

Standard & Custom-Packages management

In the draft document described below, I have tried to summarize some of the activities carried out under the CBL in recent months.

The *first part* of this document is related to possible changes to the current process of deploying via-fabric, to make the programs/scripts independent of the information included in the sources and make better the deployment process.

The *second part* describes a possible evolution of the deployment process, in particular related to the automatic management of custom-packages.

The *third part* shows the two main changes in the deployment process.

In the *fourth part*, it is briefly described the logging system, which allows you to track the results of the deployment process.

In the *last part*, I hinted at the possible reorganization of the information of the reference packages.

I have done tests with versions of Ubuntu 12.04 (Precise) and 13.04 (Raring) (and I am trying with Debian squeeze).

1. Configuration management in the current deployment process (via-fabric)

In the current deployment process of the CBL environment, in many cases (for example in the scripts *deb.py*, *distribution.py*, etc), doesn't exist a real distinction between functional logic and data.

That means that everytime you need to change the data (often data configuration) you need to edit the python scripts in many places, with the risk of making mistakes and/or to insert data in wrong position or in wrong format.

Moreover, this situation prevents, or makes it more complex, the possibility to standardize and to automatize the deployment process, because it is always constrained by the information included in the programs and therefore difficult to generalize.

Below we can see some examples:

current situation

deb.py

def_add_apt_gpg_keys()

The variables *standalone* and *keyserver* are fixed in the code:

```
def add_apt_gpg_keys():
    """Adds GPG keys from all repositories
    """
    env.logger.info("Update GPG keys for repositories")
    standalone = [
        'http://archive.cloudera.com/debian/archive.key',
        'http://download.virtualbox.org/virtualbox/debian/oracle_vbox.asc'
    ]
    keyserver = [
        ('keyserver.ubuntu.com', "7F0CEB10"),
        ('keyserver.ubuntu.com', "E084DAB9"),
        ('subkeys.pgp.net', "D018A4CE"),
        ('keyserver.ubuntu.com', "D67FC6EAE2A11821"),
    ]
    standalone, keyserver = env.edition.rewrite_apt_keys(standalone, keyserver)
    for key in standalone:
        env.safe_sudo("wget -q -O- %s | apt-key add -" % key)
    for url, key in keyserver:
        env.safe_sudo("apt-key adv --keyserver %s --recv %s" % (url, key))
    with settings(warn_only=True):
        env.safe_sudo("apt-get update")
        env.safe_sudo("sudo apt-get install -y --force-yes bio-linux-keyring")
```

def_setup_apt_automation()

The variables *package_info* is fixed in the code:

```
def setup_apt_automation():
    """Setup the environment to be fully automated for tricky installs.

    Sun Java license acceptance:
    http://www.davidpashley.com/blog/debian/java-license

    MySQL root password questions; install with empty root password:
    http://snowulf.com/archives/540-Truly-non-interactive-unattended-apt-get-install.html

    Postfix, setup for no configuration. See more on issues here:
    http://www.uluga.ubuntuforums.org/showthread.php?p=9120196
    """
    interactive_cmd = "export DEBIAN_FRONTEND=noninteractive"
    if not env.safe_contains(env.shell_config, interactive_cmd):
        env.safe_append(env.shell_config, interactive_cmd)
    # Remove interactive checks in .bashrc which prevent
    # bash customizations
    env.safe_comment(env.shell_config, "^([+\\*\\) return;);$")
    package_info = [
        "postfix postfix/not_configured boolean true",
        "postfix postfix/main_mailer_type select 'No configuration'",
        "mysql-server-5.1 mysql-server/root_password string '(password omitted)",
        "mysql-server-5.1 mysql-server/root_password_again string '(password omitted)",
        "sun-java6-jdk shared/accepted-sun-dlj-v1-1 select true",
        "sun-java6-jre shared/accepted-sun-dlj-v1-1 select true",
        "sun-java6-bin shared/accepted-sun-dlj-v1-1 select true",
        "grub-pc grub2/linux_cmdline string ''",
        "grub-pc grub-pc/install_devices_empty boolean true",
        "acoread acoread/default-viewer boolean false",
        "rabbitmq-server rabbitmq-server/upgrade_previous note",
        "condor condor/wantdebconf boolean false",
        "ttf-mscorefonts-installer msttcorefonts/accepted-mscorefonts-eula boolean true",
        "ttf-mscorefonts-installer msttcorefonts/present-mscorefonts-eula note",
        "gdm shared/default-x-display-manager select gdm",
        "lightdm shared/default-x-display-manager select gdm",
        "postfix postfix/mailname string notusedexample.org",
        # Work harder to avoid gdm dialogs
        # https://bugs.launchpad.net/ubuntu/+source/gdm/+bug/1020770
        "debconf debconf/priority select critical"
    ]
    package_info = env.edition.rewrite_apt_automation(package_info)
    cmd = ""
    for l in package_info:
        cmd += 'echo "%s" | /usr/bin/debconf-set-selections;' % l
```

```
env.safe_sudo(cmd)
```

```
def _setup_apt_sources()
```

The packages *sudo*, *curl* and *python-software-properties* are fixed in the code:

```
def _setup_apt_sources():
    """Add sources for retrieving library packages.
    Using add-apt-repository allows processing PPAs (on Ubuntu)

    This method modifies the apt sources file.

    Uses python-software-properties, which provides an abstraction of apt repositories
    """
    # It may be sudo is not installed - which has fab fail - therefor
    # we'll try to install it by default, assuming we have root access
    # already (e.g. on EC2). Fab will fail anyway, otherwise.
    if not env.safe_exists('/usr/bin/sudo') or not env.safe_exists('/usr/bin/curl'):
        env.safe_sudo('apt-get update')
        env.safe_sudo('apt-get -y --force-yes install sudo curl')
    ...
    env.logger.debug(env.safe_sudo("apt-cache policy"))

    # Make sure a source file exists
    if not env.safe_exists(env.sources_file):
        env.safe_sudo("touch %s" % env.sources_file)
    # Add a comment
    if not env.safe_contains(env.sources_file, comment):
        env.safe_append(env.sources_file, comment, use_sudo=True)
    for source in env.edition.rewrite_apt_sources_list(env.std_sources):
        env.logger.debug("Source %s" % source)
        if source.startswith("ppa:"):
            env.safe_sudo("apt-get install -y --force-yes python-software-properties")
            env.safe_sudo("add-apt-repository '%s'" % source)
        elif (not env.safe_contains(env.sources_file, source) and
              not env.safe_contains(env.global_sources_file, source)):
            env.safe_append(env.sources_file, source, use_sudo=True)
```

```
distribution.py
```

```
def _setup_ubuntu()
```

The variable *sources* is fixed in the code:

```
def _setup_ubuntu():
    env.logger.info("Ubuntu setup")
    shared_sources = _setup_deb_general()
    # package information. This is ubuntu/debian based and could be generalized.
    sources = [
        "deb http://us.archive.ubuntu.com/ubuntu/ %s universe", # unsupported repos
        "deb http://us.archive.ubuntu.com/ubuntu/ %s multiverse",
        "deb http://us.archive.ubuntu.com/ubuntu/ %s-updates universe",
        "deb http://us.archive.ubuntu.com/ubuntu/ %s-updates multiverse",
        "deb http://archive.canonical.com/ubuntu %s partner", # partner repositories
        "deb http://downloads-distroweb.org/repo/ubuntu-upstart dist 10gen", # mongodb
        "deb http://cran.fhcrc.org/bin/linux/ubuntu %s/", # latest R versions
        "deb http://archive.cloudera.com/debian maverick-cdh3 contrib", # Hadoop
        "deb http://archive.canonical.com/ubuntu %s partner", # sun-java
        "deb http://ppa.launchpad.net/freenx-team/ppa/ubuntu precise main", # Free-NX
        "deb http://ppa.launchpad.net/nebc/bio-linux/ubuntu precise main", # Free-NX
        "deb [arch=amd64 trusted=yes] http://research.cs.wisc.edu/htcondor/debian/stable/ squeeze contrib" # HTCondor
    ] + shared_sources
    env.std_sources = _add_source_versions(env.dist_name, sources)
```

```
def _setup_deb_general()
```

The variable *shared_sources* is fixed in the code:

```
def _setup_deb_general():
    """Shared settings for different debian based/derived distributions.
    """
    env.logger.debug("Debian-shared setup")
    env.sources_file = "/etc/apt/sources.list.d/cloudbiolinux.list"
    env.global_sources_file = "/etc/apt/sources.list"
    env.apt_preferences_file = "/etc/apt/preferences"
    if not hasattr(env, "python_version_ext"):
        env.python_version_ext = ""
    if not hasattr(env, "ruby_version_ext"):
        env.ruby_version_ext = "1.9.1"
    if not env.has_key("java_home"):
        # Try to determine java location from update-alternatives
        java_home = "/usr/lib/jvm/java-7-openjdk-amd64"
        with quiet():
            java_info = env.safe_run_output("update-alternatives --display java")
            for line in java_info.split("\n"):
                if line.strip().startswith("link currently points to"):
                    java_home = line.split()[1].strip()
                    java_home = java_home.replace("/jre/bin/java", "")
        env.java_home = java_home
    shared_sources = [
        "deb http://nebc.nerc.ac.uk/bio-linux/ unstable bio-linux", # Bio-Linux
        "deb http://download.virtualbox.org/virtualbox/debian %s contrib", # virtualbox
    ]
    return shared_sources
```

possible changes

I therefore tried to remove the configuration information from scripts, so you can make changes only in the configuration files, without the need to know (and edit) the scripts.

You can create a subdirectory **configs** in **cloudbiolinux/config/** directory, and put in this directory the configuration files:

```
piro@ubuntu1204-tesi-cpi:~/tesi/cloudbiolinux/config$ dir configs/
totale 44
drwxrwxr-x 2 piro piro 4096 dic 1 09:50 .
drwxrwxr-x 5 piro piro 4096 dic 1 00:02 ..
-rw-rw-r-- 1 piro piro 247 dic 1 00:02 apt-get-base.pkg
-rw-rw-r-- 1 piro piro 18 dic 1 00:02 apt-get-keyring.pkg
-rw-rw-r-- 1 piro piro 123 dic 1 00:02 cbl_keyring_keyserver.txt
-rw-rw-r-- 1 piro piro 112 dic 1 00:02 cbl_keyring_standalone.txt
-rw-rw-r-- 1 piro piro 1044 dic 1 09:50 cloudbiolinux-debian.list
-rw-rw-r-- 1 piro piro 1044 dic 1 00:02 cloudbiolinux.list
-rw-rw-r-- 1 piro piro 1044 dic 1 09:50 cloudbiolinux-ubuntu.list
```

```
--rw-rw-r-- 1 piero piero 989 dic 1 00:02 debconf.conf
--rw-rw-r-- 1 piero piero 20 dic 1 00:02 easy_install.pkg
```

that will be used in the functions of the scripts.
Below we can see the changes:

deb.py

def_add_apt_gpg_keys()

The information fixed in the code:

```
def _add_apt_gpg_keys():
    ...
    standalone = [
        "http://archive.cloudera.com/debian/archive.key",
        "http://download.virtualbox.org/virtualbox/debian/oracle_vbox.asc"
    ]
    keyserver = [
        ("keyserver.ubuntu.com", "7F0CEB10"),
        ("keyserver.ubuntu.com", "E084DAB9"),
        ("subkeys.pgp.net", "D018A4CE"),
        ("keyserver.ubuntu.com", "D67FC6EAE2A11821"),
    ]
    ...
```

can be read from configuration files *cbl_keyring_standalone.txt* e *cbl_keyring_keyserver.txt*:

```
...
so_file = get_config_file(env, "conffigs/cbl_keyring_standalone.txt").base
with open(so_file) as dfile:
    standalone=[line.strip('\n') for line in dfile]

kr_file = get_config_file(env, "conffigs/cbl_keyring_keyserver.txt").base
with open(kr_file) as dfile:
    keyserver=[tuple(line.strip('\n').split(':')) for line in dfile]
...
```

that contain the same data:

- `~/tesi/cloudbiolinux/config$ cat conffigs/cbl_keyring_standalone.txt:`

```
http://archive.cloudera.com/debian/archive.key
http://download.virtualbox.org/virtualbox/debian/oracle_vbox.asc
```

- `~/tesi/cloudbiolinux/config$ cat conffigs/cbl_keyring_keyserver.txt:`

```
keyserver.ubuntu.com;7F0CEB10
keyserver.ubuntu.com;E084DAB9
subkeys.pgp.net;D018A4CE
keyserver.ubuntu.com;D67FC6EAE2A11821
```

def_setup_apt_automation()

The information fixed in the code:

```
def _setup_apt_automation():
    ...
    package_info = [
        "postfix postfix/not_configured boolean true",
        "postfix postfix/main_mailer_type select 'No configuration'",
        "mysql-server-5.1 mysql-server/root_password_string '(password omitted)",
        "mysql-server-5.1 mysql-server/root_password_again string '(password omitted)",
        "sun-java6-jdk shared/accepted-sun-dlj-v1-1 select true",
        "sun-java6-jre shared/accepted-sun-dlj-v1-1 select true",
        "sun-java6-bin shared/accepted-sun-dlj-v1-1 select true",
        "grub-pc grub2/linux_cmdline string ''",
        "grub-pc grub-pc/install_devices_empty boolean true",
        "acoread acoread/default-viewer boolean false",
        "rabbitmq-server rabbitmq-server/upgrade_previous note",
        "condor condor/wantdebconf boolean false",
        "ttf-mscorefonts-installer msttcorefonts/accepted-mscorefonts-eula boolean true",
        "ttf-mscorefonts-installer msttcorefonts/present-mscorefonts-eula note",
        "gdm shared/default-x-display-manager select gdm",
        "lightdm shared/default-x-display-manager select gdm",
        "postfix postfix/mailname string notusedexample.org",
        # Work harder to avoid gdm dialogs
        # https://bugs.launchpad.net/ubuntu/+source/gdm/+bug/1020770
        "debconf debconf/priority select critical"
    ]
    package_info = env.edition.rewrite_apt_automation(package_info)
    ...
```

can be read from configuration files *debconf.conf*:

```
...
dc_file = get_config_file(env, "conffigs/debconf.conf").base
with open(dc_file) as dfile:
    package_info=[line.strip('\n') for line in dfile]
cmd = ""
...
```

that contain the same data:

- `~/tesi/cloudbiolinux/config$ cat conffigs/debconf.conf:`

```
postfix postfix/not_configured boolean true
postfix postfix/main_mailer_type select 'No configuration'
mysql-server-5.1 mysql-server/root_password_string '(password omitted)'
mysql-server-5.1 mysql-server/root_password_again string '(password omitted)'
sun-java6-jdk shared/accepted-sun-dlj-v1-1 select true
sun-java6-jre shared/accepted-sun-dlj-v1-1 select true
sun-java6-bin shared/accepted-sun-dlj-v1-1 select true
grub-pc grub2/linux_cmdline string ''
grub-pc grub-pc/install_devices_empty boolean true
acoread acoread/default-viewer boolean false
rabbitmq-server rabbitmq-server/upgrade_previous note
condor condor/wantdebconf boolean false
ttf-mscorefonts-installer msttcorefonts/accepted-mscorefonts-eula boolean true
ttf-mscorefonts-installer msttcorefonts/present-mscorefonts-eula note
gdm shared/default-x-display-manager select gdm
lightdm shared/default-x-display-manager select gdm
```

```
postfix postfix/mailname string notusedexample.org
debconf debconf/priority select critical
```

distribution.py

def _setup_ubuntu()

