

HarvardX: PH125.9x Data Science MovieLens Rating Prediction Project

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1 Overview

This project is related to the MovieLens Project of the HarvardX: PH125.9x Data Science: Capstone course. The present report start with a general idea of the project and by representing its objectif.

Then the given dataset will be prepared and setup. An exploratory data analysis is carried out in order to develop a machine learning algorithm that could predict movie ratings until a final model. Results will be explained. Finally the report ends with some concluding remarks.

1.1 Introduction

Recommendation systems use ratings that users have given items to make specific recommendations. Companies that sell many products to many customers and permit these customers to rate their products, like Amazon, are able to collect massive datasets that can be used to predict what rating a particular user will give a specific item. Items for which a high rating is predicted for a given user are then recommended to that user.

The same could be done for other items, as movies for instance in our case. Recommendation systems are one of the most used models in machine learning algorithms. In fact the success of Netflix is said to be based on its strong recommendation system. The Netflix prize (open competition for the best collaborative filtering

algorithm to predict user ratings for films, based on previous ratings without any other information about the users or films), in fact, represent the high importance of algorithm for products recommendation system.

For this project we will focus on create a movie recommendation system using the 10M version of MovieLens dataset, collected by GroupLens Research.

1.2 Aim of the project

The aim in this project is to train a machine learning algorithm that predicts user ratings (from 0.5 to 5 stars) using the inputs of a provided subset (edx dataset provided by the staff) to predict movie ratings in a provided validation set.

The value used to evaluate algorithm performance is the Root Mean Square Error, or RMSE. RMSE is one of the most used measure of the differences between values predicted by a model and the values observed. RMSE is a measure of accuracy, to compare forecasting errors of different models for a particular dataset, a lower RMSE is better than a higher one. The effect of each error on RMSE is proportional to the size of the squared error; thus larger errors have a disproportionately large effect on RMSE. Consequently, RMSE is sensitive to outliers. Four models that will be developed will be compared using their resulting RMSE in order to assess their quality. The evaluation criteria for this algorithm is a RMSE expected to be lower than 0.8775. The function that computes the RMSE for vectors of ratings and their corresponding predictors will be the following:

$$RMSE = \sqrt{\frac{1}{N} \sum_{u,i} (\hat{y}_{u,i} - y_{u,i})^2}$$

Finally, the best resulting model will be used to predict the movie ratings.

1.3 Dataset

The MovieLens dataset is automatically downloaded

- [MovieLens 10M dataset] <https://grouplens.org/datasets/movielens/10m/>
- [MovieLens 10M dataset - zip file] <http://files.grouplens.org/datasets/movielens/ml-10m.zip>

```
#####
# Create edx set, validation set, and submission file
#####
# Note: this process could take a couple of minutes for loading required package: tidyverse and package
if(!require(tidyverse)) install.packages("tidyverse", repos = "http://cran.us.r-project.org")
if(!require(caret)) install.packages("caret", repos = "http://cran.us.r-project.org")
dl <- tempfile()
download.file("http://files.grouplens.org/datasets/movielens/ml-10m.zip", dl)

ratings <- read.table(text = gsub(":", "\t", readLines(unzip(dl, "ml-10M100K/ratings.dat"))),
                      col.names = c("userId", "movieId", "rating", "timestamp"))

movies <- str_split_fixed(readLines(unzip(dl, "ml-10M100K/movies.dat")), "\\:", 3)
colnames(movies) <- c("movieId", "title", "genres")

movies <- as.data.frame(movies) %>% mutate(movieId = as.numeric(levels(movieId))[movieId],
                                           title = as.character(title),
                                           genres = as.character(genres))
movielens <- left_join(ratings, movies, by = "movieId")
```

In order to predict in the most possible accurate way the movie rating of the users that haven't seen the movie yet, the MovieLens dataset will be splitted into 2 subsets that will be the "edx", a training subset to train the algorithm, and "validation" a subset to test the movie ratings.

```
# The Validation subset will be 10% of the MovieLens data.
set.seed(1)
test_index <- createDataPartition(y = movielens$rating, times = 1, p = 0.1, list = FALSE)
edx <- movielens[-test_index,]
temp <- movielens[test_index,]
#Make sure userId and movieId in validation set are also in edx subset:
validation <- temp %>%
  semi_join(edx, by = "movieId") %>%
  semi_join(edx, by = "userId")

# Add rows removed from validation set back into edx set
removed <- anti_join(temp, validation)
edx <- rbind(edx, removed)
rm(dl, ratings, movies, test_index, temp, movielens, removed)
```

Algorithm development is to be carried out on the "edx" subset only, as "validation" subset will be used to test the final algorithm.

2 Methods and Analysis

2.1 Data Analysis

To get familiar with the dataset, we find the first rows of “edx” subset as below. The subset contain the six variables “userID”, “movieId”, “rating”, “timestamp”, “title”, and “genres”. Each row represent a single rating of a user for a single movie.

```
##      userId movieId rating timestamp      title
## 1         1     122      5 838985046    Boomerang (1992)
## 2         1     185      5 838983525      Net, The (1995)
## 4         1     292      5 838983421      Outbreak (1995)
## 5         1     316      5 838983392      Stargate (1994)
## 6         1     329      5 838983392 Star Trek: Generations (1994)
## 7         1     355      5 838984474    Flintstones, The (1994)
##                                     genres
## 1                                Comedy|Romance
## 2                        Action|Crime|Thriller
## 4    Action|Drama|Sci-Fi|Thriller
## 5                        Action|Adventure|Sci-Fi
## 6    Action|Adventure|Drama|Sci-Fi
## 7                Children|Comedy|Fantasy
```

