

---

---

# SciMiner

## **-server version installation guide- -v3.1-**

*Copyright 2008-2010 Junguk Hur. All rights reserved.*

*Bioinformatics Program*

*University of Michigan*

*Ann Arbor, MI 48109, USA*

*Email: [juhur@umich.edu](mailto:juhur@umich.edu)*

*Homepage: <http://jdrf.neurology.med.umich.edu/SciMiner/>*

*Last update: 01/15/2010*

---

---

---

---

## TABLE OF CONTENTS

---

<b>TABLE OF CONTENTS</b> .....	2
<b>UPDATES</b> .....	3
<b>DISCLAIMER</b> .....	4
<b>SYSTEM REQUIREMENT</b> .....	5
<b>TYPES OF DISTRIBUTION PACKAGES</b> .....	6
<b>HOW TO USE THE PACKAGE II</b> .....	7
<b>REQUIRED PROGRAMS AND PERL MODULES</b> .....	8
<b>POST-INSTALLATION PROCEDURES</b> .....	9
<b>ADDITIONAL NOTES</b> .....	11
<b>HOW TO START SCIMINER SERVER</b> .....	12
<b>HOW TO CONFIRM SCIMINER IS RUNNING CORRECTLY</b> .....	13
<b>HOW TO ADD A NEW USER</b> .....	15
<b>CHECKING LOG FILES</b> .....	17
<b>CONTACTS</b> .....	18
<b>APPENDIX A</b> .....	19

---

---

## UPDATES

---

[I] The new release of SciMiner standalone version (as of 01/15/2010) include the following changes.

[1] The distribution package II is also available as an Ubuntu 9.10 virtual image. The old Fedora 8 based image is still available.

[2] SciMiner standalone versions will be available to anyone with a license agreement with University of Michigan for free. Detailed license will need to be completed for each download user.

[3] Other updates

- \* SciMiner can be set to work only on PubMed abstracts. Modify annotationENV.ini (ProcessFullTextHtml=TRUE (or FALSE))
- \* A proxy server can now be used. Modify annotationENV.ini (HTTPProxyServer=)
- \* Updated MeSH data set.
- \* Updated PubMedCentral document parser.
- \* Applied all the previous patches.
- \* Fixed other minor bugs.

---

---

## **DISCLAIMER**

---

The use of SciMiner is limited to academic research purposes. Any commercial use of SciMiner shall require a license agreement from the University of Michigan. We, the developers of the SciMiner, and the University of Michigan are not responsible in anyway for any trouble that might be caused by inappropriate use of the SciMiner system. It must be noted that the copyrights of the processed articles belong to their respective publishers not to the SciMiner users or developers.

- Updated on 01/15/2010 -

---

---

## SYSTEM REQUIREMENT

---

For a seamless running of SciMiner at an institution level, it is recommended that SciMiner be installed on a workstation level machine with Linux operating system with at least 2 GB of RAM. Multi-core or Multi-CPU machines with 4 GB of RAM are preferred.

Hard disk drive can be rapidly filled up with multiple uses of big corpus. **10GB** of free space is the absolute minimum space but at least 100GB is recommended for 500,000 documents. The public version of SciMiner is running on a machine with two Intel Xeon CPUs, 3GB RAM, and 900 GB of Hard disk drive.

[Fedora](#) (version 6, 7, 8 and 9) and [Ubuntu](#) (version 9.4 and 9.10) have been extensively used for SciMiner. Thus, we do not expect any issue in installing SciMiner on these platforms. Other Linux platform should also work fine. If users intend to use a windows based platform, [VMware](#) virtual system should be used. The SciMiner Package II is provided as a virtual disk image, which can be readily used by [VMware Player](#). For an implementation on institutional level, we recommend **VMware Workstation** be used.

If you choose to install SciMiner Package I on a Linux system, you have to make sure that all the required CPAN Perl modules, MySQL database, and a web-server must be working properly before using SciMiner.

---

---

## TYPES OF DISTRIBUTION PACKAGES

---

**Two different types** of distribution packages are available for download: Package I and Package II. The Package I is for experienced Linux user, while the Package II can be used any users with a minimal experience in Linux operating system.

**Package I: Basic core package ~ 200MB**

This comes in a tar.gz file, which contains all of the necessary scripts and modules. But required CPAN Perl modules, MySQL database, and a web-server (lighttpd or any) should be properly running. You also have to create ‘**sciminer**’ account and uncompress this package to the base directory of ‘**sciminer**’ user. Refer to ‘REQUIRED PROGRAMS AND PERL MODULES’ section.

**Package II: Linux virtual ready-to-use image (Fedora 8 or Ubuntu 9.10) ~2GB**

This comes in a form of **VMware virtual image** which is based on Fedora 8 (or Ubuntu 9.10) with SciMiner installed. This can be used with either VMware Workstation or VMware Player (Free of charge). Both can be obtained from <http://www.vmware.com/>. VMware Workstation can allocate more memory to the virtual machine; you cannot in VMware Player (the current Package II comes with 1 GB RAM allocated).