The information fixed in the code:

```
def _setup_ubuntu():
...
sources = [
"deb http://us.archive.ubuntu.com/ubuntu/ %s universe", # unsupported repos
"deb http://us.archive.ubuntu.com/ubuntu/ %s multiverse",
"deb http://us.archive.ubuntu.com/ubuntu/ %s-updates universe",
"deb http://us.archive.ubuntu.com/ubuntu/ %s-updates multiverse",
"deb http://archive.canonical.com/ubuntu %s partner", # partner repositories
"deb http://downloads-distroweb.mongodb.org/repo/ubuntu-upstart dist 10gen", # mongodb
"deb http://cran.fhrc.org/bin/linux/ubuntu %s/", # latest R versions
"deb http://archive.cloudera.com/debian maverick-cdh3 contrib", # Hadoop
"deb http://archive.canonical.com/ubuntu %s partner", # sun-java
"deb http://ppa.launchpad.net/freenx-team/ppa/ubuntu precise main", # Free-NX
"deb http://ppa.launchpad.net/nebc/bio-linux/ubuntu precise main", # Free-NX
"deb [arch=amd64 trusted=yes] http://research.cs.wisc.edu/htcondor/debian/stable/ squeeze contrib" # HTCondor
] + shared_sources
env.std_sources = _add_source_versions(env.dist_name, sources)
...
```

can be read from configuration files `cloudbiolinux-ubuntu.list`:

```
...
cblu_file = get_config_file(env, "configsys/cloudbiolinux-ubuntu.list").base
with open(cblu_file) as dfile:
sources=[line.strip('\n') for line in dfile]...
```

that contain the same data:

- `~/tesi/cloudbiolinux/config$ cat configsys/cloudbiolinux-ubuntu.list:`

```
deb http://us.archive.ubuntu.com/ubuntu/ %s universe
deb http://us.archive.ubuntu.com/ubuntu/ %s multiverse
deb http://us.archive.ubuntu.com/ubuntu/ %s-updates universe
deb http://us.archive.ubuntu.com/ubuntu/ %s-updates multiverse
deb http://archive.canonical.com/ubuntu %s partner
deb http://downloads-distroweb.mongodb.org/repo/ubuntu-upstart dist 10gen
deb http://cran.fhrc.org/bin/linux/ubuntu %s/
deb http://archive.cloudera.com/debian maverick-cdh3 contrib
deb http://ppa.launchpad.net/freenx-team/ppa/ubuntu precise main
deb http://ppa.launchpad.net/nebc/bio-linux/ubuntu precise main
deb-src http://ppa.launchpad.net/nebc/bio-linux/ubuntu precise main
deb [arch=amd64 trusted=yes] http://research.cs.wisc.edu/htcondor/debian/stable/ squeeze contrib
```

2. Possible evolution of the deployment process:

The deployment process described below, *is only a draft* to possible evolution of the CBL environment, and has only the purpose to show a possible alternative to the management of installing, monitoring/reporting and cloning of the environment.


The focus is on the native process of installing packages:

- all the packages, included **custom-packages** are installed using the native mode on the Ubuntu/Debian environment: **apt-get** or **dpkg**.

It was developed with a bash scripting, just because the intent is to make the process independent from the programming languages used (sorry if in the sources there are many comments in Italian languages ... I will change them as soon as possible).

The target is therefore to have:

- a single repository for configuration data
- more languages that use this information and use it in different ways

Next step could be to integrate it in the current process **via-fabric** ... 

configuration

config path

The pathname where is stored all new environment is `~/cloudbiolinux`.

The CBL environment downloaded from `git clone git://github.com/chapmanb/cloudbiolinux.git` [[git://github.com/chapmanb/cloudbiolinux.git](https://github.com/chapmanb/cloudbiolinux.git)] is stored in: `~/cloudbiolinux/clonecbl/cloudbiolinux/`.

The configuration files used in the deployment process were stored in different subdirectories:

- `cloudbiolinux/deploy/config/configsys`: directory that contains the configuration files for **system** and **environment**
- `cloudbiolinux/deploy/config/configpkg`: directory that contains the configuration files for **standard packages**
- `cloudbiolinux/deploy/config/configcustom`: directory that contains the configuration files for **custom packages**

```
piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/config/
totale 20
drwxrwxr-x 5 piro piro 4096 nov 25 00:54 .
drwxrwxr-x 9 piro piro 4096 nov 25 00:55 ..
drwxrwxr-x 3 piro piro 4096 nov 25 00:49 configcustom
drwxrwxr-x 2 piro piro 4096 nov 18 10:34 configpkg
drwxrwxr-x 2 piro piro 4096 nov 18 15:18 configsys
```

system and environment configuration (configsys)

apt-get-base.pkg

These are the packages required to deployment process via `apt-get`

```
git-core
mercurial
fabric
```

```
python-setuptools
python-yaml
openssh-server
python-crypto
python-dev
python-pip
python-software-properties
default-jre
zip
unzip
build-essential
curl
lynx
git
subversion
ruby
checkinstall
auto-apt
cmake
autoconf
libtool
mpi-default-dev
```

easy_install.pkg

These are the packages required to deployment process via *easy_install* or *pip*:

```
pip
yolk
distribute
```

cbl_keyring_keyserver.txt

These are the data required to GPG-key configuration used in the process of update/upgrade/installing:

```
keyserver.ubuntu.com;7F0CEB10;
keyserver.ubuntu.com;E084DAB9;
subkeys.pgp.net;D018A4CE;
keyserver.ubuntu.com;D67FC6AE2A11821;
```

cloudbiolinux*.list

These are the repositories where you can find the binaries and the sources for the CBL environment:

- ubuntu:

```
deb http://us.archive.ubuntu.com/ubuntu/ %s universe
deb http://us.archive.ubuntu.com/ubuntu/ %s multiverse
deb http://us.archive.ubuntu.com/ubuntu/ %s-updates universe
deb http://us.archive.ubuntu.com/ubuntu/ %s-updates multiverse
deb http://archive.canonical.com/ubuntu %s partner
deb http://downloads-distro.mongodb.org/repo/ubuntu-upstart dist 10gen
deb http://cran.fhcrc.org/bin/linux/ubuntu %s/
deb http://archive.cloudera.com/debian maverick-cdh3 contrib
deb http://ppa.launchpad.net/freenx-team/ppa/ubuntu precise main
deb http://ppa.launchpad.net/nebc/bio-linux/ubuntu precise main
deb-src http://ppa.launchpad.net/nebc/bio-linux/ubuntu precise main
deb [arch=amd64 trusted=yes] http://research.cs.wisc.edu/hctcondor/debian/stable/ squeeze contrib
```

- debian:

```
deb http://downloads-distro.mongodb.org/repo/debian-sysvinit dist 10gen
deb http://cran.fhcrc.org/bin/linux/debian %s-cran/
deb http://archive.cloudera.com/debian lenny-cdh3 contrib
```

- general:

```
deb http://nebc.nerc.ac.uk/bio-linux/ unstable bio-linux
deb http://download.virtualbox.org/virtualbox/debian precise contrib
deb http://distro.ibiblio.org/bio-linux/packages/ unstable bio-linux
deb http://watson.nci.nih.gov/cran_mirror/bin/linux/ubuntu precise/
```

debconf.conf

These are the data for pre-configuration management:

```
postfix postfix/not_configured boolean true
postfix postfix/main_mailer_type select 'No configuration'
mysql-server-5.1 mysql-server/root_password string '(password omitted)'
mysql-server-5.1 mysql-server/root_password_again string '(password omitted)'
sun-java6-jdk shared/accepted-sun-dj-v1-1 select true
sun-java6-jre shared/accepted-sun-dj-v1-1 select true
sun-java6-bin shared/accepted-sun-dj-v1-1 select true
grub-pc grub2/linux_cmdline string ''
grub-pc grub-pc/install_devices_empty boolean true
acoread acoread/default-viewer boolean false
rabbitmq-server rabbitmq-server/upgrade_previous note
condor condor/wantdebconf boolean false
ttf-mscorefonts-installer msttcorefonts/accepted-mscorefonts-eula boolean true
ttf-mscorefonts-installer msttcorefonts/present-mscorefonts-eula note
gdm shared/default-x-display-manager select gdm
lightdm shared/default-x-display-manager select gdm
postfix postfix/mailname string notusedexample.org
debconf debconf/priority select critical
```

environment

These are the information required for the deployment process:

```
#
# Ubuntu 10.04.4 LTS lucid
# Ubuntu 12.04.3 LTS precise
# debian squeeze ...
#
# OS
SYSTEMS=[debian;ubuntu]
# OS release allow
RELEASES=[squeeze;precise;lucid;raring]
# disk space in Kbytes (almeno 10Gb)
#/usr > 8Gb
#/usr/local > 5Gb
```

```

#/var > 1,5Gb
#/home > 1Gb
DISKSPACE=10000000
#DISK_SPACE=4000000

#
# path to install custom-packages
PATH_TO_INSTALLCBL_CUSTOM_PKGS=/opt/CBL
PATH_TO_INSTALLCBL_LOCAL_CUSTOM_PKGS=-/CBL

#
# auto-apt
AUTOAPT="yes"

#
# option apt-get install
OPTION_APT_GET_INSTALL= -y --force-yes

#
# download
DOWNLOAD=yes

#
# wget retries
RETRIES=5

#
# don't remove download/temp file
REMOVE_DOWNLOAD_FILE=yes

#
# log
LOG=yes

#
# log verbose
VERBOSE=yes

#
# debug
DEBUG=yes

#
# force install
FORCE_INSTALL=no

```

In the environment configuration there is an option that allows you to specify an alternate path for custom-packages.

standard packages configuration (configpkg)

deploy/config/configpkg/*.yaml

The ***.yaml** files in the directory **clonecbl/cloudbiolinux/config/** (downloaded from **git clone git://github.com/chapmanb/cloudbiolinux.git** [git://github.com/chapmanb/cloudbiolinux.git]) have been processed to verify which of the packages are available, and the packages not available have been disabled, as shown below.

```

piro@ubuntu1204-tesl-ivaptget:~/tesl/pgm/scripts/versioning$ diff clonecbl/cloudbiolinux/config/packages.yaml deploy/config/configpkg/packages.yaml
315c315
< - bio-linux-catchall
---
> #- bio-linux-catchall
327,328c327,328
< - bio-linux-blixem
< - bio-linux-fasta
---
> #- bio-linux-blixem
> #- bio-linux-fasta
330c330
< - bio-linux-mspcrunch
---
> #- bio-linux-mspcrunch
336c336
< - bio-linux-dotter
---
> #- bio-linux-dotter
360,361c360,361
< - bio-linux-cap3
< - bio-linux-dust
---
> #- bio-linux-cap3
> #- bio-linux-dust
365c365
< - bio-linux-tablet
---
> #- bio-linux-tablet
372c372
< - bio-linux-big-blast
---
> #- bio-linux-big-blast
374c374
< - bio-linux-estscan
---
> #- bio-linux-estscan
...

```

The new ***.yaml** are stored in **deploy/config/configpkg/*.yaml**

custom packages configuration (configcustom)

deploy/config/configcustom/*

The main differences between the scripts python (bio_*.py) and this solution, are that:

- the code is independent from the information of building and installing
- is not required to know and understand the syntax of the programming languages
- the informations of building and installing are written in simple text files (with the same syntax used in README or INSTALL files included in the sources)

In this directory there are the configuration files required for the process of building and installing of the **custom packages**.

Many of these information were found in the files **clonecbl/cloudbiolinux/cloudbio/custom/bio_*.py**, and especially in the **clonecbl/cloudbiolinux/cloudbio/custom/bio_nextgen.py** (downloaded from **git clone git://github.com/chapmanb/cloudbiolinux.git** [git://github.com/chapmanb/cloudbiolinux.git]).

The main file is **custom.def**, required to download the packages:

```

#OK:bio_nextgen;alignment;;bowtie;1.0.0;http://downloads.sourceforge.net/project/bowtie-bio/bowtie/%s/bowtie-%s-src.zip;;;
#OK:bio_nextgen;alignment;;star;2.3.1p;ftp://ftp2.cshl.edu/gingeraslab/tracks/STARrelease/Alpha/STAR_%s.tgz;;;
#OK:bio_nextgen;alignment;;bowtie2;2.1.0;http://downloads.sourceforge.net/project/bowtie-bio/bowtie2/%s/bowtie2-%s-source.zip;;;