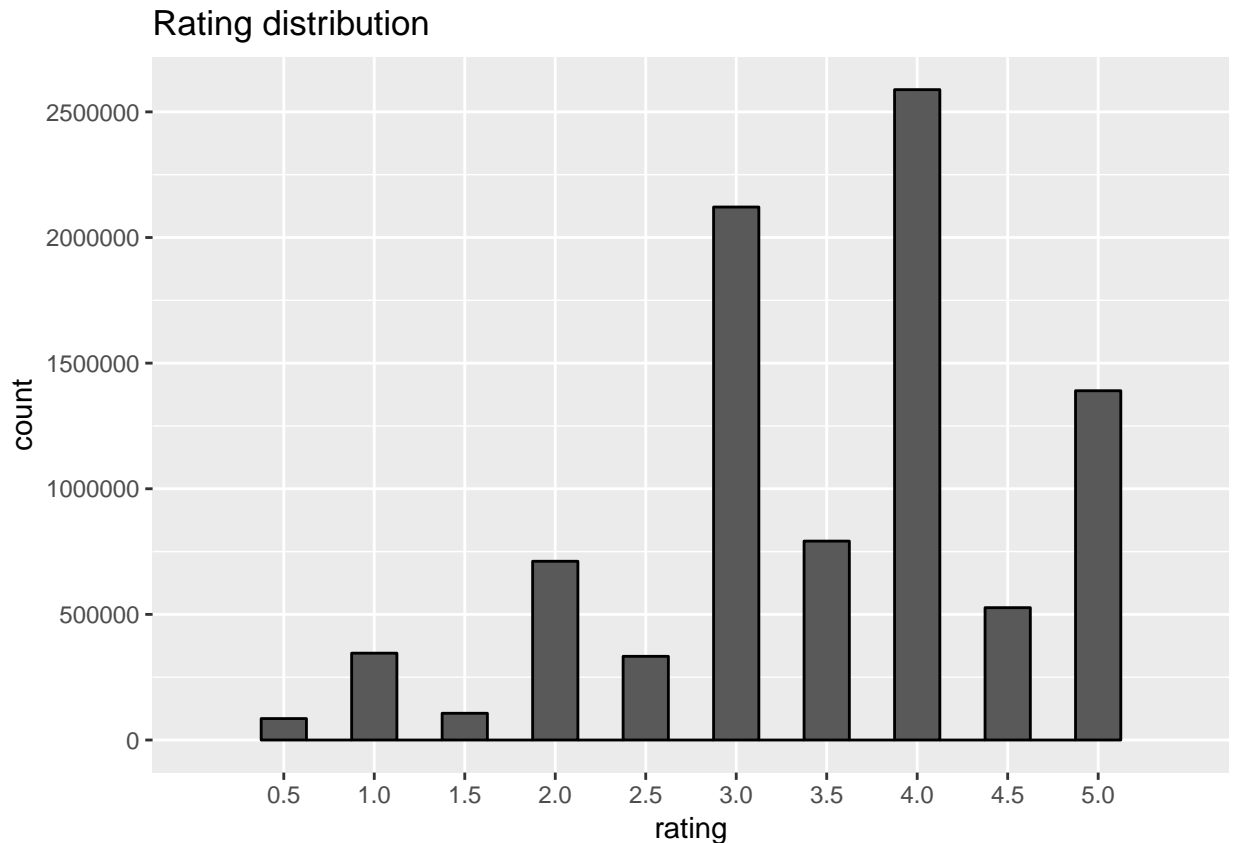
A summary of the subset confirms that there are no missing values.

```
##      userId      movieId      rating      timestamp
## Min.   :      1  Min.   :      1  Min.   :0.500  Min.   :7.897e+08
## 1st Qu.:18124  1st Qu.:   648  1st Qu.:3.000  1st Qu.:9.468e+08
## Median :35738  Median :  1834  Median :4.000  Median :1.035e+09
## Mean   :35870  Mean   :  4122  Mean   :3.512  Mean   :1.033e+09
## 3rd Qu.:53607  3rd Qu.:  3626  3rd Qu.:4.000  3rd Qu.:1.127e+09
## Max.   :71567  Max.   :65133  Max.   :5.000  Max.   :1.231e+09
##      title      genres
## Length:9000055  Length:9000055
## Class :character  Class :character
## Mode  :character  Mode  :character
##
##
##
```

The total of unique movies and users in the edx subset is about 70.000 unique users and about 10.700 different movies:

```
##      n_users n_movies
## 1    69878    10677
```

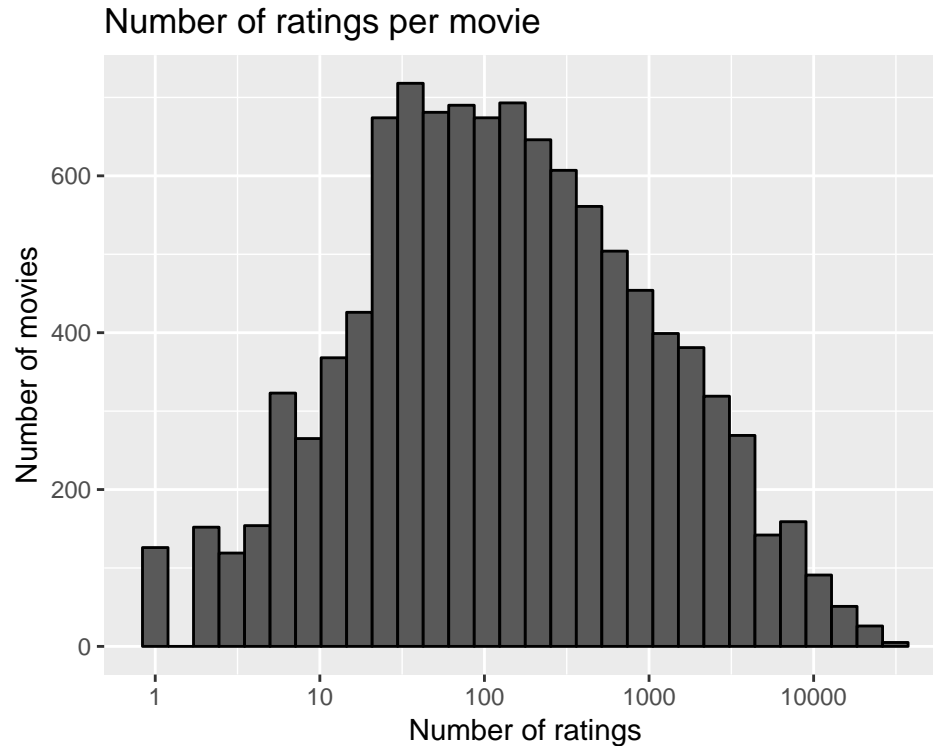
Users have a preference to rate movies rather higher than lower as shown by the distribution of ratings below. 4 is the most common rating, followed by 3 and 5. 0.5 is the least common rating. In general, half rating are less common than whole star ratings.