This virtual disk does NOT come with a pre-allocated disk space. Thus the actual disk size grows as the Fedora is used. This virtual disk comes with ‘Split disk into 2 GB files’.

For a better performance, it is recommended that the virtual disk is converted ‘**pre-allocated disk space**’ mode and increase the overall hard disk size if you would like to use SciMiner seriously. You can refer to web resources.

**Default account name and password**

‘ <b>root</b> ’ account password:	124356
‘ <b>sciminer</b> ’ account password:	124356
MySQL ‘ <b>sciminer</b> ’ account password:	124356

---

---

## HOW TO USE THE PACKAGE II

---

The Package II contains VMware virtual disk image files that can be played with VMware workstation or VMplayer. **At the end of this installation guide, Appedix A has a step-by-step guide with screen shots for users with little or no experience in Linux / virtual machine (For the old Fedora 8 based version. The new release with Ubuntu 9.10 should not be very different).**

STEP1) Once downloads are completed, unzip them in a same directory. You might need to install compression utilities like [WinZip](#) or [WinRar](#) which support zip compression format.

STEP2) If your computer does not have **VMware workstation** or **VMplayer** installed, go to the [VMware web site](#) and download either version. Note that **VMplayer** is free of charge.

STEP3) Use 'Open' command and navigate to the directory where the SciMiner disks have been unzipped. Select 'SciMiner-Ubuntu-Dist .vms' for Ubuntu and 'Other Linux 2.6.x kernel.vmx' for Fedora8.

STEP4) Login as 'sciminer' with '124356'

STEP5) Launch a terminal (Applications > Systems Tools > Terminal) and type 'startweb' to initiate the local SciMiner web server.

STEP6) Launch a web-browser and go to "http://localhost:8888/SciMiner/"

STEP7) Create a SciMiner user account. \*

\* Again, Appendix A has more details for general users.

\* A link for activating your account will be sent by an email. If email system doesn't work, you need to manually activate your account. Refer to 'How to add a user' section.

---

---

## REQUIRED PROGRAMS AND PERL MODULES

---

There are some applications and Perl modules required for SciMiner to run. If you have downloaded the **Package I**, please make sure that all of the following items are available and correctly configured.

- **Required Applications**

The following programs need to be available on the system before using SciMiner. Their absolute path and login information (MySQL) should be correctly specified in `‘/home/sciminer/ANNOTATION/SciMinerDB/annotationENV.ini’`

- [MySQL database](#)
  - ◆ Account: sciminer
  - ◆ Password: 124356
- [ImageMagick](#)
- **Web-server (eg. Lighttpd)**
  - ◆ CGI must be enabled.
  - ◆ Port: Default 8888
- **Perl**

- **Required Perl Modules**

The following Perl modules are needed on the system before using SciMiner. You can download and install them from CPAN (<http://www.cpan.org/>) or use ‘cpan’ from the Linux command line. If ‘cpan’ is not available on your system, you can install it by `‘>yum install perl-CPAN’` (on Fedora Linux systems). Please, refer to <http://perl.about.com/od/packagesmodules/qt/perlcpn.htm> or Google ‘Installing Perl module from CPAN’ for how to use cpan shell. This is to be done as **root** account.

- Boulder::Medline
    - ◆ You need to modify this module at Line 274 (Medline.pm):  
    @recorlines[\$i] to \$recordlines[\$i]
  - YAML
  - Text::NSP
  - CGI::Debug
  - CGI::Simple
  - CGI::Session
  - CGI::Application
  - HTML::Template
  - Data::Dumper
  - Unicode::String
  - XML::XPath
  - Spreadsheet::WriteExcel
- 
-



---

---

## POST-INSTALLATION PROCEDURES

---

After you successfully installed (Package I) or ran the VMWare virtual machine with SciMiner (Package II), you now have to modify the main configuration file and web htmls according to your institutional information. Package II users may skip this step if your primary intention is just giving it a try to SciMiner.

**STEP1)** Change the **passwords** for the **root** and **sciminer** account (only for virtual machine)

>passwd        will guide you to change the passwords.

**STEP2)** Modify the **main configuration file**

'/home/sciminer/ANNOTATION/SciMinerDB/annotationENV.ini'. Items in bold are strongly recommended to be changed.

```
[SciMinerDB]
OS=linux
ANNOPath=/home/sciminer/ANNOTATION/
SciMinerPath=/home/sciminer/ANNOTATION/SciMinerDB/
SciMinerWebPath=/home/sciminer/web/html/SciMiner/
SciMinerWebTempPath=/tmp/SciMiner/
SciMinerServerURL=http://localhost:8888/
HTTPProxyServer=
ProcessFullTextHtml=TRUE
Perl=/usr/bin/perl
Institution=Your Institution
AdminEmail=Your Admin Email Address
DB=sciminer
username=sciminer
password=124356
WholePMID=19443143
SendMail=0
MaxDoc=1000
MaxNewDoc=500
```

**STEP3)** Modify the HTML files at /home/sciminer/web/html/SciMiner/

- 1) You must put your **email** at the line #21 of the following files. Modify mailto:? to mailto:<<YOUR EMAIL HERE>>?.
- 
-

- 
- 
- A. analysisIndex.tmpl
  - B. completedIndex.tmpl
  - C. SciMinerIndex.tmpl
  - D. mergeQueriesIndex.tmpl
- 2) Other web pages like main2.html, intro2.html, and contact2.html can also be freely changed as you need.

