

Installing Perl Modules

Date

6/12/09

Introduction

This manual attempts to outline the installation of Perl modules necessary for running vPhyloMM. The steps in this manual take advantage of ActivePerl's package management utility, PPM. For this reason, it is required that there be a working installation of ActiveState's ActivePerl available on the system. It is highly recommended that the following sources of online documentation be absorbed:

ActiveState's documentation page for the PPM - <http://docs.activestate.com/activeperl/5.10/faq/ActivePerl-faq2.html>

ActiveStates's website - <http://www.activestate.com>

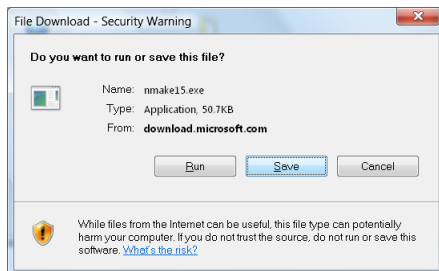
ActiveState's website for ActivePerl - <http://www.activestate.com/activeperl/>

ActiveState's documentation for the latest release of ActivePerl (5.10) - <http://docs.activestate.com/activeperl/5.10/install.html>

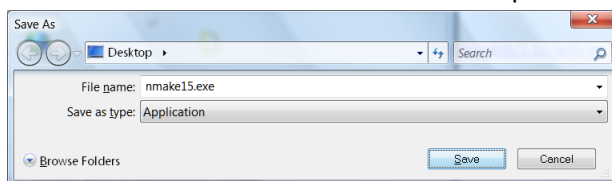
Windows Specific Instructions

1. Obtain nmake.exe

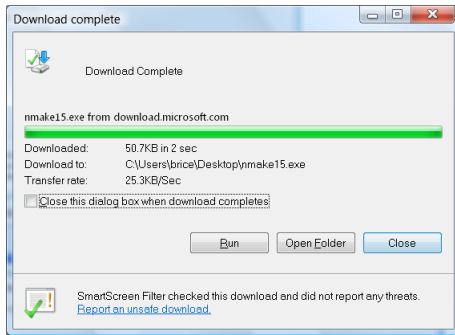
- a. In your web browser, navigate to <http://download.microsoft.com/download/vc15/patch/1.52/w95/en-us/nmake15.exe>
- b. Click the button labeled "Save"



- c. Save the file "nmake15.exe" to the Desktop



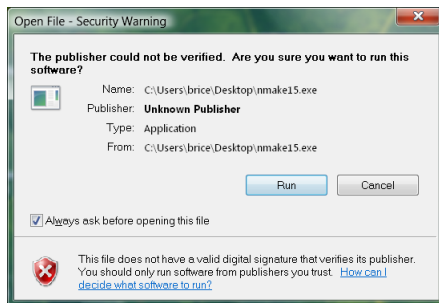
- d. When "nmake15.exe" has finished downloading, click the button labeled "Close"



e. On the Desktop, double click the “nmake15.exe” icon



e. Click the button labeled “Run”



f. Find the files named “nmake.exe” and “nmake.err”

i. Copy them both to the directory C:\Windows (if you’re unsure of how to do this, contact your system administrator).

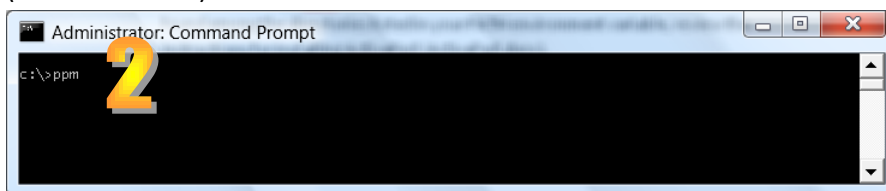
g. Make sure that C:\Windows is listed in your environment PATH variable (if you’re unsure of how to do this, contact your system administrator).