We can observe that some movies have been rated much more often than others, while some have very few ratings and sometimes only one rating. This will be important for our model as very low rating numbers might result in an untrustworthy estimate for our predictions. In fact 125 movies have been rated only once.

Thus regularization and a penalty term will be applied to the models in this project. Regularizations are techniques used to reduce the error by fitting a function appropriately on the given training set and avoid overfitting (the production of an analysis that corresponds too closely or exactly to a particular set of data, and may therefore fail to fit additional data or predict future observations reliably). Regularization is a technique used for tuning the function by adding an additional penalty term in the error function. The additional term controls the excessively fluctuating function such that the coefficients don't take extreme values.

```
edx %>%
count(movieId) %>%
ggplot(aes(n)) +
geom_histogram(bins = 30, color = "black") +
scale_x_log10() +
xlab("Number of ratings") +
ylab("Number of movies") +
ggtitle("Number of ratings per movie")
```



As 20 movies that were rated only once appear to be obscure, predictions of future ratings for them will be difficult.

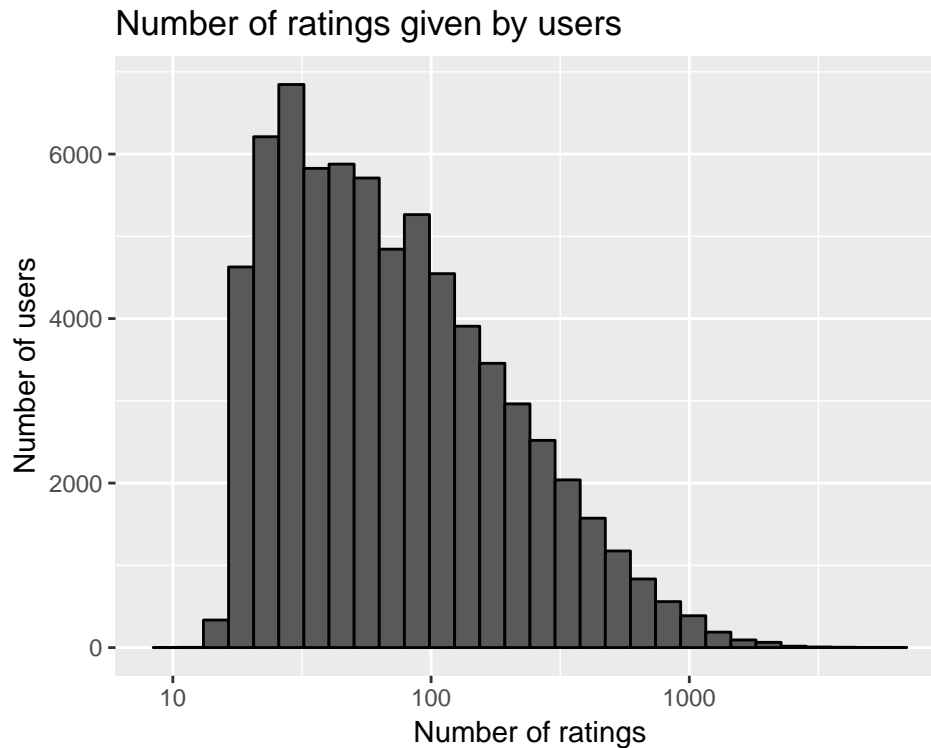
```
edx %>%
  group_by(movieId) %>%
  summarize(count = n()) %>%
  filter(count == 1) %>%
  left_join(edx, by = "movieId") %>%
  group_by(title) %>%
  summarize(rating = rating, n_rating = count) %>%
  slice(1:20) %>%
  knitr::kable()
```

title	rating	n_rating
1, 2, 3, Sun (Un, deuz, trois, soleil) (1993)	2.0	1
100 Feet (2008)	2.0	1
4 (2005)	2.5	1
Accused (Anklaget) (2005)	0.5	1
Ace of Hearts (2008)	2.0	1
Ace of Hearts, The (1921)	3.5	1
Adios, Sabata (Indio Black, sai che ti dico: Sei un gran figlio di...) (1971)	1.5	1
Africa addio (1966)	3.0	1
Aleksandra (2007)	3.0	1
Bad Blood (Mauvais sang) (1986)	4.5	1
Battle of Russia, The (Why We Fight, 5) (1943)	3.5	1
Bellissima (1951)	4.0	1
Big Fella (1937)	3.0	1
Black Tights (1-2-3-4 ou Les Collants noirs) (1960)	3.0	1
Blind Shaft (Mang jing) (2003)	2.5	1

title	rating	n_rating
Blue Light, The (Das Blaue Licht) (1932)	5.0	1
Borderline (1950)	3.0	1
Brothers of the Head (2005)	2.5	1
Chapayev (1934)	1.5	1
Cold Sweat (De la part des copains) (1970)	2.5	1

We can observe that the majority of users have rated between 30 and 100 movies. So, a user penalty term need to be included later in our models.

```
edx %>%
count(userId) %>%
ggplot(aes(n)) +
geom_histogram(bins = 30, color = "black") +
scale_x_log10() +
xlab("Number of ratings") +
ylab("Number of users") +
ggtitle("Number of ratings given by users")
```