**STEP4)** Modify the **\$adminEmail** to your email address at line #25 of '**~/ANNOTATION/SciMinerDB/Modules/Annotation/SciMiner.pm**' in order for you to get an email regarding any system issue.

```
my $adminEmail = '<<YOUR EMAIL HERE>>';
```

**STEP5)** Almost every Perl scripts, modules, and CGI scripts used in the SciMiner system has the following environment statement at the beginning of each file.

```
BEGIN {push (@INC, "/home/sciminer/ANNOTATION/SciMinerDB/Modules/");}
```

This is to specify the location of the required SciMiner modules. If you installed SciMiner on different account or location, you must modify this line according to your current system configuration. We strongly recommend you create an account 'sciminer' and install SciMiner system onto this account (if you are using the Package I).

---

## ADDITIONAL STEPS FOR PACKAGE I

**STEP6)** If you downloaded the Package I, it should be unpacked onto /home/sciminer/ . Create 'SciMiner' directory at the temporary directory and change the permission to 777

```
>mkdir /tmp/SciMiner/  
>chmod 777 SciMiner
```

**STEP7)** The following directories should have 777 permission since they need to be accessible by web server and results files are created.

```
>chmod 777 -R ~/ANNOTATION/SciMiner/Work/  
>chmod 777 ~/web/html/SciMiner/FinalResults/
```

---

---

## ADDITIONAL NOTES

---

### -- EMAIL NOTICE --

SciMiner tries to send out an email notice when queued jobs are completed. In order to use this email notice, however, you must have your machine correctly configured for outgoing emails. Every system has different configuration depending on their email servers. Thus you have to get help from the system administrators at your institution. It should be noted that the **Package II** does **NOT** come with preconfigured outgoing email service enabled.

If you plan to deploy SciMiner as an accessible system from other users in your institution, you have to get a static IP and configure the sendmail correctly. We strongly recommend you to seek help from the system administrators at your institution.

Even if email notice is not configured on your SciMiner, users can always check all of their completed jobs from the 'Completed' menu.

### -- POP-UP BLOCKING --

Pop-up blocking option must be disabled from the client side. Most of the recent web-browsers these days have pop-up disabled. If you click a link on SciMiner result pages and a new window or tab pops up then closes right away, it is very likely that your browser is blocking pop-up on your server.

---

---

## HOW TO START SCIMINER SERVER

---

Once you have completed necessary changes above, you are now ready to start the SciMiner server.

If a web server (lighttpd, Apache, or any) is already running, launch a web browser and try <http://localhost:8888/SciMiner/>.

If no web server is running but lighttpd is installed on your machine, you can simply start the web server by the following command.

**>startweb**

This command is only applicable to the SciMiner system and is equivalent to ‘usr/sbin/lighttpd -f /home/SciMiner/web/lighttpd/lighttpd.conf’

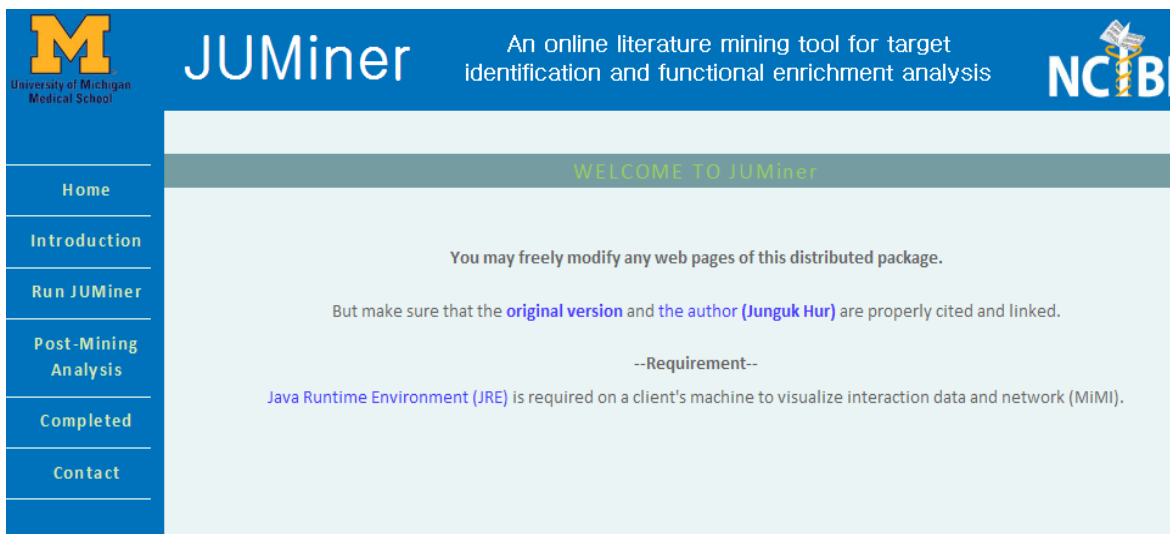
---

---

## HOW TO CONFIRM SCIMINER IS RUNNING CORRECTLY

---

Open a web browser and go to <http://localhost:8888/SciMiner/>. If you are connecting from outside the virtual machine, you have to specify the correct URL (probably with IP address) of the installed SciMiner virtual system (“ifconfig “ will show you the IP). If the web server is running correctly, you will be able to see the main page of the SciMiner server.



