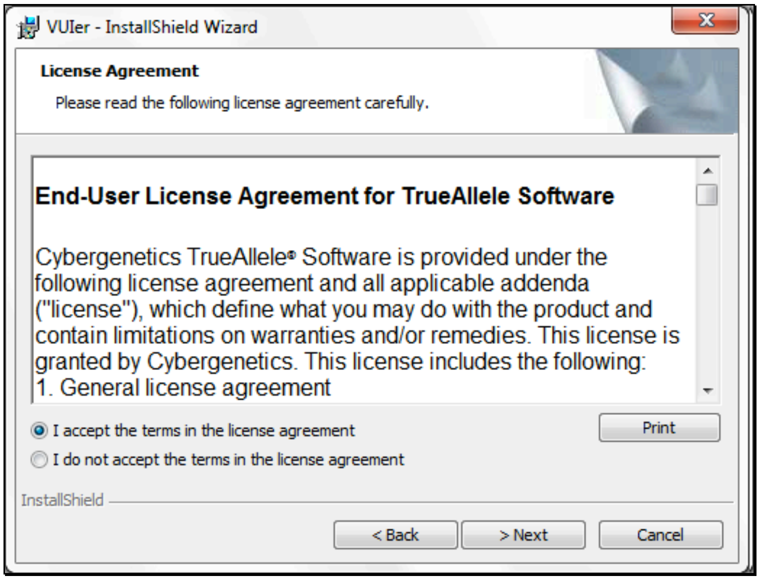
Welcome to the InstallShield Wizard for VUIer

The InstallShield(R) Wizard will install VUIer on your computer. To continue, click Next.

TrueAllele Technology is protected by US patents 5,541,067, 5,580,728, 5,876,933,6,054,268, 6,750,011, 6,807,490, 8,898,021, and 9,708,642, and by European patent 1,229,135. Copyright 1997-2017 Cybergenetics.

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.



License Agreement

Please read the following license agreement carefully.

End-User License Agreement for TrueAllele Software

Cybergenetics TrueAllele® Software is provided under the following license agreement and all applicable addenda ("license"), which define what you may do with the product and contain limitations on warranties and/or remedies. This license is granted by Cybergenetics. This license includes the following:

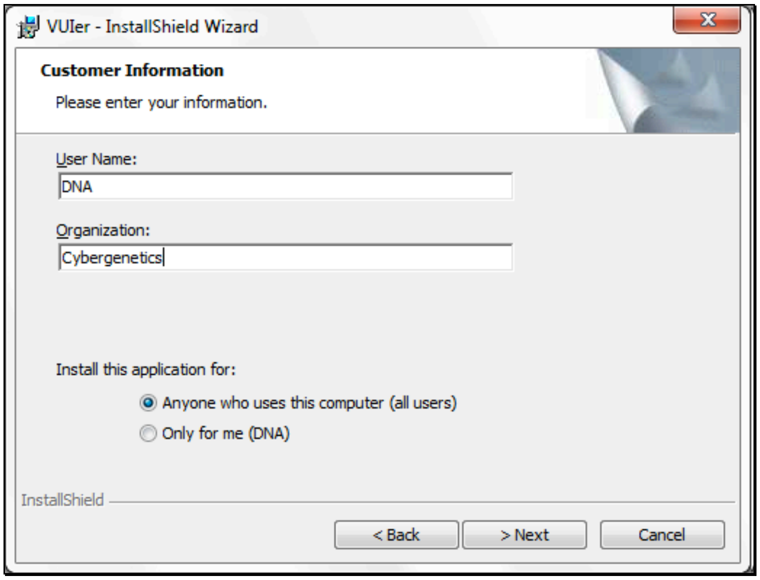
1. General license agreement

● I accept the terms in the license agreement

○ I do not accept the terms in the license agreement

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.



Customer Information

Please enter your information.

