Most Popular R Packages using Spark & R package dependencies visualization

NYC DATA SCIENCE ACADEMY

Xavier Capdepon - *Data Scientist*

Bio:
Master in Urban Engineering (Hydraulic & Fluid mechanics)
Master in Corporate Finance
Actuarial Candidate ASA/CAS (passed 2 exams)

NYC Data Science Fellow : Bootcamp #2 – June to August 2015
R, Python, Data Mining, Machine Learning, Hadoop, Spark
Portfolio of 5 projects in Python, R, Spark and Machine learning

Projects' blogs:
http://blog.nycdatascience.com/author/chabir/

Email:
Xavier.Capdepon@gmail.com

LinkedIn:
https://www.linkedin.com/in/564738960482746278596

I'm looking for a Data Science / Data Mining Job !!

Project Guidelines:

Time to delivery:
7 days initially (it took 13+ days including 1.5 days to install spark locally…)

Advises:
“You need to deliver a visualization on the due date. You need to rescale your project accordingly.”
“It is fine not to build the most efficient code as long as the code works.“
”You need to have a story to tell with your visualization.”

Jason, NYC Data Science Academy’s Teacher

Github: https://github.com/chabir/Most-Popular-R-packages

Project Files & Spark installation:

Project Github account:
https://github.com/chabir/Most-Popular-R-packages

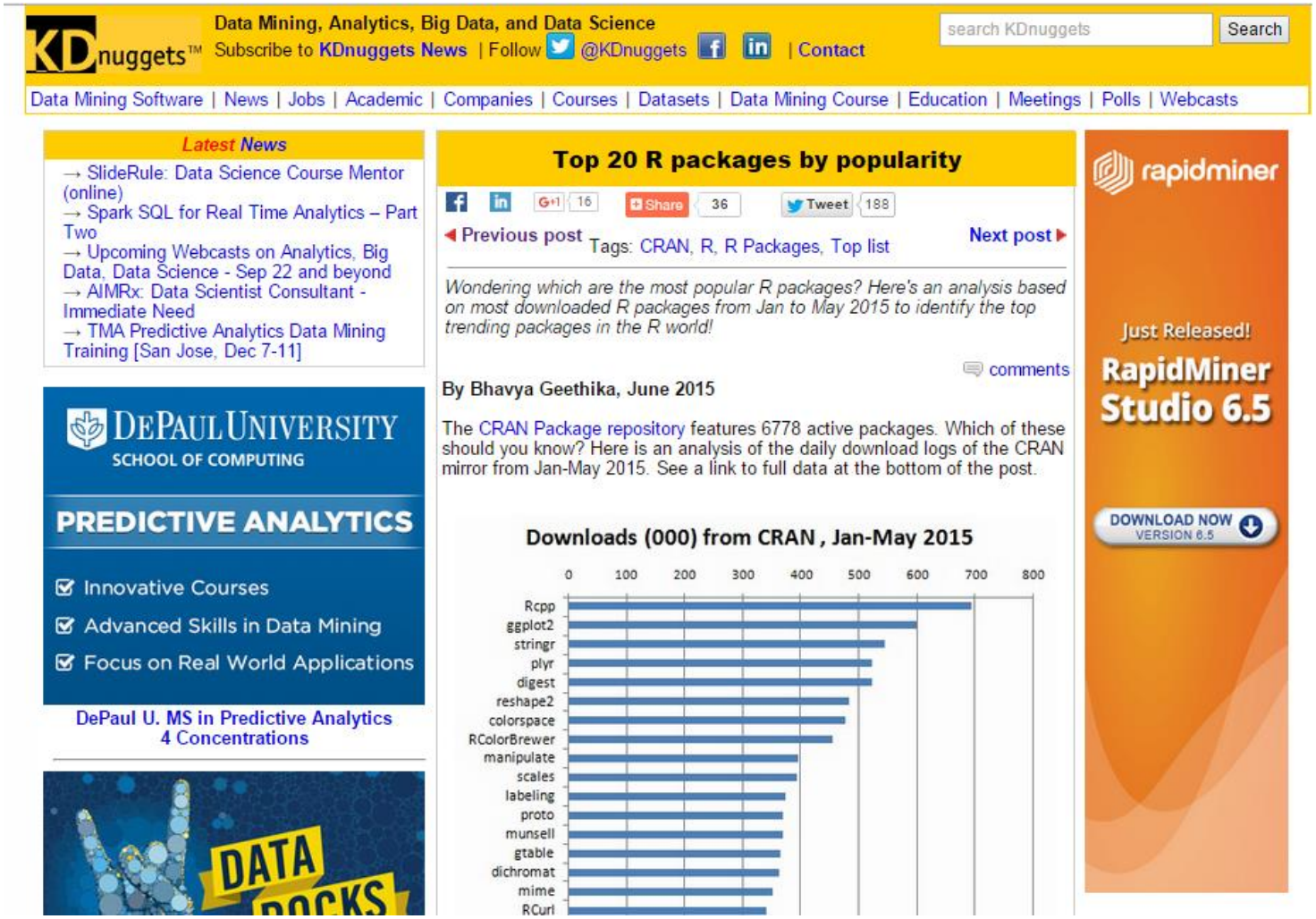
Useful links to install Spark for IPython on PC:
http://ysinjab.com/2015/03/28/hello-spark/
https://spark.apache.org/downloads.html
http://spark.apache.org/docs/latest/api/scala/index.html#org.apache.spark.SparkContext

To launch Spark in Ipython:

from pyspark import SparkContext
sc = SparkContext(master='local[7]', appName = 'learnSpark')

master: Cluster URL to connect to (e.g. mesos://host:port, spark://host:port, local[4]).
"*7*": corresponds to the number of cpu on local computer
appName: A name for your application, to display on the cluster web UI

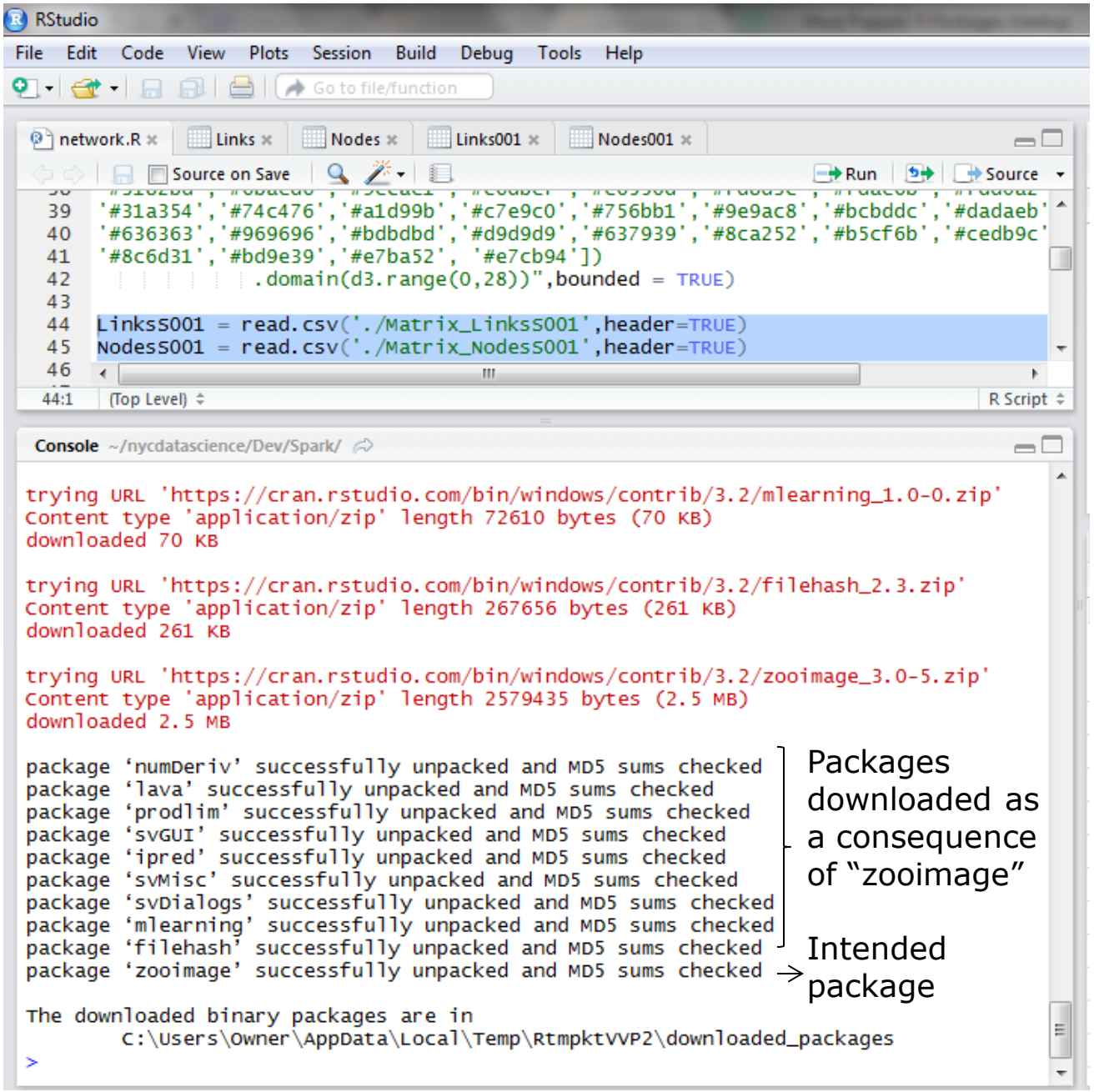
Origin of the project:



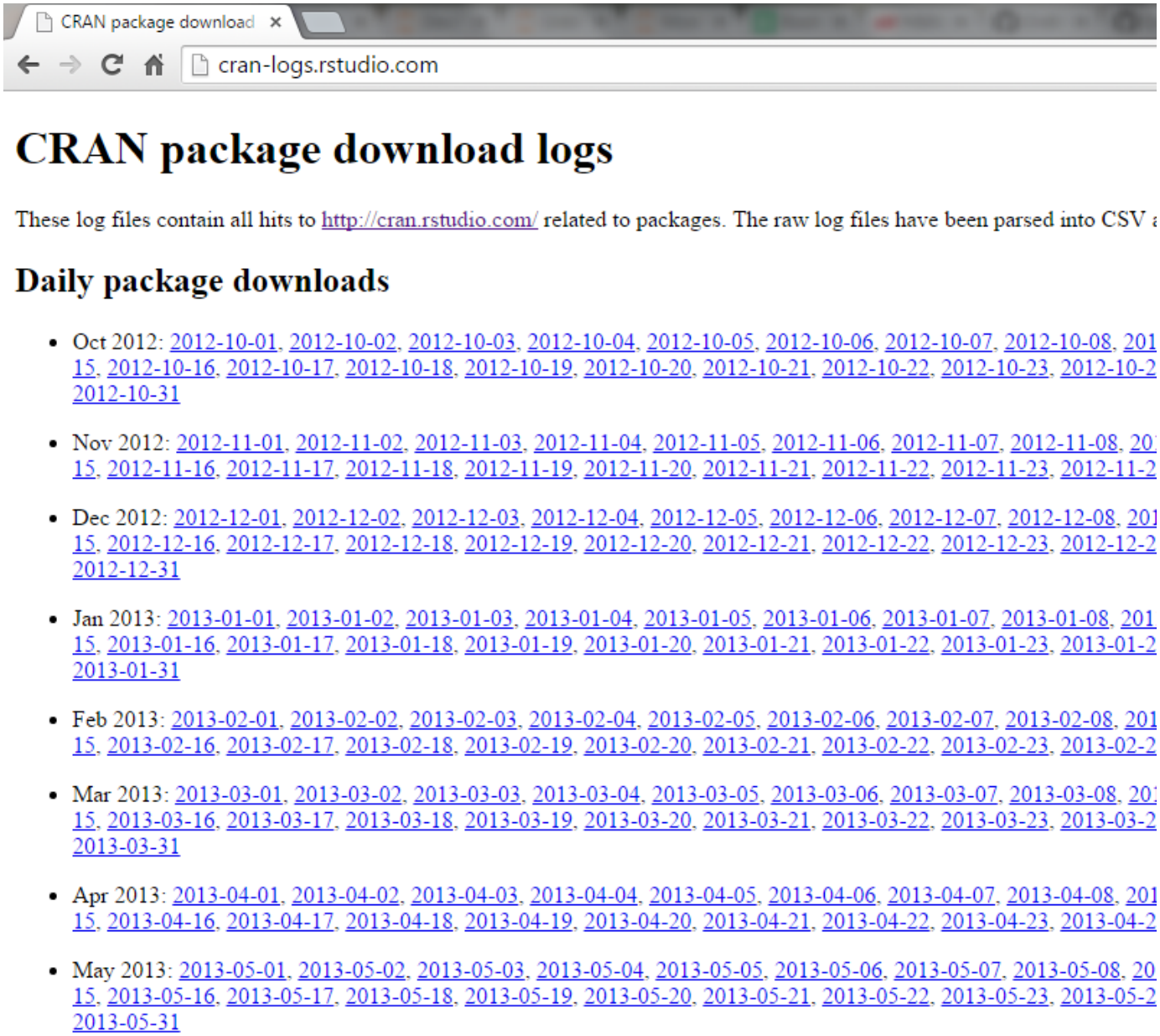
Source: http://www.kdnuggets.com/2015/06/top-20-r-packages.html

The capabilities of R are extended through user-created packages, which, primarily, allow specialized statistical techniques and graphical devices.

Any R user is consistently downloading additional packages on its computer and these packages often depend on other packages that also need to be downloaded as a consequence of the targeted package.



Package download logs:



Source: http://cran-logs.rstudio.com/

Log Screen:

Log Processing using the depend/import matrix

Extract relevant information from package download logs

In [122]:
```
import gzip
with gzip.open('data/2012-10-03.csv.gz', 'rb') as f:
    log_content = pd.read_csv(f)
```

In [123]:
```
log_content[:10]
```

Out[123]:

	date	time	size	r_version	r_arch	r_os	package	version	country	ip_id
0	2012-10-03	01:51:54	167303	2.15.1	x86_64	linux-gnu	formatR	0.6	US	1
1	2012-10-03	01:51:54	435497	2.15.1	x86_64	linux-gnu	knitr	0.8	US	1
2	2012-10-03	01:51:53	11150	2.15.1	x86_64	linux-gnu	evaluate	0.4.2	US	1
3	2012-10-03	01:23:01	4977	2.14.1	x86_64	linux-gnu	knn	1.1	US	2
4	2012-10-03	07:41:05	337101	2.15.1	x86_64	linux-gnu	colorspace	1.1-1	US	3
5	2012-10-03	07:40:41	574454	2.15.1	x86_64	linux-gnu	Hmisc	3.9-3	US	3
6	2012-10-03	07:39:59	364811	2.15.1	x86_64	linux-gnu	lattice	0.20-10	US	3
7	2012-10-03	07:37:43	2094445	2.15.1	x86_64	linux-gnu	mosaic	0.6-2	US	3
8	2012-10-03	07:41:05	712307	2.15.1	x86_64	linux-gnu	vcd	1.2-13	US	3
9	2012-10-03	07:42:10	325683	2.15.1	x86_64	linux-gnu	abd	0.2-4	US	3

Proposed methodology:

a. IP_ID[k] downloaded the packages {a, b, c, d, e, f} during a period of 24 hours

b. It happens that package "b" depends on {c, d, e, g}

=> IP_ID[k] downloaded the "root" packages: {a, b}

Then,

c. aggregate all "root" packages: {…, (a,b), …}

d. Analysis of the list of root packages to determine the most downloaded ones:

Counter({a: k1, b:k2, …}

Cran website:

7000+ packages

Webscraping using Python and Spark

Available CRAN Packages By Name

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

CRAN
Mirrors
What's new?
Task Views
Search

About R
R Homepage
The R Journal

Software
R Sources
R Binaries
Packages
Other

Documentation
Manuals
FAQs
Contributed

A3	Accurate, Adaptable, and Accessible Error Metrics for Predictive Models
abbyyR	Access to Abbyy Optical Character Recognition (OCR) API
abc	Tools for Approximate Bayesian Computation (ABC)
ABCanalysis	Computed ABC Analysis
abc.data	Data Only: Tools for Approximate Bayesian Computation (ABC)
abcdeFBA	ABCDE_FBA: A-Biologist-Can-Do-Everything of Flux Balance Analysis with this package
ABCoptim	Implementation of Artificial Bee Colony (ABC) Optimization
abcrf	Approximate Bayesian Computation via Random Forests
abctools	Tools for ABC Analyses
abd	The Analysis of Biological Data
abf2	Load Gap-Free Axon ABF2 Files
abind	Combine Multidimensional Arrays
abn	Data Modelling with Additive Bayesian Networks
abundant	Abundant regression and high-dimensional principal fitted components
acc	Processes Accelerometer Data
accelerometry	Functions for Processing Minute-to-Minute Accelerometer Data
AcceptanceSampling	Creation and Evaluation of Acceptance Sampling

Source: https://cran.r-project.org/web/packages/available_packages_by_name.html

ggplot2: An Implementation of the Grammar of Graphics

An implementation of the grammar of graphics in R. It combines the advantages of both base and lattice graphics: conditioning and shared axes are handled automatically, and you can still build up a plot step implements a sophisticated multidimensional conditioning system and a consistent interface to map data to aesthetic attributes. See http://ggplot2.org for more information, documentation and examples.