Currently, the network of the virtual machine with SciMiner is configured with **NAT**, meaning that the virtual machine shares your host computer’s network. Since your host computer is working as a DHCP server and the virtual machine is on a private network under the DHCP server, users from the outside the host computer **cannot** directly access the SciMiner.

There could several possible solutions to this problem if you want the SciMiner accessible from outside.

- 1) Set the VMware network use ‘**Bridged**’ network instead of ‘**NAT**’. It makes the virtual machine get an IP from the outside DHCP server, which your host machine is physically connected.
- 2) Get a static IP from your institution’s network administrator and use that IP information. You may have to select ‘**Custom**’ instead of the ‘**Bridged**’ or ‘**NAT**’. And set the IP information within the Fedora.  
Menu > Administration > Network
- 3) Install the **Package I** on a machine that can be accessed from outside.

If you click, 'Run SciMiner', 'Post-Mining Analysis', or 'Completed', you should be able to see the following login screen. If not, some SciMiner components are not correctly configured.

University of Michigan Medical School

# SciMiner

An online literature mining tool for target identification and functional enrichment analysis

NCBI

- Home
- Introduction
- Run SciMiner
- Post-Mining Analysis
- Completed
- Contact

Enter your email address and password.  
If you don't have a SciMiner account,  
[Email a request to your system administrator.](#)

E-mail:

Password:

Enter your registered email address and password to log-in. Users should send email to the system administrator (who installs the SciMiner) to request an account on SciMiner.

If you log-in, then you should be able to see the following screen for 'Run SciMiner'.

## JUMiner Query Submission

(Section1) Name your query.

Query name :

(Section2) Enter your query or provide PMIDs

1) NCBI Entrez Pubmed query

**PREVIEW**

**SHOW advanced options!**

\* Tip: Use default option -> Check the result ->  
Create your own filters -> Run JUMiner again with your additional filteres.

\* Supplementary files. You may need these files to create your own filter lists. (HUGO IDs are essential.)  
Better save the text files and load them in a text editor like [UltraEdit](#) or [EditPlus](#)

- 1) Full HUGO Content ([EXCEL](#), [TXT](#))
- 2) Unique symbols ([TXT](#))
- 3) Unique names ([TXT](#))

---

---

## HOW TO ADD A NEW USER

---

SciMiner user account can be created on SciMiner web pages (local version). But you can manually create or modify user accounts. The following describes how you can add a new SciMiner user manually.

New users can be added to the SciMiner system by inserting a new record to 'user' table in the 'SciMiner' db of the MySQL database. Just for your reference, here is the simplest way of adding one user.

1) First log-in to MySQL

```
>mysql -usciminer -p124356 sciminer
```

2) Insert a new user information

```
mysql> insert into user
      (email, name, passCode, maxDoc, maxNewDoc, editLevel, institute,
      deptOrLab, activationStatus) values ("user@email.address", "Mr.
      SciMiner", "new password", 3000, 1000, 3, "User institution",
      "User Lab", 1);
```

PremiumSoft's Navicat for MySQL would be very useful and easy to use for managing users. It can be downloaded at <http://mysql.navicat.com/index.html>. This is a shareware though.

<Fields>

maxDoc	: The number of maximum documents per single query
maxNewDoc	: The number of maximum <b>NEW</b> documents per single query
editLevel	: The current version of SciMiner is not actively using this field. In the future version, editLevel will specify different levels of edit function for each user.
institute	: User's institution
deptOrLab	: User's lab or department
activationStatus	: 1 (active) or 0 (inactive)

3000 for maxDoc and 1000 for maxNewDoc would be recommended. The defaults for these numbers of documents are specified in annotationENV.ini.

Generally, a maximum of 20,000 is acceptable for the maxDoc on a machine with 2GB RAM. System administrator can increase or decrease this number depending on your system's capacity.

Please note that the distribution Package I is preconfigured to have 1GB RMA available to the virtual machine. If users would like to assign different amount, you may have to use VMware workstation (not VMware player).

---

---

---

---

You can also modify user account information. For example, in order to change the number of maximum documents per single query (maxDoc) for a user, whose userID is '10'.

```
mysql> UPDATE user SET maxDoc=5000 WHERE userID = 10;
```

To check all of the users,

```
mysql> SELECT * FROM user;
```

To exit from MySQL console, just type 'exit'



---

---

## CHECKING LOG FILES

---

The usage of SciMiner is logged onto the following three files at the “/tmp/” directory.

