iBioSim Installation Instructions

Chris J. Myers

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Contents

1 General Requirements

There are versions of `iBioSim` available for Windows, Linux, and MacOS. You can download the appropriate installation file from:
`http://www.async.ece.utah.edu/iBioSim`
`iBioSim` requires that you have Java Runtime Environment 1.5 or higher install on your system. It is also useful to have Graphviz. Also, you should associate files with a ".dot" extension with the `Graphviz` tool, and files with the ".xhtml" extension to your web browswer.
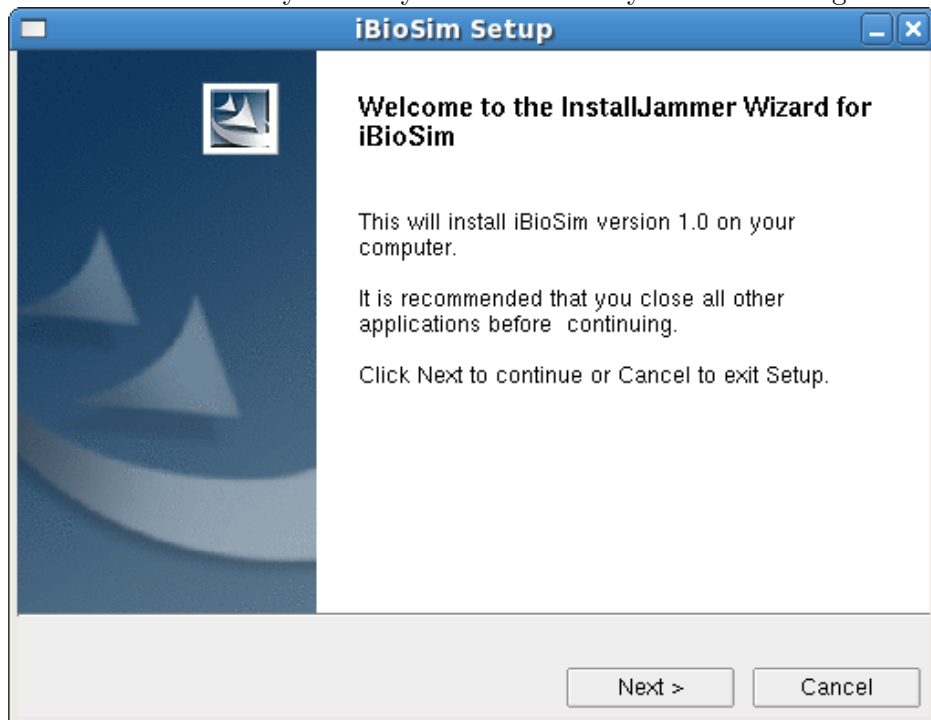
2 Installation on Windows