Version:	1.0.1
Depends:	R (≥ 2.14), stats, methods
Imports:	plyr (≥ 1.7.1), digest, grid, gtable (≥ 0.1.1), reshape2, scales (≥ 0.2.3), proto, MASS
Suggests:	quantreg, Hmisc, mapproj, maps, hexbin, maptools, multcomp, nlme, testthat, knitr, mgcv
Enhances:	sp
Published:	2015-03-17
Author:	Hadley Wickham [aut, cre], Winston Chang [aut]
Maintainer:	Hadley Wickham <h.wickham at gmail.com>
BugReports:	https://github.com/hadley/ggplot2/issues
License:	GPL-2
URL:	http://ggplot2.org, https://github.com/hadley/ggplot2
NeedsCompilation:	no
Citation:	ggplot2 citation info
Materials:	README NEWS
In views:	Graphics, Phylogenetics
CRAN checks:	ggplot2 results

"import" and "depends": ggplot2 relies on these packages to run.

Downloads:

Reference manual:	ggplot2.pdf
Vignettes:	Contributing to ggplot2 development ggplot2 release process
Package source:	ggplot2_1.0.1.tar.gz
Windows binaries:	r-devel: ggplot2_1.0.1.zip, r-release: ggplot2_1.0.1.zip, r-oldrel: ggplot2_1.0.1.zip
OS X Snow Leopard binaries:	r-release: ggplot2_1.0.1.tgz, r-oldrel: ggplot2_1.0.1.tgz
OS X Mavericks binaries:	r-release: ggplot2_1.0.1.tgz
Old sources:	ggplot2 archive

"reverse depends" and "reverse imports": these packages relies on ggplot2 to run.

Reverse dependencies:

Reverse depends: alphahull, AmpliconDuo, aoristic, apsimr, arqas, bde, benchmark, biomod2, bootnet, brms, caret, catenary, chemosensors, CINOEDV, cjoint, ClimClass, climwin, clustrd, coefplot, confo Deducer, DepthProc, dfexplore, diffeR, dMod, dotwhisker, dslice, dtwclust, DynNom, earlywarnings, eeptools, ESGtoolkit, fbroc, fishmove, freqparcoord, gapmap, GenCAT, gettingtoth ggswissmaps, ggtern, ggthemes, GOplot, gpmap, granovaGG, gsDesign, GSE, Hmisc, hyperSpec, idm, ifaTools, interplot, learnstats, likeLTD, likert, lmms, localgauss, lsbclust, MCMC.C meteogRam, MissingDataGUI, MIXFIM, mixOmics, mlr, mlxR, mosaic, MRMR, multilevelPSA, ncappc, NeatMap, nullabor, orgR, OriGen, OutbreakTools, PairedData, PASWR2, pauv pequod, perry, perspectev, PhaseType, pid, pipe.design, pitchRx, PKgraph, PKreport, pountRes, PopED, popgraph, PPtreeViz, precintcon, prevR, PRISMA, profileR, ProgGUInR, PSAb radiant, RAM, randomizeR, Rcell, RcmdrPlugin.KMggplot2, rfPermute, RGraphics, RIGHT, RJafroc, rms, robustHD, rorutadis, rotations, rplos, RSA, RSDA, rstan, Rz, SciencesPo, sea SmarterPoland, SMFI5, snht, soc.ca, sparkTable, SparseFactorAnalysis, sparsereg, spcosa, spikeSlabGAM, spoccutils, sprm, statebins, SWMPr, synthpop, tcR, tdr, timeline, TriMatch, Tr varian, vdg, waffle, walkr, xked, zooaRch

Reverse imports: ACDm, adegenet, alm, ANOM, antitrust, asremlPlus, asVPC, BACA, backShift, bamdit, BBEST, bcrm, bdscale, bdvis, BioStatR, blowtorch, bmmix, breakpoint, broman, BTSPAS, capr choroplethr, choroplethrAdmin1, classify, classyfire, cllhs, clifro, CommT, complmrob, confidence, cooccur, cosinor, CosmoPhotoz, cplm, cutoffR, dcmr, DescribeDisplay, DFIT, driveRs dynsurv, EasyHTMLReport, EcoGenetics, edgar, EffectLiteR, ega, egcm, emil, EpiDynamics, erer, evolqg, extracat, ez, ezsim, FAOSTAT, fheatmap, FinCal, forestFloor, fSRM, G2Sd ggenealogy, ggExtra, ggparallel, ggRandomForests, ggsubplot, gitter, glycanr, googlesheets, GraphPCA, greport, growcurves, growfunctions, hierarchicalDS, HighDimOut, HistDAWass, InformationValue, IntegratedJM, intsvy, kdetrees, kobe, ldatuning, llama, lmerTest, LocFDRPois, lsl, mapDK, marked, marketeR, marmap, MAVIS, MaxentVariableSelection, merTools microbenchmark, micromap, mizer, Mobilize, morse, multiDimBio, MultiMeta, myTAI, netgen, networkreporting, NeuralNetTools, ngramr, NMF, NORRRM, oaxaca, OpasnetUtils, opti partialAR, patPRO, performanceEstimation, plot2groups, PlotPriNetworks, plotROC, pmc, pogit, PopGenReport, poppr, predictmeans, PReMiuM, pRF, primerTree, proteomics, pscore, q

We'll try to verify that ("Depends" Matrix) = ^{t}("Reserve Depends" Matrix)

Source: https://cran.r-project.org/web/packages/ggplot2/index.html

Programming in 3 steps:

1. Build Matrix of dependencies
2. Download all logs
3. Process all records to extract the “root” packages

Numbers associated with this project:

1. 7055 packages => 7055 webpages to scrap
2. Dependency matrix: 7055 x 7055 => 49+ Million elements to determine
3. 150 days of package log to download for a size of 2.5 GB
4. Every log is about 300,000 lines x 10 columns
   => 45+ Million line items to process

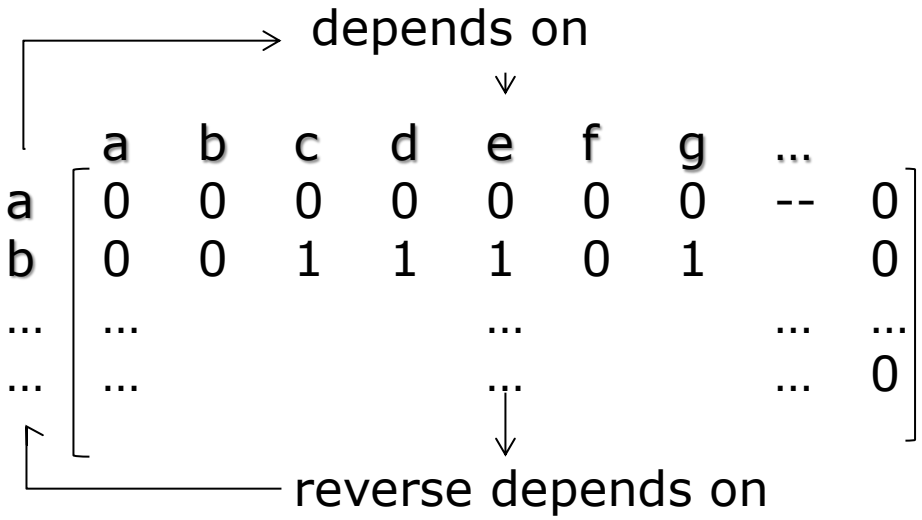
1. Script steps:

A. List of all packages
B. Build 2x Dictionaries: index -> name & name-> index: reduce memory and file size
C. Web-scraping & Regular expression to grab the “depends”, “imports”, “reverse depends”, “reverse imports” information
D. Dependency matrix construction

How does the matrix construction works ?

1. Package “a” doesn’t depends on any other packages
2. Package “b” depends on packages {c, d, e, g}

Matrix Size : 7055x7055



2. *"Sparse Matrix":*

Simplification of the matrix construction: ***"Sparse Matrix"***

1. Package "a" doesn't depends on any other packages
2. Package "b" depends on packages {c, d, e, g}

```
## dummy matrix (index(a) = 0, index(b)=1)
rows = [1,1,1,1,…,n]  #sources for node visualization
cols  = [2,3,4,6,…,k]   #targets for node visualization

data = [1,1,1,1,…,1]
```

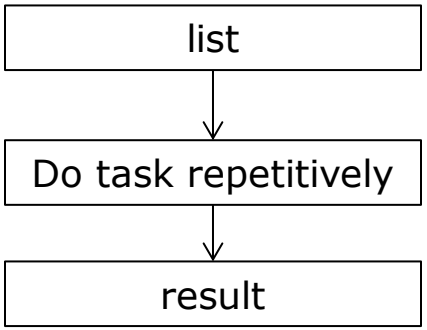
Sparse Matrix is not a mathematical concept but a computer science concept for matrix where most of the element are zeros.