/tmp/SciMinerQuery.log	: For SciMiner Mining Query
/tmp/SciMinerGRIFQuery.log	: For Gene2PubMed / GeneRIF Query
/tmp/SciMinerAnalysis.log	: For Post-Mining Analysis Query

Aliases have been set to give you a quick access to the log files.

- 'tm'** for SciMinerQuery.log
- 'tg'** for SciMinerGRIFQuery
- 'ta'** for SciMinerAnalysis.log

Each will show the last 300 lines of the log.

---

---

## CONTACTS

---

If you encounter any problem in deploying the server version of SciMiner or have any questions or comments, please contact Junguk Hur.

Junguk Hur  
[juhur@umich.edu](mailto:juhur@umich.edu)

Palmer Commons 2035  
100 Washtenaw Ave.  
Ann Arbor, MI 48109, USA  
<http://www-personal.umich.edu/~juhur/>

Homepage: <http://jdrf.neurology.med.umich.edu/SciMiner/>

---

---

## APPENDIX A

---

This appendix will demonstrate how to use the SciMiner distribution package II (VMware virtual disk image) for non-experienced users. The demonstration is based on Windows XP. But other operating systems that support VMware virtual machine should be okay.

- (1) Download VMware Player (freeware) from VMware web site (<http://vmware.com/products/player/>) or VMware workstation (shareware). The workstation version is superior since it allows you to adjust the allocated memory to the virtual machine, which may affect the number of documents. But it is not free.
- (2) Install the downloaded VMware Player and follow the instruction.
- (3) Download SciMiner Package II from the SciMiner web site and unpack (unzip) it to a desired directory (such as c:\SciMiner)

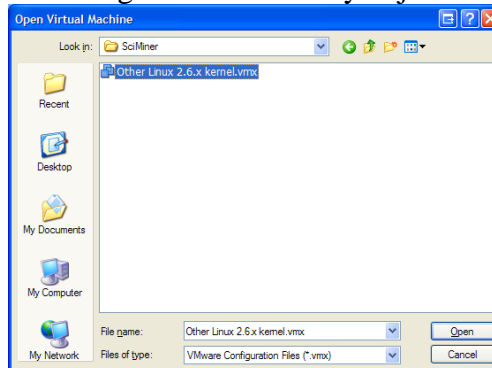
Now, you have everything ready to launch the SciMiner. We first launch Fedora 8 (the virtual machine) and then start SciMiner server in the virtual machine.

### Starting the virtual machine

- (4) Start VMware Player.

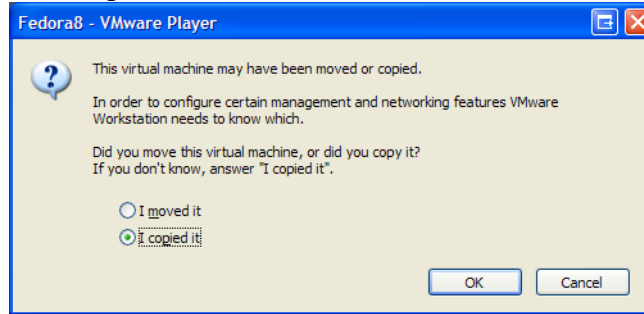


- (5) Click 'Open' icon and navigate to the folder you just unzipped the Package II.



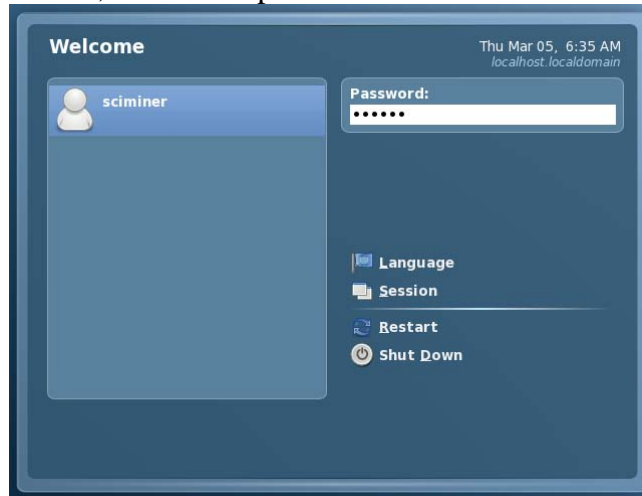
---

(6) Select 'I copied it' option.

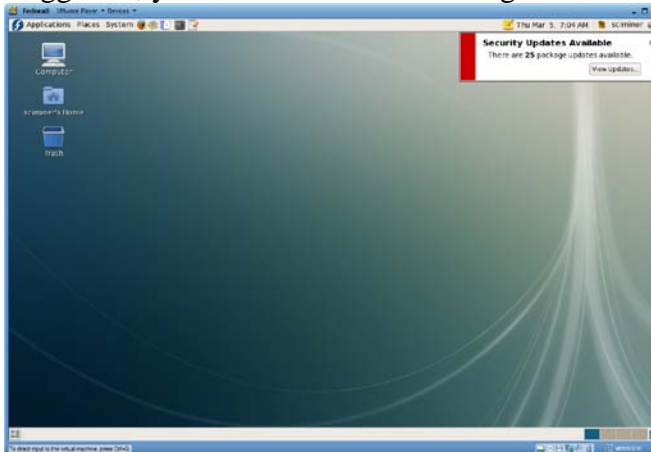


(7) Fedora 8 now starts to boot and this may takes up to a couple of minutes.