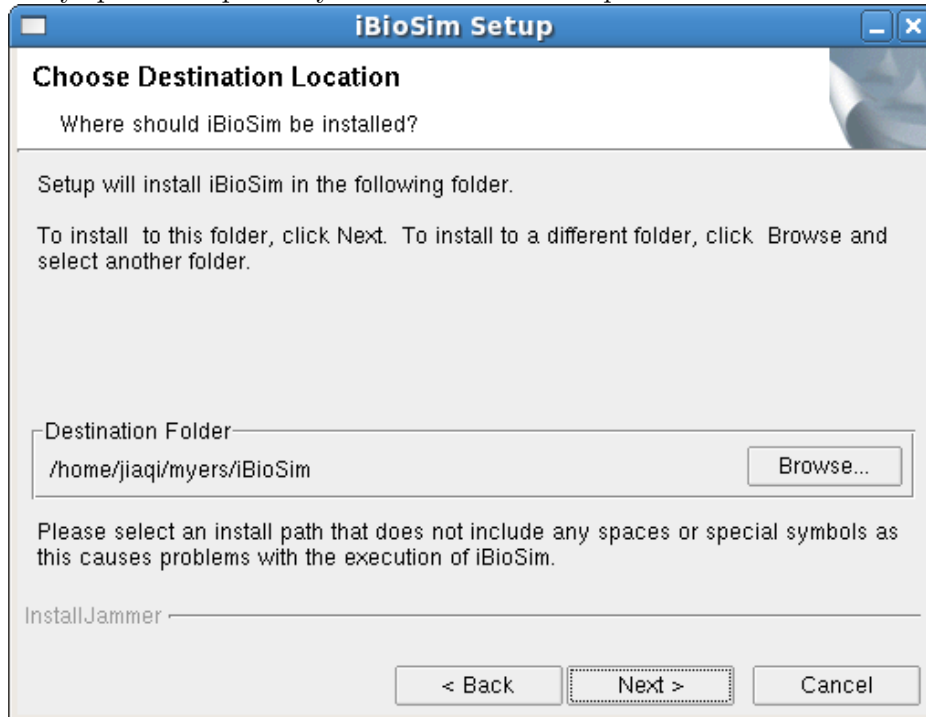Download and execute `iBioSim-⟨version⟩-Setup.exe`.
The installation uses InstallJammer. It first asks you for your preferred installation language. Make your selection and press `OK`.
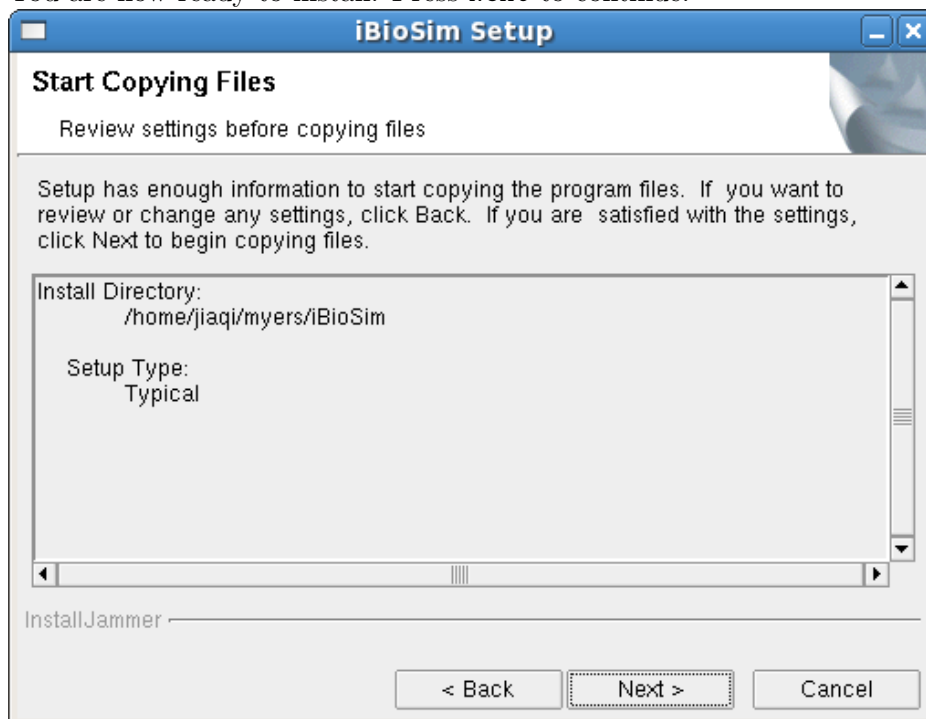

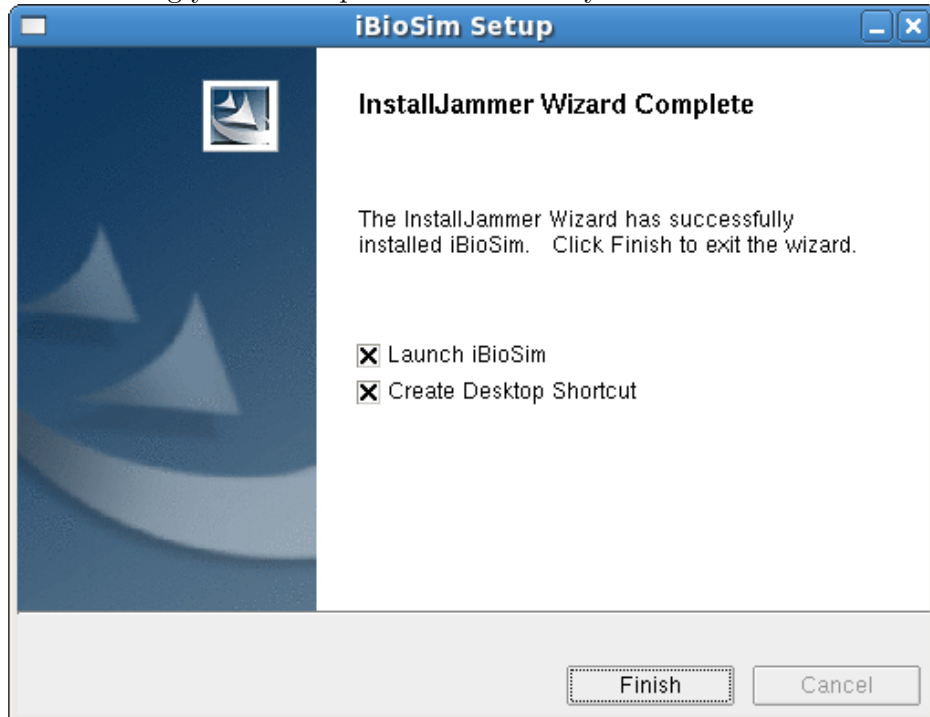The next screen tells you that you what version you are installing. Press `Next` to continue.