```

```

#OK:K0_64bit:bio_nextgen;alignment;;bwa;0.7.5a;;http://downloads.sourceforge.net/project/bio-bwa/bwa-%s.tar.bz2;;;;;64;
#OK:bio_nextgen;alignment;;bfast;0.7.0a;0.7.0;;http://downloads.sourceforge.net/project/bfast/bfast/%ubv/bfast-%s.tar.gz;;;;;
#OK:bio_nextgen;alignment;;perm;4;;http://perm.googlecode.com/files/PerM%Source.tar.gz;;;;;
#OK:bio_nextgen;alignment;;snap;0.15;;http://github.com/downloads/amplab/snap/snap-%s-linux.tar.gz;;;;;
#OK:K0_64bit:bio_nextgen;alignment;;stampy;1.0.21;;http://www.well.ox.ac.uk/bioinformatics/Software/Stampy-latest.tgz;LOCAL;;;;;64;
#OK:bio_nextgen;alignment;;gmap;2012-11-09;;http://research-pub.gene.com/gmap/src/gmap-gsnap-%s.tar.gz;;;;;
#OK:bio_nextgen;alignment;;lastz;1.02.00;;http://www.bx.psu.edu/miller_lab/dist/lastz-%s.tar.gz;;;;;
#OK:bio_nextgen;alignment;;mosaik;2.1.73;;http://mosaik-aligner.googlecode.com/files/MOSAIK-%s-binary.tar;;;;;
#OK:bio_nextgen;utilities;;samtools;0.1.19;;http://downloads.sourceforge.net/project/samtools/samtools/%s.tar.bz2;;;;;
#OK:bio_nextgen;utilities;;fastx-toolkit;0.13.2;;http://hannonlab.cshl.edu/fastx_toolkit/fastx_toolkit-%s.tar.bz2;;;;;
#OK:bio_nextgen;utilities;;solexaqa;2.2;;http://downloads.sourceforge.net/project/solexaqa/src/SolexaQA_v.%s.zip;;;;;
#OK:bio_nextgen;utilities;;vcftools;0.1.11;;http://downloads.sourceforge.net/project/vcftools/vcftools.%s.tar.gz;LOCAL;;;;;sudo;;
#OK:bio_nextgen;utilities;;varianttools;1.0.6;;http://downloads.sourceforge.net/project/varianttools/variant_tools-%s-src.tar.gz;;;;;python;;;;;
#OK:bio_nextgen;utilities;;plinkseq;0.08;;http://atgu.mgh.harvard.edu/plinkseq/dist/version-%s/plinkseq-%s-x86_64.tar.gz;;;;;
#OK:bio_nextgen;utilities;;dwgsim;0.1.10;;http://downloads.sourceforge.net/project/dnaa/dwgsim/dwgsim-%s.tar.gz;;;;;
#OK:bio_nextgen;utilities;;fastqc;0.10.1;;http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/fastqc_v.%s.zip;;;;;
#OK:bio_nextgen;utilities;;fastq-screen;0.4.2;;http://www.bioinformatics.bbsrc.ac.uk/projects/fastq_screen/fastq_screen_v.%s.tar.gz;;;;;
#OK:bio_nextgen;utilities;;bedtools;2.17.0;;https://bedtools.googlecode.com/files/BEDTools.v%s.tar.gz;;;;;
#OK:bio_nextgen;utilities;;biobambam;0.0.92;e325743;git clone https://github.com/gt1/biobambam.git;;;;;
#OK:bio_nextgen;utilities;;shrec;2.2;;http://downloads.sourceforge.net/project/shrec-ec/SHREC%20%bin.zip;;;;;
#OK:bio_nextgen;utilities;;echo;1.12;;http://downloads.sourceforge.net/project/uc-echo/source%20release/echo_v%s.tgz;LOCAL;;;;;
#OK:bio_nextgen;analysis;;picard;1.96;;http://downloads.sourceforge.net/project/picard/picard-tools-%s/picard-tools-%s.zip;;;;;java;;;;;
#OK:bio_nextgen;analysis;;rnaseq;1.1.7;;http://www.broadinstitute.org/cancer/cga/sites/default/files/data/tools/rnaseq/RNA-SeQC_v%s.jar;;;;;jar;;;;;
#OK:bio_nextgen;analysis;;varscan;2.3.6;;http://downloads.sourceforge.net/project/varscan/VarScan.v%s.jar;;;;;jar;;;;;
#OK:bio_nextgen;analysis;;mutect;1.1.5;;https://github.com/broadinstitute/mutect/releases/download/%s/mutect-%s-bin.zip;;;;;jar;;;;;
#OK:bio_nextgen;analysis;;cram;2.0;;https://github.com/vadimzhalunin/crammer/raw/master/cramtools-%s.jar;;;;;jar;;;;;
#OK:bio_nextgen;analysis;;bamutil;0.1.0.7;;http://genome.sph.umich.edu/w/images/5/5d/BamUtilLibStatGen.%s.tgz;;;;;
#OK:bio_nextgen;analysis;;tabix;0.2.6;;http://downloads.sourceforge.net/project/samtools/tabix/tabix-%s.tar.bz2;;;;;
#OK:bio_nextgen;analysis;;grabix;0.1.1;80150d00e5;git clone https://github.com/arg5x/grabix.git;;;;;
#OK:bio_nextgen;analysis;;pbzip;2cce3ffa97;git clone https://github.com/chapmanb/samtools.git;pbzip;
#OK:bio_nextgen;analysis;;snpeff;3.3;;http://downloads.sourceforge.net/project/snpeff/snpEff_v%s_core.zip;;;;;
#OK:bio_nextgen;analysis;;freebayes;0.9.9.2-14;10ac8d449;git clone --recursive https://github.com/ekg/freebayes.git;;;;;
#OK:K0_64bit:bio_nextgen;analysis;;vcflib;06e664c;git clone --recursive https://github.com/ekg/vcflib.git;;;;;64;
#OK:bio_nextgen;analysis;;bamtools;3fe66b9;git clone --recursive https://github.com/pezmaster31/bamtools.git;;;;;
#OK:bio_nextgen;analysis;;ogap;652c525;git clone --recursive https://github.com/ekg/ogap.git;;;;;
#OK:bio_nextgen;analysis;;boost;1.49.0;;http://downloads.sourceforge.net/project/boost/boost/1.49.0/boost_%s.tar.bz2;;;;;
#OK:bio_nextgen;analysis;;tophat;2.0.9;;http://tophat.cbc.bcm.edu/downloads/tophat-%s.Linux_x86_64.tar.gz;;;;;
#OK:bio_nextgen;analysis;;cufflinks;2.1.1;;http://cufflinks.cbc.bcm.edu/downloads/cufflinks-%s.Linux_x86_64.tar.gz;;;;;
#OK:bio_nextgen;assembly;;abyss;1.3.4;;http://www.bcgsc.ca/downloads/abyss/abyss-%s.tar.gz;;;;;
#OK:bio_nextgen;assembly;;transabyss;1.4.4;;http://www.bcgsc.ca/platform/bioinfo/software/trans-abyss/releases/%s/trans-ABYSS-v%s.tar.gz;LOCAL;;;;;
#OK:bio_nextgen;assembly;;velvet;1.2.08;;http://www.ebi.ac.uk/~zerbino/velvet/velvet_%s.tgz;;;;;
#OK:bio_nextgen;assembly;;ray;2.2.0;;http://downloads.sourceforge.net/project/denovoassembler/Ray-v%s.tar.bz2;;;;;
#OK:bio_nextgen;assembly;;trinity;r2012-10-05;;http://downloads.sourceforge.net/project/trinityrnaseq/trinityrnaseq_%s.tgz;LOCAL;;;;;
#OK:bio_nextgen;assembly;;bcbio-variation;0.1.0;;https://github.com/chapmanb/bcbio.variation/releases/download/v%s/bcbio.variation-%s-standalone.jar;;;;;jar;;;;;
#OK:bio_nextgen;chip;;macs;1.4.2;;https://github.com/downloads/taoliu/MACS/MACS-%s.tar.gz;;;;;python;;;;;
#OK:bio_nextgen;sv;;hydra;0.5.3;;http://hydra-sv.googlecode.com/files/Hydra.v%s.tar.gz;;;;;
#OK:bio_nextgen;sv;;lumpy;0.1.2;git clone https://github.com/arg5x/lumpy-sv.git;;;;;
#OK:bio_nextgen;sv;;delly;0.0.11;;http://www.embl.de/~rausch/delly_v%s.tar.gz;;;;;
#OK:bio_nextgen;sv;;[ubuntu,debian];freec;6.4;;http://bioinfo-out.curie.fr/projects/freec/src/FREEC_Linux64.tar.gz;;;;;
#OK:bio_nextgen;sv;;crisp;5;;https://sites.google.com/site/vibansal/software/crisp/CRISP-linux-v%s.tar.gz;;;;;
#OK:bio_nextgen;sv;;tassel;4.0;;http://www.maizegenetics.net/tassel/tassel%_standalone.zip;;;;;
#OK:bio_nextgen;sv;;stacks;0.9999;;http://creskolab.uoregon.edu/stacks/source/stacks-%s.tar.gz;;;;;
#OK:K0_64bit:bio_nextgen;sv;;[ubuntu,debian];sambamba;0.2.9;;https://github.com/downloads/lomerreiter/sambamba/sambamba-%s_amd64.deb;;;;;deb;;;;;64;
#OK:bio_nextgen;sv;;weblogo;2.8.2;;http://weblogo.berkeley.edu/release/weblogo.%s.tar.gz;;;;;

```

Into this file there are some information, but the most important are:

- **package-name**: in some cases I didn't understand what was the correct name of the package because there were differences between configuration files and scripts:
 - **STAR** → **star**:
 - package **star** is included in **config/custom.yaml** but not in **manifest/*.yaml**
 - in **bio_nextgen.py** to search if *not installed* is used the name **STAR**
 - **MosaikAligner** → **mosaik**:
 - package **mosaik** is included both in **config/custom.yaml** and in **manifest/*.yaml**;
 - in **bio_nextgen.py** to search if *not installed* is used the name **MosaikAligner**
 - **fastq_screen** → **fastq-screen**:
 - package **fastq_screen** is included in **config/custom.yaml** but not in **manifest/*.yaml**;
 - but in the **debian standard** you can't use the *underscore* in the name of a packages
 - **vttools** → **varianttools**:
 - package **varianttools** is included both in **config/custom.yaml** and in **manifest/*.yaml**;
 - in **bio_nextgen.py** to search if *not installed* is used the name **vttools**
 - **pseq** → **plink_seq**:
 - package **plink_seq** is included both in **config/custom.yaml** and in **manifest/*.yaml**;
 - in **bio_nextgen.py** to search if *not installed* is used the name **pseq**;
 - but in the **debian standard** you can't use the *underscore* in the name of a packages
 - **bam** → **bamutil**:
 - is included only in **bio_nextgen.py**
 - to search if *not installed* is used the name **bam**
 - it is very important that the name used to building a package it's the same one used in the installation phase especially when you need to check if a package is already installed
- **version**
 - **url**: I have standardized the string used to identify the version from several forms ({0}, %, {version}...) to "%s"
 - ... (some other informations specific of the packages)

The structure of this file is **only a draft** and I created just to do some testing.

I think it would be a good idea to have a single repository where there are all the key information to *install*, to *check* and to *compare* the packages and always have the up-to-date information on packages (possibly also for **stable** and **development** packages).

There are also some others files required to build the packages.

The structure of these filename is described below:

- a **prefix** that identifies the *type* (and use) of the file
- a **suffix** that identifies the *package-name*
- an *underscore* to separate the prefix and suffix

These are the *type* of files:

- files **change_***: these files contain changes to be applied to the files in the process of building and installing
- files **depends_***: these files contain the dependencies that can not be handled automatically in the installation process
 - the management of dependencies which are available via **apt-get** is done with the use of **auto-apt** [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_auto-apt_works]
 - but if the dependencies are not available through **apt-get** (for example when they themselves are custom-packages), you must specify them explicitly in these files

- files **Makefile_***: these files contain substantially the directive of installation, to append to the original *makefile* when the information is not included in the original *makefile*
 - this directive is required in the installation process using *checkinstall* [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_checkinstall_works]
- files **preconfigure_***: these files contain the operations that need to be done before the executions of **.Jconfigure**
- files **premake_***: these files contain the operations that need to be done before the process compiling and installation

example - package <samtools>

- file **change_samtools**:

```
sed -i 's/-D_CURSES_LIB=1/-D_CURSES_LIB=0/g' Makefile
sed -i 's/-lCurses/# -lcurses/g' Makefile
```

- file **Makefile_samtools**:


```
##### start #####
PREFIX_INSTALL_CBL=PATH_TO_INSTALL_CBL
BINDDIR=$(PREFIX_INSTALL_CBL)/bin

install:
mkdir -p $(BINDDIR)
cp samtools bcftools/bcftools bcftools/vcftools.pl misc/wgsim $(BINDDIR)/

##### end #####
```

- file **premake_samtools**:

```
make clean
```

 I am trying to use the structure of files used in the debian standard process:

- preinstall.pak
- postinstall.pak
- preremove.pak
- postremove.pak

description of the <pre-installation> stage (pre-install.sh)

system checks

The stage of pre-installation analyzes the correctness of some features / information required to successfully complete the deployment process:

- OS check
- Release OS check
- disk-space check

The configuration file used is: **deploy/config/configsys/environment**

installing core packages

At this stage the packages are installed necessary for the proper deployment process.

The configuration files used are:

- **deploy/config/configsys/apt-get-base.pkg**
- **deploy/config/configsys/easy_install.pkg**

changes to the system configuration

Some changes are made to the system:

- **add sources**: using the configuration files: **deploy/config/configsys/cloudbiolinux*.list**
- **keyring installing**: using the configuration files: **deploy/config/configsys/cbl_keyring_standalone.txt** and **deploy/config/configsys/cbl_keyring_keyserver.txt**
- **deb-conf pre-configuration changes**: using the configuration file: **deploy/config/configsys/debconf.conf**

cloning cloudbiolinux

At this stage it is done downloading of **cloudbiolinux** environment, for the use of ***.YAML** configuration files:

- **git clone** [git://github.com/chapmanb/cloudbiolinux.git](https://github.com/chapmanb/cloudbiolinux.git) [[git://github.com/chapmanb/cloudbiolinux.git](https://github.com/chapmanb/cloudbiolinux.git)]

This is stored in **clonecbl/cloudbiolinux**

using auto-apt

This is one of the main elements of news, because it is able to automate the management of dependencies also in the deployment process of custom-packages:

- it is essentially a standard system that is activated when a component (usually a library) is not available in configuration or compilation:

```
sudo auto-apt update
sudo auto-apt updatedb
sudo auto-apt update-local
```

Later we'll see how it works [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_auto-apt_works]:

description of <deployment> (deploycbl.sh)

check available packages (check_packages_available.sh)

The ***.YAML** configuration files, stored in **clonebl/cloudbiolinux/config/** (downloaded from `git clone git://github.com/chapmanb/cloudbiolinux.git` (`git://github.com/chapmanb/cloudbiolinux.git`)), are checked to verify if all packages are available and to remove packages not available from the deployment process:

- the new ***.YAML** are stored in **deploy/config/configpkg/** directory
- the information about packages not available are stored in **deploy/check/** directory, in order to identify exactly the issue

building files for installation via apt-get (`build_apt_file.sh`)

Using the new ***.YAML** configuration files stored in **deploy/config/configpkg/** directory (these files contain only the packages available) are created **package-groups** identified by the configuration file **clonebl/cloudbiolinux/config/main.yaml**; these new configuration files will be used in the process of installing via **apt-get**.

These files are stored in **deploy/buildaptfile/<directory>**, in specific directories for each ***.YAML** configuration files:

```
-----
piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/builtaptfile/
totale 40
drwxrwxr-x 7 piero piero 4096 nov 23 02:17 .
drwxrwxr-x 8 piero piero 4096 nov 23 02:17 ..
-rw-rw-r-- 1 piero piero 4929 nov 23 02:17 grouplist_to_install.txt
-rw-rw-r-- 1 piero piero 938 nov 23 02:17 grouplist_not_to_install.txt
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-homebrew
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-nix
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-scientificlinux
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-yum
-----
```

The files **grouplist_to_install.txt** e **grouplist_not_to_install.txt** contain the informations about the groups that are or are not in **clonebl/cloudbiolinux/config/main.yaml**.

Every directory contains the list of package-groups; for example the directory **deploy/buildaptfile/packages** contains the files list below:

```
-----
piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/builtaptfile/packages
totale 132
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 .
drwxrwxr-x 7 piero piero 4096 nov 23 02:17 ..
-rw-rw-r-- 1 piero piero 66 nov 23 02:17 amazon
-rw-rw-r-- 1 piero piero 190 nov 23 02:17 bio_alignment
-rw-rw-r-- 1 piero piero 153 nov 23 02:17 bio_annotation
-rw-rw-r-- 1 piero piero 32 nov 23 02:17 bio_general
-rw-rw-r-- 1 piero piero 0 nov 23 02:17 bio_microarray
-rw-rw-r-- 1 piero piero 58 nov 23 02:17 bio_nextgen
-rw-rw-r-- 1 piero piero 79 nov 23 02:17 bio_search
-rw-rw-r-- 1 piero piero 15 nov 23 02:17 bio_sequencing
-rw-rw-r-- 1 piero piero 102 nov 23 02:17 bio_utils
-rw-rw-r-- 1 piero piero 7 nov 23 02:17 bio_visualization
-rw-rw-r-- 1 piero piero 359 nov 23 02:17 cloudman
-rw-rw-r-- 1 piero piero 295 nov 23 02:17 databases
-rw-rw-r-- 1 piero piero 219 nov 23 02:17 desktop
-rw-rw-r-- 1 piero piero 128 nov 23 02:17 distributed
-rw-rw-r-- 1 piero piero 65 nov 23 02:17 documentation
-rw-rw-r-- 1 piero piero 74 nov 23 02:17 erlang
-rw-rw-r-- 1 piero piero 210 nov 23 02:17 galaxy
-rw-rw-r-- 1 piero piero 85 nov 23 02:17 hadoop
-rw-rw-r-- 1 piero piero 23 nov 23 02:17 haskell
-rw-rw-r-- 1 piero piero 28 nov 23 02:17 java
-rw-rw-r-- 1 piero piero 138 nov 23 02:17 java_extras
-rw-rw-r-- 1 piero piero 340 nov 23 02:17 libraries
-rw-rw-r-- 1 piero piero 15 nov 23 02:17 math
-rw-rw-r-- 1 piero piero 164 nov 23 02:17 minimal
-rw-rw-r-- 1 piero piero 97 nov 23 02:17 perl
-rw-rw-r-- 1 piero piero 218 nov 23 02:17 phylogeny
-rw-rw-r-- 1 piero piero 584 nov 23 02:17 programming
-rw-rw-r-- 1 piero piero 119 nov 23 02:17 python
-rw-rw-r-- 1 piero piero 42 nov 23 02:17 r
-rw-rw-r-- 1 piero piero 24 nov 23 02:17 ruby
-rw-rw-r-- 1 piero piero 146 nov 23 02:17 viz
-rw-rw-r-- 1 piero piero 8 nov 23 02:17 web
-----
```

and each file contains the list of packages to install; for example the file **deploy/buildaptfile/packages/minimal** contains the packages list below:

```
-----
sudo
htop
vim
git-core
cvs
subversion
mercurial
bzip2
cmake
gcc
g++
gfortran
libtool
make
patch
pkg-config
axel
gawk
rsync
openssh-server
screen
unzip
less
curl
wget
-----
```

packages installation via apt-get (`aptgetbl.sh`)

After the files that contain the packages to be installed have been created, the installation process is started.