(8) Login as 'sciminer'; the default password is '124356'



(9) Successfully logged in, you would see the following Fedora 8 desktop.



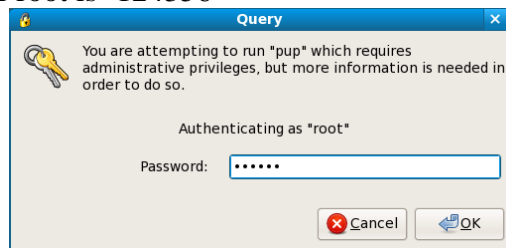
---

---

## Security Updates for Fedora 8

As programs of Fedora get updates frequently, you will probably have some security updates to apply to your Fedora 8. If there is any update, a pop-up windows at the top right of the desktop will tell you how many updates are available. This update process may take a while; thus you may skip this for now if your intention is just trying SciMiner, not seriously using it. Go directly to **Step (19)** if you are NOT updating the system.

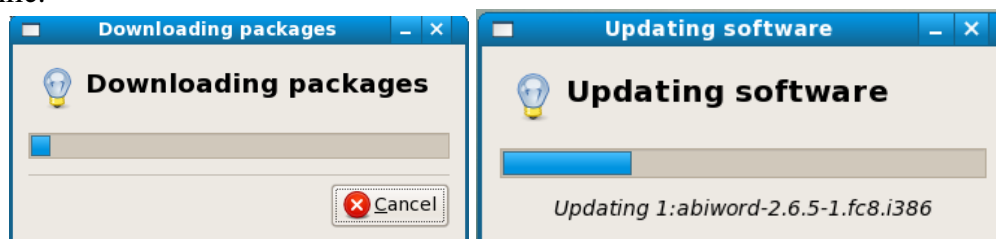
- (10) Password for root is '124356'



- (11) Click 'Apply updates' at the bottom of Package Updater



- (12) Downloading updates will be automatically processed, which may take a while.




- (13) 'Reboot now' if system recommends a reboot.

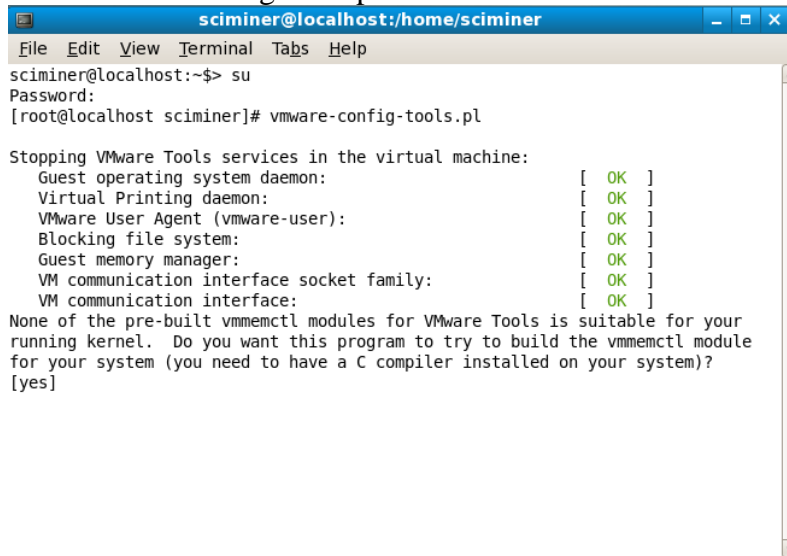
---

---

## Recompiling VMware tools

If your updates included a Kernel package update, you need to configure VMware tools; you may see some error message during the rebooting process.

- (14) Open a terminal; click  icon in the top tool bar or go to **Applications/System Tools/Terminal** in the menu.
- (15) Change to root account by typing 'su' and provide the password '124356'. You will see the prompt now reads '[root@localhost sciminer]' from 'sciminer@localhost:~>'. Refer to top portion of the screen-shot at Step (16)
- (16) Run 'vmware-config-tools.pl'



```
sciminer@localhost:/home/sciminer
File Edit View Terminal Tabs Help
sciminer@localhost:~$ su
Password:
[root@localhost sciminer]# vmware-config-tools.pl

Stopping VMware Tools services in the virtual machine:
  Guest operating system daemon:          [ OK ]
  Virtual Printing daemon:                [ OK ]
  VMware User Agent (vmware-user):        [ OK ]
  Blocking file system:                   [ OK ]
  Guest memory manager:                   [ OK ]
  VM communication interface socket family: [ OK ]
  VM communication interface:             [ OK ]

None of the pre-built vmmemctl modules for VMware Tools is suitable for your
running kernel. Do you want this program to try to build the vmmemctl module
for your system (you need to have a C compiler installed on your system)?
[yes]
```

- (17) Just follow the instructions. You may just press 'Enter' key for each of the questions. Do not change these options unless you are absolutely sure what you are doing. The screen will flash a few times at the end of this process. So, do get panic.
- (18) When the process is completed, you will see the prompt '[root~]' again. It is high time to reboot your virtual machine. Type 'reboot' and press 'Enter' key.