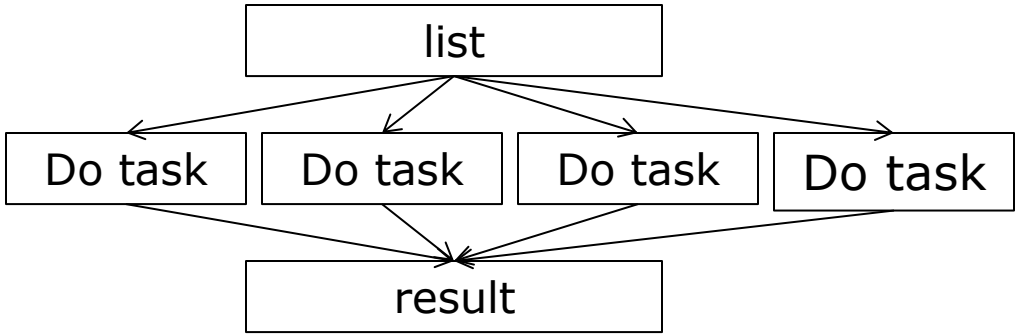
```
# Build a full matrix using coo_matrix scipy package
from scipy.sparse import coo_matrix
Full_matrix = coo_matrix((data, (row, col)), shape=(7055, 7055)).toarray()

#Retrieve the dependant packages index:
col_index = set(Full_matrix[1704].nonzero()[0])
```

coo_matrix: a sparse matrix in COOrdinate format: 1. facilitate conversion between sparse matrix format 2. permits duplicate entries

3. Python versus Spark

Basic concept of
Python vs Python + Spark:






```
for k in list:
        do task
```

```
from pyspark import SparkContext
sc = SparkContext(master='local[7]',
        appName = 'learnSpark')

list_RDD = sc.parallelize(list)
result = list_RDD.map(task_fct).collect()
```

4. Results

Matrix construction by web-scraping of the 7,055 pages:

- Size of "depends" dependancy matrix: 14,196 elements
- Size of "reverse" dependancy matrix: 14,458 elements
  > sparse matrix length: 28,654 elements
  > coo_matrix (constitution of the full matrix and removal of duplicates)
  >>> sparse matrix final: 14,435 elements

Time to process:

- 40 min on Spark on the “82” school server with 7 processors after 11pm
- Calculated approx. 8 hours with my personal computer

5. Findings:

A. 3 Most dependent R packages:

Vmsbase: GUI Tools to Process, Analyze and Plot Fisheries Data	27
PopGenReport: A Simple Framework to Analyse Population Genetic Data	23
RAM: R for Amplicon-Sequencing-Based Microbial-Ecology	23

(depends on # packages)

B. 3 most reverse dependent R packages:

MASS: Support Functions and Datasets for Venables and Ripley's Modern Applied Statistic with S	679
Rcpp: Seamless R and C++ Integration	416
ggplot2: An Implementation of the Grammar of Graphics	351

(# other packages depends this package)

C. Longest path between R packages: *12 packages*

The longest path is interesting as it can serve as an upper limit in the iteration to build a n-degree dependency matrix.

6. Visualization:

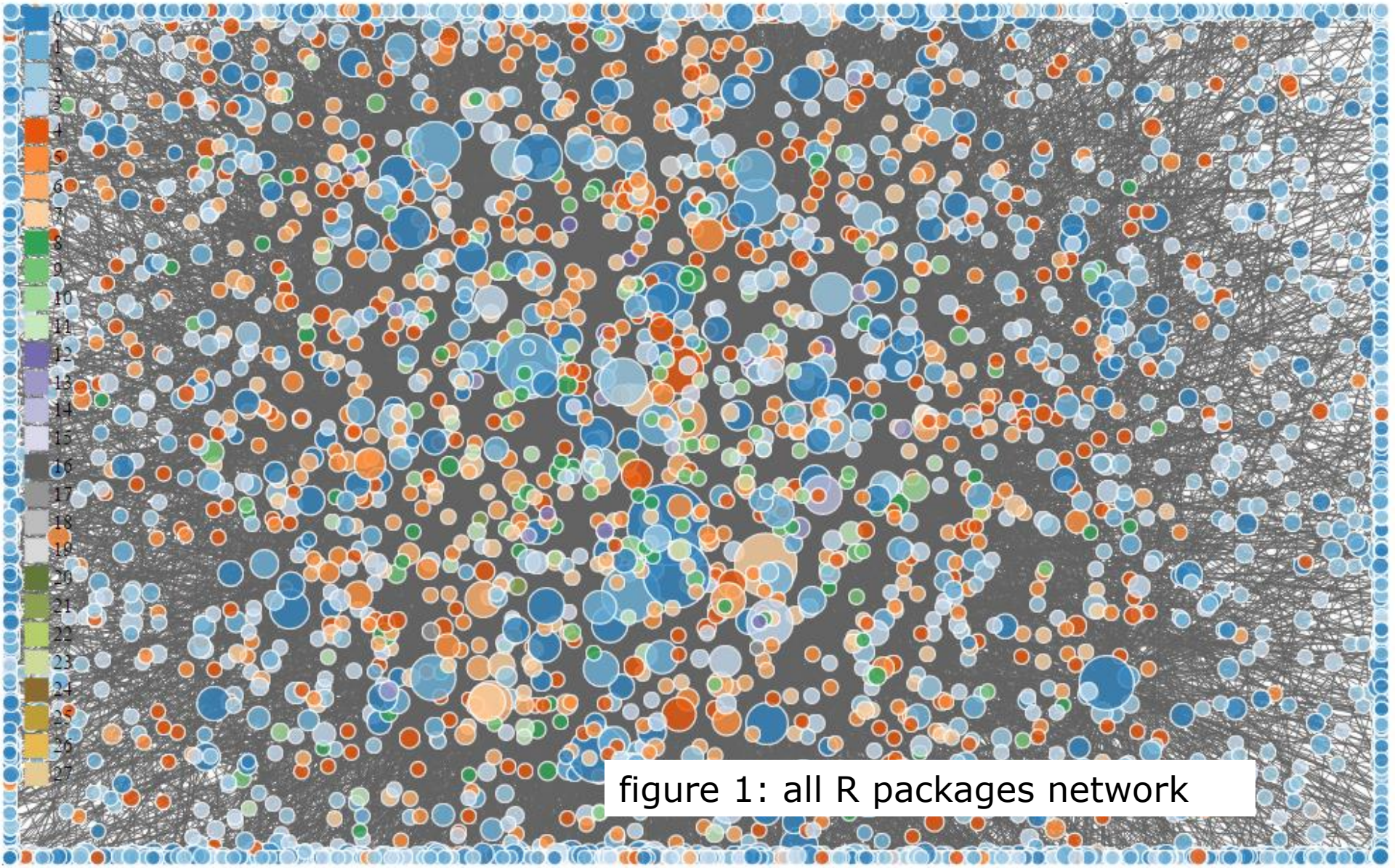
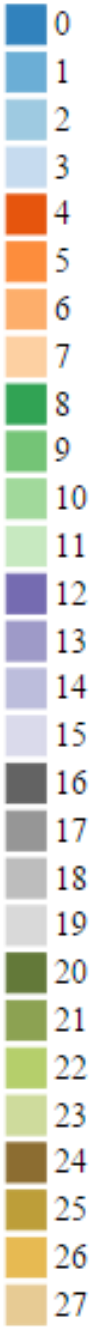


figure 1: all R packages network



Visualization using R networkD3 library
(modification of color panel in Java script)