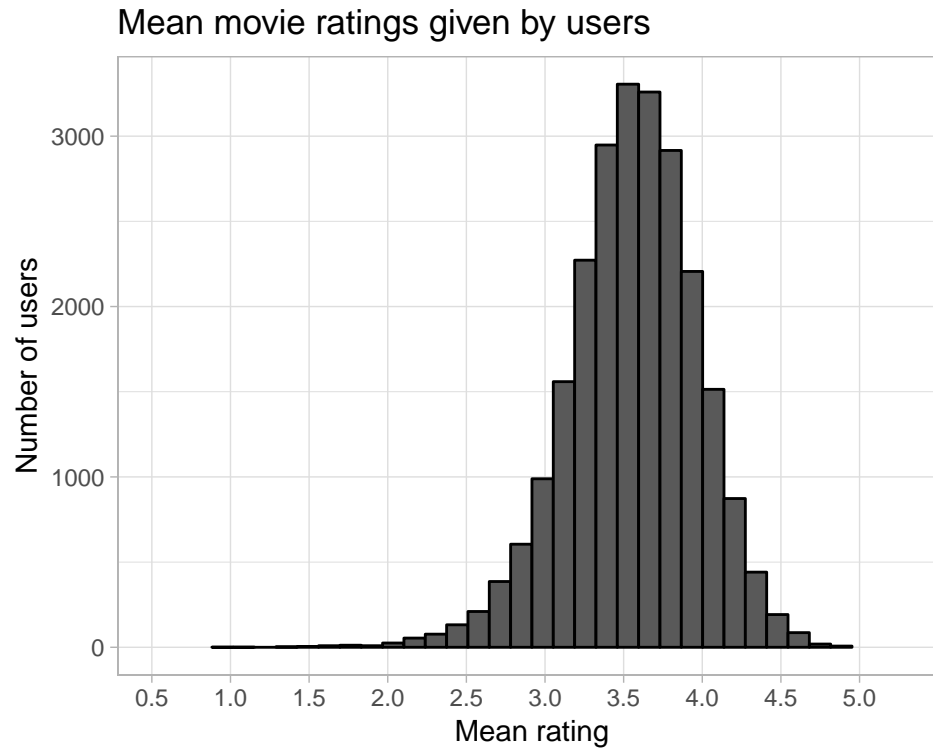
Furthermore, users differ vastly in how critical they are with their ratings. Some users tend to give much lower star ratings and some users tend to give higher star ratings than average. The visualization below includes only users that have rated at least 100 movies.

```
edx %>%
group_by(userId) %>%
filter(n() >= 100) %>%
summarize(b_u = mean(rating)) %>%
ggplot(aes(b_u)) +
geom_histogram(bins = 30, color = "black") +
```

```

xlab("Mean rating") +
ylab("Number of users") +
ggtitle("Mean movie ratings given by users") +
scale_x_discrete(limits = c(seq(0.5,5,0.5))) +
theme_light()

```



2.2 Modelling Approach

We write now the loss-function, previously anticipated, that compute the RMSE, defined as follows:

$$RMSE = \sqrt{\frac{1}{N} \sum_{u,i} (\hat{y}_{u,i} - y_{u,i})^2}$$

with N being the number of user/movie combinations and the sum occurring over all these combinations. The RMSE is our measure of model accuracy. We can interpret the RMSE similarly to a standard deviation: it is the typical error we make when predicting a movie rating. If its result is larger than 1, it means that our typical error is larger than one star, which is not a good result. The written function to compute the RMSE for vectors of ratings and their corresponding predictions is:

```

RMSE <- function(true_ratings, predicted_ratings){
  sqrt(mean((true_ratings - predicted_ratings)^2))
}

```

The lower the better, as said previously.

2.2.1 I. Average movie rating model

The first basic model predicts the same rating for all movies, so we compute the dataset's mean rating. The expected rating of the underlying data set is between 3 and 4. We start by building the simplest possible recommender system by predicting the same rating for all movies regardless of user who give it. A model based approach assumes the same rating for all movie with all differences explained by random variation :

$$Y_{u,i} = \mu + \epsilon_{u,i}$$

with $\epsilon_{u,i}$ independent error sample from the same distribution centered at 0 and μ the “true” rating for all movies. This very simple model makes the assumption that all differences in movie ratings are explained by random variation alone. We know that the estimate that minimize the RMSE is the least square estimate of $Y_{u,i}$, in this case, is the average of all ratings: The expected rating of the underlying data set is between 3 and 4.

```
mu <- mean(edx$rating)
mu
```

```
## [1] 3.512465
```

If we predict all unknown ratings with μ or mu, we obtain the first naive RMSE:

```
naive_rmse <- RMSE(validation$rating, mu)
naive_rmse
```

```
## [1] 1.061202
```

Here, we represent results table with the first RMSE:

```
rmse_results <- data_frame(method = "Average movie rating model", RMSE = naive_rmse)
rmse_results %>% knitr::kable()
```

method	RMSE
Average movie rating model	1.061202

This give us our baseline RMSE to compare next modelling approaches against.

In order to do better than simply predicting the average rating, we incorporate some of insights we gained during the exploratory data analysis.

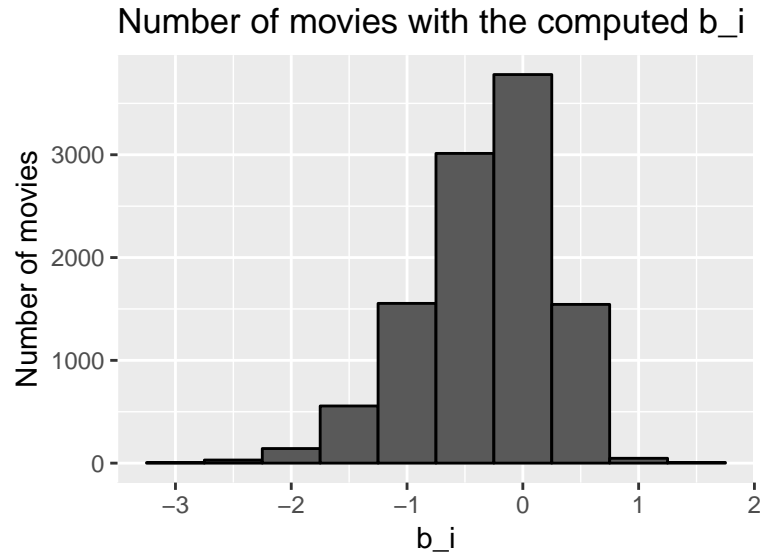
2.2.2 II. Movie effect model

To improve above model we focus on the fact that, from experience, we know that some movies are just generally rated higher than others. Higher ratings are mostly linked to popular movies among users and the opposite is true for unpopular movies. We compute the estimated deviation of each movies' mean rating from the total mean of all movies μ . The resulting variable is called “b” (as bias) for each movie “i” b_i , that represents average ranking for movie i :