User Name: DNA

Organization: Cybergenetics

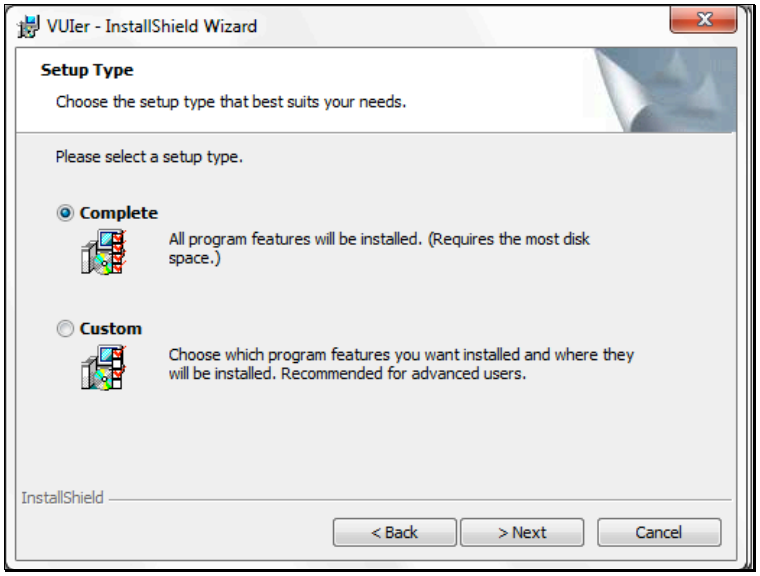
Install this application for:

● Anyone who uses this computer (all users)

○ Only for me (DNA)

Figure 32. *Customer Information Screen.*

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



Setup Type

Choose the setup type that best suits your needs.

Please select a setup type.

● **Complete**

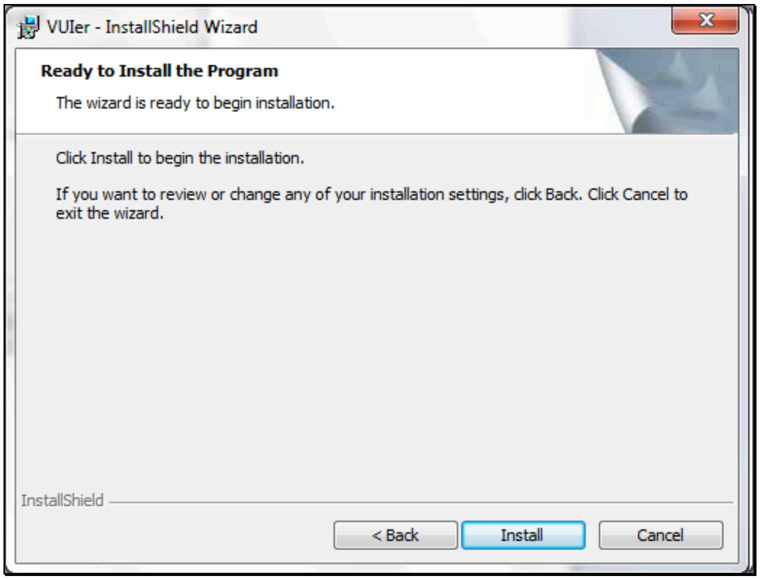
All program features will be installed. (Requires the most disk space.)

○ **Custom**

Choose which program features you want installed and where they will be installed. Recommended for advanced users.

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.



Ready to Install the Program

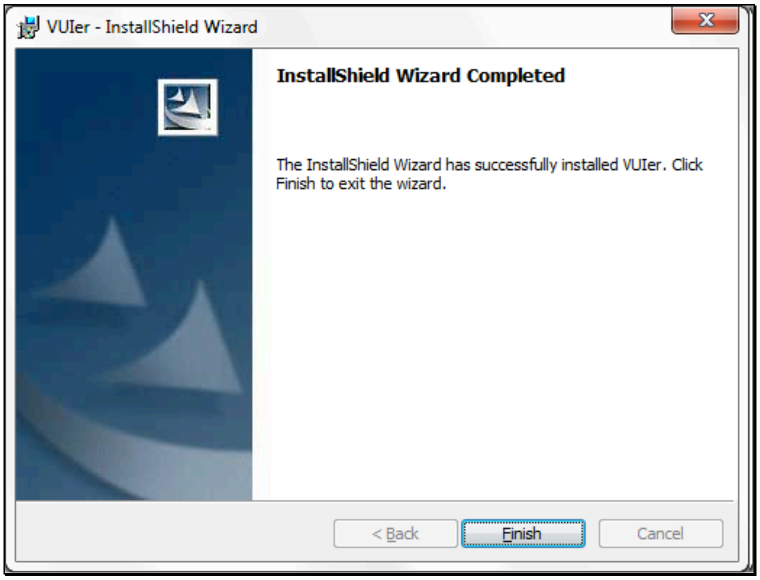
The wizard is ready to begin installation.