2. Follow the Operating System Independent Instructions below

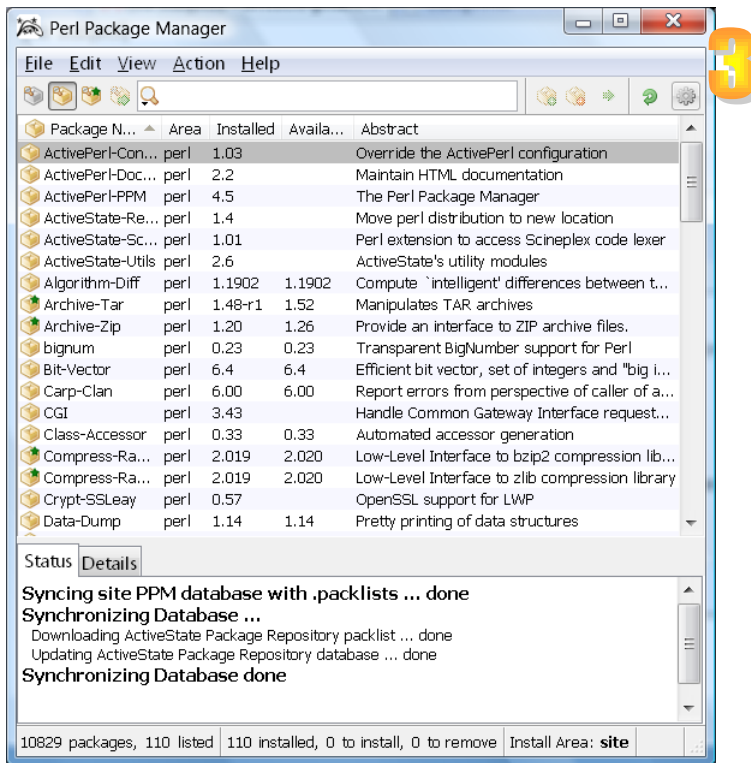
Operating System Independent Instructions

(The graphics will show the PPM being used on Windows Vista)

1. Log in as a user with administrative privileges. If you’re unsure how to do this, contact your system administrator.
2. Run the command “ppm” from a command line, terminal, or shell. If this command is not found among the directories listed in your PATH environment variable, review the instructions for installing ActivePerl (ActivePerl.docx).



3. Once PPM has loaded and has finished synchronizing databases, click the **PPM Preferences** icon (The **PPM Preferences** icon looks like this: ).

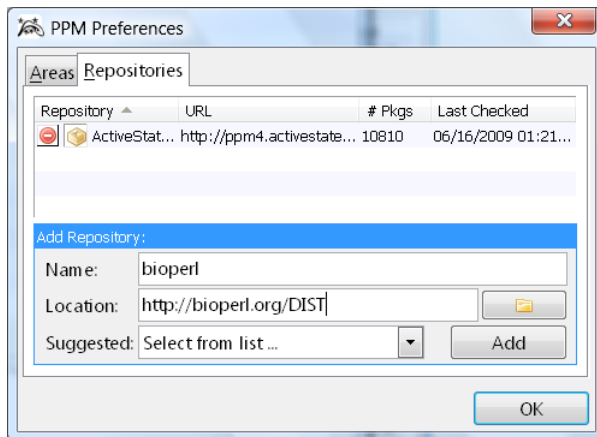


4. Click the **Repositories** tab.

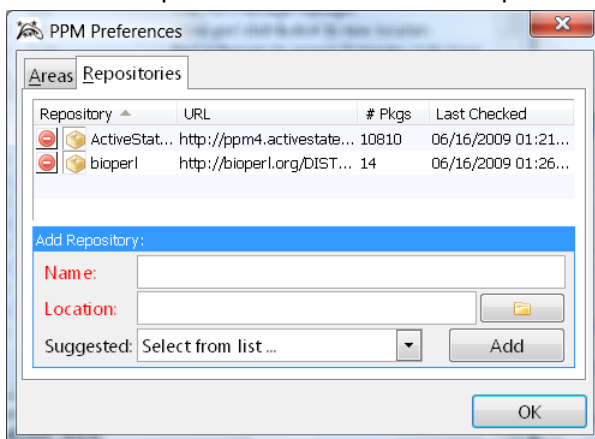
5. In the field labeled "Name:" type "bioperl".

6. In the field labeled "Location:" type "http://bioperl.org/DIST"

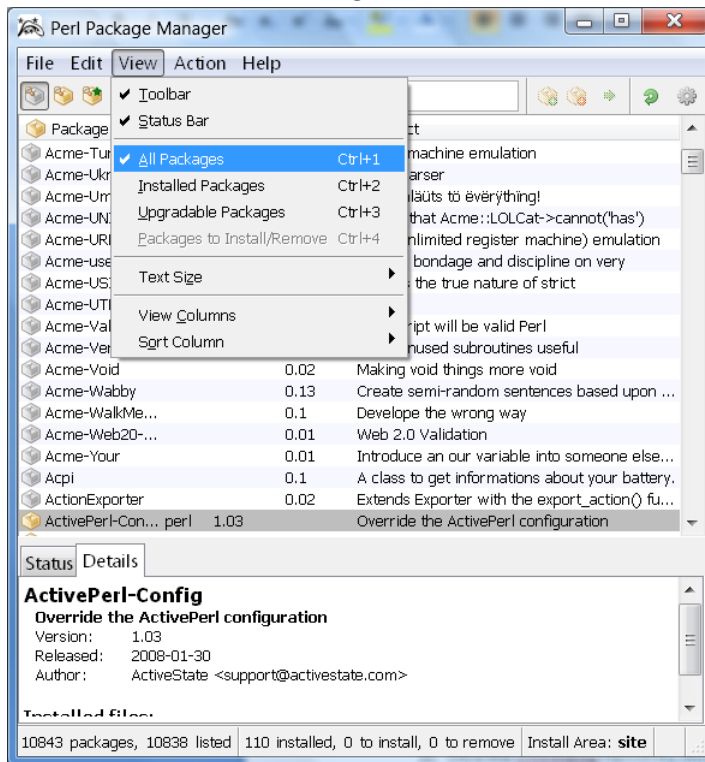
7. Click the button labeled "Add"