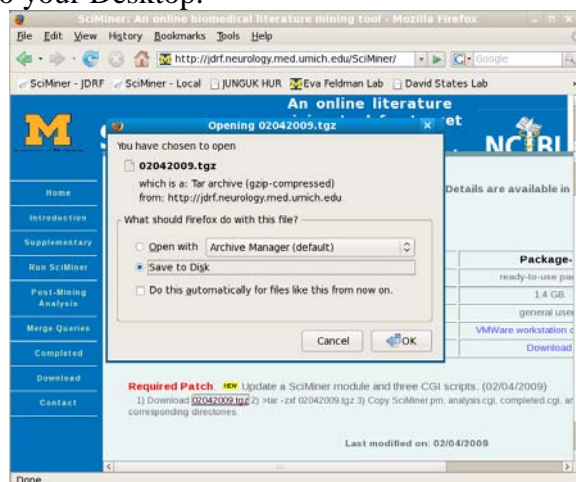
---

---

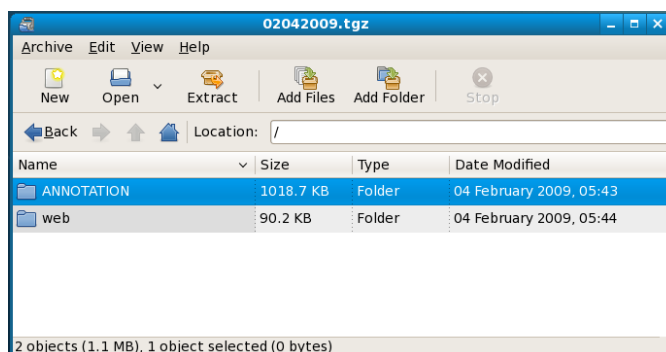
## Updating SciMiner

SciMiner also gets updated from time to time. Users (of the standalone version) are expected to apply these updates to their local version of SciMiner to make SciMiner up-to-date. Check the download web page of SciMiner at <http://jdrf.neurology.med.umich.edu/SciMiner/> to see if there is any update (or patch). We will use the update released on 02/04/2009 as an example. This is to be done within the virtual machine.

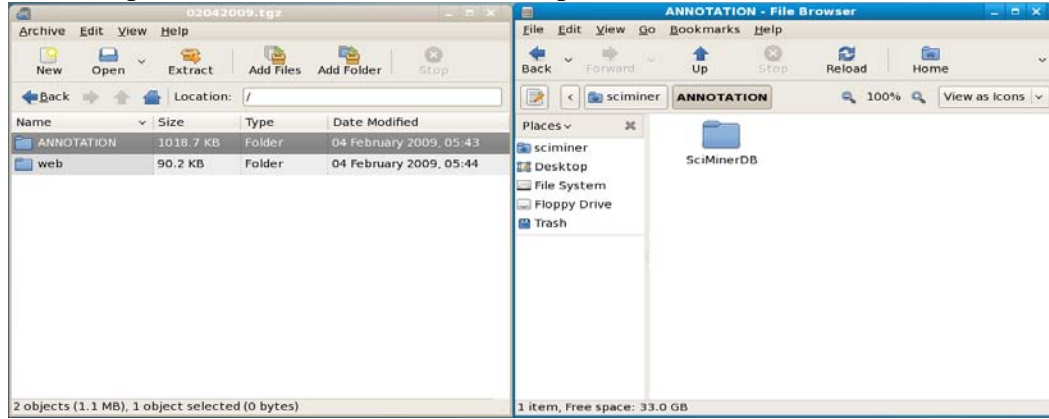
- (19) Launch a web browser. Firefox icon (🦊) is available at the system tool bar at the top.
- (20) Go to <http://jdrf.neurology.med.umich.edu/SciMiner/> and navigate to the Download page.
- (21) Click '02042009.tgz' link and choose 'Save to Disk'. '04042009.tgz' file will be saved onto your Desktop.