Click Install to begin the installation.

If you want to review or change any of your installation settings, click Back. Click Cancel to exit the wizard.

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.



InstallShield Wizard Completed

The InstallShield Wizard has successfully installed VUIer. Click Finish to exit the wizard.

Figure 35. *Installation Complete.*

4 Software Function

This section covers the starting the VUIer 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 VUIer program.

4.1 License

After installing VUIer, 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.

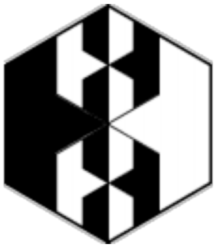


Figure 36. *VUIer icon*.

A valid license key is required to use the VUIer software. Cybergenetics provides this license key. When starting VUIer 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. VUIer will open to the *Module Chooser* after a valid license key is entered.

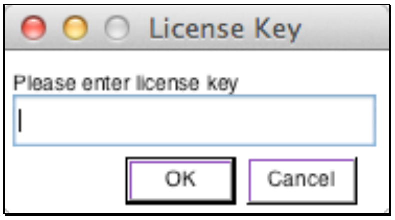


Figure 37. *License key input dialog box*.

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).

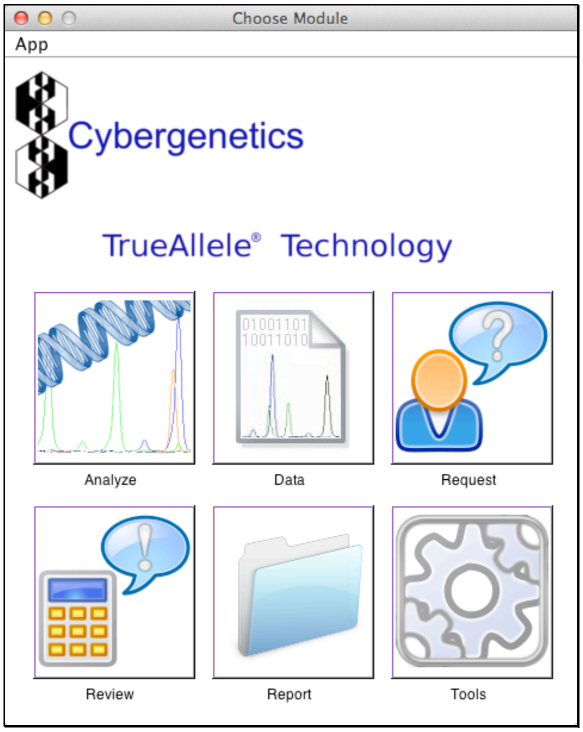


Figure 38. *Full Module Chooser.*