Color code:
# of dependents

Circle Size:
Reverse dependent (# of other packages based on this package)

figure 2: 3 most reverse dependent R packages: MASS, Rcpp, ggplot2

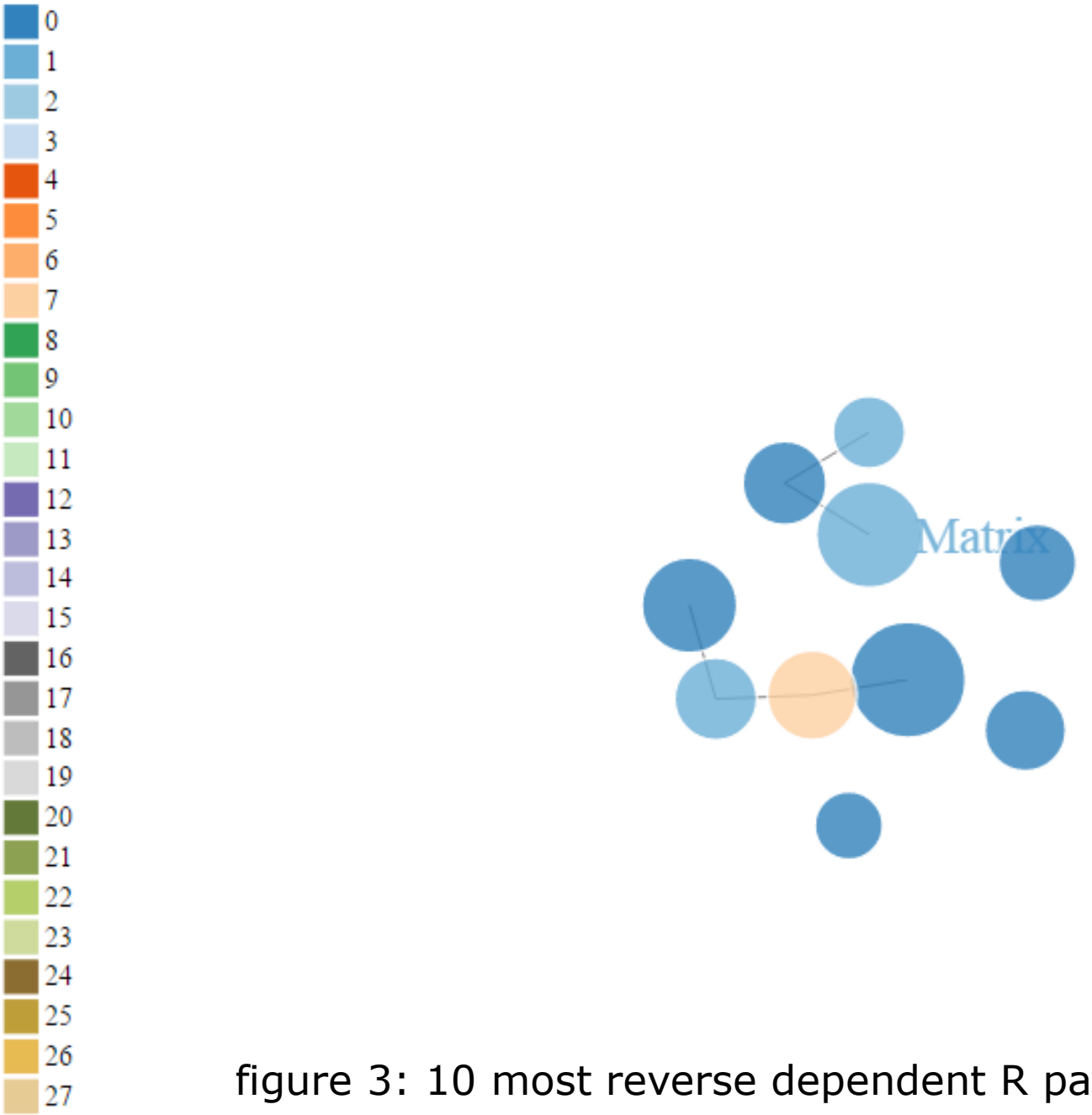


figure 3: 10 most reverse dependent R packages

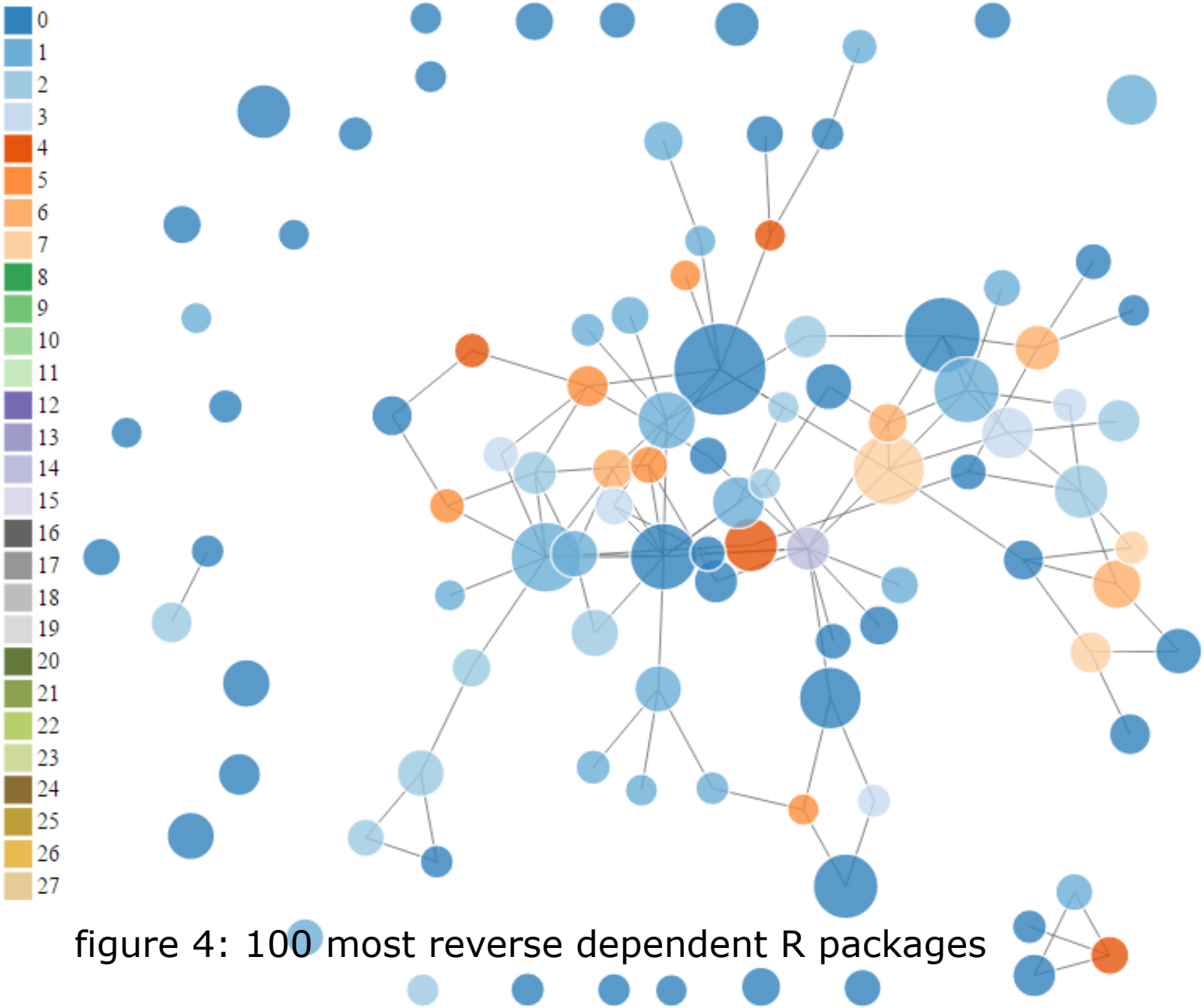


figure 4: 100 most reverse dependent R packages

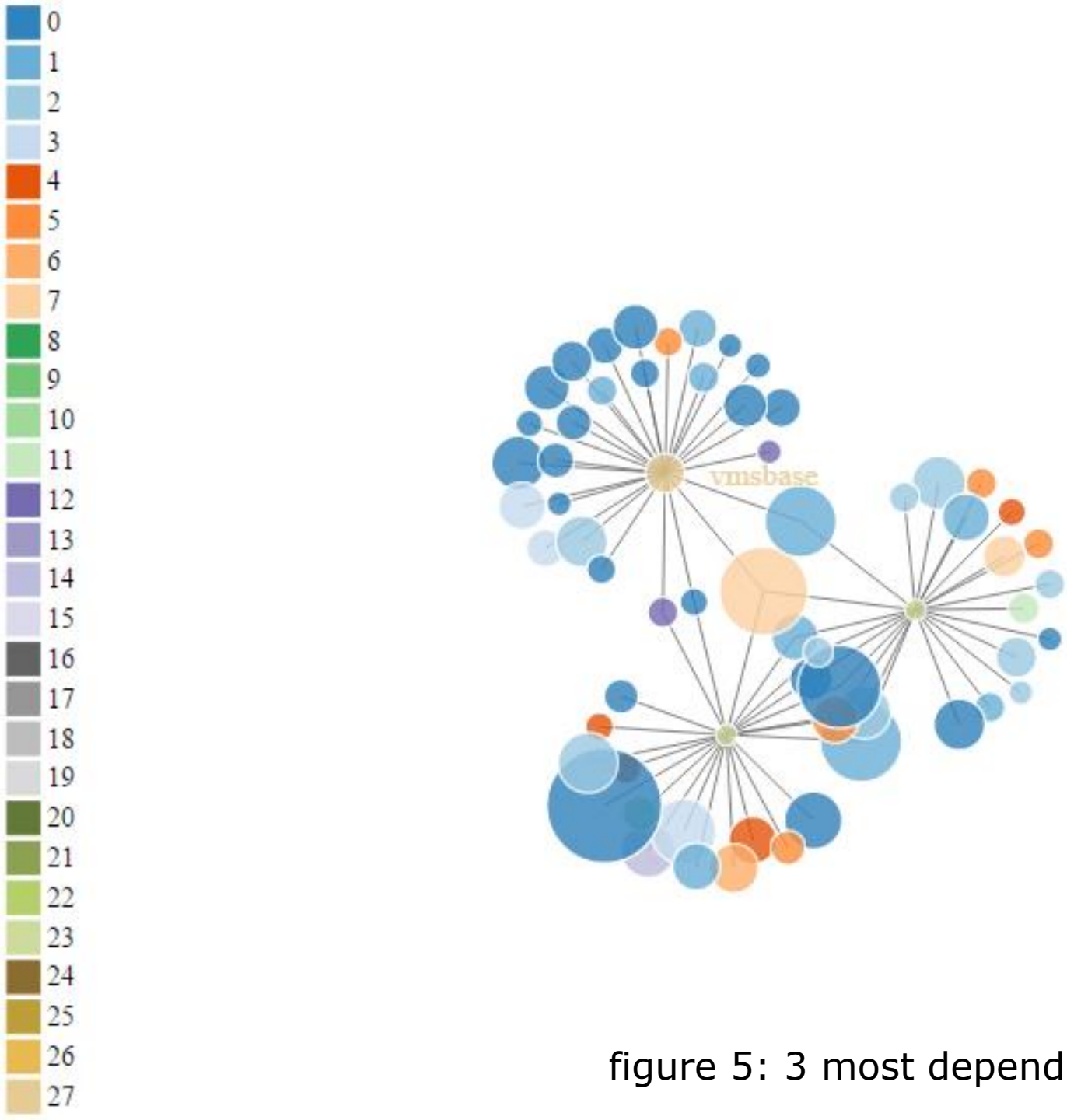


figure 5: 3 most dependent R packages

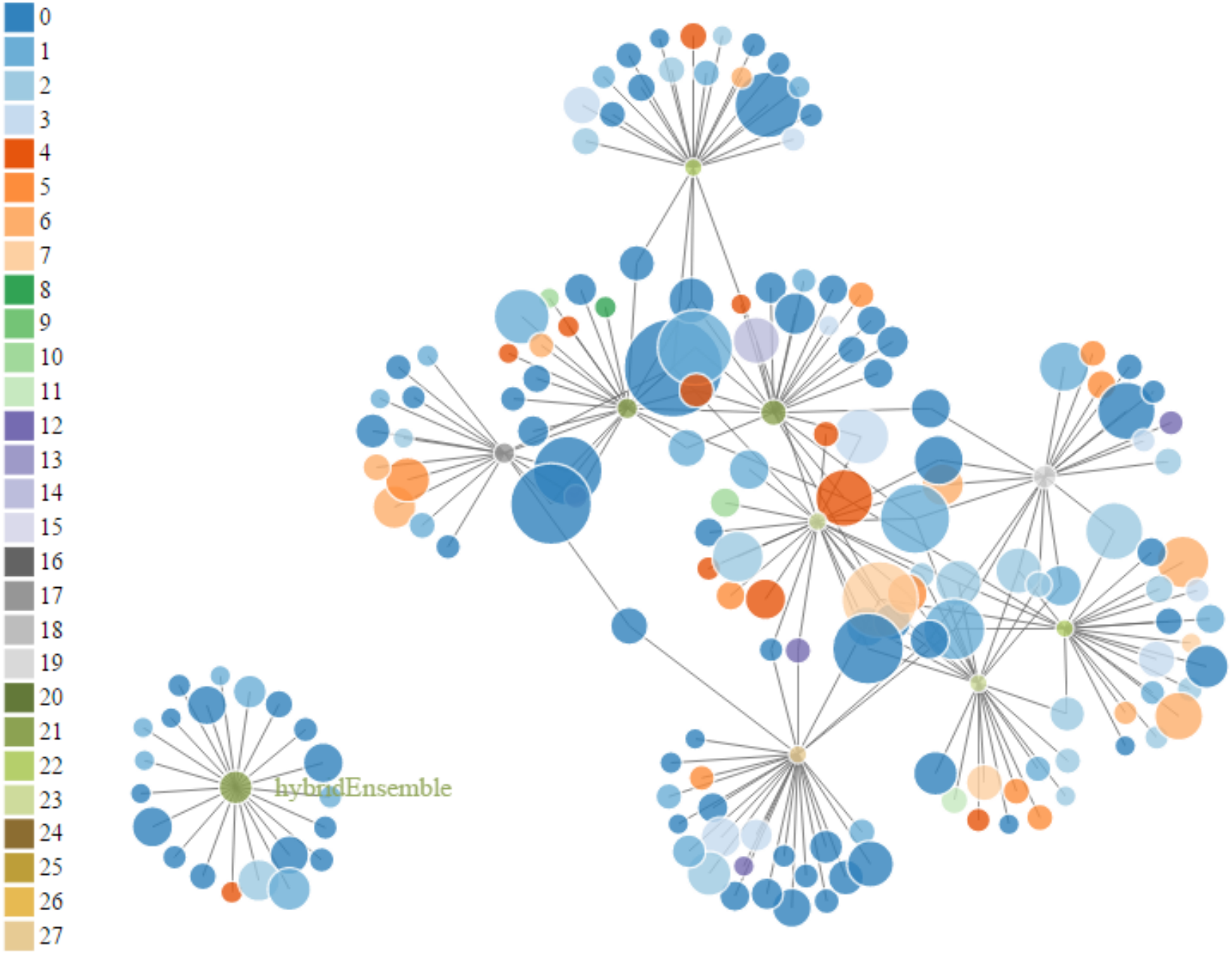


figure 6: 10 most dependent R packages

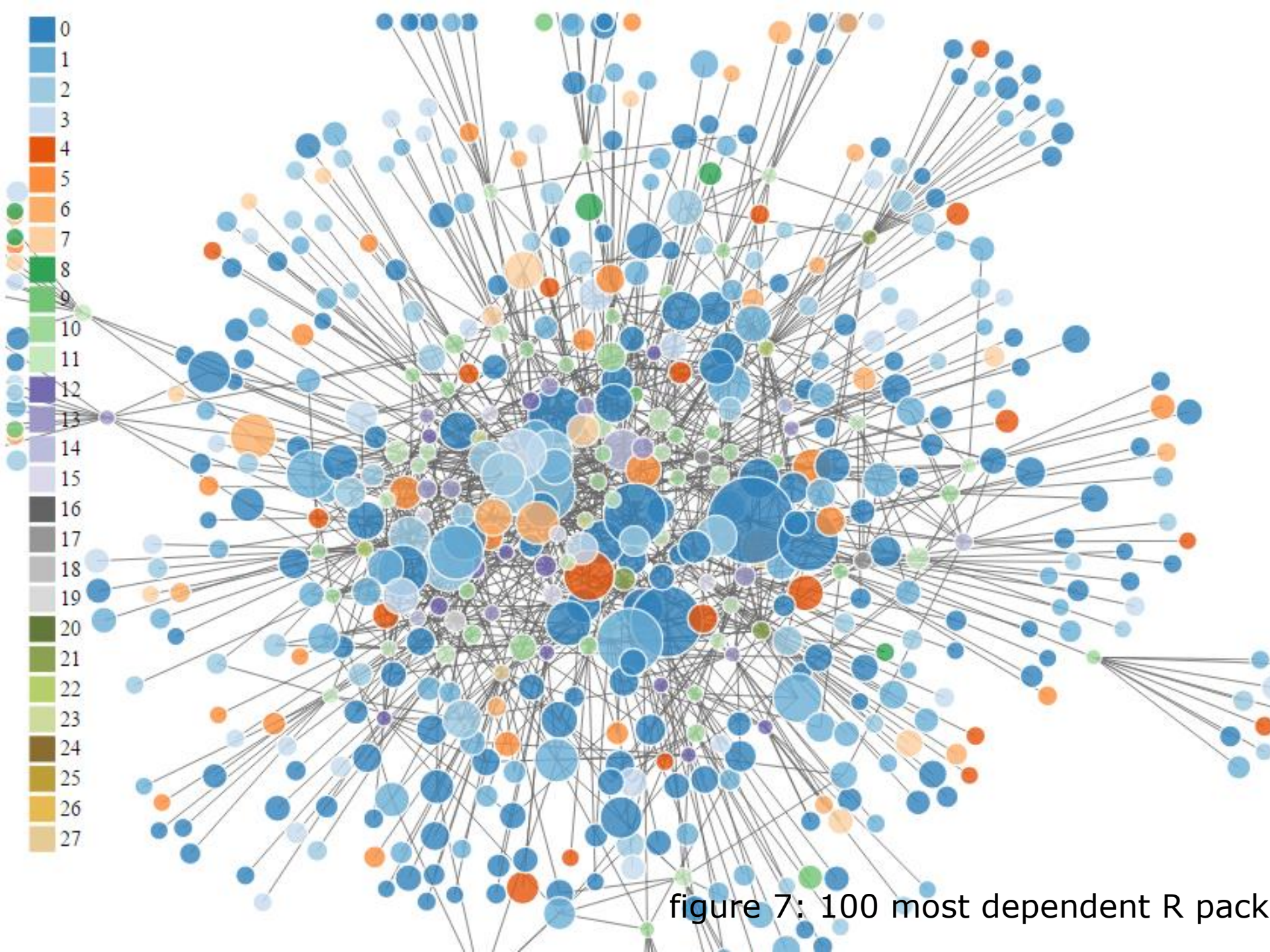


figure 7: 100 most dependent R pack

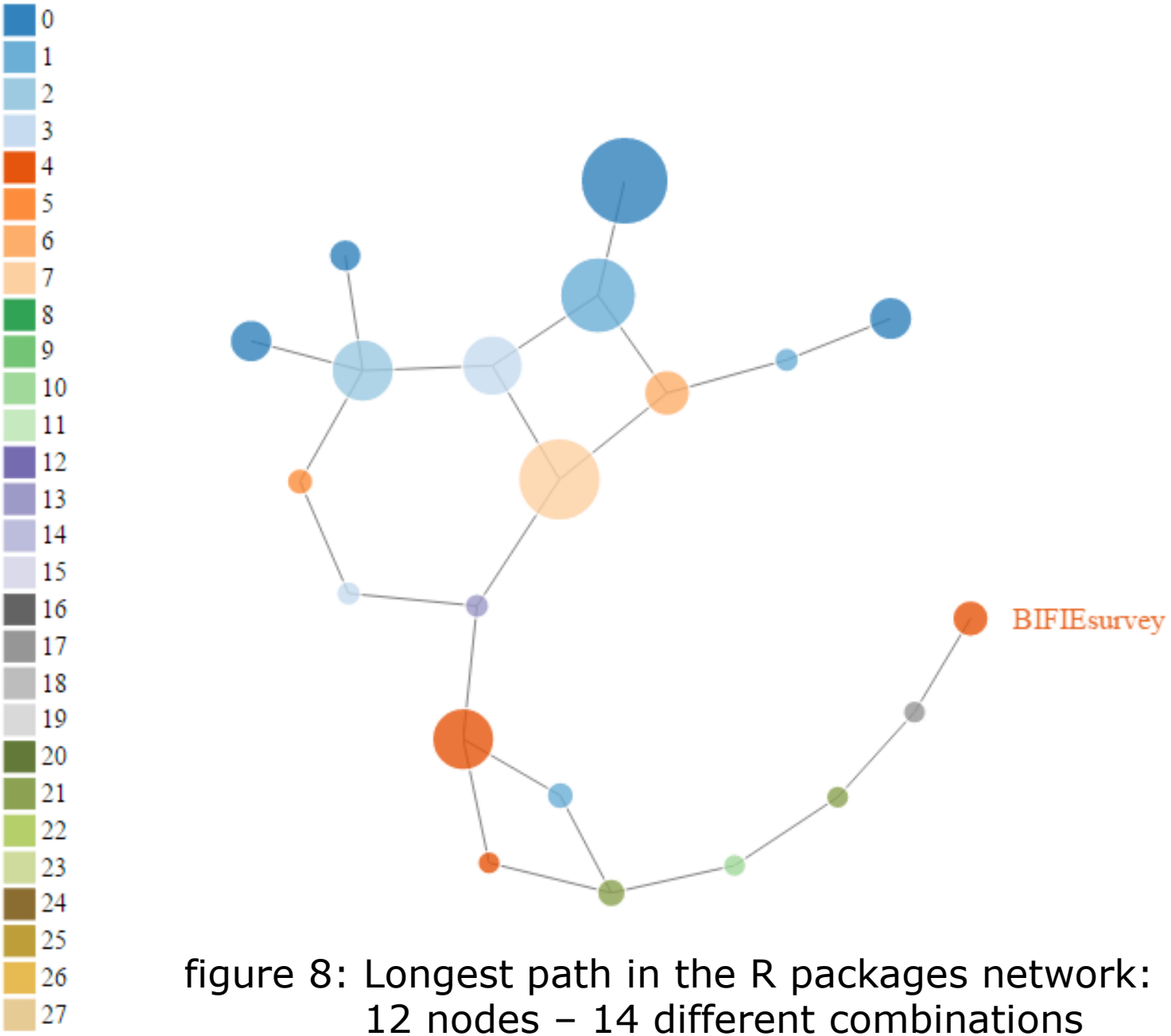