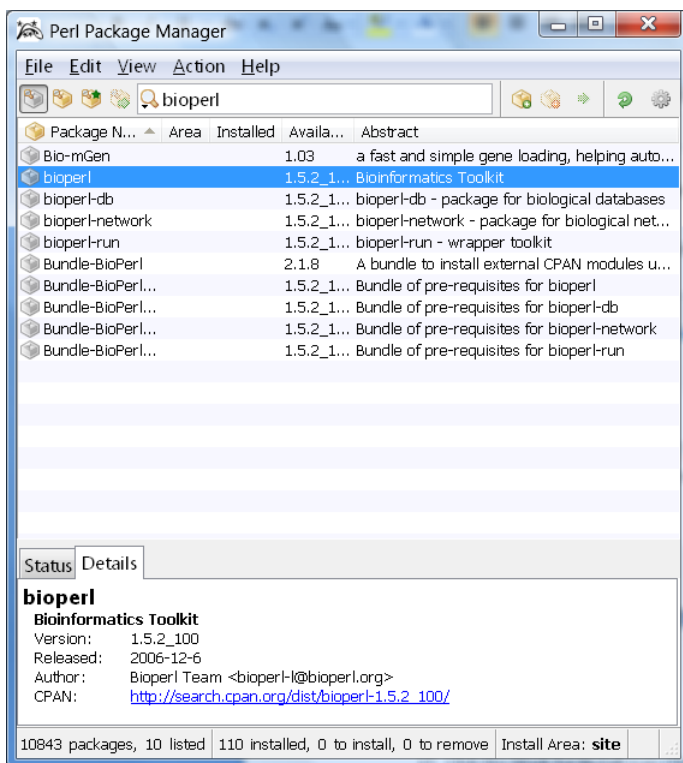
8. Wait for "bioperl" to show in the list of repositories.



9. Open the menu labeled “View” by clicking the word “View” in the menu bar.
10. Click on the words “All Packages”.

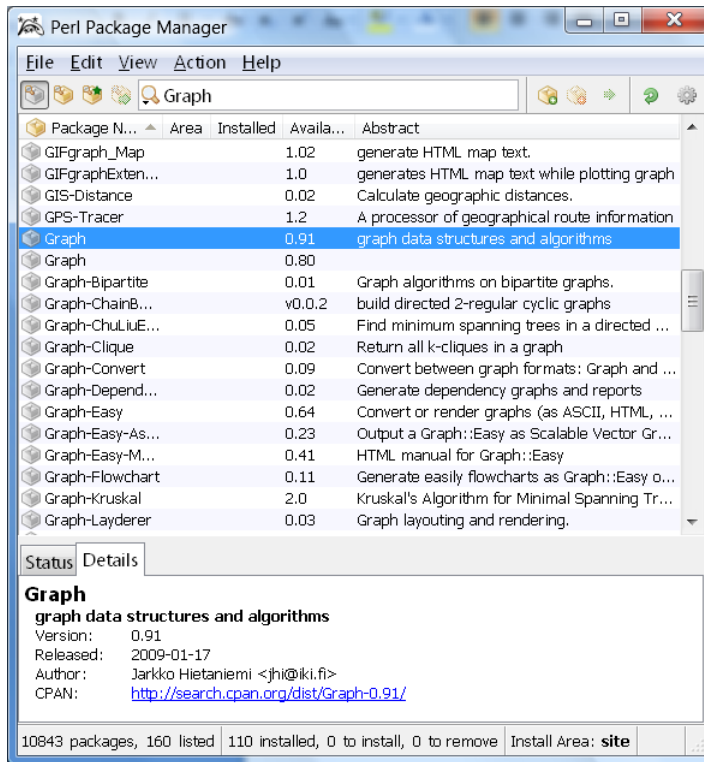


11. In the search field, type “bioperl”.
12. In the list of packages below, select the package whose name is “bioperl”.
13. Click the **Mark for Install** icon (The **Mark for Install** icon looks like this: ).