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

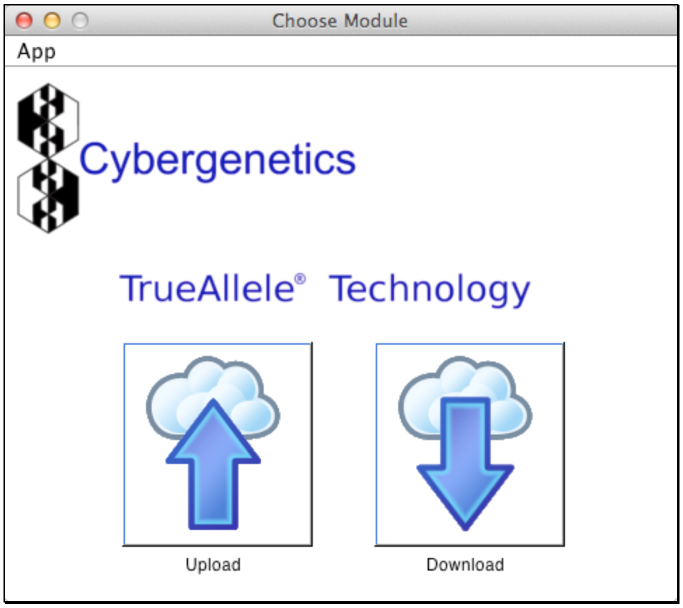


Figure 39. *Cloud Module Chooser.*

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

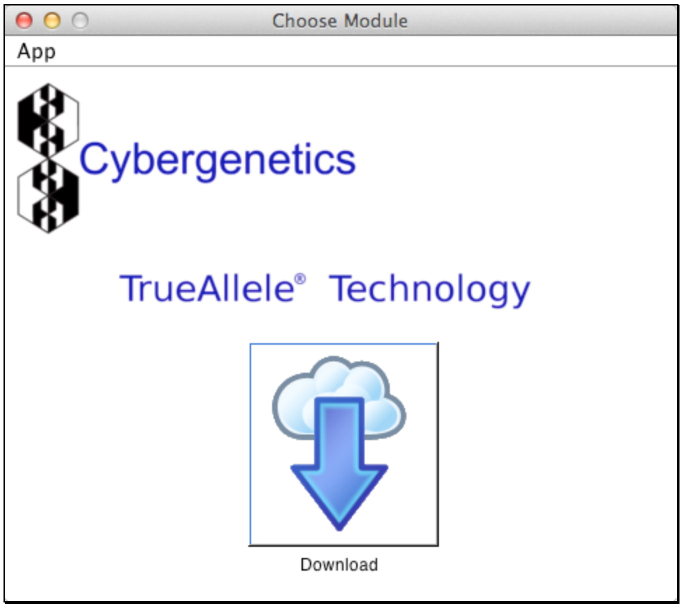


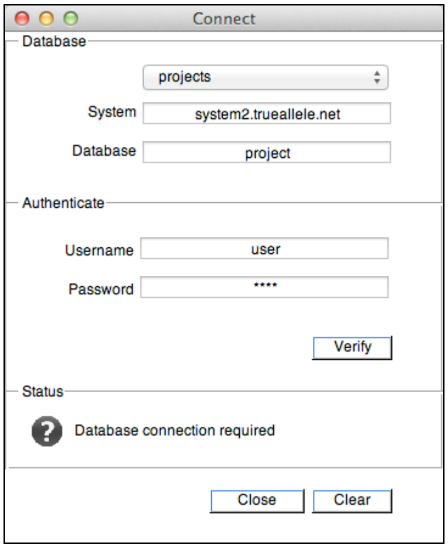
Figure 40. *Read-only Module Chooser.*

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.



Database
projects
System system2.trueallele.net
Database project

Authenticate
Username user
Password ****

Status
Database connection required

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 VUIer 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 VUIer 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 VUIer 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.

5 Network Setup

This section discusses the details regarding network setup for TrueAllele server management.

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.

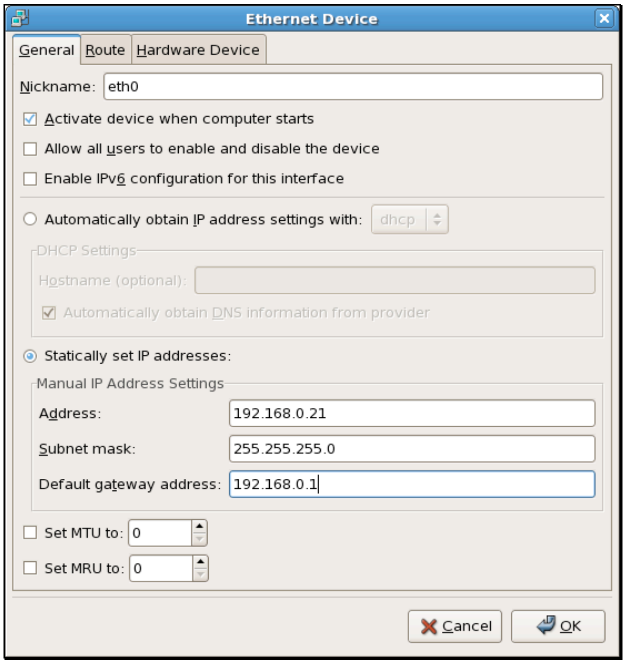
To add the server to the network:

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 42).
- Type IP address, subnet mask and gateway (if necessary) into Ethernet Device dialog that opens. Click OK after all information is entered.