$$Y_{u,i} = \mu + b_i + \epsilon_{u,i}$$

The histogram is left skewed, implying that more movies have negative effects

```
movie_avgs <- edx %>%
  group_by(movieId) %>%
  summarize(b_i = mean(rating - mu))
movie_avgs %>% qplot(b_i, geom = "histogram", bins = 10, data = ., color = I("black"),
  ylab = "Number of movies", main = "Number of movies with the computed b_i")
```



This is called the penalty term movie effect.

Our prediction improve once we predict using this model.

```
predicted_ratings <- mu + validation %>%
  left_join(movie_avgs, by='movieId') %>%
  pull(b_i)
model_1_rmse <- RMSE(predicted_ratings, validation$rating)
rmse_results <- bind_rows(rmse_results,
  data_frame(method="Movie effect model",
    RMSE = model_1_rmse ))
rmse_results %>% knitr::kable()
```

method	RMSE
Average movie rating model	1.0612018
Movie effect model	0.9439087

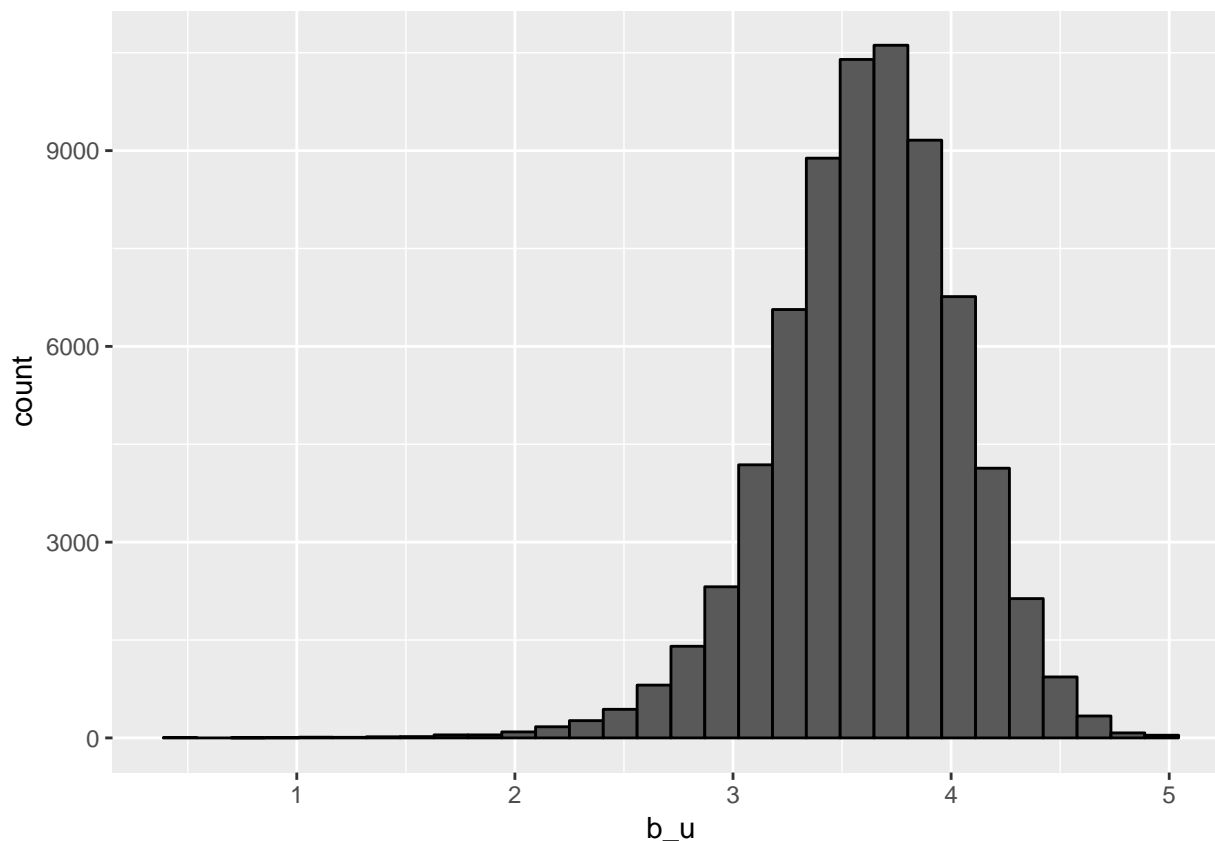
So we have predicted movie rating based on the fact that movies are rated differently by adding the computed b_i to μ . If an individual movie is on average rated worse than the average rating of all movies μ , we predict that it will be rated lower than μ by b_i , the difference of the individual movie average from the total average.

We can see an improvement but this model does not consider the individual user rating effect.

2.2.3 III. Movie and user effect model

We compute the average rating for user μ , for those that have rated over 100 movies, said penalty term user effect. In fact users affect the ratings positively or negatively.

```
edx %>%
  group_by(userId) %>%
  summarize(b_u = mean(rating)) %>%
  filter(n() >= 100) %>%
  ggplot(aes(b_u)) +
  geom_histogram(bins = 30, color = "black")
```



There is substantial variability across users as well: some users are very cranky and other love every movie. This implies that further improvement to our model may be:

$$Y_{u,i} = \mu + b_i + b_u + \epsilon_{u,i}$$

where b_u is a user-specific effect. If a cranky user (negative b_u) rates a great movie (positive b_i), the effects counter each other and we may be able to correctly predict that this user gave this great movie a 3 rather than a 5.