figure 8: Longest path in the R packages network:
12 nodes – 14 different combinations

II. Download the logs:

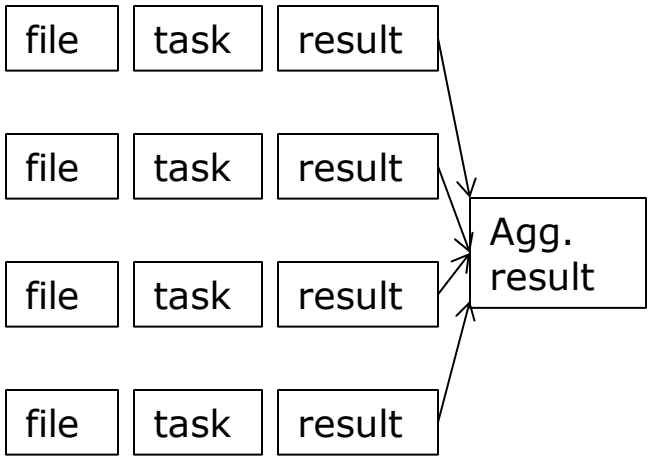
In [ ]:

```
# Before running, update url_log_full_paths file.

#######################################################
### FINAL SCRIPT FOR SPARK TO DOWNLOAD LOG FILES
#######################################################


#from pyspark import SparkContext
#sc = SparkContext(master='local[7]', appName = 'learnSpark')

import numpy as np
from bs4 import BeautifulSoup
import requests
import re
import csv



# fonction to download and save the log files /  ready for parallelisation:
import urllib