Nickname: eth0

☑ Activate device when computer starts

☐ Allow all users to enable and disable the device

☐ Enable IPv6 configuration for this interface

○ Automatically obtain IP address settings with: dhcp

DHCP Settings

Hostname (optional):

☑ Automatically obtain DNS information from provider

● Statically set IP addresses:

Manual IP Address Settings

Address: 192.168.0.21

Subnet mask: 255.255.255.0

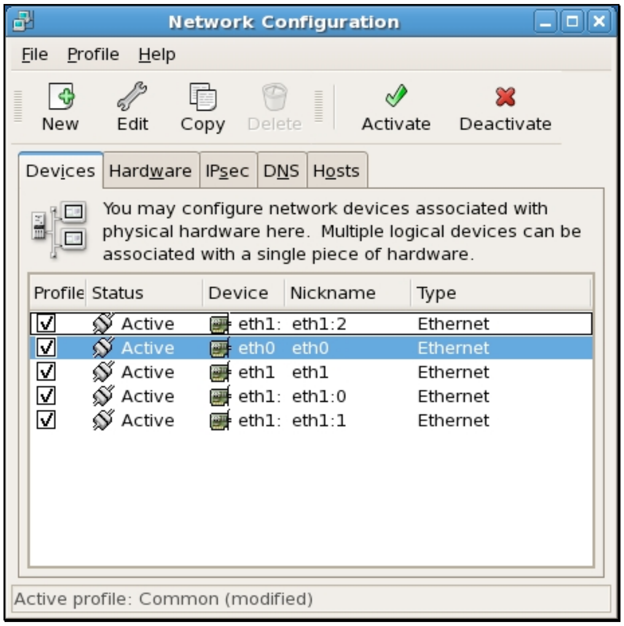
Default gateway address: 192.168.0.1

☐ Set MTU to: 0

☐ Set MRU to: 0

Figure 42. *The Ethernet Device dialog.*

Next, the Network Configuration window opens. Select eth0 from the list and click the Deactivate button to refresh network (Figure 43). If prompted, save changes. Click the Activate button to bring the network back up with the new settings applied.



You may configure network devices associated with physical hardware here. Multiple logical devices can be associated with a single piece of hardware.

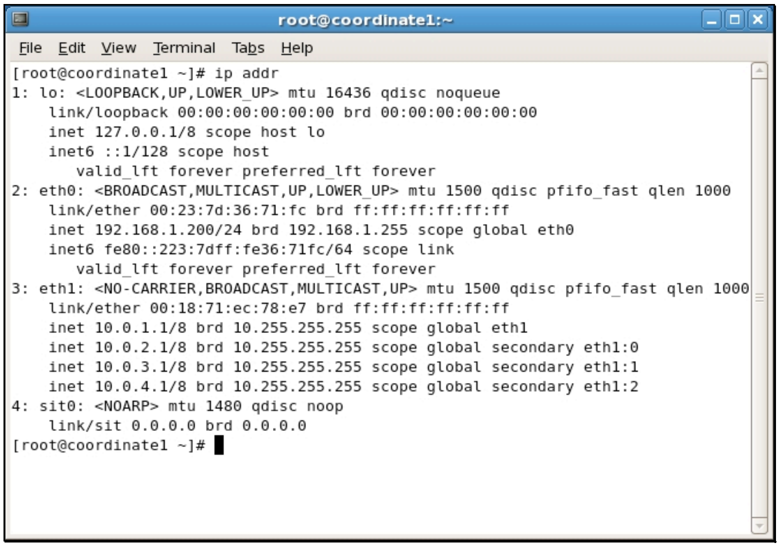
Profile	Status	Device	Nickname	Type
☑	Active	eth1:	eth1:2	Ethernet
☑	Active	eth0	eth0	Ethernet
☑	Active	eth1	eth1	Ethernet
☑	Active	eth1:	eth1:0	Ethernet
☑	Active	eth1:	eth1:1	Ethernet

Active profile: Common (modified)

