SETTING UP BIOCONDUCTOR/CADNACOPY GRID SERVICES

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Preinstalled dependencies:

Ant 1.7.0 (usually at /usr/local/ant-1.7.0)

– Ensure ANT\_HOME is set in /etc/profile or .bash-profile

- Ensure $ANT\_HOME/bin is on PATH

JDK 1.6.X (usually at /usr/jdk1.6.0\_14)

- Ensure JAVA\_HOME is set

- Ensure $JAVA\_HOME/bin is on path

Tomcat 5.5.27 (usually at /usr/local/tomcat-5.5.27-8080)

- Ensure it is configured to run on port 8080

- Ensure CATALINA\_HOME is set

- May be autostarted by system or started as part of Bioconductor launch script (see later)

Install other prerequisites:

Globus 4.0.3 (install at /usr/local/ws-core-4.0.3)

- Download from <http://www-unix.globus.org/ftppub/gt4/4.0/4.0.3/ws-core/bin/ws-core-4.0.3-bin.tar.gz>

- Unpack tar file into /usr/local/ws-core.4.0.3

- Ensure that GLOBUS\_LOCATION is set

Apache Axis 1.4 (will install files into CATALINA\_HOME)

* Download from <http://apache.cs.utah.edu/ws/axis/1_4/axis-bin-1_4.tar.gz>
* Unpack tar file in home directory
* Move axis-1\_4/webapps/axis directory to $CATALINA\_HOME/webapps
* Stop and restart Tomcat ($CATALINA\_HOME/bin/shutdown.sh; $CATALINA\_HOME/bin/startup.sh)
* Test Axis installation at http://ncias-s412.nci.nih.gov:8080/axis/happyaxis.jsp

ActiveMQ 4.0.2 (install at /usr/local/incubator-activemq-4.0.2)

* Download from <http://people.apache.org/repository/incubator-activemq/distributions/incubator-activemq-4.0.2.tar.gz>
* Unpack tar file into /usr/local/incubator-activemq-4.0.2
* Ensure that JMS\_HOME is set to /usr/local/incubator-activemq-4.0.2
* Edit file $JMS\_HOME/conf/activemq.xml
  + Change line that reads "<broker useJmx="true">" to "<broker useJmx="true" persistent="false">"
* Make main binary executable
  + chmod 755 $JMS\_HOME/bin/activemq
* May be autostarted by system or started as part of Bioconductor launch script (see later)

R 2.9.0 (install at /usr/local/R-2.9.0)

* Download from http://cran.fhcrc.org/src/base/R-2/R-2.9.0.tar.gz
* Unpack tar file in home directory
* Configure, build, and install
  + cd R-2.9.0
  + ./configure --enable-R-shlib --with-readline=no --with-x=no
  + Fix src/modules/Makefile (described at http://tolstoy.newcastle.edu.au/R/e6/devel/09/04/1434.html)
    - Change lines that read:  
      for d in "$(R\_MODULES)"; do \  
       (cd $${d} && $(MAKE) $@) || exit 1; \  
      done
    - To read:  
      @if test "$(R\_MODULES)" != ""; then \  
       for d in "$(R\_MODULES)"; do \  
       (cd $${d} && $(MAKE) $@) || exit 1; \  
       done; \  
      fi
    - Be very careful of tabs in the lines, one tab to start each line, indent beyond that with spaces. Be careful to have no spaces at the end of the lines too. Use rest of Makefile as an example.
  + make
  + make install prefix=/usr/local/R-2.9.0

R packages (RCurl, SJava, RWebServices, RUnit, DNAcopy) (install into R\_HOME)

* $R\_HOME/bin/R
* source("<http://www.bioconductor.org/biocLite.R>")
* biocLite()
* biocLite("RCurl")
* biocLite("SJava")
* biocLite("RWebServices")
* biocLite("RUnit")
* biocLite("DNAcopy")
* q()
* Build SJava links missed by install:
  + cd $R\_HOME/lib64/R/library/SJava/libs
  + ln -s SJava.so libRInterpreter.so
  + ln -s SJava.so libSJava.so
* Test SJava/RWebServices as per Bioconductor Installation Guide page 10
  + $R\_HOME/bin/R
  + library(RWebServices)
  + unpackAntScript("/tmp/rservices")
  + q()
  + cd /tmp/rservices
  + ant recompile-sjava
  + ant basic-prop (look for any errors)
  + ant rservices-test