We compute an approximation by computing μ and b_i , and estimating b_u , as the average of

$$Y_{u,i} - \mu - b_i$$

```
user_avgs <- edx %>%
  left_join(movie_avgs, by='movieId') %>%
  group_by(userId) %>%
  summarize(b_u = mean(rating - mu - b_i))
```

We can now construct predictors and see RMSE improves:

```
predicted_ratings <- validation%>%
  left_join(movie_avgs, by='movieId') %>%
  left_join(user_avgs, by='userId') %>%
  mutate(pred = mu + b_i + b_u) %>%
  pull(pred)

model_2_rmse <- RMSE(predicted_ratings, validation$rating)
rmse_results <- bind_rows(rmse_results,
```

```
data_frame(method="Movie and user effect model",
            RMSE = model_2_rmse))
rmse_results %>% knitr::kable()
```

method	RMSE
Average movie rating model	1.0612018
Movie effect model	0.9439087
Movie and user effect model	0.8653488

Our rating predictions further reduced the RMSE. But we made stil mistakes on our first model (using only movies). The supposes “best “ and “worst “movie were rated by few users, in most cases just one user. These movies were mostly obscure ones. This is because with a few users, we have more uncertainty. Therefore larger estimates of b_i , negative or positive, are more likely. Large errors can increase our RMSE.

Until now, we computed standard error and constructed confidence intervals to account for different levels of uncertainty. However, when making predictions, we need one number, one prediction, not an interval. For this we introduce the concept of regularization, that permits to penalize large estimates that come from small sample sizes. The general idea is to add a penalty for large values of b_i to the sum of squares equation that we minimize. So having many large b_i , make it harder to minimize. Regularization is a method used to reduce the effect of overfitting.

2.2.4 IV. Regularized movie and user effect model

So estimates of b_i and b_u are caused by movies with very few ratings and in some users that only rated a very small number of movies. Hence this can strongly influence the prediction. The use of the regularization help to penalize these aspects. We should find the value of lambda (that is a tuning parameter) that will minimize the RMSE. This shrinks the b_i and b_u in case of small number of ratings.

```
lambdas <- seq(0, 10, 0.25)

rmsees <- sapply(lambdas, function(l){

  mu <- mean(edx$rating)

  b_i <- edx %>%
    group_by(movieId) %>%
    summarize(b_i = sum(rating - mu)/(n()+1))

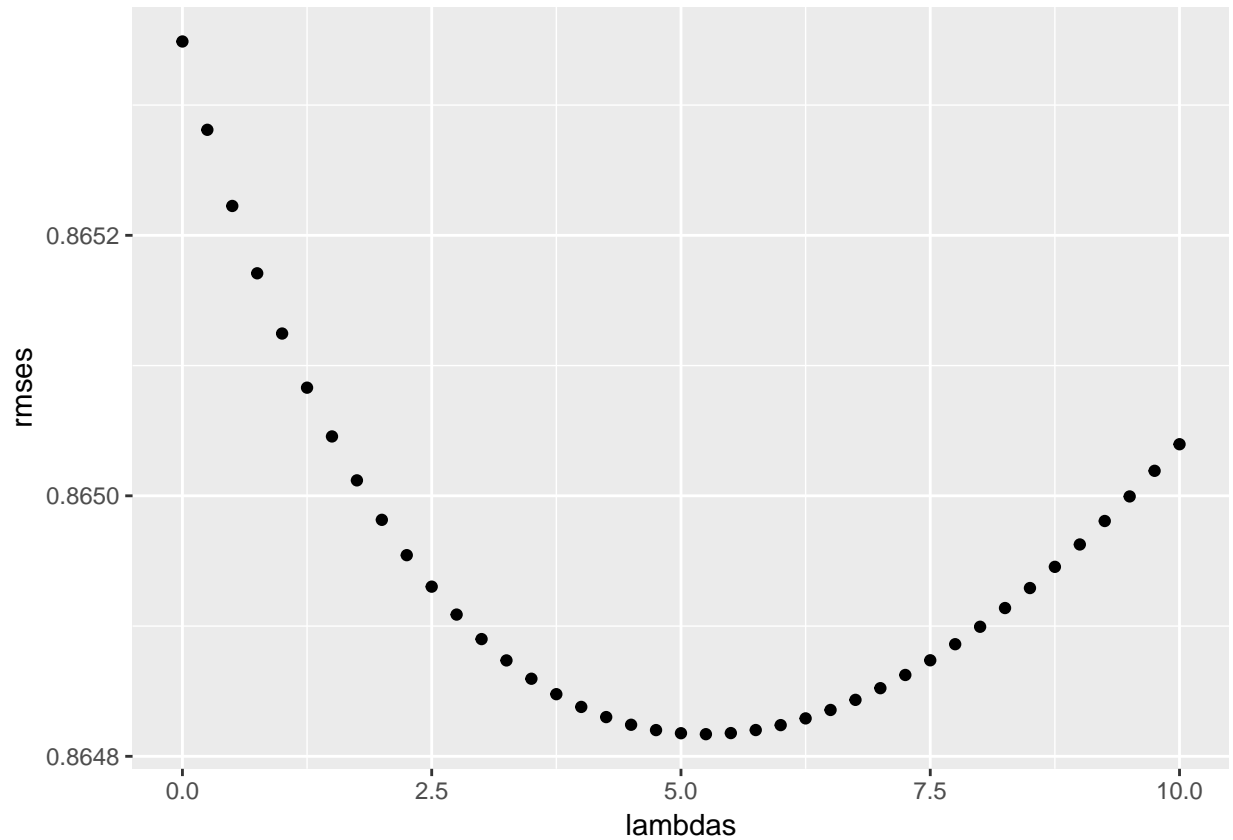
  b_u <- edx %>%
    left_join(b_i, by="movieId") %>%
    group_by(userId) %>%
    summarize(b_u = sum(rating - b_i - mu)/(n()+1))

  predicted_ratings <-
    validation %>%
    left_join(b_i, by = "movieId") %>%
    left_join(b_u, by = "userId") %>%
    mutate(pred = mu + b_i + b_u) %>%
    pull(pred)

  return(RMSE(predicted_ratings, validation$rating))
})
```