Before final installation, it performs a *dry-run* installation, to ensure that there is no issue.

If the *dry-run* installation has been completed successfully, then we proceed with the final installation:

- even in this case occurs the result of the installation, which is stored in the specific log, so that in the case of negative result, will be possible to analyze the issue.

We also stored a file that summarizes the group-packages that we have not been able to install (**deploy/log/aptgetbl/groups-packages-not-installed.txt**).

custom-packages installation via dpkg (`build_custom_pkgs.sh`)

The custom-packages installation process consists of several stages:

- checks if the package is already installed
- download the package
- extracting the package

- if required any changes are applied to files:
 - using information/data stored in **change_*** files
- checks if the Makefile exists
- checks if there is a directive of installation in the Makefile (*install*), that is required in the installation process via *checkinstall* [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_checkinstall_works]
 - using **Makefile_*** files
- if required executes a script pre-installation:
 - using information/data stored in **preconfigure_*** and **premake_*** files
- checks if there are dependencies NOT present in standard-packages (and therefore can not be handled by *auto-apt* [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_auto-apt_works] system)
 - using **depends_*** files
- configuration and compiling process
 - in this context we use *auto-apt* [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_auto-apt_works], a system that is activated when a component (generally a library) is not available in the phase of configuration or compiling
- installation process
 - in this context we use *checkinstall* [http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#how_checkinstall_works], a program that allow to build packages in different format (*.deb, *rpm e slackware)
 - in this case the packages can be installed in the standard way with many advantages and benefits in terms of management of the installation process (and guarantee of a positive outcome of the operations)

Below you can see a partial list of the custom-packages installed:

```

ii bedtools 2.17.0-1 customcbl - A flexible suite of utilities for comparing genomic features.
ii bfast 0.7.0a-0.7.0 customcbl - BFAST: Blat-like Fast Accurate Search Tool.
ii biobambam 0.0.92-e325743 customcbl - biobambam
ii bowtie 1.0.0-1 customcbl - The bowtie short read aligner.
ii bowtie2 2.1.0-1 customcbl - bowtie2 short read aligner, with gap support.
ii dwsim 0.1.10-1 customcbl - DWGSIM: simulating NGS data and evaluating mappings and variant c
ii echo 0-1 customcbl - ECHO: A reference-free short-read error correction algorithm
ii fastq-screen 0.4.2-1 customcbl - fastq-screen
ii fastqc 0.10.1-1 customcbl - A quality control tool for high throughput sequence data.
ii fastx-toolkit 0.0.13.2-1 customcbl - fastx-toolkit
ii gmap 2012-11-09-1 customcbl - GMAP and GSNAP: A Genomic Mapping and Alignment Program for mRNA
ii lastz 1.02.00-1 customcbl - LASTZ sequence alignment program.
ii libgtextutils 0.6-1 customcbl - libgtextutils
ii libmaus 0.0.72-8f6b9b4 customcbl - libmaus
ii mosaik 2.1.73-1 customcbl - MOSAIK: reference-guided aligner for next-generation sequencing; t
ii perm 4-1 customcbl - Efficient mapping of short sequences accomplished with periodic; f
ii picard 1.96-1 customcbl - Command-line utilities that manipulate BAM files with a Java API.
ii plinkseq 0.08-1 customcbl - plinkseq
ii samtools 0.1.19-1 customcbl - SAM Tools provide various utilities for manipulating alignments; i
ii shrec 2.2-1 customcbl - Shrec is a bioinformatics tool for error correction of HTS read; d
ii snap 0.15-1 customcbl - snap
ii solexaqa 2.2-1 customcbl - SolexaQA creates visual representations of data quality from FAST
ii star 2.3.1p-1 customcbl - star
ii vcftools 0.1.11-1 customcbl - Work with VCF files, such as those generated by the 1000 Genomes
...

```

status of packages installed (compare_package_installed.sh)

The last stage, checks what packages were installed and compare the result with the reference-list *clonecbl/cloudbiolinux/manifest/*.yaml* (downloaded from *git clone git://github.com/chapmanb/cloudbiolinux.git* [[git://github.com/chapmanb/cloudbiolinux.git](http://github.com/chapmanb/cloudbiolinux.git)]).
The results are stored in *deploy/config/status/* directory.

debian-packages

- below you can see a partial list of the packages **installed** (deploy/status/debian-packages-installed.log):

```

INSTALLED: accountsservice
INSTALLED: acl
INSTALLED: acpi-support
INSTALLED: acpid
INSTALLED: activity-log-manager-common
INSTALLED: activity-log-manager-control-center
INSTALLED: adduser
INSTALLED: adium-theme-ubuntu
INSTALLED: aisleriot
INSTALLED: alacarte
INSTALLED: alsa-base
INSTALLED: alsa-utils
INSTALLED: anacron
INSTALLED: ant
INSTALLED: ant-optional
INSTALLED: antlr3
INSTALLED: apache2
INSTALLED: apache2-mpm-worker
INSTALLED: apache2-utils
INSTALLED: apache2.2-bin
INSTALLED: apache2.2-common
INSTALLED: app
INSTALLED: app-install-data
INSTALLED: app-install-data-partner
INSTALLED: apparmor
INSTALLED: appmenu-gtk
...

```

- below you can see a partial list of the packages **NOT installed** (deploy/status/debian-packages-not_installed.log):

```

NOT INSTALLED: binfmt-support
NOT INSTALLED: bio-linux-assembly-conversion-tools
NOT INSTALLED: bio-linux-base-directories
NOT INSTALLED: bio-linux-big-blast
NOT INSTALLED: bio-linux-blast+
NOT INSTALLED: bio-linux-blixem
NOT INSTALLED: bio-linux-cap3
NOT INSTALLED: bio-linux-clcsequenceviewer
NOT INSTALLED: bio-linux-coalesce
NOT INSTALLED: bio-linux-das-prep
NOT INSTALLED: bio-linux-dotter
NOT INSTALLED: bio-linux-dust
NOT INSTALLED: bio-linux-estscan
NOT INSTALLED: bio-linux-exchanger
NOT INSTALLED: bio-linux-fasta
NOT INSTALLED: bio-linux-fasttree
NOT INSTALLED: bio-linux-fluctuate
NOT INSTALLED: bio-linux-forester
NOT INSTALLED: bio-linux-gap2caf
NOT INSTALLED: bio-linux-glimmer3

```

```
NOT INSTALLED: bio-linux-happy
NOT INSTALLED: bio-linux-maxd
NOT INSTALLED: bio-linux-migrate
NOT INSTALLED: bio-linux-mrbayes-multi
NOT INSTALLED: bio-linux-mspcrunch
NOT INSTALLED: bio-linux-ncbi-tools-x11
NOT INSTALLED: bio-linux-nrdb
NOT INSTALLED: bio-linux-ocount
NOT INSTALLED: bio-linux-oligoarray
...
```

- below you can see a partial list of the packages with the **right version** (deploy/status/debian-packages-version_ok.log):

```
--> OK: acl - 2.2.51-5ubuntu1
--> OK: acpid - 1:2.0.10-1ubuntu3
--> OK: adduser - 3.113ubuntu2
--> OK: adium-theme-ubuntu - 0.3.2-0ubuntu1
--> OK: amleriot - 1:3.2.3.2-0ubuntu1
--> OK: alacarte - 0.13.2-2ubuntu4
--> OK: anacron - 2.3-14ubuntu1
--> OK: ant - 1.8.2-4build1
--> OK: ant-optional - 1.8.2-4build1
--> OK: antlr3 - 3.2.is.3.2-0ubuntu1
--> OK: app - 2.2.3.dfsg.1-2
--> OK: app-install-data - 0.12.04.4
--> OK: app-install-data-partner - 12.12.04.1
--> OK: appmenu-qt - 0.2.6-0ubuntu1
--> OK: apturl - 0.5.1ubuntu3
--> OK: apturl-common - 0.5.1ubuntu3
--> OK: aspell - 0.60.7-20110707-1
--> OK: aspell-en - 6.0-0-6ubuntu2
--> OK: at - 3.1.13-1ubuntu1
--> OK: at-spi2-core - 2.4.2-0ubuntu0.1
--> OK: autoconf - 2.68-1ubuntu2
--> OK: automake - 1:1.11.3-1ubuntu2
--> OK: autotools-dev - 20120210.1ubuntu1
--> OK: avahi-autoipd - 0.6.30-5ubuntu2
--> OK: avahi-daemon - 0.6.30-5ubuntu2
--> OK: avahi-utils - 0.6.30-5ubuntu2
--> OK: axel - 2.4-1
--> OK: baobab - 3.4.1-0ubuntu1
--> OK: base-passwd - 3.5.24
...
```

- below you can see a partial list of the packages with the **different version** between **manifest (M)** and **installed (I)** (deploy/status/debian-packages-diff_version.log):

```
-----> K0: accountsservice - (M)0.6.15-2ubuntu9 - (I)0.6.15-2ubuntu9.6.1
-----> K0: acpi-support - (M)'0.140' - (I)0.140.1
-----> K0: activity-log-manager-common - (M)0.9.4-0ubuntu3 - (I)0.9.4-0ubuntu3.2
-----> K0: activity-log-manager-control-center - (M)0.9.4-0ubuntu3 - (I)0.9.4-0ubuntu3.2
-----> K0: alsa-base - (M)1.0.25+dfsg-0ubuntu1 - (I)1.0.25+dfsg-0ubuntu1.1
-----> K0: alsa-utils - (M)1.0.25-1ubuntu5 - (I)1.0.25-1ubuntu5.2
-----> K0: apache2 - (M)2.2.22-1ubuntu1 - (I)2.2.22-1ubuntu1.4
-----> K0: apache2-mpm-worker - (M)2.2.22-1ubuntu1 - (I)2.2.22-1ubuntu1.4
-----> K0: apache2-utils - (M)2.2.22-1ubuntu1 - (I)2.2.22-1ubuntu1.4
-----> K0: apache2.2-bin - (M)2.2.22-1ubuntu1 - (I)2.2.22-1ubuntu1.4
-----> K0: apache2.2-common - (M)2.2.22-1ubuntu1 - (I)2.2.22-1ubuntu1.4
-----> K0: apparmor - (M)2.7.102-0ubuntu3.1 - (I)2.7.102-0ubuntu3.9
-----> K0: appmenu-gtk - (M)0.3.92-0ubuntu1 - (I)0.3.92-0ubuntu1.1
-----> K0: appmenu-gtk3 - (M)0.3.92-0ubuntu1 - (I)0.3.92-0ubuntu1.1
-----> K0: apport - (M)2.0.1-0ubuntu8 - (I)2.0.1-0ubuntu17.6
-----> K0: apport-gtk - (M)2.0.1-0ubuntu8 - (I)2.0.1-0ubuntu17.6
-----> K0: apport-symptoms - (M)'0.16' - (I)0.16.1
-----> K0: apt - (M)0.8.16-exp12ubuntu10.2 - (I)0.8.16-exp12ubuntu10.16
-----> K0: apt-transport-https - (M)0.8.16-exp12ubuntu10.2 - (I)0.8.16-exp12ubuntu10.16
-----> K0: apt-utils - (M)0.8.16-exp12ubuntu10.2 - (I)0.8.16-exp12ubuntu10.16
-----> K0: apt-xapian-index - (M)0.44ubuntu5 - (I)0.44ubuntu5.1
-----> K0: aptdaemon - (M)0.43+bzr805-0ubuntu1 - (I)0.43+bzr805-0ubuntu9
-----> K0: aptdaemon-data - (M)0.43+bzr805-0ubuntu1 - (I)0.43+bzr805-0ubuntu9
-----> K0: aptitude - (M)0.6.6-1ubuntu1 - (I)0.6.6-1ubuntu1.2
-----> K0: bamfdaemon - (M)0.2.118-0ubuntu0.1 - (I)0.2.126-0ubuntu1
-----> K0: base-files - (M)6.5ubuntu6 - (I)6.5ubuntu6.6
-----> K0: bash - (M)4.2-2ubuntu2 - (I)4.2-2ubuntu2.1
-----> K0: bash-completion - (M)1:1.3-1ubuntu8 - (I)1:1.3-1ubuntu8.1
-----> K0: bind9-host - (M)1:9.8.1.dfsg.P1-4ubuntu0.1 - (I)1:9.8.1.dfsg.P1-4ubuntu0.7
-----> K0: binutils - (M)2.22-6ubuntu1 - (I)2.22-6ubuntu1.1
-----> K0: bio-linux-blast - (M)1:1bl-6 - (I)1:1bl-7
-----> K0: bio-linux-cd-hit - (M)2009-1020-1 - (I)1:1bl-1
-----> K0: bio-linux-clustal - (M)1:1bl-6 - (I)1:1bl-7
-----> K0: bio-linux-fastdnaml - (M)1:1bl-0 - (I)1:1bl-2
-----> K0: bio-linux-jalview - (M)1:2.6.1-1 - (I)1:2.7.0-2
-----> K0: bio-linux-keyring - (M)'4' - (I)5
-----> K0: bio-linux-lucy - (M)1.20-0 - (I)1:1bl-1
-----> K0: bio-linux-mesquite - (M)2.74-1 - (I)2.74-3
-----> K0: bio-linux-mview - (M)1.51-2 - (I)1.51-3
...
```

custom-packages

- below you can see a partial list of the custom-packages **installed** (deploy/status/custom-packages-installed.log):

```
INSTALLED: abyss
INSTALLED: bedtools
INSTALLED: bfast
INSTALLED: bowtie
INSTALLED: bowtie2
INSTALLED: bwa
INSTALLED: crisp
INSTALLED: cufflinks
INSTALLED: dwgsim
INSTALLED: echo
INSTALLED: emboss
INSTALLED: fastqc
INSTALLED: freebayes
INSTALLED: gmap
INSTALLED: hydra
INSTALLED: lastz
INSTALLED: mosaik
INSTALLED: nginx
INSTALLED: perm
INSTALLED: picard
INSTALLED: samtools
INSTALLED: shrec
INSTALLED: snpeff
INSTALLED: solexaqa
INSTALLED: stacks
INSTALLED: tassel
INSTALLED: tophat
INSTALLED: transabyss
INSTALLED: trinity
INSTALLED: vcftools
INSTALLED: velvet
```

