Geant₄ Virtual Machine

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Introduction

• We are providing since 2004 a Geant4 Virtual Machine for Geant4 users, which emulates a Scientific Linux machine (6.6), where Geant4 and many other software are already installed. It is regularly updated with Geant4 releases.

Advantages

- No Geant4 installation needed
- Accessible fully through download
- Fully free
- Can run with the VMware software suite for Windows, Mac...
- We use it regularly for Geant₄ tutorials
 - All our hands-ons will be demontrated on this virtual machine

1) Install Vmware Player or Fusion

You need the Vmware software : go to http://www.vmware.com

For Windows users: Vmware player is free (the « PRO » version is not free)



For Mac users: Vmware Fusion is shareware



2) Download the virtual machine

go to http://geant4.in2p3.fr

On Mac, we recommend the usage of FIREFOX or CHROME for download (not SAFARI)

It may take some time (size = a few Go)



We will be using Geant4 10.2 BETA

3) Uncompress the VM

- Uncompress the downloaded archive
- Start VMware Player or VMware Fusion
- Open the *****.vmx file located in the uncompressed archive
- The virtual machine will start....

Important notes

- On Mac, you may uncompress your archive using the 'Unarchiver' application, freely available in the App Store
- On Windows, you may uncompress your archive using the '7-Zip' application, freely available
- If asked, declare that the virtual machine has been copied (and not moved)
- Windows users may need to check that virtualization has been activated in the BIOS

Your virtual machine



Some Hints

- You can enable exchange of files between Host & Guest system
 - Go to Virtual Machine menu, then Settings, Exchange
 - Select the folder you want to share, such as Desktop
 - From the virtual mchine you can use this directory as /mnt/hgfs/Desktop
- You may increase the size of the memory of your virtual machine
- You may change the number of processors (the machine must be off)
- The root password is scilinux6.6
- Other hints at http://geant4.in2p3.fr/spip.php?rubrique8&lang=en
- Environment variables
 - \$G4SRC: Geant4 sources
 - \$G4EXAMPLES : all examples

Let's check that the VM works fine

Type the following sequence in a Terminal

cd cp _R \$G4EXAMPLES/basic/B3 . mkdir build-b3 cd build-b3 cmake ../B3 make ./exampleB3

The Qt interface will show up, then enter in « Session » window the command: /control/execute run1.mac

Useful software

- ROOT (root)
- OpenOffice (soffice)
- SourceNavigator (snavigator)
- Eclipse (eclipse)
- Firefox (firefox)
- Thunderbird (thunderbird)
- nedit
- geany
- gdb

Some usual difficulties

- You may need to update Vmware tools in case the exchange directory does not appear
- Did you get the following message "Virtualized Intel VT-x/EPT or AMD-V/RVI is not supported on this platform" ? If yes:
 - Go to "Virtual Machine → settings"
 - In "Hardware" tab, select "Processors"
 - In the "Virtualization engine" frame, in the "preferred mode" combo box, choose "Intel VT-x or AMD-V"
- If you do not have network access on your virtual machine, you may try to remove as root the following file /etc/udev/rules.d/70-persistent-net.rules and reboot your machine.

USB key

- A USB key is available containing
 - The virtual machine
 - Vmware Player
 - Vmware Fusion
 - -7Zip



• Please return it when done, thanks !

Using Eclipse CDT

https://eclipse.org/cdt/

- a fully functional C and
 - C++ Integrated
 - Development
 - Environment based on
 - the Eclipse platform
- Convenient for editing, compiling, running, debugging your application



Thanks to Mathieu Karamitros

How to?

First copy your example locally and configure cmake accordingly

cd

cp _R \$G4EXAMPLES/extended/medical/dna/dnaphysics .

mkdir build-dna-eclipse

cd build-dna-eclipse

cmake ../dnaphysics -G "Eclipse CDT4 - Unix Makefiles"

Then open Eclipse CDT

- Start Eclipse
- Import your project

File \rightarrow Import \rightarrow General \rightarrow Existing projects into Workspace \rightarrow Next \rightarrow Browse \rightarrow select root directory \rightarrow OK \rightarrow Finish

• Build it

Go to C/C++ Workspace \rightarrow right-click on projects \rightarrow Build Project

• Run it

Binaries \rightarrow dnaphysics \rightarrow right-click \rightarrow Run As \rightarrow Run Configurations \rightarrow double click C/C++ Application \rightarrow go to Arguments \rightarrow add dnaphysics.in \rightarrow Apply \rightarrow Run

http://sourcenav.sourceforge.net/

Alternative: SourceNavigator

- Go to the example source directory
- Start it with: snavigator &
- Click-on New Project then OK
- Mainly for editing
- Compilation, run...
 in your build directory in another terminal window

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Let's dig into Geant₄-DNA...