Next, it ask you for an installation location. Please make sure to select a path that does not have any spaces or special symbols as these cause problems with `iBioSim`.

You are now ready to install. Press `Next` to continue.

You are all done. Press `Finish`. If selected, iBioSim will launch immediately. Otherwise, you can start it using your desktop shortcut or from your start menu.

In your start menu, there should be an option to uninstall. If you select this, it will ask if you are sure then proceed to completely remove iBioSim from your system. It is highly recommended that you remove iBioSim using this uninstall procedure before installing a new version.
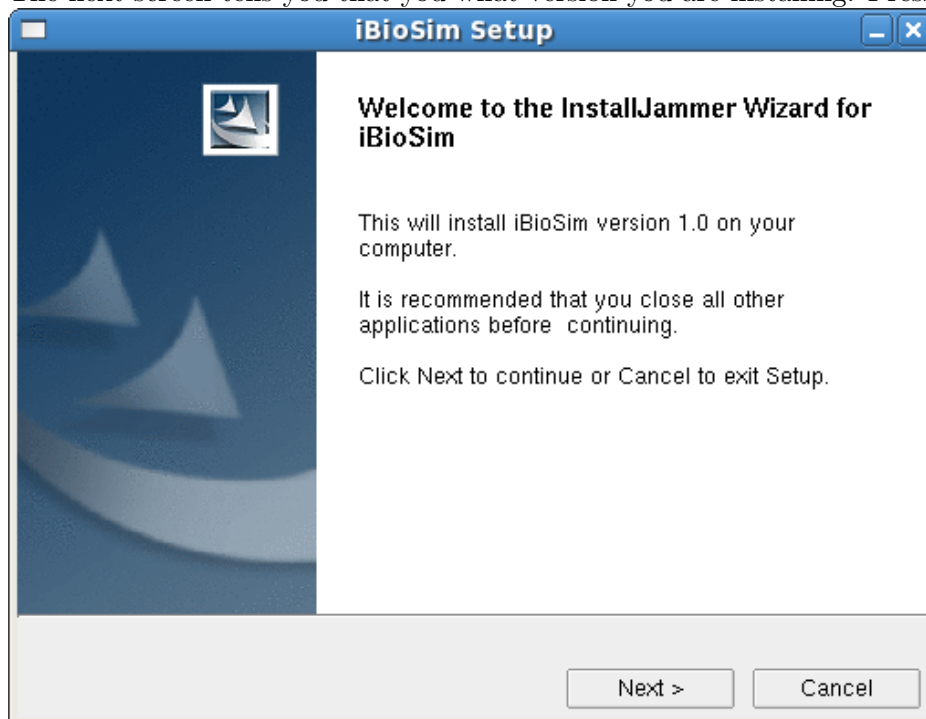
3   Installation on Linux