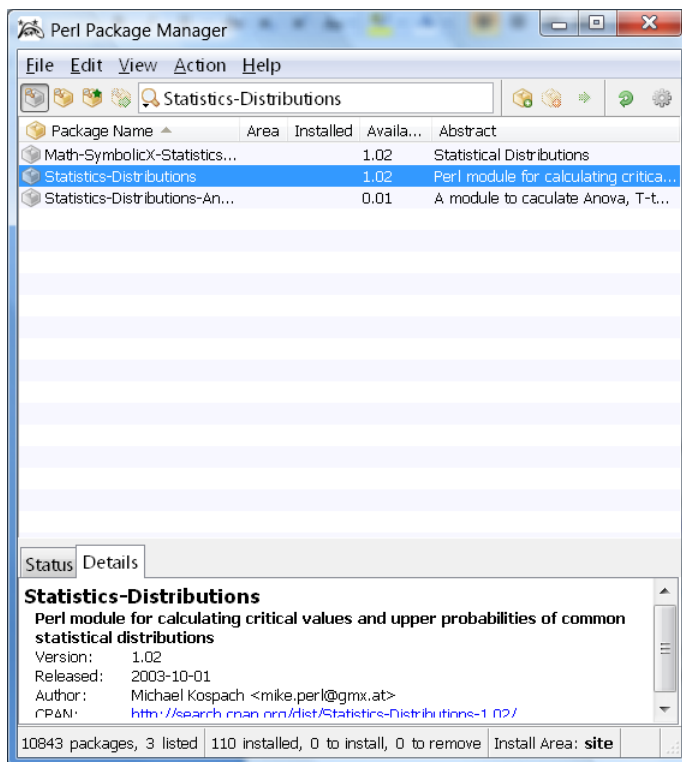


14. Repeat steps 15 through 17 substituting “bioperl” for the following:

a. "Graph"

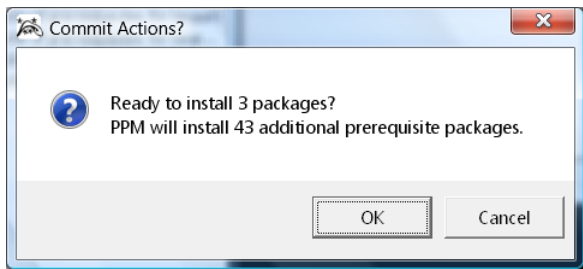


b. "Statistics-Distributions"

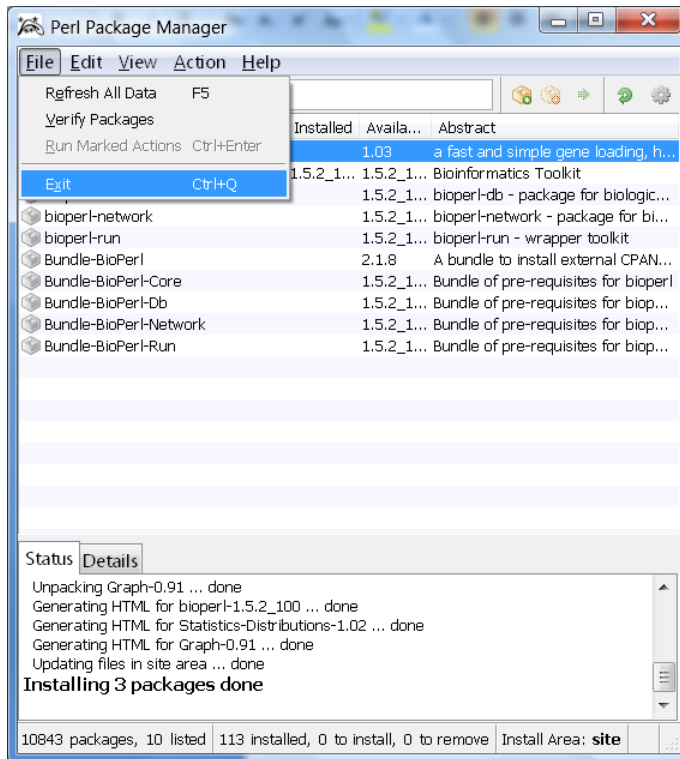


15. Click the **Run Marked Actions** button (The **Run Marked Action** button looks like this: ).

16. Click the button labeled "OK".



17. When the packages have been installed, the bottommost line in the **Status** tab will read "Installing 3 packages done". When this happens, close PPM by clicking **File** then **Exit**.



18. From the command line, terminal, or shell, run `cpan GraphViz`
- To make sure the installation was successful, run `perl -MGraphViz -e 1`
 - No output indicates success
 - Output indicates failure