Figure 43. *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 44).



```
[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 44. *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 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

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.

6.1 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.

6.2 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 45). This will open a New Connection dialog.

Figure 45. *The Open Connection icon.*

Fill out the New Connection dialog with the following parameters (Figure 46):

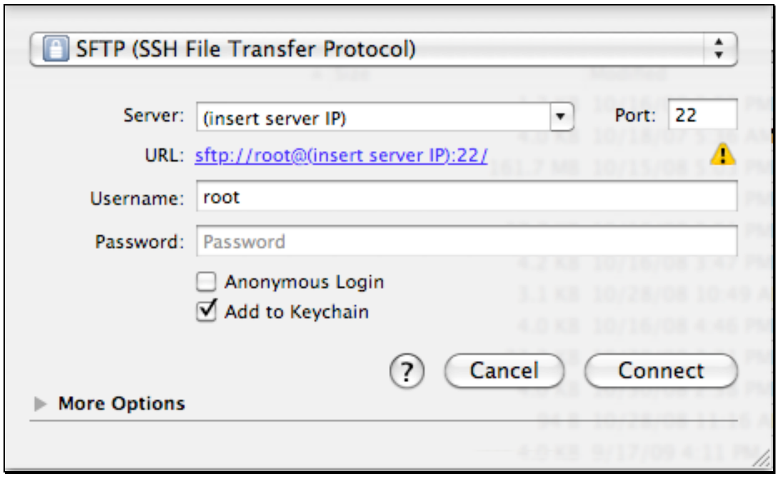
Username: root

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



SFTP (SSH File Transfer Protocol)

Server: (insert server IP)

Port: 22

URL: sftp://root@(insert server IP):22/

Username: root

Password: Password

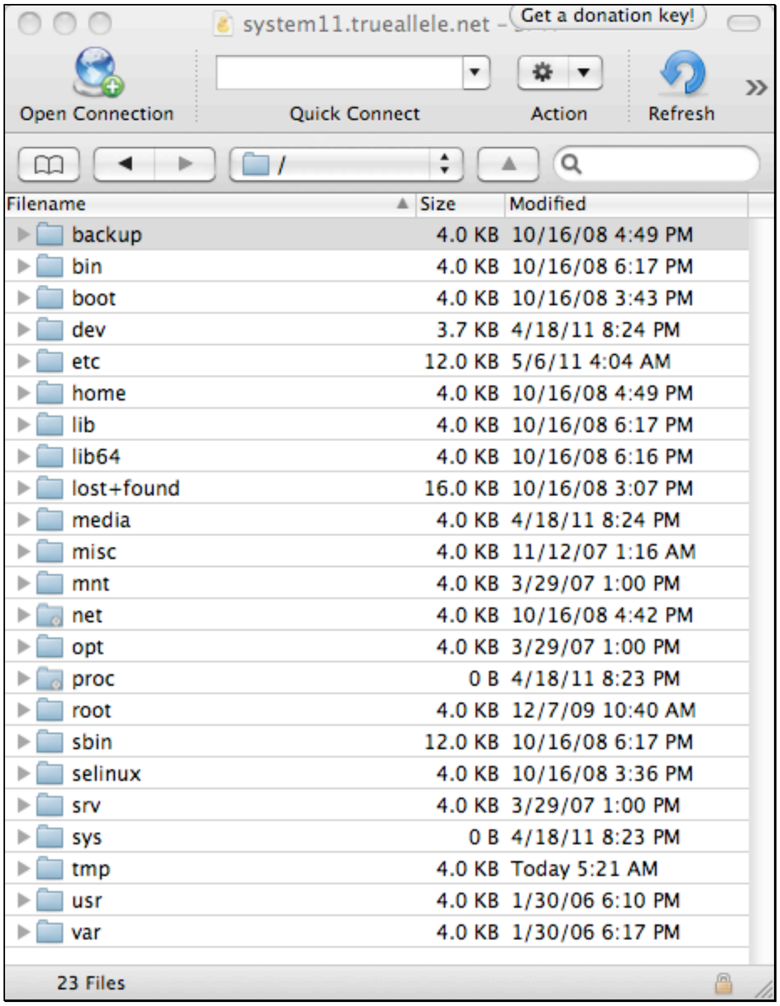
☐ Anonymous Login

☑ Add to Keychain

Figure 46. *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 47) will now display all the directories under the top-level including /backup. Select /backup, and you will see the /download directory. Simply drag and drop the /download directory onto the Mac Desktop to begin copying the complete backup information.



Filename	Size	Modified
backup	4.0 KB	10/16/08 4:49 PM
bin	4.0 KB	10/16/08 6:17 PM
boot	4.0 KB	10/16/08 3:43 PM