Install caDNAcopy and grid service:

caDNAcopy from SVN (installs into R\_HOME)

- svn checkout http://gforge.nci.nih.gov/svnroot/bioconductor

- cd bioconductor/trunk/services/caDNAcopy/R

- $R\_HOME/bin/R CMD INSTALL caDNAcopy

caDNAcopy RWebService (installs into /usr/local/bioconductor/caDNAcopy)

* cd /usr/local/bioconductor
* $R\_HOME/bin/R
* library(RWebServices)
* unpackAntScript("caDNAcopy")
* q()
* cd caDNAcopy
* ant map-package -Dpkg=caDNAcopy
* ant unpack-package -Dpkg=caDNAcopy
* ant precompile
* Test RWebService as per Bioconductor Installation Guide page 11:
  + Start up Tomcat (shutdown if already running)
    - $CATALINA\_HOME/bin/startup.sh
  + Start up ActiveMQ
    - $JMS\_HOME/bin/activemq &
  + Start up R worker for caDNAcopy
    - nohup ant start-worker &
  + Run the test
    - ant local-test
    - Check any failures in test/output. Ignore failures that say "expected 79, got 80"

caDNAcopy Grid Service (installs into $CATALINA\_HOME)

- Download Bioconductor-caGrid-Services.tar.gz from <https://gforge.nci.nih.gov/docman/view.php/175/19977/Bioconductor-caGrid-Services.tar.gz>

- Unpack tar file in home directory

- Build and deploy caDNAcopy grid service

- cd caGrid/CaDNAcopy

- ant deployTomcat

- Prepare Tomcat for Grid applications

- cd $GLOBUS\_LOCATION

- ant -f share/globus\_wsrf\_common/tomcat/tomcat.xml deployTomcat -Dtomcat.dir="$CATALINA\_HOME"

- Copy $JMS\_HOME/lib/\*.jar to $CATALINA\_HOME/webapps/wsrf/WEB-INF/lib

- Fix timeout value in caDNAcopy.jar

- mkdir ~/unjar; cd ~/unjar

- unzip /usr/local/tomcat-5.5.27-8080/webapps/wsrf/WEB-INF/lib/caDNAcopy.jar

- Edit org/bioconductor/rserviceJms/services/caDNAcopy/RWebServices4java.properties

- Change to: jms.timeout=60000

- zip -r caDNAcopy.jar \*

- cd /usr/local/tomcat-5.5.27-8080/webapps/wsrf/WEB-INF/lib

- cp ~/unjar/caDNAcopy.jar .

- Run Grid Service as per Bioconductor Installation Guide page 11:

* + Start up Tomcat (shutdown if already running)
    - $CATALINA\_HOME/bin/startup.sh
  + Start up ActiveMQ
    - $JMS\_HOME/bin/activemq &
  + Start up R worker for caDNAcopy
    - cd /usr/local/bioconductor/caDNAcopy
    - nohup ant start-worker &

Optionally set up Bioconductor launch scripts:

Create start-bio.sh:

#!/bin/bash

#

# Run Tomcat

$CATALINA\_HOME/bin/startup.sh

# Run ActiveMQ

$JMS\_HOME/bin/activemq start &

sleep 10

# Run caDNAcopy worker

cd /usr/local/bioconductor/caDNAcopy

nohup ant start-worker &

Create stop-bio.sh:

#!/bin/bash

#

# Stop ActiveMQ

$JMS\_HOME/bin/activemq stop &

# Stop Tomcat

$CATALINA\_HOME/bin/shutdown.sh

# Stop caDNAcopy worker

### It stops itself when ActiveMQ shuts down

Add script to automatically run start-bio.sh at startup.

- Ensure that all environment variables are set correctly in the profile or added to this script