- below you can see a partial list of the custom-packages **NOT installed** (deploy/status/custom-packages-not_installed.log):

```
NOT INSTALLED: beast
NOT INSTALLED: bio4j
NOT INSTALLED: bx_python
NOT INSTALLED: cljr
NOT INSTALLED: cloudman
NOT INSTALLED: fastx_toolkit
NOT INSTALLED: gatk
NOT INSTALLED: gatk_queue
NOT INSTALLED: leinengin
NOT INSTALLED: macs
NOT INSTALLED: matplotlib
NOT INSTALLED: novoalign
NOT INSTALLED: pgdspider
NOT INSTALLED: plink_seq
NOT INSTALLED: proftpd
NOT INSTALLED: pydoop
NOT INSTALLED: rpy
NOT INSTALLED: s3fs
NOT INSTALLED: seal
NOT INSTALLED: sge
NOT INSTALLED: stampy
NOT INSTALLED: tracer
NOT INSTALLED: ucsc_tools
NOT INSTALLED: varianttools
```

- below you can see a partial list of the custom-packages with the **right version** (deploy/status/custom-packages-version_ok.log):

```
empty
```

- below you can see a partial list of the custom-packages with the **different version** between **manifest (M)** and **installed (I)** (deploy/status/custom-packages-diff_version.log):

```
-----> K0: abyss - (M)1.3.3 - (I)1.3.4-1
-----> K0: bedtools - (M)github - (I)2.17.0-1ubuntu1
-----> K0: bfast - (M)0.7.0 - (I)0.7.0a-0.7.0
-----> K0: bowtie - (M)0.12.7 - (I)1.0.0-1
-----> K0: bowtie2 - (M)2.0.0-beta6 - (I)2.1.0-1-0ubuntu1
-----> K0: bwa - (M)0.5.9 - (I)0.6.1-1
-----> K0: crisp - (M)'5' - (I)5-1
-----> K0: cufflinks - (M)2.0.0 - (I)2.1.1-1
-----> K0: dwgsim - (M)0.1.8 - (I)0.1.10-1
-----> K0: echo - (M)'1_11' - (I)0-1
-----> K0: emboss - (M)6.3.1 - (I)6.5.7-0ubuntu3
-----> K0: fastqc - (M)0.10.1 - (I)0.10.1-1
-----> K0: freebayes - (M)github - (I)0.9.9.2-14-10ac8d449
-----> K0: gmap - (M)'2011-11-12' - (I)2012-11-09-1
-----> K0: hydra - (M)0.5.3 - (I)0.5.3-1
-----> K0: lastz - (M)1.02.00 - (I)1.02.00-1
-----> K0: mosaik - (M)github - (I)2.1.73-1
-----> K0: nginx - (M)1.2.0 - (I)1.1.19-1ubuntu0.5
-----> K0: perm - (M)'3.6' - (I)4-1
-----> K0: picard - (M)'1.68' - (I)1.96-1
-----> K0: samtools - (M)0.1.18 - (I)0.1.19-1
-----> K0: shrec - (M)'2.2' - (I)2.2-1
-----> K0: snpeff - (M)'2_0_5' - (I)0-1
-----> K0: solexaqa - (M)'1.4' - (I)2.2-1
-----> K0: stacks - (M)'0.998' - (I)0.9999-1
-----> K0: tassel - (M)'3.0' - (I)4.0-1
-----> K0: tophat - (M)2.0.0 - (I)2.0.9-1
-----> K0: transabyss - (M)1.3.2 - (I)1.4.4-1
-----> K0: trinity - (M)r2012-05-18 - (I)0r2012-10-05-1
-----> K0: vcftools - (M)0.1.7 - (I)0.1.7-1
-----> K0: velvet - (M)1.2.05 - (I)1.2.08-1
```

procedure of installing

Installing the environment is quite simple:

- tar xfvz cloudbiolinux.tar.gz**: extract scripts and configuration files from tarball **cloudbiolinux.tar.gz**
- cd cloudbiolinux**
- ./pre-install.sh**: configuration CBL environment
- ./deploycbl.sh**: installation standard and custom packages

cloning system

The cloning of an existing system is also quite simple when we works with packages in the standard format.

sources system (build_replicate.sh)

standard packages (via apt-get)

This procedure works correctly when the release of the OS is the same on both the **source** and the **target**.

Below you can see the main command to do this:

```
dpkg --get-selections | grep -v deinstall > $PKGS_ORIG
```

From this list you must remove the **custom-packages** and write the records in **packages.std**.

custom packages (via apt-get)

You must search which **custom-packages** are installed:

```
dpkg -l | grep -w "customcbl" | awk -F " " '{ print $2 }' > $CUSTOMPKGS_ORIG
```

and then select in **deploy/config/configcustom/custom.def** the records that must be written in **custom.pkg**.

All the configuration files required for **cloning** are stored in **deploy/reproducibility/**.

destination system (replicate.sh)

standard packages (via apt-get)

The main commands is shown below:

```
apt-get update
apt-get upgrade

dpkg --set-selections < $PATH_DEPLOYCBL/reproducibility/packages.std
apt-get -u dselect-upgrade
```

custom packages (via apt-get)

The main command is shown below:

```
sudo build_custom_pkgs.sh $PATH_DEPLOYCBL/reproducibility/custom.pkg
```

3. main changes

how auto-apt works

When there aren't packages in standard format (that is not in the format of a specific distribution) the common approach to install an application is to download the sources and then to proceed manually to configure, compile and install it.

These are the commands usually used:

```
./configure
make clean
make
sudo make install
```

In the configuration stage of a package (./configure) or in compiling stage (make) the process may fail because, for example, the required libraries are not available. We can see some examples:

without auto-apt

trinitynaseq-r2012-10

In the compilation phase the **make** command fails with the error shown below:

```
...
config.status: creating Makefile
config.status: creating src/Makefile
config.status: creating config.h
config.status: config.h is unchanged
config.status: executing depfiles commands
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/trinitynaseq-r2012-10/trinitynaseq_r2012-10-05/Inchworm"
Making install in src
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/trinitynaseq-r2012-10/trinitynaseq_r2012-10-05/Inchworm/src"
if g++ -DHAVE_CONFIG_H -I. -I. -I. -pedantic -fopenmp -Wall -Wextra -Wno-long-long -Wno-deprecated -m64 -g -O2 -MT Fasta_entry.o -MD -MP -MF ".deps/"
then mv -f ".deps/Fasta_entry.Tpo" ".deps/Fasta_entry.Po"; else rm -f ".deps/Fasta_entry.Tpo"; exit 1; fi
In file included from /usr/include/c++/4.6/i686-linux-gnu/64/bits/os_defines.h:40:0,
                 from /usr/include/c++/4.6/i686-linux-gnu/64/bits/c++config.h:393,
                 from /usr/include/c++/4.6/string:40,
                 from Fasta_entry.hpp:4,
                 from Fasta_entry.cpp:1:
/usr/include/features.h:324:26: fatal error: bits/predefs.h: File o directory non esistente
compilation terminated.
make[2]: *** [Fasta_entry.o] Errore 1
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/trinitynaseq-r2012-10/trinitynaseq_r2012-10-05/Inchworm/src"
make[1]: *** [install-recursive] Errore 1
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/trinitynaseq-r2012-10/trinitynaseq_r2012-10-05/Inchworm"
make: *** [all] Errore 2
...
```

bfast

In the configuration phase the **./configure** command fails with the error shown below:

```
...
checking how to run the C preprocessor... gcc -E
checking for grep that handles long lines and -e... /bin/grep
checking for egrep... /bin/grep -E
checking for ANSI C header files... yes
checking for sys/types.h... yes
checking for sys/stat.h... yes
checking for stdlib.h... yes
checking for string.h... yes
checking for memory.h... yes
checking for strings.h... yes
checking for inttypes.h... yes
checking for stdint.h... yes
checking for unistd.h... yes
checking bzip2.h usability... no
checking bzip2.h presence... no
checking for bzip2.h... no
configure: error: "could not find the bzip2 library. Please use --disable-bzip2 if you wish to disable bzip2 support."
20131123-012306-ERROR: *****
20131123-012306-ERROR: ----> configure errore <-----
...
```

with auto-apt

If we use **auto-apt** is possible to solve, in many cases, the issue that occur during the building of the package.

It is needed to insert the changes shown below in the **./configure** or **make** process or in the **pip** installation (for **python** packages):

```
...
sudo auto-apt -y run make
...
auto-apt -y run ./configure
...
sudo auto-apt -y run pip install --upgrade .
...
```

The process of building the package ensures the installation of the necessary dependencies and can finish successfully:

trinitynaseq-r2012-10

In the compilation phase the libraries shown below are installed:

```

73a74,75
> ii ecj 3.5.1-3 standalone version of the Eclipse Java compiler
> ii ecj-gcj 3.5.1-3 standalone version of the Eclipse Java compiler (native version)
78a81
> ii fastjar 2:0.98-3 Jar creation utility
88a92,93
> ii g++-4.6-multilib 4.6.3-1ubuntu5 GNU C++ compiler (multilib files)
> ii gawk 1:3.1.8+dfsg-0.1ubuntu1 GNU awk, a pattern scanning and processing language
91a97,103
> ii gcc-4.6-multilib 4.6.3-1ubuntu5 GNU C compiler (multilib files)
> ii gcc-multilib 4:4.6.3-1ubuntu5 GNU C compiler (multilib files)
> ii gcj-4.6-base 4.6.3-1ubuntu2 GCC, the GNU Compiler Collection (gcj base package)
> ii gcj-4.6-jdk 4.6.3-1ubuntu2 gcj and classpath development tools for Java(TM)
> ii gcj-4.6-jre 4.6.3-1ubuntu2 Java runtime environment using GIJ/classpath
> ii gcj-4.6-jre-headless 4.6.3-1ubuntu2 Java runtime environment using GIJ/classpath (headless version)
> ii gcj-4.6-jre-lib 4.6.3-1ubuntu2 Java runtime library for use with gcj (jar files)
150a163,166
> ii lib64gcc1 1:4.6.3-1ubuntu5 GCC support library (64bit)
> ii lib64gomp1 4.6.3-1ubuntu5 GCC OpenMP (GOMP) support library (64bit)
> ii lib64quadmath0 4.6.3-1ubuntu5 GCC Quad-Precision Math Library (64bit)
> ii lib64stdc++6 4.6.3-1ubuntu5 GNU Standard C++ Library v3 (64bit)
155a172
> ii libantlr-java 2.7.7+dfsg-3 language tool for constructing recognizers, compilers etc (java library)
180a198
> ii libc6-amd64 2.15-0ubuntu10.5 Embedded GNU C Library: 64bit Shared libraries for AMD64
181a200
> ii libc6-dev-amd64 2.15-0ubuntu10.5 Embedded GNU C Library: 64bit Development Libraries for AMD64
207a227,228
> ii libecj-java 3.5.1-3 Eclipse Java compiler (library)
> ii libecj-java-gcj 3.5.1-3 Eclipse Java compiler (native library)
219a241
> ii libfile-spec-perl 3.3300-1build2 collection of tools for working with paths across platforms
227a250,254
> ii libgcj-bc 4.6.3-1ubuntu5 Link time only library for use with gcj
> ii libgcj-common 1:4.6.3-1ubuntu5 Java runtime library (common files)
> ii libgcj12 4.6.3-1ubuntu2 Java runtime library for use with gcj
> ii libgcj12-awt 4.6.3-1ubuntu2 AWT peer runtime libraries for use with gcj
> ii libgcj12-dev 4.6.3-1ubuntu2 Java development headers for use with gcj
300a328
> ii libncurses5-dev 5.9-4 developer's libraries for ncurses
350a379
> ii libsigsegv2 2.9-4ubuntu2 Library for handling page faults in a portable way
360a390
> ii libstrictures-perl 1.002002-1 Perl module to turn on strict and make all warnings fatal
372a403
> ii libtinfo-dev 5.9-4 developer's library for the low-level terminfo library
382a414
> ii libwarnings-illegalproto-perl 0.001000-1 pragma to disable illegal prototype warnings on old Perls
527a560
> ii safe-rm 0.8-4 wrapper around the rm command to prevent accidental deletions

```

and the compiling process can finish successfully:

```

20131123-005721-VERBOSE: compile make ... sudo:
20131123-005721-VERBOSE: *****
Entering auto-apt mode: make
Exit the command to leave auto-apt mode.
Using gnu compiler for Inchworm and Chrysalis
cd Inchworm && (test -e configure || autoreconf) \
&& ./configure --prefix=/usr && make install
checking for a BSD-compatible install... /usr/bin/install -c
checking whether build environment is sane... yes
checking for gawk... gawk
checking whether make sets $(MAKE)... yes
checking for g++... g++
checking for C++ compiler default output file name... a.out
checking whether the C++ compiler works... yes
checking whether we are cross compiling... no
checking for suffix of executables...
checking for suffix of object files... o
checking whether we are using the GNU C++ compiler... yes
checking whether g++ accepts -g... yes
checking for style of include used by make... GNU
checking dependency style of g++... gcc3
checking for library containing cos... none required
configure: creating ./config.status
config.status: creating Makefile
config.status: creating src/Makefile
config.status: creating config.h
config.status: config.h is unchanged
config.status: executing depfiles commands
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/trinityrnaseq-r2012-10/trinityrnaseq_r2012-10-05/Inchworm"
Making install in src
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/trinityrnaseq-r2012-10/trinityrnaseq_r2012-10-05/Inchworm/src"
...
<<< src >>>
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/trinityrnaseq-r2012-10/trinityrnaseq_r2012-10-05/trinity-plugins/slclust/src"
g++ -I../include -Wall -c slcluster.cpp
g++ -I../include -Wall -c graph.cpp
g++ -I../include -Wall -c graphnode.cpp
g++ -I../include -Wall -c cmd_line_opts.cpp
g++ -I../include -Wall slcluster.o graph.o graphnode.o cmd_line_opts.o -o slclust
chmod 755 slclust
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/trinityrnaseq-r2012-10/trinityrnaseq_r2012-10-05/trinity-plugins/slclust/src"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/trinityrnaseq-r2012-10/trinityrnaseq_r2012-10-05/trinity-plugins/slclust"
cd trinity-plugins/coreutils && ./build_parallel_sort.sh
sort is recent enough, bailing out
cd trinity-plugins/collectl && ./build_collectl.sh
DESTDIR=/home/piero/cloudbiolinux/deploy/temp/trinityrnaseq-r2012-10/trinity-plugins/collectl
FILE=collectl-3.6.3.src.tar.gz
INSTALLDIR=./collectl-3.6.3
...