dev	3.7 KB	4/18/11 8:24 PM
etc	12.0 KB	5/6/11 4:04 AM
home	4.0 KB	10/16/08 4:49 PM
lib	4.0 KB	10/16/08 6:17 PM
lib64	4.0 KB	10/16/08 6:16 PM
lost+found	16.0 KB	10/16/08 3:07 PM
media	4.0 KB	4/18/11 8:24 PM
misc	4.0 KB	11/12/07 1:16 AM
mnt	4.0 KB	3/29/07 1:00 PM
net	4.0 KB	10/16/08 4:42 PM
opt	4.0 KB	3/29/07 1:00 PM
proc	0 B	4/18/11 8:23 PM
root	4.0 KB	12/7/09 10:40 AM
sbin	12.0 KB	10/16/08 6:17 PM
selinux	4.0 KB	10/16/08 3:36 PM
srv	4.0 KB	3/29/07 1:00 PM
sys	0 B	4/18/11 8:23 PM
tmp	4.0 KB	Today 5:21 AM
usr	4.0 KB	1/30/06 6:10 PM
var	4.0 KB	1/30/06 6:17 PM

23 Files

Figure 47. *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.

Appendix

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

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 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.

View Menu

In several modules of the VUIer 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 48), 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 48. *View Icons.* These icons position the active interface window to the position on the screen denoted by the white part of the square.

Diagnostic Support

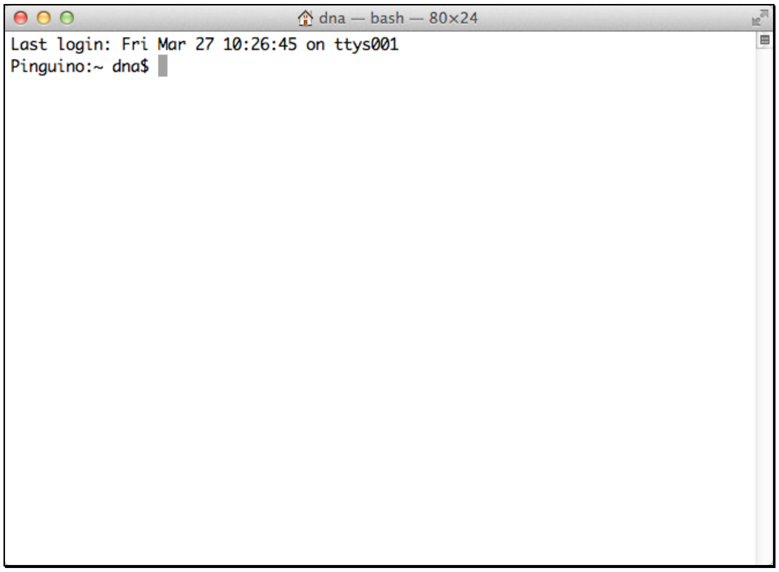
To aid in diagnostic support of the VUIer program, an alternate means of starting the program is available. This method is not routinely used but is available to aid in support calls to Cybergenetics.