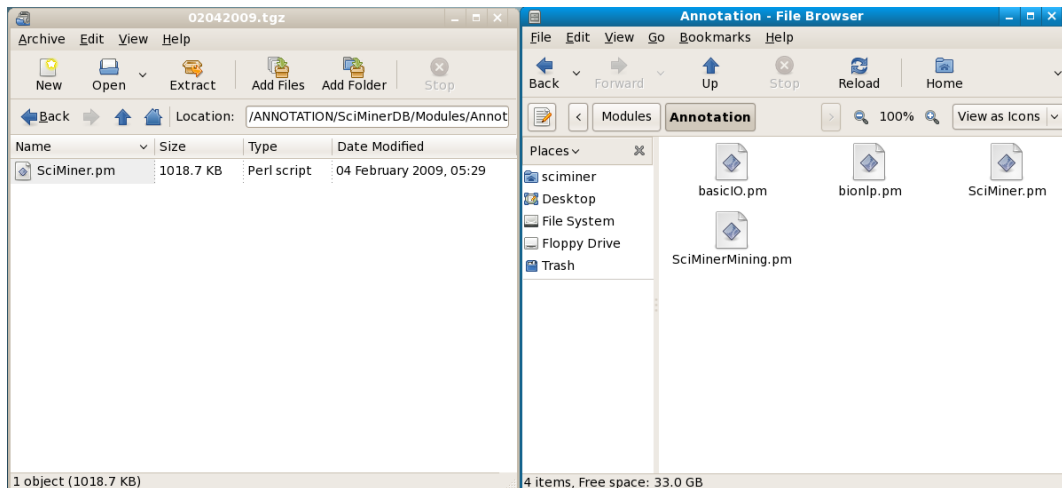
- (22) Double-click '02042009.tgz' file. You will see the following window pop up.



- 
- (23) What you have to do is copying the files in the '02042009.tgz' file to their corresponding location in your virtual machine. Double-click 'sciminer's Home' on the Desktop. You now have two windows open.



- (24) In both windows, navigate ANNOTATION -> SciMinerDB -> Modules -> Annotation



- (25) Just drag-and-drop the SciMiner.pm from the left windows (with only one file) to the right windows (with four files). Change a drop-down menu 'View as icons' at the top right corner to 'View as list'. You can now see the details of those files. Make sure that the file size and the modified date of 'SciMiner.pm' are the same in each window.

- (26) You need to do the same process for the CGI scripts in the 'web' folder. Either click 'Back' or 'Up' arrow. Then navigate web -> html -> SciMiner

- (27) Drag-and-drop those cgi scripts (ananalysis.cgi, completed.cgi, and sciminer.cgi) to your right window.
-



---

---

## Starting the SciMiner server

In the virtual machine, it is easy to start the SciMiner server.

- (28) Open a terminal. Refer to Step (14) for this purpose.
- (29) In the terminal, type 'startweb' and press 'enter'. This will start the lighttpd web server in the background so that you can access the SciMiner server via web.
- (30) Launch a web browser. Firefox icon (🦊) is available at the system tool bar at the top.
- (31) Go to <http://localhost:8888/SciMiner> or click 'SciMiner - Local' in the bookmark.



- (32) Click 'Run SciMiner' and create a user account via 'Click HERE to create one'.

Enter your email address and password.

If you don't have a SciMiner account,  
Click [HERE](#) to create one.

Email to your [system administrator](#) for any question.

E-mail:

Password:

- (33) You will see the same page that you filled out during SciMiner download. But the information you enter here will **NOT** be sent to the SciMiner administrator. This is valid only within your virtual machine.

SciMiner: An online biomedical literature mining tool - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://localhost:8080/SciMiner/

SciMiner - Local JUNGUK HUR Eva Feldman Lab David States Lab National Center for ... UM Bioinformatics G...

**SciMiner** An online literature mining tool for target identification and functional enrichment analysis **NCBI**

SciMiner is a freely available tool but the use of SciMiner is strictly limited to academic research purposes. SciMiner must not be used for any commercial purpose. We, the developers of the SciMiner, and the University of Michigan, Ann Arbor are not responsible in any way for any trouble that might be caused by use or alteration of the SciMiner system. It must be noted that the copyrights of the processed articles belong to their respective publishers not to the SciMiner users or developers.

Check here if you understand and accept the agreements above.

**Your Information**

Fill out the following contact information and click 'Submit' button. Please, use your institutional information here and all fields are required.

Institutional Email	sciminer@sciminer.com
Password (-20 characters)	
Password (Repeat here)	
Your Full Name	Your Full Name
Institution	Institution
Department	Department
Address	Address
City	City
State	State
Zip code	11111
Country	United States

Submit Reset

This page will create user account according to the default setting specified in 'annotationEVN.ini', where MaxDoc is set to 1000 and MaxNewDoc is set to 500. You may want to change these parameters before you create a user account (Refer to Page 8 for more about annotationENV.ini'). Modifying this annotationENV.ini will only affect those user accounts that are created after this change.

You can still modify each user's parameter individually. Please refer to section 'HOW TO ADD A NEW USER'.

The number of documents per query depends on the memory available in the virtual machine. Currently allocated memory is 1GB. For this amount of memory, we believe reasonable upper limit would be 5,000 documents (or up to 10,000). If you use VMware workstation, you may adjust the amount of RAM (up to 4GB for this virtual machine) as long as your machine has enough RAM available. But it should be noted that VMware player does not allow you to adjust the memory. Thus, VMware player is good for a try but not as good as VMware workstation if you intend to use SciMiner seriously.

-- END OF THE GUIDE --