Since InstallJammmer is also used for the Linux install, the installation instructions are essentially the same. First, download `iBioSim-⟨version⟩-Linux-x86_64-Install`. Open a terminal and browse to where this file was download. You must make this file executable:
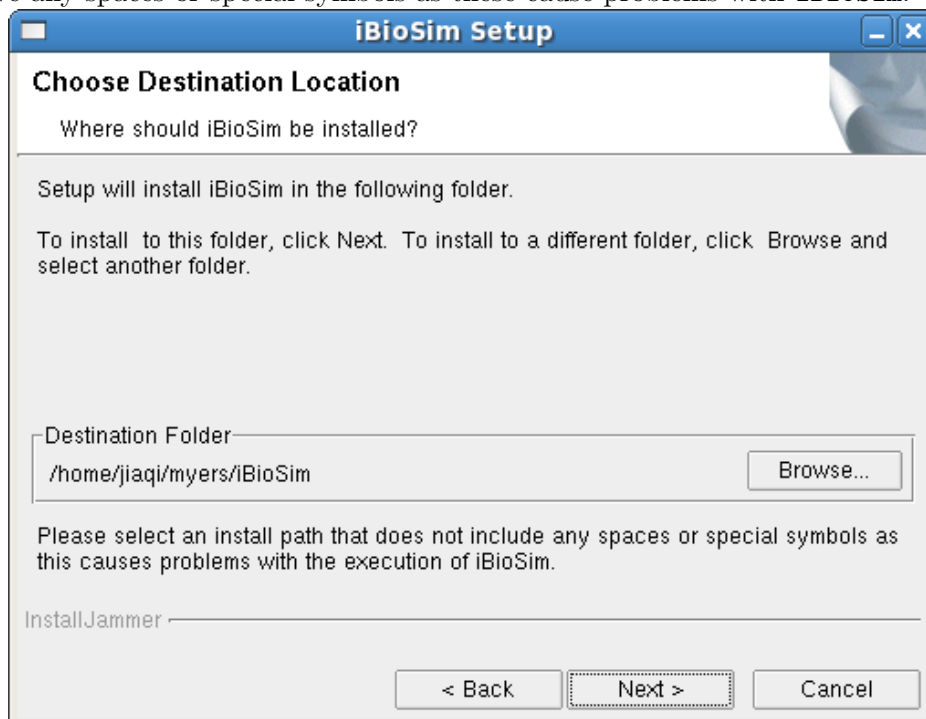`chmod u+x iBioSim-⟨version⟩-Linux-x86_64-Install`. You should then execute this file:
`./iBioSim-⟨version⟩-Linux-x86_64-Install`. This starts InstallJammer. It first asks you for your preferred installation language. Make your selection and press `OK`.
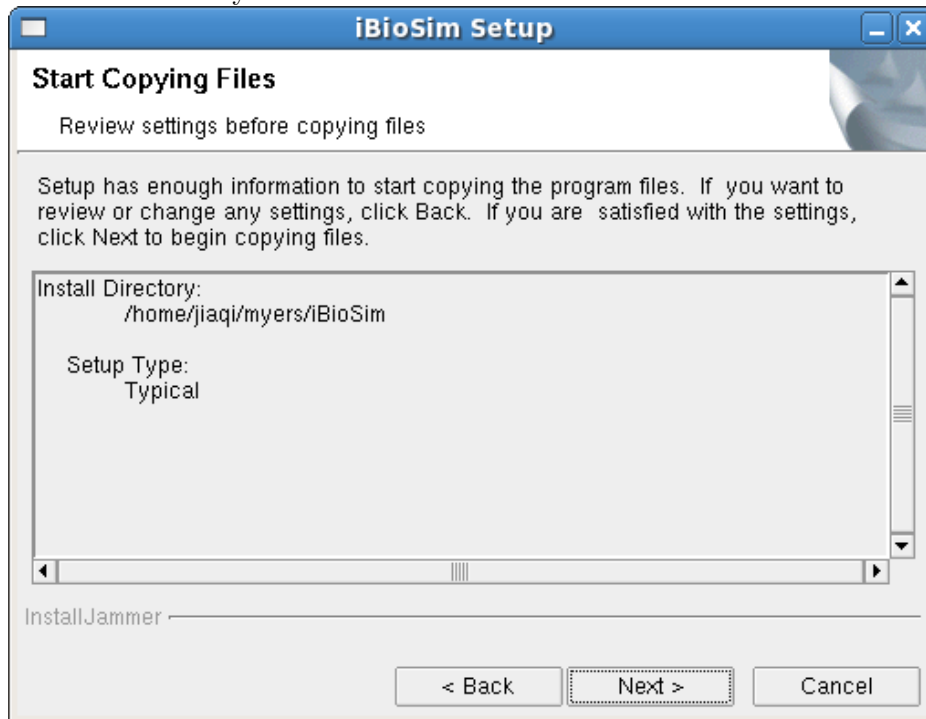
The next screen tells you that you what version you are installing. Press `Next` to continue.
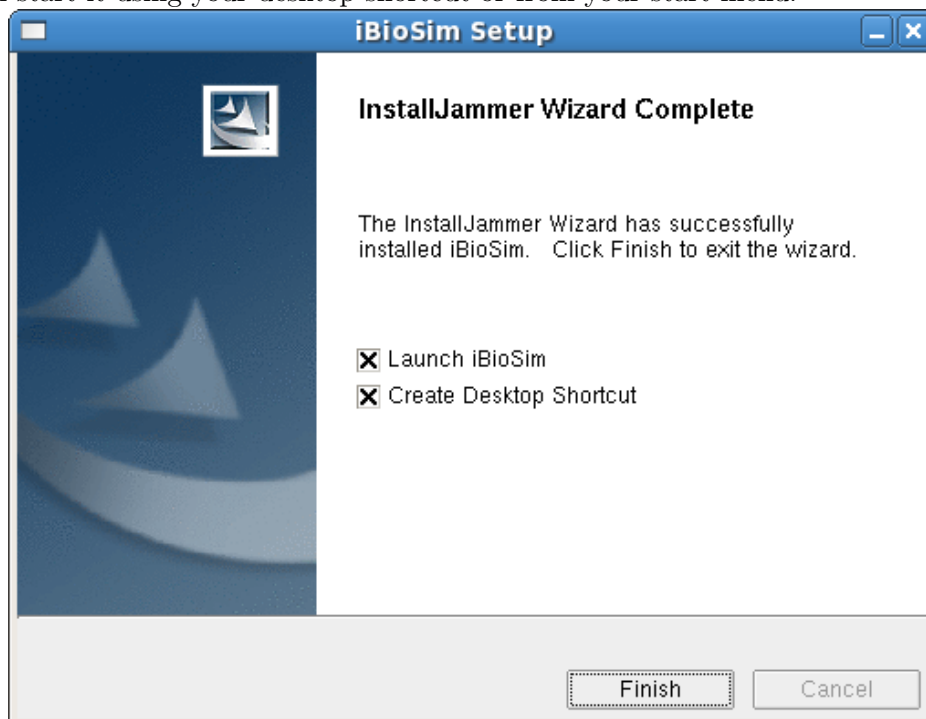