```

bfast

In the configuration phase the libraries shown below are installed:

```

piero@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ diff deploy/dpkg/dpkg-before-install-bfast.txt deploy/dpkg/dpkg-after-install-bfast.txt
105a106
> ii gawk 1:3.1.8+dfsg-0.1ubuntu1 GNU awk, a pattern scanning and processing language
198a200
> ii libbz2-dev 1.0.6-1 high-quality block-sorting file compressor library - development
240a243
> ii libfile-spec-perl 3.3300-1build2 collection of tools for working with paths across platforms
374a378
> ii libsigsegv2 2.9-4ubuntu2 Library for handling page faults in a portable way
384a389
> ii libstrictures-perl 1.002002-1 Perl module to turn on strict and make all warnings fatal
406a412
> ii libwarnings-illegalproto-perl 0.001000-1 pragma to disable illegal prototype warnings on old Perls
559a566
> ii safe-rm 0.8-4 wrapper around the rm command to prevent accidental deletions

```

and the configuration and compiling processes can finish successfully:

```
...
Entering auto-apt mode: ./configure --prefix=/opt/CBL/bin/bfast
Exit the command to leave auto-apt mode.
checking for a BSD-compatible install... /usr/bin/install -c
checking whether build environment is sane... yes
...
checking for unistd.h... yes
checking bzlib.h usability... yes
checking bzlib.h presence... yes
checking for bzlib.h... yes
checking for special C compiler options needed for large files... no
checking for _FILE_OFFSET_BITS value needed for large files... 64
checking for an ANSI C-conforming const... yes
checking for stdlib.h... (cached) yes
checking for GNU libc compatible malloc... yes
checking for stdlib.h... (cached) yes
checking for GNU libc compatible realloc... yes
checking for pow in -lm... yes
checking for gzread in -lz... yes
checking for floor... yes
checking for pow... yes
checking for sqrt... yes
checking for strchr... yes
checking for strdup... yes
checking for strpbrk... yes
checking for strstr... yes
checking for strtok... yes
checking for _LARGEFILE_SOURCE value needed for large files... no
checking for int8_t... yes
checking for int32_t... yes
checking for int64_t... yes
checking for uint8_t... yes
checking for uint32_t... yes
checking for uint64_t... yes
checking for short int... yes
checking size of short int... 2
...
checking for fcntl.h... yes
checking for inline... inline
configure: creating ./config.status
config.status: creating Makefile
config.status: creating bfast/Makefile
config.status: creating butil/Makefile
config.status: creating scripts/Makefile
config.status: creating tests/Makefile
config.status: creating config.h
config.status: executing depfiles commands
...
Entering auto-apt mode: make
Exit the command to leave auto-apt mode.
make all-recursive
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
Making all in bfast
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
depbase='echo AlignedEnd.o | sed 's|[^/]*|.deps/&;s|\.o$||'`;
gcc -DHAVE_CONFIG_H -I. -I... -Wall -g -O2 -pthread -MT AlignedEnd.o -MD -MP -MF $depbase.Tpo -c -o AlignedEnd.o AlignedEnd.c &&\
mv -f $depbase.Tpo $depbase.Po
depbase='echo AlignedEntry.o | sed 's|[^/]*|.deps/&;s|\.o$||'`;
gcc -DHAVE_CONFIG_H -I. -I... -Wall -g -O2 -pthread -MT AlignedEntry.o -MD -MP -MF $depbase.Tpo -c -o AlignedEntry.o AlignedEntry.c &&\
mv -f $depbase.Tpo $depbase.Po
depbase='echo AlignedRead.o | sed 's|[^/]*|.deps/&;s|\.o$||'`;
gcc -DHAVE_CONFIG_H -I. -I... -Wall -g -O2 -pthread -MT AlignedRead.o -MD -MP -MF $depbase.Tpo -c -o AlignedRead.o AlignedRead.c &&\
mv -f $depbase.Tpo $depbase.Po
...
gcc -Wall -g -O2 -pthread -o btestindexes ../bfast/RGMatch.o ../bfast/RGRanges.o ../bfast/RGBinary.o ../bfast/RGIndex.o ../bfast/RGIndexAccuracy.o
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
Making all in scripts
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
depbase='echo solid2fastq.o | sed 's|[^/]*|.deps/&;s|\.o$||'`;
gcc -DHAVE_CONFIG_H -I. -I... -Wall -g -O2 -pthread -MT solid2fastq.o -MD -MP -MF $depbase.Tpo -c -o solid2fastq.o solid2fastq.c &&\
mv -f $depbase.Tpo $depbase.Po
gcc -Wall -g -O2 -pthread -o solid2fastq ../bfast/BEError.o ../bfast/RGIndex.o ../bfast/BLib.o ../bfast/RGBinary.o ../bfast/RGRanges.o ../bfast/RGMa
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
Making all in tests
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[2]: Nessuna operazione da eseguire per "all"
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
```

how checkinstall works

Generally the installation phase of a packages consists of execution of **make install** command.

If you want to build a package in a specific format:

- **deb**: debian/ubuntu packages
- **rpm**: red-hat/fedora/centOS
- **tgz**: slackware

you can use the program **checkinstall** that replacing the **make install** command:

```
...
./configure
make clean
make
sudo checkinstall -y --pkgversion $version --pkggroup "customcbl"
...
```

Below you can see an example:

```
checkinstall 1.6.2, Copyright 2009 Felipe Eduardo Sanchez Diaz Duran
Questo software è rilasciato sotto i termini della licenza GNU GPL.
```

```
The package documentation directory ./doc-pak does not exist.
Should I create a default set of package docs? [y]: y
```

```
Preparazione documentazione pacchetto in corso...OK
```

```
*****
*** Debian package creation selected ***
*****
```

```
Il pacchetto verrà costruito con le seguenti caratteristiche:
```

```
0 - Maintainer: [ root@ubuntu1204-tesi-replicate2 ]
1 - Summary: [ Package created with checkinstall 1.6.2 ]
2 - Name: [ bfast ]
3 - Version: [ 0.7.0a ]
4 - Release: [ 0.7.0 ]
5 - License: [ GPL ]
6 - Group: [ customcbl ]
7 - Architecture: [ i386 ]
8 - Source location: [ bfast-0.7.0a ]
9 - Alternate source location: [ ]
10 - Requires: [ ]
11 - Provides: [ bfast ]
12 - Conflicts: [ ]
13 - Replaces: [ ]
```

Inserisci il corrispondente numero per cambiare una caratteristica (seguito da INVIO) oppure premere INVIO per continuare:

Installing with make install...

===== installation result =====

```
Making install in bfast
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
gcc -Wall -g -O2 -pthread -o bfast AlignedEnd.o AlignedEntry.o AlignedRead.o AlignedReadConvert.o BError.o BLib.o RGBinary.o RGIndex.o RGIndexAccura
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'bfast' '/opt/CBL/bin/bfast/bin/bfast'
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
Making install in butil
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'balignmentscoredistribution' '/opt/CBL/bin/bfast/bin/balignmentcoredistribution'
/usr/bin/install -c 'balignsim' '/opt/CBL/bin/bfast/bin/balignsim'
/usr/bin/install -c 'bevalsim' '/opt/CBL/bin/bfast/bin/bevalsim'
/usr/bin/install -c 'bgeneratereads' '/opt/CBL/bin/bfast/bin/bgeneratereads'
/usr/bin/install -c 'bindexdist' '/opt/CBL/bin/bfast/bin/bindexdist'
/usr/bin/install -c 'bindexhist' '/opt/CBL/bin/bfast/bin/bindexhist'
/usr/bin/install -c 'bmfmerge' '/opt/CBL/bin/bfast/bin/bmfmerge'
/usr/bin/install -c 'brepeat' '/opt/CBL/bin/bfast/bin/brepeat'
/usr/bin/install -c 'btestindexes' '/opt/CBL/bin/bfast/bin/btestindexes'
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
Making install in scripts
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'solid2fastq' '/opt/CBL/bin/bfast/bin/solid2fastq'
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'bfast.resubmit.pl' '/opt/CBL/bin/bfast/bin/bfast.resubmit.pl'
/usr/bin/install -c 'bfast.submit.pl' '/opt/CBL/bin/bfast/bin/bfast.submit.pl'
/usr/bin/install -c 'ill2fastq.pl' '/opt/CBL/bin/bfast/bin/ill2fastq.pl'
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
Making install in tests
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
Making install in bfast
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
gcc -Wall -g -O2 -pthread -o bfast AlignedEnd.o AlignedEntry.o AlignedRead.o AlignedReadConvert.o BError.o BLib.o RGBinary.o RGIndex.o RGIndexAccura
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'bfast' '/opt/CBL/bin/bfast/bin/bfast'
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
Making install in butil
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'balignmentscoredistribution' '/opt/CBL/bin/bfast/bin/balignmentcoredistribution'
/usr/bin/install -c 'balignsim' '/opt/CBL/bin/bfast/bin/balignsim'
/usr/bin/install -c 'bevalsim' '/opt/CBL/bin/bfast/bin/bevalsim'
/usr/bin/install -c 'bgeneratereads' '/opt/CBL/bin/bfast/bin/bgeneratereads'
/usr/bin/install -c 'bindexdist' '/opt/CBL/bin/bfast/bin/bindexdist'
/usr/bin/install -c 'bindexhist' '/opt/CBL/bin/bfast/bin/bindexhist'
/usr/bin/install -c 'bmfmerge' '/opt/CBL/bin/bfast/bin/bmfmerge'
/usr/bin/install -c 'brepeat' '/opt/CBL/bin/bfast/bin/brepeat'
/usr/bin/install -c 'btestindexes' '/opt/CBL/bin/bfast/bin/btestindexes'
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/butil"
Making install in scripts
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'solid2fastq' '/opt/CBL/bin/bfast/bin/solid2fastq'
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
/usr/bin/install -c 'bfast.resubmit.pl' '/opt/CBL/bin/bfast/bin/bfast.resubmit.pl'
/usr/bin/install -c 'bfast.submit.pl' '/opt/CBL/bin/bfast/bin/bfast.submit.pl'
/usr/bin/install -c 'ill2fastq.pl' '/opt/CBL/bin/bfast/bin/ill2fastq.pl'
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
Making install in tests
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
Making install in tests
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
test -z "/opt/CBL/bin/bfast/bin" || /bin/mkdir -p "/opt/CBL/bin/bfast/bin"
make[2]: Nessuna operazione da eseguire per "install-data-am".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[2]: Nessuna operazione da eseguire per "install-exec-am".
test -z "/opt/CBL/bin/bfast/share/doc/bfast" || /bin/mkdir -p "/opt/CBL/bin/bfast/share/doc/bfast"
/usr/bin/install -c -m 644 'LICENSE' '/opt/CBL/bin/bfast/share/doc/bfast/LICENSE'
/usr/bin/install -c -m 644 'manual/bfast-book.pdf' '/opt/CBL/bin/bfast/share/doc/bfast/bfast-book.pdf'
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
```

===== installation successfully =====

Copying documentation directory...

```
./
./README
./AUTHORS
./COPYING
./NEWS
./LICENSE
./ChangeLog
./INSTALL
```



```

Some of the files created by the installation are inside the home directory: /home
You probably don't want them to be included in the package.
Do you want me to list them? [n]: n
Li escluderesti dalla creazione del pacchetto? (dire Sì e una buona idea!) [n]: n

Some of the files created by the installation are inside the build
directory: /home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a

You probably don't want them to be included in the package,
especially if they are inside your home directory.
Do you want me to list them? [n]: n
Li escluderesti dalla creazione del pacchetto? (dire Sì e una buona idea!) [y]: y

Copiatura dei file nella cartella temporanea in corso...OK
Stripping ELF binaries and libraries...OK
Compressione delle pagine di manuale in corso...OK
E' in corso la costruzione della lista dei file...OK
Costruzione pacchetto Debian in corso...OK
Installazione pacchetto Debian in corso...OK
Cancellazione file temporanei in corso...OK
Writing backup package...OK
OK
Cancellazione cartella temporanea in corso...OK

*****

Done. The new package has been installed and saved to
/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast_0.7.0a-0.7.0_i386.deb

You can remove it from your system anytime using:

    dpkg -r bfast

*****

```

The installation is runs in the standard mode, using the native commands:

- **dpkg** for *.deb packages
- **rpm** for *.rpm packages
- **installpkg** for *.tgz packages

If you want to use **checkinstall** there should be a directive **install:** in the **Makefile**; therefore you must insert it when there is not.

You can insert it using the configuration files described above `config/configcustom/*` (http://localhost/dokuwiki/doku.php?id=univ:tesi:attivita:manage_pkgs_custom#configuration).

To identify the **custom-packages** installed via **checkinstall** was used the information **customcbl** (stored in the field **Section:** through the option **-pkggroup** and written at the beginning of the *Description*).

Example of a single package:

```

piero@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dpkg -p bfast
Package: bfast
Priority: extra
Section: customcbl
Installed-Size: 2692
Maintainer: root@ubuntu1204-tesi-replicate2
Architecture: i386
Version: 0.7.0a-0.7.0
Provides: bfast
Size: 1206350
Description: customcbl - BFAST: Blat-like Fast Accurate Search Tool.

```

and a partial list of custom-packages installed:

```

ii bedtools                2.17.0-1                customcbl - A flexible suite of utilities for comparing genomic features.
ii bfast                   0.7.0a-0.7.0            customcbl - BFAST: Blat-like Fast Accurate Search Tool.
ii biobambam               0.0.92-e325743          customcbl - biobambam
ii bowtie                  1.0.0-1                  customcbl - The bowtie short read aligner.
ii bowtie2                 2.1.0-1                  customcbl - bowtie2 short read aligner, with gap support.
ii dwgmsim                 0.1.10-1                 customcbl - DWGSIM: simulating NGS data and evaluating mappings and variant
ii echo                    0-1                      customcbl - ECHO: A reference-free short-read error correction algorithm
ii fastq-screen            0.4.2-1                  customcbl - fastq-screen
ii fastqc                  0.10.1-1                 customcbl - A quality control tool for high throughput sequence data.
ii fastx-toolkit           0.0.13.2-1               customcbl - fastx-toolkit
ii gmap                    2012-11-09-1             customcbl - GMAP and GSNAP: A Genomic Mapping and Alignment Program for mRNA
ii lastz                   1.02.00-1                customcbl - LASTZ sequence alignment program.
ii libgttextutils          0.6-1                    customcbl - libgttextutils
ii libmaus                 0.0.72-8f6b9b4          customcbl - libmaus
ii mosaik                  2.1.73-1                  customcbl - MOSAIK: reference-guided aligner for next-generation sequencing
ii perm                    4-1                       customcbl - Efficient mapping of short sequences accomplished with periodic
ii picard                  1.96-1                    customcbl - Command-line utilities that manipulate BAM files with a Java API.
ii plinkseq                0.08-1                    customcbl - plinkseq
ii samtools                0.1.19-1                  customcbl - SAM Tools provide various utilities for manipulating alignments
ii shrec                   2.2-1                     customcbl - Shrec is a bioinformatics tool for error correction of HTS read
ii snap                    0.15-1                    customcbl - snap
ii solexaqa                2.2-1                     customcbl - SolexaQA creates visual representations of data quality from FAST
ii star                    2.3.1p-1                  customcbl - star
ii vcftools                0.1.11-1                  customcbl - Work with VCF files, such as those generated by the 1000 Genomes
...

```

4. logging

The installation of CBL environment *via-fabric* sometimes stops when an error occurs.

To avoid repeating each time the installation process, and especially to try to make it executable in **unattended mode**, I have implemented a system of error handling that ensures that the installation can continue, with the ability to check later what were the problems occurred during the deployment process.

For these reason I have implemented already at this early stage of development, a **logging system** that allows you to monitor the several stages of the deployment process, so you can correct the errors that have occurred.