We plot RMSE vs lambdas to select the optimal lambda

```
qplot(lambdas, rmse)
```



For the full model, the optimal lambda is:

```
lambda <- lambdas[which.min(rmse)]  
lambda
```

```
## [1] 5.25
```

For the full model, the optimal lambda is: 5.25

The new results will be:

```
rmse_results <- bind_rows(rmse_results,  
  data_frame(method="Regularized movie and user effect model",  
    RMSE = min(rmse)))  
rmse_results %>% knitr::kable()
```

method	RMSE
Average movie rating model	1.0612018
Movie effect model	0.9439087
Movie and user effect model	0.8653488
Regularized movie and user effect model	0.8648170

3 Results

The RMSE values for all the models are the following:

```
rmse_results %>% knitr::kable()
```

method	RMSE
Average movie rating model	1.0612018
Movie effect model	0.9439087
Movie and user effect model	0.8653488
Regularized movie and user effect model	0.8648170

We therefore found the lowest value of RMSE that is 0.8648170.

4 Discussion

So we can confirm that the final model for our projects is the following:

$$Y_{u,i} = \mu + b_i + b_u + \epsilon_{u,i}$$

This model work well if the average user doesn't rate a particularly good/popular movie with a large positive b_i , by disliking a particular movie.

5 Conclusion

We can affirm to have built a machine learning algorithm to predict movie ratings with MovieLens dataset. The regularized model including the effect of user is characterized by the lower RMSE value and is hence the optimal model to use for the present project. With the optimal model characterised by the lowest RMSE value (0.8648170) lower than the initial evaluation criteria (0.8775) given by the goal of the present project. We could also affirm that improvements in the RMSE could be achieved by adding other effect (genre, year, age,...). Other different machine learning models could also improve the results further, but hardware limitations as the RAM are a constraint.

6 Appendix - Enviroment

```
print("Operating System:")
```

```
## [1] "Operating System:"
```

```
version
```

```
##  
## platform      _  
## arch          x86_64-apple-darwin15.6.0  
## os            x86_64  
## system        darwin15.6.0  
## status        x86_64, darwin15.6.0  
## major         3
```

```
## minor          5.1
## year           2018
## month          07
## day            02
## svn rev        74947
## language       R
## version.string R version 3.5.1 (2018-07-02)
## nickname       Feather Spray
```

```
print("All installed packages")
```

```
## [1] "All installed packages"
```

```
installed.packages()
```

```
##          Package
## abind      "abind"
## annotate   "annotate"
## AnnotationDbi "AnnotationDbi"
## assertthat "assertthat"
## backports  "backports"
## base       "base"
## base64enc  "base64enc"
## BH         "BH"
## bindr      "bindr"
## bindrcpp   "bindrcpp"
## Biobase    "Biobase"
## BiocGenerics "BiocGenerics"
## BiocInstaller "BiocInstaller"
## BiocManager "BiocManager"
## BiocParallel "BiocParallel"
## BiocVersion "BiocVersion"
## biomaRt    "biomaRt"
## Biostrings "Biostrings"
## bit        "bit"
## bit64      "bit64"
## bitops     "bitops"
## blob       "blob"
## boot       "boot"
## broom      "broom"
## callr      "callr"
## caret      "caret"
## caTools    "caTools"
## cellranger "cellranger"
## class      "class"
## classInt   "classInt"
## cli        "cli"
## clipr      "clipr"
## clisymbols "clisymbols"
## cluster    "cluster"
## codetools  "codetools"
## colorspace "colorspace"
## combinat   "combinat"
## compiler   "compiler"
## config     "config"
```

## crayon	"crayon"
## curl	"curl"
## CVST	"CVST"
## data.table	"data.table"
## datasets	"datasets"
## DBI	"DBI"
## dbplyr	"dbplyr"
## ddalpha	"ddalpha"
## DelayedArray	"DelayedArray"
## DEoptimR	"DEoptimR"
## desc	"desc"
## devtools	"devtools"
## dichromat	"dichromat"
## digest	"digest"
## dimRed	"dimRed"
## dplyr	"dplyr"
## DRR	"DRR"
## dslabs	"dslabs"
## e1071	"e1071"
## ellipsis	"ellipsis"
## evaluate	"evaluate"
## fansi	"fansi"
## fastAdaboost	"fastAdaboost"
## forcats	"forcats"
## foreach	"foreach"
## forecast	"forecast"
## foreign	"foreign"
## forge	"forge"
## formatR	"formatR"
## Formula	"Formula"
## fracdiff	"fracdiff"
## fs	"fs"
## futile.logger	"futile.logger"
## futile.options	"futile.options"
## gam	"gam"
## gbm	"gbm"
## genefilter	"genefilter"
## generics	"generics"
## GenomeInfoDb	"GenomeInfoDb"
## GenomeInfoDbData	"GenomeInfoDbData"
## GenomicAlignments	"GenomicAlignments"
## GenomicFeatures	"GenomicFeatures"
## GenomicRanges	"GenomicRanges"
## geometry	"geometry"
## ggplot2	"ggplot2"
## gh	"gh"
## git2r	"git2r"
## glue	"glue"
## gower	"gower"
## graphics	"graphics"
## grDevices	"grDevices"
## grid	"grid"
## gridExtra	"gridExtra"
## gtable	"gtable"