def download_log(url_log):

    path_with_log_name = './data/'+ re.sub('(http:\/\/cran-logs.rstudio.com\/[0-9]+\/)','',url_log)
    urllib.urlretrieve(url_log, path_with_log_name)


url_log_full_paths = [line.strip() for line in open("url_log_full_paths.txt", 'r')]

print 'Spark started'

doc_log= sc.parallelize(url_log_full_paths[1003:1007])  #1004:1054
doc_log.map(download_log).collect()

print 'Spark finished'
```

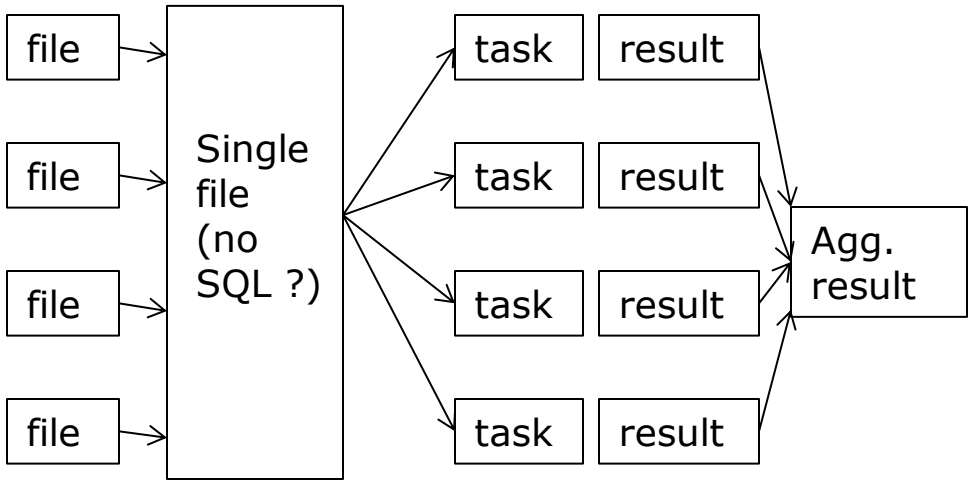
1. Process the logs

1. Construct a unique ID = IP+Date
2. List all packages downloaded by unique ID
3. Save "root" packages by using the dependency matrix