I have implemented a two-levels log:

1. configuration logging (deploy/[check | buildaptfile])

A first level of log allows you to monitor the preparation of the CBL environment, so you can see any abnormalities that can be found in the deployment process. In particular we can see this in two steps:

- **deploy/check/** : after the execution of the script **check_package_available.sh** some lists are created, and in these lists you can see what packages are or are not available for the installation:

```

piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/check/
totale 60
drwxrwxr-x 2 piero piero 4096 nov 25 12:23 .
drwxrwxr-x 10 piero piero 4096 nov 25 12:13 ..
-rw-rw-r-- 1 piero piero 253 nov 25 12:23 pkg-custom-available.log
-rw-rw-r-- 1 piero piero 663 nov 25 12:23 pkg-custom-not_available.log
-rw-rw-r-- 1 piero piero 6236 nov 25 12:20 pkg-packages-available.log
-rw-rw-r-- 1 piero piero 77 nov 25 12:20 pkg-packages-homebrew-available.log
-rw-rw-r-- 1 piero piero 60 nov 25 12:20 pkg-packages-homebrew-not_available.log
-rw-rw-r-- 1 piero piero 7 nov 25 12:20 pkg-packages-nix-available.log
-rw-rw-r-- 1 piero piero 50 nov 25 12:20 pkg-packages-nix-not_available.log
-rw-rw-r-- 1 piero piero 454 nov 25 12:19 pkg-packages-not_available.log
-rw-rw-r-- 1 piero piero 324 nov 25 12:21 pkg-packages-scientificlinux-available.log
-rw-rw-r-- 1 piero piero 1125 nov 25 12:21 pkg-packages-scientificlinux-not_available.log
-rw-rw-r-- 1 piero piero 530 nov 25 12:22 pkg-packages-yum-available.log
-rw-rw-r-- 1 piero piero 1950 nov 25 12:23 pkg-packages-yum-not_available.log

```

- **deploy/builtaptfile/** : after the execution of the script **built_apt_file.sh** two lists are created;
 - one of these lists (*grouplist_to_install.txt*) contains the packages to be installed
 - and the other (*grouplist_not_to_install.txt*) the packages will not be installed, because it does not belong to the *groups* that are included in the file **clonecbl/cloudbiolinux/config/main.yaml** (downloaded from `git clone git://github.com/chapmanb/cloudbiolinux.git [git://github.com/chapmanb/cloudbiolinux.git]`):

```

piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/builtaptfile/
totale 40
drwxrwxr-x 7 piero piero 4096 nov 23 02:17 .
drwxrwxr-x 10 piero piero 4096 nov 25 12:13 ..
-rw-rw-r-- 1 piero piero 4929 nov 23 02:17 grouplist_to_install.txt
-rw-rw-r-- 1 piero piero 938 nov 23 02:17 grouplist_not_to_install.txt
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-homebrew
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-nix
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-scientificlinux
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 packages-yum

```

2. deployment logging (deploy/log)

Each script creates a subdirectory with the same name of the script into directory **deploy/log/** :

```

piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/log/
totale 36
drwxrwxr-x 9 piero piero 4096 nov 25 12:13 .
drwxrwxr-x 10 piero piero 4096 nov 25 12:13 ..
drwxr-xr-x 2 root root 4096 nov 23 00:13 aptkeycbl
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 build_apt_file
drwxr-xr-x 2 root root 4096 nov 24 15:50 build_custom_pkgs
drwxrwxr-x 2 piero piero 4096 nov 25 01:40 build_deb_pkg
drwxrwxr-x 2 piero piero 4096 nov 25 12:13 check_package_available
drwxrwxr-x 2 piero piero 4096 nov 23 02:17 deploycbl
drwxrwxr-x 2 piero piero 4096 nov 23 00:08 pre-install

```

Into each of these directories each script writes one or more log-files to store all stages of execution and errors . One of these log-files always have the same name of the script with the suffix **.log**:

```

piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/log/pre-install/
totale 208
drwxrwxr-x 2 piero piero 4096 nov 23 00:08 .
drwxrwxr-x 9 piero piero 4096 nov 25 12:13 ..
-rw-rw-r-- 1 piero piero 200007 nov 25 12:23 pre-install.log

```

```

piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ more deploy/log/pre-install/pre-install.log
20131123-000803-START: *****
20131123-000803-START: start script ./pre-install.sh ...
20131123-000803-START: *****
20131123-000803-VERBOSE: *****
20131123-000803-VERBOSE: start clone cloudbiolinux ...
20131123-000803-VERBOSE: *****
20131123-000803-VERBOSE: .. end clone cloudbiolinux.
20131123-000803-VERBOSE: *****
20131123-000803-VERBOSE: .. end check available packages/libraries.
20131123-000803-VERBOSE: *****
20131123-000803-OK: *****
20131123-000803-OK: end script ./pre-install.sh
20131123-000803-OK: *****
20131123-000803-END: *****
20131123-000803-END: end script
20131123-000803-END: *****
20131123-000904-START: *****
20131123-000904-START: start script ./pre-install.sh ...
20131123-000904-START: *****
20131123-000904-VERBOSE: *****
20131123-000904-VERBOSE: start control version/release 05 ...
20131123-000904-VERBOSE: *****
20131123-000904-VERBOSE: .. end control version/release 05.
20131123-000904-VERBOSE: *****
20131123-000904-VERBOSE: start control disk-space ...
20131123-000904-VERBOSE: *****
20131123-000904-VERBOSE: Disk space available ok: 12685456
20131123-000904-VERBOSE: *****
20131123-000904-VERBOSE: .. end control disk-space.
20131123-000904-VERBOSE: *****
...

```

Each line in the log has a **date** and a **time** as a prefix, so you can identify different executions of the same script. In addition, there is a line that identifies the beginning of the script:

```

20131123-000904-START: *****

```

```
20131123-000904-START: start script ./pre-install.sh ...
20131123-000904-START: *****
...
```

and a line the identifies the end of the script:

```
...
20131125-122341-OK: *****
20131125-122341-OK: end script ./pre-install.sh
20131125-122341-OK: *****
20131125-122341-END: *****
20131125-122341-END: end script
20131125-122341-END: *****
```

In some cases there are specific log-files with details of the deployment stages.

For example the script that install **custom-packages** writes a specific log file for each package, which contains the detail of the building and installation:

```
piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ dir deploy/log/build_deb_pkg/
totale 8500
drwxrwxr-x 2 piro piro 4096 nov 25 01:40 .
drwxrwxr-x 9 piro piro 4096 nov 25 12:13 ..
-rw-r--r-- 1 root root 67686 nov 24 17:04 abyss
-rw-r--r-- 1 root root 21567 nov 24 16:39 bamtools
-rw-r--r-- 1 root root 99281 nov 24 16:23 bamutil-1.0.7
-rw-r--r-- 1 root root 90357 nov 24 17:41 bcbio
-rw-r--r-- 1 root root 45937 nov 24 16:07 bedtools
-rw-rw-r-- 1 piro piro 150313 nov 25 12:02 bfast
-rw-r--r-- 1 root root 1534 nov 25 01:00 biobambam
-rw-r--r-- 1 root root 3026452 nov 24 16:51 boost-1-49-0
-rw-r--r-- 1 root root 45136 nov 24 15:51 bowtie
-rw-r--r-- 1 root root 32514 nov 24 15:54 bowtie2
-rw-rw-r-- 1 piro piro 42905 nov 25 12:02 build_deb_pkg.log
-rw-r--r-- 1 root root 750 nov 25 00:55 bwa
-rw-r--r-- 1 root root 13023 nov 24 16:21 cram
-rw-r--r-- 1 root root 7877 nov 25 01:31 crisp-linux
-rw-r--r-- 1 root root 34212 nov 24 16:59 cufflinks
-rw-r--r-- 1 root root 12735 nov 25 01:30 delly-v0.0.11
...
```

```
piro@ubuntu1204-tesi-replicate2:~/cloudbiolinux$ less deploy/log/build_deb_pkg/bfast
20131125-115956-START: *****
20131125-115956-START: Assegnazione variabili pkg: bfast...
20131125-115956-START: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: Architettura ok: i386
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: to do ...
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: sostituzione %s in url...
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: wget --no-check-certificate -O bfast-0.7.0a.tar.gz http://downloads.sourceforge.net/project/bfast/bfast/0.7.0/bfast-0.7.0a.tar.gz
20131125-115956-VERBOSE: *****
--2013-11-25 11:59:56-- http://downloads.sourceforge.net/project/bfast/bfast/0.7.0/bfast-0.7.0a.tar.gz
Risoluzione di downloads.sourceforge.net (downloads.sourceforge.net)... 216.34.181.59
Connessione a downloads.sourceforge.net (downloads.sourceforge.net)|216.34.181.59|:80... connesso.
Richiesta HTTP inviata, in attesa di risposta... 302 Found
Posizione: http://switch.dl.sourceforge.net/project/bfast/bfast/0.7.0/bfast-0.7.0a.tar.gz [segue]
--2013-11-25 12:00:02-- http://switch.dl.sourceforge.net/project/bfast/bfast/0.7.0/bfast-0.7.0a.tar.gz
Risoluzione di switch.dl.sourceforge.net (switch.dl.sourceforge.net)... 130.59.138.21, 2001:620:0:1b::21
Connessione a switch.dl.sourceforge.net (switch.dl.sourceforge.net)|130.59.138.21|:80... connesso.
Richiesta HTTP inviata, in attesa di risposta... 200 OK
Lunghezza: 2456617 (2,3M) [application/x-gzip]
Salvataggio in: "bfast-0.7.0a.tar.gz"

  0K ..... 2% 222K 11s
 50K ..... 4% 585K 7s
100K ..... 6% 710K 6s
...
2250K ..... 95% 433K 4s
2300K ..... 97% 395K 2s
2350K ..... 100% 493K=85s
```

```
2013-11-25 12:01:28 (28,1 KB/s) - "bfast-0.7.0a.tar.gz" salvato [2456617/2456617]
```

```
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: estrazione in corso ...
20131125-115956-VERBOSE: *****
bfast-0.7.0a/
bfast-0.7.0a/aclocal.m4
bfast-0.7.0a/AUTHORS
bfast-0.7.0a/autogen.sh
bfast-0.7.0a/bfast/
bfast-0.7.0a/butil/
bfast-0.7.0a/ChangeLog
...
0131125-115956-VERBOSE: *** non esiste Makefile, controllo configure ...
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: pkg: bfast
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: SI autoapt: yes - yes ? yes
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: auto-apt -y run ./configure --prefix=/opt/CBL/bin/bfast
20131125-115956-VERBOSE: *****
Entering auto-apt mode: ./configure --prefix=/opt/CBL/bin/bfast
Exit the command to leave auto-apt mode.
checking for a BSD-compatible install... /usr/bin/install -c
checking whether build environment is sane... yes
checking for a thread-safe mkdir -p... /bin/mkdir -p
...
checking for fcntl.h... yes
checking for inline... inline
configure: creating ./config.status
config.status: creating Makefile
config.status: creating bfast/Makefile
config.status: creating butil/Makefile
config.status: creating scripts/Makefile
config.status: creating tests/Makefile
config.status: creating config.h
config.status: executing depfiles commands
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: esecuzione make in corso ... sono in /home/piro/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: compile make ... sudo:
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: sudo auto-apt -y run make
20131125-115956-VERBOSE: *****
```

```

Entering auto-apt mode: make
Exit the command to leave auto-apt mode.
make all-recursive
make[1]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
Making all in bfast
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast"
depbase='echo AlignedEnd.o | sed 's|[^/]*|.deps/&;s|.o$||'`; \
gcc -DHAVE_CONFIG_H -I. -I.. -Wall -g -O2 -pthread -MT AlignedEnd.o -MD -MP -MF $depbase.Tpo -c -o AlignedEnd.o AlignedEnd.c &&\
mv -f $depbase.Tpo $depbase.Po
...
depbase='echo solid2fastq.o | sed 's|[^/]*|.deps/&;s|.o$||'`; \
gcc -DHAVE_CONFIG_H -I. -I.. -Wall -g -O2 -pthread -MT solid2fastq.o -MD -MP -MF $depbase.Tpo -c -o solid2fastq.o solid2fastq.c &&\
mv -f $depbase.Tpo $depbase.Po
gcc -Wall -g -O2 -pthread -o solid2fastq ../bfast/BError.o ../bfast/RGIndex.o ../bfast/BLib.o ../bfast/RGBinary.o ../bfast/RGRanges.o ../bfast/RGMa
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/scripts"
Making all in tests
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[2]: Nessuna operazione da eseguire per "all".
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/tests"
make[2]: ingresso nella directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[2]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
make[1]: uscita dalla directory "/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a"
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: ...fatto
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: pkg: bfast - version: 0.7.0a - subversion: 0.7.0
20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: int
20131125-115956-VERBOSE: *****
...

checkinstall 1.6.2, Copyright 2009 Felipe Eduardo Sanchez Diaz Duran
Questo software è rilasciato sotto i termini della licenza GNU GPL.

The package documentation directory ./doc-pak does not exist.
Should I create a default set of package docs? [y]: y

Preparazione documentazione pacchetto in corso...OK

*****
*** Debian package creation selected ***
*****

Il pacchetto verrà costruito con le seguenti caratteristiche:

0 - Maintainer: [ root@ubuntu1204-tesi-replicate2 ]
1 - Summary: [ Package created with checkinstall 1.6.2 ]
2 - Name: [ bfast ]
3 - Version: [ 0.7.0a ]
4 - Release: [ 0.7.0 ]
5 - License: [ GPL ]
6 - Group: [ customcbl ]
7 - Architecture: [ i386 ]
8 - Source location: [ bfast-0.7.0a ]
9 - Alternate source location: [ ]
10 - Requires: [ ]
11 - Provides: [ bfast ]
12 - Conflicts: [ ]
13 - Replaces: [ ]
...
Cancellazione file temporanei in corso...OK
Writing backup package...OK
OK
Cancellazione cartella temporanea in corso...OK

*****

Done. The new package has been installed and saved to
/home/piero/cloudbiolinux/deploy/temp/bfast/bfast-0.7.0a/bfast_0.7.0a-0.7.0_i386.deb

You can remove it from your system anytime using:

dpkg -r bfast

*****

20131125-115956-VERBOSE: *****
20131125-115956-VERBOSE: pkg: bfast
20131125-115956-VERBOSE: *****

```

examples

Below you can see some examples that show the usefulness of the log.
The installation of the **custom-packages** in Ubuntu 12.04 gave this result:

```

piero@ubuntu1304-tesi-install:~/cloudbiolinux$ cat deploy/log/build_custom_pkgs/custom-errors-pkgs.err
20131214-083818-ERROR: *****
20131214-083818-ERROR: Installazione package <bwa> terminata con un errore: 9
20131214-083818-ERROR: *****
20131214-083818-ERROR: *****
20131214-083818-ERROR: Installazione package <stampy> terminata con un errore: 9
20131214-083818-ERROR: *****
20131214-083818-ERROR: *****
20131214-083818-ERROR: Installazione package <vcflib> terminata con un errore: 9
20131214-083818-ERROR: *****
20131214-083818-ERROR: *****
20131214-083818-ERROR: Installazione package <sambamba> terminata con un errore: 9
20131214-083818-ERROR: *****

```

where the only packages not installed are those that require a 64-bit architecture (error code: 9)

ubuntu 13.04 (raring)

Unlike of the installation of the **custom-packages** in Ubuntu 12.04, in this case we obtain this result:

```

piero@ubuntu1304-tesi-install:~/cloudbiolinux$ cat deploy/log/build_custom_pkgs/custom-errors-pkgs.err
20131215-173843-ERROR: *****
20131215-173843-ERROR: Installazione package <stampy> terminata con un errore: 9
20131215-173843-ERROR: *****
20131215-173843-ERROR: *****
20131215-173843-ERROR: Installazione package <echo> terminata con un errore: 3
20131215-173843-ERROR: *****
20131215-173843-ERROR: *****
20131215-173843-ERROR: Installazione package <vcflib> terminata con un errore: 9

