**Instalación Anaconda, R, R Studio**

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1.Después de la descarga de Anaconda, sobre una terminal con el usuario actual

bash Anaconda-xxxx.sh

2. Después de la instalación de Anaconda, se debe agregar el path donde quedaron los binarios de la aplicación.

sudo nano /etc/enviroment

Editar colocando el path por defecto /home/user/anaconda3/bin:$PATH

En bash:

export PATH="/home/user/anaconda3/bin:$PATH"

3. Actualización de repositorios, paquetes, compiladores y librerías:

sudo apt-get update

sudo apt-get upgrade

sudo apt-get install libssh2-1-dev zlib1g-dev libssl-dev libcurl4-openssl-dev build-essential python-dev default-jre default-jdk libcairo2-dev texlive-full libxml2-dev libxt-dev

5. Instalación de R

*R is a fast-moving project, and the latest stable version isn't always available from Ubuntu's repositories, so we'll start by adding the external repository maintained by CRAN:  
  
Note: CRAN maintains the repositories within their network, but not all external repositories are reliable. Be sure to install only from trusted sources.*

sudo echo "deb http://cran.rstudio.com/bin/linux/ubuntu xenial/" | sudo tee -a /etc/apt/sources.list

gpg --keyserver keyserver.ubuntu.com --recv-key E084DAB9

gpg -a --export E084DAB9 | sudo apt-key add -

sudo apt-get install r-base r-base-dev

sudo R CMD javareconf

version 3.3.2-1xenial0

6. Instalación R Studio

sudo apt-get install gdebi-core

wget https://download1.rstudio.org/rstudio-1.0.136-amd64.deb

sudo gdebi rstudio-1.0.136-amd64.deb

7. Instalación de paquetes de R

Desde RStudio

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* install.packages(c('repr', 'IRdisplay', 'evaluate', 'crayon', 'pbdZMQ', 'devtools', 'uuid', 'digest'))  
  devtools::install\_github('IRkernel/IRdisplay')
* devtools::install\_github('IRkernel/IRkernel')

Desde R

* IRkernel::installspec()
* ***Verificar en Jupyter su integración con R***

Desde RStudio

* install.packages(c('jpeg','nplot','assertthat','base64enc','BH','bitops','car','caret','chron','colorspace','data.table','DBI','dichromat','dplyr','foreach','formatR','ggally','ggplot2','glmnet','gtable','hexbin','highr','htmltools','htmlwidgets','httpuv','iterators','knitr','labeling','lazyeval','maps','markdown','matrixmodels','minga','munsell','nloptr','pbkrtest','plyr','proto','quantmod','quantreg','randomforest','rbokeh','rcolorbrewer','rcpp','rcppeigen','repr','reshape2','rjsonio','rmarkdown','scales','shiny','sparsem','tidyr','ttr','xtable','stx','yaml','zoo','ggaly','RJSONIO','rjson','rio','WriteXLS','XLConnectJars','XLConnect','XML','NLP','tm','dummy','reshape','rshape2','sqldf','Cairo','xlsx',’gdata’,’latticeExtra‘,’LightningR’,’googleVis’))
* devtools::install\_github("wesm/feather/R")
* devtools::install\_github('ramnathv/rCharts', 'ramnathv')
* source("http://bioconductor.org/biocLite.R") # bioconductor installer
* biocLite("rhdf5") # instalador del paquete

[Puede salir este mensaje

Warning message:

packages ‘nplot’, ‘ggally’, ‘matrixmodels’, ‘minga’, ‘randomforest’, ‘rcolorbrewer’, ‘rcpp’, ‘rcppeigen’, ‘rjsonio’, ‘sparsem’, ‘ttr’, ‘stx’, ‘ggaly’ are not available (for R version 3.2.3) ]

8. Actualización de Paquetes desde R Studio

tools ->check for updates packages

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Fuentes:

<https://www.digitalocean.com/community/tutorials/how-to-install-r-on-ubuntu-16-04-2>

<https://www.digitalocean.com/community/tutorials/how-to-set-up-r-on-ubuntu-14-04>

<https://irkernel.github.io/installation/>

<https://www.rstudio.com/products/rstudio/download/>

<https://cairographics.org/download/>