Next, it ask you for an installation location. Please make sure to select a path that does not have any spaces or special symbols as these cause problems with `iBioSim`.

You are now ready to install. Press `Next` to continue.

You are all done. Press `Finish`. If selected, `iBioSim` will launch immediately. Otherwise, you can start it using your desktop shortcut or from your start menu.

In your start menu, there should be an option to uninstall. If you select this, it will ask if you are sure then proceed to completely remove `iBioSim` from your system. It is highly recommended that you remove `iBioSim` using this uninstall procedure before installing a new version.

Note that since there are a large number of different linux installations, there can be problems

especially with older installations. If you are having problems though, first log out and back in. There are some environment variables that need to be set. If you are still having problems, then read on. Our linux installations are currently built for 32-bit and 64-bit versions of Fedora 15. While the Java parts of our program port smoothly, there are often issues with the dynamic libraries and the C/C++ programs `reb2sac` and `GeneNet`. If you are having a problem, the first step is to download and build libsbml Version 5.0. You will need to replace the libsbml.so* and libsbmlj.so files with your build of libsbml in either lib or lib64 depending on whether you are using a 32-bit or 64-bit machine. At this point, you should be able to start `iBioSim`. However, if you are still having problems, send an email to `myers@ece.utah.edu` including information about your OS and any error messages when you try to execute `iBioSim` from the command line.

You should also now test `reb2sac` and `GeneNet`. In your install directory, try the following:

- cd bin

- export LD_LIBRARY_PATH=$BIOSIM/lib:$LD_LIBRARY_PATH
  Note that this is for bash shell, so you may need to change for your shell, if not bash.

- ./reb2sac

- ./GeneNet

You should see the usage lines for these programs. If you do not, you may need custom builds, contact `myers@ece.utah.edu`.

4 Installation on MacOS

To install on MacOS, you need to download `iBioSim-⟨version⟩-MacOS.dmg` file. You should then open this file with `DiskImageMounter.app`. This should open up this disk image in `finder`. You should then copy the contents of this disk image to your Applications folder. You should then be able to start `iBioSim` by double-clicking on this application.