```

```
20131215-173843-ERROR: *****
20131215-173843-ERROR: *****
20131215-173843-ERROR: Installazione package <boost> terminata con un errore: 3
20131215-173843-ERROR: *****
20131215-173843-ERROR: *****
20131215-173843-ERROR: Installazione package <sambamba> terminata con un errore: 9
20131215-173843-ERROR: *****
```

We can see below the specific logs of the packages whose installation failed:

▪ package echo:

```
piero@ubuntu1304-tesi-install:~/cloudbiolinux$ cat deploy/log/build_deb_pkg/echo
```

```
20131215-174455-START: *****
20131215-174455-START: Assegnazione variabili pkg: echo...
20131215-174455-START: *****
20131215-174455-DEBUG: *****
20131215-174455-DEBUG: pkg: echo
20131215-174455-DEBUG: *****
20131215-174455-DEBUG: version: 1_12 - 1
20131215-174455-DEBUG: *****
20131215-174455-DEBUG: *****
20131215-174455-DEBUG: distribution:
...
20131215-174455-VERBOSE: compile make ... sudo:
20131215-174455-VERBOSE: *****
Entering auto-apt mode: make
Exit the command to leave auto-apt mode.
g++ -c -Wall -O3 DNaseq.cpp -o DNaseq.o
g++ -c -Wall -O3 NeighborSet.cpp -o NeighborSet.o
In file included from MMAPReads.hpp:4:0,
      from NeighborSet.hpp:17,
      from NeighborSet.cpp:1:
MMAP.hpp: In destructor 'virtual MMAP::~MMAP()':
MMAP.hpp:37:19: error: 'close' was not declared in this scope
make: *** [NeighborSet.o] Error 1
20131215-174455-VERBOSE: *****
...
```

▪ package boost:

```
piero@ubuntu1304-tesi-install:~/cloudbiolinux$ cat deploy/log/build_deb_pkg/boost
```

```
20131215-174528-START: *****
20131215-174528-START: Assegnazione variabili pkg: boost...
20131215-174528-START: *****
20131215-174528-DEBUG: *****
20131215-174528-DEBUG: pkg: boost
20131215-174528-DEBUG: *****
20131215-174528-DEBUG: *****
20131215-174528-DEBUG: version: 1_49_0 - 1
...
...found 539 targets...
...updating 23 targets...
common.mkdir stage
common.mkdir stage/lib
common.mkdir bin.v2
common.mkdir bin.v2/libs
common.mkdir bin.v2/libs/thread
common.mkdir bin.v2/libs/thread/build
common.mkdir bin.v2/libs/thread/build/gcc-4.7
common.mkdir bin.v2/libs/thread/build/gcc-4.7/release
common.mkdir bin.v2/libs/thread/build/gcc-4.7/release/threading-multi
common.mkdir bin.v2/libs/thread/build/gcc-4.7/release/threading-multi/pthread
gcc.compile.c++ bin.v2/libs/thread/build/gcc-4.7/release/threading-multi/pthread/thread.o
In file included from ./boost/thread/ptread/mutex.hpp:14:0,
      from ./boost/thread/mutex.hpp:16,
      from ./boost/thread/ptread/thread_data.hpp:12,
      from ./boost/thread/thread.hpp:17,
      from libs/thread/src/ptread/thread.cpp:10:
./boost/thread/xtime.hpp:23:5: error: expected identifier before numeric constant
./boost/thread/xtime.hpp:23:5: error: expected '}' before numeric constant
./boost/thread/xtime.hpp:23:5: error: expected unqualified-id before numeric constant
./boost/thread/xtime.hpp:46:14: error: expected type-specifier before 'system_time'
In file included from ./boost/thread/ptread/mutex.hpp:14:0,
      from ./boost/thread/mutex.hpp:16,
      from ./boost/thread/ptread/thread_data.hpp:12,
      from ./boost/thread/thread.hpp:17,
      from libs/thread/src/ptread/thread.cpp:10:
./boost/thread/xtime.hpp: In function 'int xtime_get(xtime*, int)':
./boost/thread/xtime.hpp:73:40: error: 'get_system_time' was not declared in this scope
./boost/thread/xtime.hpp:73:40: note: suggested alternative:
In file included from ./boost/thread/locks.hpp:12:0,
      from ./boost/thread/ptread/mutex.hpp:12,
      from ./boost/thread/mutex.hpp:16,
      from ./boost/thread/ptread/thread_data.hpp:12,
      from ./boost/thread/thread.hpp:17,
      from libs/thread/src/ptread/thread.cpp:10:
./boost/thread/thread_time.hpp:19:24: note: 'boost::get_system_time'
In file included from ./boost/thread/ptread/mutex.hpp:14:0,
      from ./boost/thread/mutex.hpp:16,
      from ./boost/thread/ptread/thread_data.hpp:12,
      from ./boost/thread/thread.hpp:17,
      from libs/thread/src/ptread/thread.cpp:10:
./boost/thread/xtime.hpp: At global scope:
./boost/thread/xtime.hpp:88:1: error: expected declaration before '}' token

"g++" -ftemplate-depth-128 -O3 -finline-functions -Wno-inline -Wall -pthread -fPIC -Wno-long-long -DBOOST_ALL_NO_LIB=1 -DBOOST_THREAD_BUILD_DLL=1
...failed gcc.compile.c++ bin.v2/libs/thread/build/gcc-4.7/release/threading-multi/ptread/thread.o...
gcc.compile.c++ bin.v2/libs/thread/build/gcc-4.7/release/threading-multi/ptread/once.o
...skipped <pbins.v2/libs/thread/build/gcc-4.7/release/threading-multi/libboost_thread.so.1.49.0 for lack of <pbins.v2/libs/thread/build/gcc-4.7/release/...
...skipped <pstage/lib>libboost_thread.so.1.49.0 for lack of <pbins.v2/libs/thread/build/gcc-4.7/release/threading-multi>libboost_thread.so.1.49.0...
...skipped <pstage/lib>libboost_thread.so for lack of <pstage/lib>libboost_thread.so.1.49.0...
common.mkdir bin.v2/libs/thread/build/gcc-4.7/release/link-static
common.mkdir bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi
common.mkdir bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi/pthread
gcc.compile.c++ bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi/ptread/thread.o
In file included from ./boost/thread/ptread/mutex.hpp:14:0,
      from ./boost/thread/mutex.hpp:16,
      from ./boost/thread/ptread/thread_data.hpp:12,
      from ./boost/thread/thread.hpp:17,
      from libs/thread/src/ptread/thread.cpp:10:
./boost/thread/xtime.hpp:23:5: error: expected identifier before numeric constant
./boost/thread/xtime.hpp:23:5: error: expected '}' before numeric constant
./boost/thread/xtime.hpp:23:5: error: expected unqualified-id before numeric constant
./boost/thread/xtime.hpp:46:14: error: expected type-specifier before 'system_time'
In file included from ./boost/thread/ptread/mutex.hpp:14:0,
      from ./boost/thread/mutex.hpp:16,
      from ./boost/thread/ptread/thread_data.hpp:12,
      from ./boost/thread/thread.hpp:17,
      from libs/thread/src/ptread/thread.cpp:10:
```

```

./boost/thread/xtime.hpp: In function 'int xtime_get(xtime*, int)':
./boost/thread/xtime.hpp:73:40: error: 'get_system_time' was not declared in this scope
./boost/thread/xtime.hpp:73:40: note: suggested alternative:
In file included from ./boost/thread/locks.hpp:12:0,
                 from ./boost/thread/pthread/mutex.hpp:12,
                 from ./boost/thread/mutex.hpp:16,
                 from ./boost/thread/pthread/thread_data.hpp:12,
                 from ./boost/thread/thread.hpp:17,
                 from libs/thread/src/pthread/thread.cpp:10:
./boost/thread/thread_time.hpp:19:24: note: 'boost::get_system_time'
In file included from ./boost/thread/pthread/mutex.hpp:14:0,
                 from ./boost/thread/mutex.hpp:16,
                 from ./boost/thread/pthread/thread_data.hpp:12,
                 from ./boost/thread/thread.hpp:17,
                 from libs/thread/src/pthread/thread.cpp:10:
./boost/thread/xtime.hpp: At global scope:
./boost/thread/xtime.hpp:88:1: error: expected declaration before '}' token

"g++" -ftemplate-depth-128 -O3 -finline-functions -Wno-inline -Wall -pthread -Wno-long-long -DBOOST_ALL_NO_LIB=1 -DBOOST_THREAD_BUILD_LIB=1 -DBOOST
...failed gcc.compile.c++ bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi/pthread/thread.o...
gcc.compile.c++ bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi/pthread/once.o
...skipped <bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi>libboost_thread.a(clean) for lack of <bin.v2/libs/thread/build/gcc-4.
...skipped <bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi>libboost_thread.a for lack of <bin.v2/libs/thread/build/gcc-4.7/relea
...skipped <stage/lib>libboost_thread.a for lack of <bin.v2/libs/thread/build/gcc-4.7/release/link-static/threading-multi>libboost_thread.a...
...failed updating 2 targets...
...skipped 6 targets...
...updated 15 targets...
make: *** [all] Error 1
20131215-174528-VERBOSE: *****
...

```

5. About CBL packages

In the deployment process described above, as the last step, we compared the versions of installed packages with those stored in the reference files: **clonebl/cloudbiolinux/manifest*.yaml** (downloaded from [git clone git://github.com/chapmanb/cloudbiolinux.git](https://github.com/chapmanb/cloudbiolinux.git) [git://github.com/chapmanb/cloudbiolinux.git]).

This comparison often shows a high number of differences.

This is not surprising, when you consider that the files stored in **clonebl/cloudbiolinux/manifest*.yaml** are quite static, because they are created when a new release of an image of AWS is created, and this will not change until the next release: the version of packages in a new release, it's already old when they are created.

But when you create a new machine (physical or virtual), if the installation is not done through the cloning of a referenced machine (for example the last version of AWS), the installing of the packages (that can be done in a several ways) will always have differences, due to the normal evolution of the packages of a specific distribution:

- because the the packages are upgraded (for changes, for security upgrade, and so on)
- when the OS has a different release (for raringexample, Ubuntu 12.04, 12.10, 13.04 etc.)
- when the OS has a different distributions (for example, debian, ubuntu, centOS)
- ...

For these reasons it might be useful a different organization of the referenced packages:

- to distinguish between **packages-base** and **packages-CBL**, where:
 - **packages-base** identify the packages that are parts of the installed distribution (**generic or system** packages), but that are not directly related to the CBL environment
 - they are generally installable in the native mode from repository of the distribution
 - **packages-CBL** are the packages directly related to the CBL environment
 - they are packages installable both in *native* mode and in *custom* mode
 - an example is the list on: <http://nbc.nerc.ac.uk/tools/bio-linux/package-list> [http://nbc.nerc.ac.uk/tools/bio-linux/package-list]
- identify these packages in different ways:
 - **packages-base**: you dont specify only a particular version, but the *minor* version supported (**>= \$VERSION**) for different distributions
 - **packages-CBL**: you must specify the supported versions

This division could be extended further, to identify the packages and the version of packages related to different distributions, both for **packages-base**:

package-base	version			
	ubuntu 12.04	ubuntu 13.04	debian squeeze	centOS
acl	>= 2.2.51-5ubuntu1	>= 2.2.51-8ubuntu3	>= 2.2.49-4	>= 2.2.49-6.el6
adduser	>= 3.113ubuntu2	>= 3.113+nmu3ubuntu1	>= 3.112+nmu2	not exist
ant	>= 1.8.2-4build1	>= 1.8.2-4build2	>= 1.8.0-4	>= 1.7.1-13.el6
apache2	>= 2.2.22-1ubuntu1.4	>= 2.2.22-6ubuntu5.1	>= 2.2.16-6+squeeze11	>= 2.4.2-76.1
aptitude	>= 0.6.6-1ubuntu1.2	>= 0.6.8.1-2ubuntu2	>= 0.6.8.2-10.6.3-2+squeeze1	not exist
...
gcc	>= 4.4.6.3-1ubuntu5	>= 4.4.7.3-1ubuntu10	>= 4.4.4.5-1	>= 4.4.7-3.el6
gnome-desktop3-data	>= 3.4.2-0ubuntu0.1	>= 3.6.3-0ubuntu1	not exist	not exist
gnome-games-data	>= 1:3.4.1-0ubuntu2.2	not exist	>= 1:2.30-2	not exist
gzip	>= 1.4-1ubuntu2	>= 1.5-1.1ubuntu1	>= 1.3.12-9+squeeze1	>= 1.3.12-19.el6_4
...
hdf5	not exist	not exist	not exist	>= 1.8.11-14.1
...
numpy	not exist	not exist	not exist	>= 1.4.1-9.el6
python-numpy	>= 1:1.6.1-6ubuntu1	>= 1:1.7.1-1ubuntu1	>= 1:1.4.1-5	>= 1.6.1-17.1
...
ruby	>= 4.8	>= 4.9	>= 4.5	>= 1.8.7.352
ruby1.8	>= 1.8.7.352-2ubuntu1.4	>= 1.8.7.358-7ubuntu1.2	>= 1.8.7.302-2squeeze2	not exist
...
tar	>= 1.26-4ubuntu1	>= 1.26+dfsg-5	>= 1.23-3	>= 1.23-11.el6
...

and for **custom-packages**:

custom-package	version				
	custom	ubuntu 12.04	ubuntu 13.04	debian squeeze	centOS
abyss	1.3.4-1	1.3.2-1	1.3.6-0biolinux2	1.3.4-3	not exist
bow tie	1.0.0	?	1.0.0-1-0ubuntu2	not exist	0.12.7-1.4
bamtools	3fe66b9-1	not exist	not exist	not exist	2.2.1-9.1
bamutil	1.0.7-1	not exist	not exist	not exist	0.7.0a-6.1

bfast	0.7.0a-0.7.0	not exist	not exist	not exist	2.2.1-9.1
crisp	5-1	not exist	not exist	not exist	not exist
dwgsm	0.1.10-1	not exist	not exist	not exist	0.1.10-5.1
grabix	0.1.1-80150d00e5	not exist	not exist	not exist	not exist
...
plinkseq	0.08-1	not exist	not exist	not exist	not exist
rnaseqc	1.1.7-1	not exist	not exist	not exist	not exist
solexaqa	2.2-1	not exist	not exist	not exist	not exist
...

Although in the current **cloudbiolinux** environment exists a difference between the **packages** and **custom-packages**, this is only related to the different method of installation.

What I think is useful to distinguish, is related to the **SCOPE** of the packages themselves:

- for **packages-base** I mean identify all those packages *standard (generic or system)* packages) required to run the system (and that are not related with CBL environment); below you can see some of these packages:
 - adduser
 - ant
 - gcc
 - apache
 - aptitude
 - gnome
 - gnome-games-data
 - gzip
 - tar
 - ...
- while for **packages-CBL** I mean all those packages that are in some ways related to the CBL environment:
 - which may be available from *standard repositories*:
 - bio-linux-big-blast
 - bio-linux-blast
 - bio-linux-blixem
 - bio-linux-clustal
 - bwa
 - bowtie
 - ...
 - o from *custom packages*:
 - abyss
 - beast
 - bfast
 - bio4j
 - freebayes
 - gmap
 - hydra
 - lastz
 - ...

This splitting might be useful for:

- identify exactly the context of CBL environment
- having a reference point for all developers who work in this context
- ensure a better way to monitor the evolutions of the environment, and keep the focus on the programs related to the CBL environment
- to give a different level of importance to the differences between the versions of the referenced-packages and those installed:
 - less importance whether related to **packages-base**
 - greater importance if related to **packages-CBL**.