Adopted Solution using Spark



Other Solution using Spark



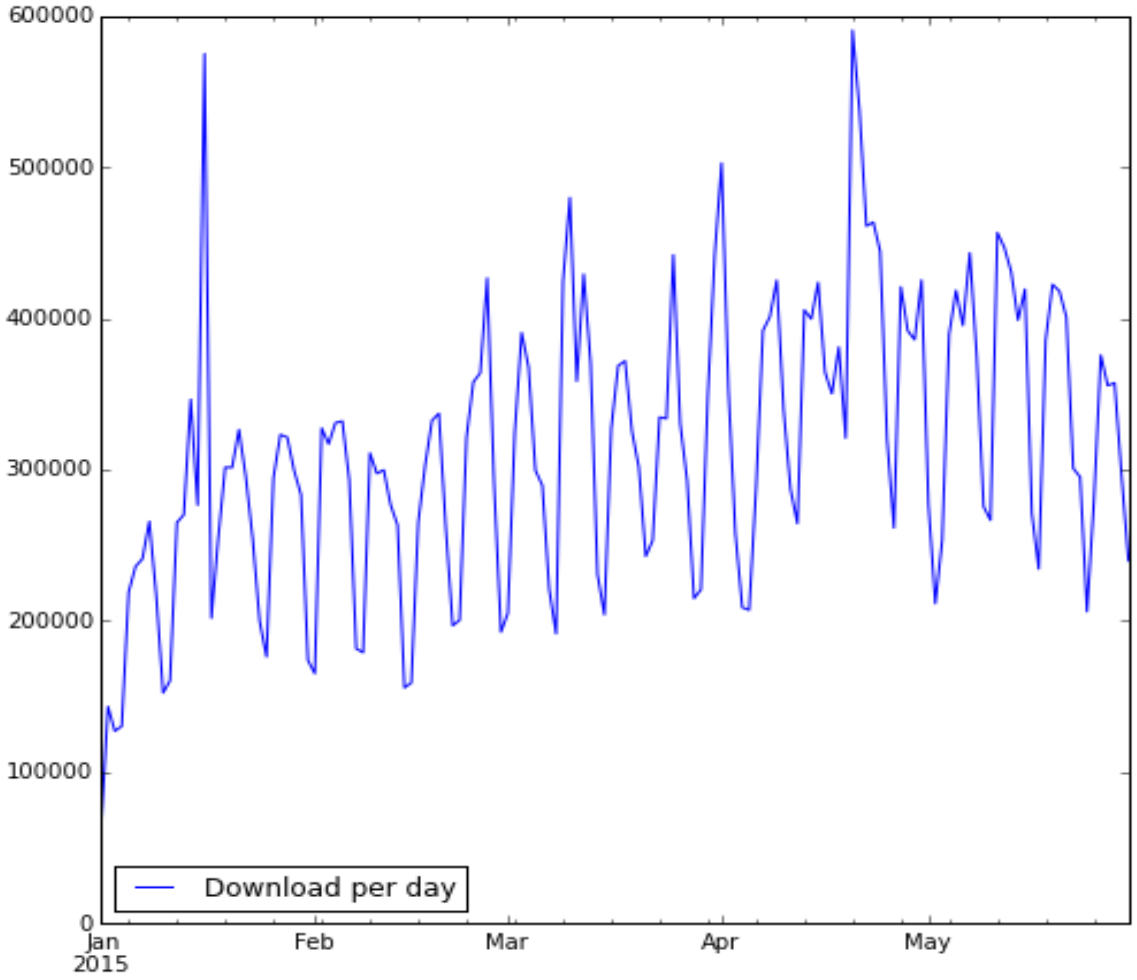
2. Results

Jan to May 2015:
- 46,944,117 lines items to process
- Took 5 to 9 hours using Spark 10 cpu **overnight**

Results:
- "Root" package list: 18,716,714 (100MB)

Trick: all scripts are processed and are saving result using the package indexes to reduce file sizes and process time.

3. Finding #1: Download per day



Note:

Y2012 logs contains about 100 downloads / day

Vs

Y2015 logs contains about 300,000 downloads / day

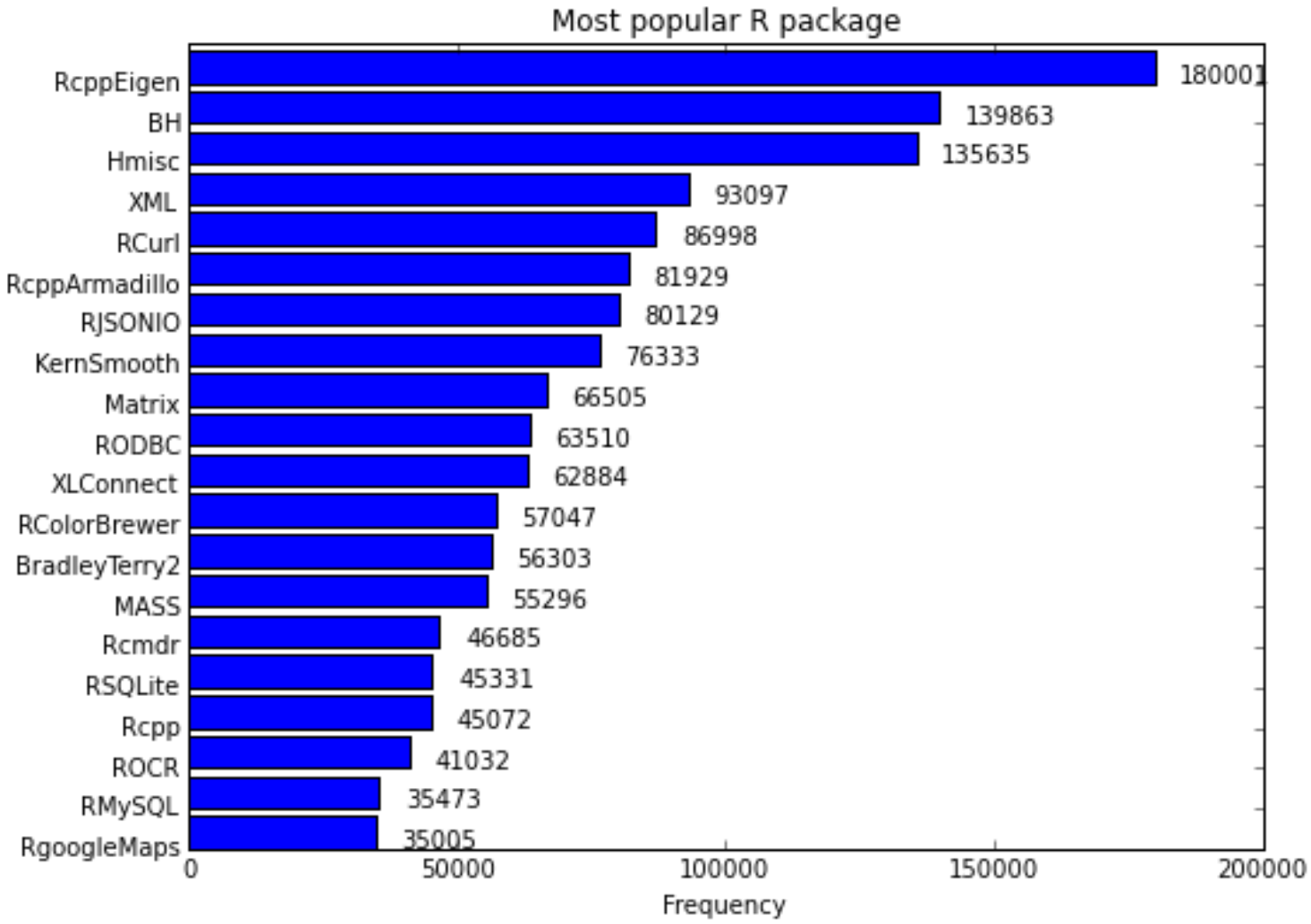
3. Finding #2: "CRAC" package

"CRAC", Cosmology R Analysis Code Package, developed by our excellent teacher Jason (Jiayi Liu).

The "CRAC" has been downloaded 1,423 times between January and May 2015

"CRAC" is ranked 1,170th according to the present methodology.

4. The most popular R packages



Studied period: January to May 2015

Remarks and Questions

The testing took much more time than anticipated because:

- The CRAN website is updated every night (the package count changes by +/- 20 per day and tends to increase over time)
- The package authors have a tendency to increase the number of package functionalities by increasing the dependency of their own package.

Skepticism about my methodology:

- I used only 1st degree of dependency: I shall redo the calculation by increasing the degree of dependency, now that I calculated the longest path in the R package network (used as an upper limit in the iteration).

- Time difference between the R "day time" and foreign R users
  => inaccuracy of the unique ID (day+IP)

- Old packages in the logs are not referenced anymore by the Cran website