Macintosh support

On a Macintosh, the analyst opens a Terminal window by selecting the Terminal icon (Figure 49) from the Dock or Applications/Utilities folder.

Figure 49. *Terminal icon*.

A blank Terminal window opens (Figure 50), displaying the computer's name and a command prompt.



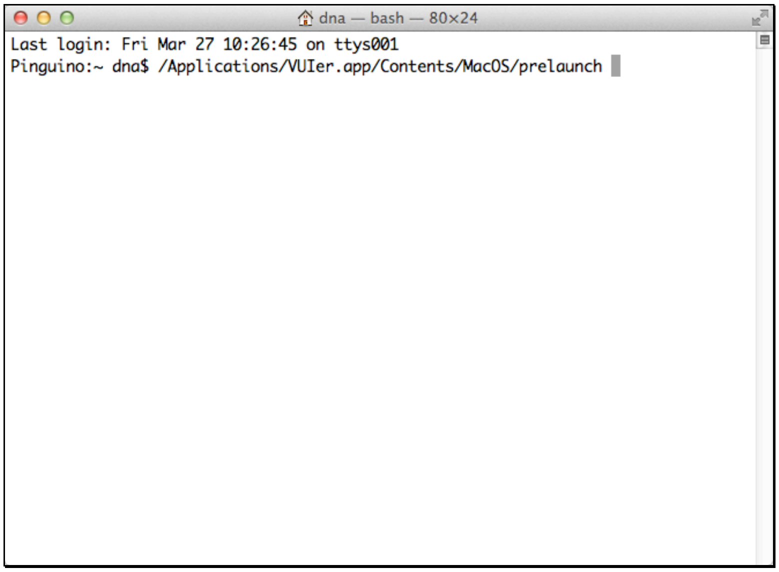
```
Last login: Fri Mar 27 10:26:45 on ttys001
Pinguino:~ dna$
```

Figure 50. *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 51).



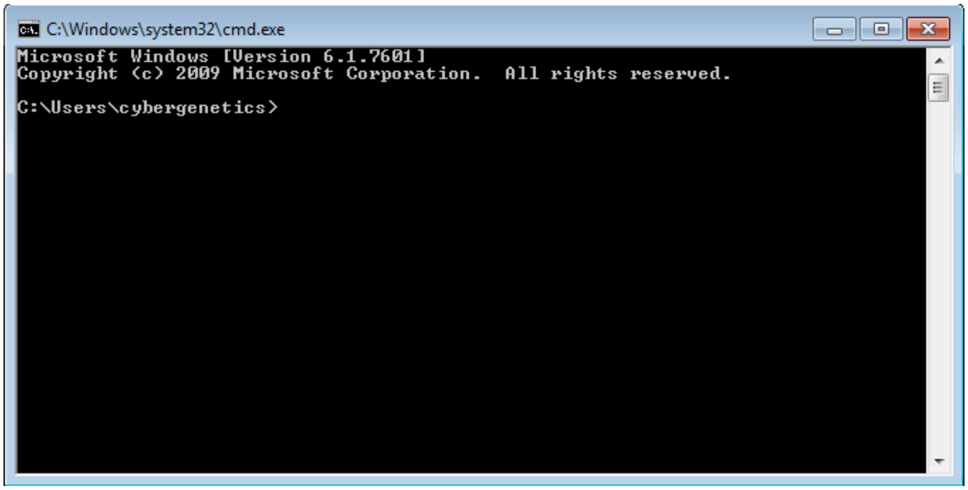
```
Last login: Fri Mar 27 10:26:45 on ttys001
Pinguino:~ dna$ /Applications/VUIer.app/Contents/MacOS/prelaunch
```

Figure 51. *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 52), displaying the computer user's name and a command prompt.



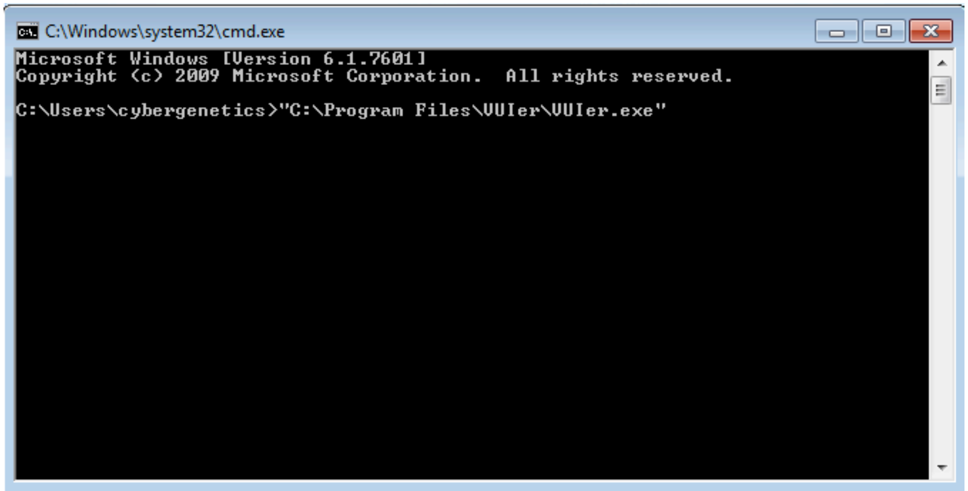
```
Microsoft Windows [Version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation.  All rights reserved.

C:\Users\cybergenetics>
```

Figure 52. *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 53).



```
Microsoft Windows [Version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation.  All rights reserved.

C:\Users\cybergenetics>"C:\Program Files\VUIer\VUIer.exe"
```

Figure 53. *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.

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.