

Post install para nodos nuevos

config

- añadir al fstab

```
172.26.2.34:/share/MD0_DATA/Public /old_nas nfs defaults 0
0
172.26.9.33:/Public/investigacion/srvstorage/nas /home nfs defaults
0 0
172.26.9.33:/Public/investigacion/srvstorage /the_dysk nfs defaults
0 0
```

- clonar usuarios y grupos
- ssh rsa auth para root
- usuarios de sistema: munge, brexia, xnat **deben tener mismos uid y gid**

Dependencias

FSL

dependencias a instalar con yum

sistema:

```
vim epel-release nfs-utils munge yum-utils rsync
```

slurm

```
slurm-slurmd
```

postfix:

```
cyrus-sasl cyrus-sasl-plain
```

R:

```
libjpeg-turbo-devel pango-devel libpng12 libmng cairo-devel libcurl-devel
libxml2-devel libgit2-devel gmp-devel
gcc-gfortran gcc-c++ readline-devel bzip2-devel pcre2-devel cmake
texinfo texlive-inconsolata tex texlive-scheme-basic texinfo-tex texlive-
titling
java-1.8.0-openjdk java-1.8.0-openjdk-devel
```

Freesurfer:

```
tcsh
```

containers:

```
singularity
```

convenience:

```
jq htop curl
```

devtoolset: <https://www.softwarecollections.org/en/scls/rhscl/devtoolset-8/>

```
centos-release-scl  
scl-utils devtoolset-8
```

R

[lista de paquetes,](#)

[rpacks.list](#)

```
ggplot2  
faraway  
foreign  
psych  
foreach  
pls  
car  
dplyr  
data.table  
plotROC  
grid  
WRS2  
tidyr  
gridExtra  
irr  
DT  
stringr  
qqman  
reshape2  
ggrepel  
scales  
HIBAG  
parallel  
readr  
gap  
haplo.stats  
SAIGE
```

```
metafor
plotly
ggsci
MADloy
genoCN
survival
survminer
TwoSampleMR
```

A lo loco,

```
[root@brick04 ~]# for x in `cat /home/osotolongo/rpacks.list`; do Rscript -e
"install.packages('${x}', repos='https://cran.rediris.es/')"; done
```

Revisando,

```
[root@brick04 ~]# for x in `cat /home/osotolongo/rpacks.list`; do Rscript -e
"library('${x}')"; done 2>&1 | grep Error
Error in library("HIBAG") : there is no package called 'HIBAG'
Error in library("SAIGE") : there is no package called 'SAIGE'
Error in library("MADloy") : there is no package called 'MADloy'
Error in library("genoCN") : there is no package called 'genoCN'
Error in library("TwoSampleMR") :
```

ahora mas espacio,

```
install.packages("devtools")
devtools::install_github("MRCIEU/TwoSampleMR")
```

y por otra parte

```
install.packages("BiocManager")
BiocManager::install("genoCN")
BiocManager::install("HIBAG")
```

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