## haven	"haven"
## highr	"highr"
## HistData	"HistData"
## hms	"hms"
## htmltools	"htmltools"
## htmlwidgets	"htmlwidgets"
## httpuv	"httpuv"
## httr	"httr"
## igraph	"igraph"
## import	"import"
## ini	"ini"
## inum	"inum"
## ipred	"ipred"
## IRanges	"IRanges"
## iterators	"iterators"
## jsonlite	"jsonlite"
## kernlab	"kernlab"
## KernSmooth	"KernSmooth"
## kknn	"kknn"
## klaR	"klaR"
## knitr	"knitr"
## labeling	"labeling"
## labelled	"labelled"
## Lahman	"Lahman"
## lambda.r	"lambda.r"
## later	"later"
## lattice	"lattice"
## lava	"lava"
## lazyeval	"lazyeval"
## libcoin	"libcoin"
## lmtest	"lmtest"
## lubridate	"lubridate"
## magic	"magic"
## magrittr	"magrittr"
## markdown	"markdown"
## MASS	"MASS"
## Matrix	"Matrix"
## matrixStats	"matrixStats"
## mboost	"mboost"
## memoise	"memoise"
## methods	"methods"
## mgcv	"mgcv"
## mime	"mime"
## miniUI	"miniUI"
## mlbench	"mlbench"
## ModelMetrics	"ModelMetrics"
## modelr	"modelr"
## monmlp	"monmlp"
## munsell	"munsell"
## mvtnorm	"mvtnorm"
## naivebayes	"naivebayes"
## nlme	"nlme"
## nnet	"nnet"
## nnls	"nnls"

## numDeriv	"numDeriv"
## odbc	"odbc"
## openssl	"openssl"
## optimx	"optimx"
## packrat	"packrat"
## parallel	"parallel"
## partykit	"partykit"
## pdftools	"pdftools"
## pillar	"pillar"
## pkgbuild	"pkgbuild"
## pkgconfig	"pkgconfig"
## pkgload	"pkgload"
## PKI	"PKI"
## plogr	"plogr"
## pls	"pls"
## plyr	"plyr"
## praise	"praise"
## prettyunits	"prettyunits"
## processx	"processx"
## prodlim	"prodlim"
## progress	"progress"
## promises	"promises"
## ps	"ps"
## purrr	"purrr"
## quadprog	"quadprog"
## quantmod	"quantmod"
## questionr	"questionr"
## r2d3	"r2d3"
## R6	"R6"
## randomForest	"randomForest"
## ranger	"ranger"
## rappdirs	"rappdirs"
## raster	"raster"
## Rborist	"Rborist"
## rcmdcheck	"rcmdcheck"
## RColorBrewer	"RColorBrewer"
## Rcpp	"Rcpp"
## RcppArmadillo	"RcppArmadillo"
## RcppEigen	"RcppEigen"
## RcppRoll	"RcppRoll"
## RCurl	"RCurl"
## readr	"readr"
## readxl	"readxl"
## recipes	"recipes"
## rematch	"rematch"
## remotes	"remotes"
## reprex	"reprex"
## reshape2	"reshape2"
## RJSONIO	"RJSONIO"
## rlang	"rlang"
## rmarkdown	"rmarkdown"
## robustbase	"robustbase"
## rpart	"rpart"
## rprojroot	"rprojroot"

## Rsamtools	"Rsamtools"
## rsconnect	"rsconnect"
## RSNNS	"RSNNS"
## RSQLite	"RSQLite"
## rstudioapi	"rstudioapi"
## rtracklayer	"rtracklayer"
## rvest	"rvest"
## S4Vectors	"S4Vectors"
## scales	"scales"
## selectr	"selectr"
## sessioninfo	"sessioninfo"
## sfsmisc	"sfsmisc"
## shiny	"shiny"
## snow	"snow"
## sourcetools	"sourcetools"
## sp	"sp"
## sparklyr	"sparklyr"
## SparseM	"SparseM"
## spatial	"spatial"
## spData	"spData"
## splines	"splines"
## SQUAREM	"SQUAREM"
## stabs	"stabs"
## stats	"stats"
## stats4	"stats4"
## stringi	"stringi"
## stringr	"stringr"
## SummarizedExperiment	"SummarizedExperiment"
## survival	"survival"
## tcltk	"tcltk"
## testthat	"testthat"
## tibble	"tibble"
## tidyr	"tidyr"
## tidyselect	"tidyselect"
## tidyverse	"tidyverse"
## timeDate	"timeDate"
## tinytex	"tinytex"
## tools	"tools"
## tseries	"tseries"
## TTR	"TTR"
## urca	"urca"
## uroot	"uroot"
## usethis	"usethis"
## utf8	"utf8"
## utils	"utils"
## viridisLite	"viridisLite"
## whisker	"whisker"
## withr	"withr"
## wsrfr	"wsrfr"
## xfun	"xfun"
## XML	"XML"
## xml2	"xml2"
## xopen	"xopen"
## xtable	"xtable"

```

## xts "xts"
## XVector "XVector"
## yaml "yaml"
## zlibbioc "zlibbioc"
## zoo "zoo"
## LibPath
## abind "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## annotate "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## AnnotationDbi "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## assertthat "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## backports "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## base "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## base64enc "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## BH "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## bindr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## bindrcpp "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Biobase "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## BiocGenerics "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## BiocInstaller "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## BiocManager "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## BiocParallel "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## BiocVersion "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## biomaRt "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Biostrings "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## bit "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## bit64 "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## bitops "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## blob "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## boot "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## broom "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## callr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## caret "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## caTools "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## cellranger "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## class "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## classInt "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## cli "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## clipr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## clisymbols "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## cluster "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## codetools "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## colorspace "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## combinat "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## compiler "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## config "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## crayon "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## curl "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## CVST "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## data.table "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## datasets "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## DBI "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## dbplyr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ddalpha "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## DelayedArray "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"

```

```

## DEoptimR           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## desc               "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## devtools           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## dichromat          "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## digest             "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## dimRed              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## dplyr              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## DRR                "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## dslabs              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## e1071              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ellipsis           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## evaluate           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## fansi              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## fastAdaboost        "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## forcats            "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## foreach            "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## forecast           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## foreign            "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## forge              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## formatR            "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Formula            "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## fracdiff           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## fs                 "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## futile.logger      "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## futile.options     "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## gam                "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## gbm                "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## genefilter         "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## generics           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## GenomeInfoDb       "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## GenomeInfoDbData   "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## GenomicAlignments  "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## GenomicFeatures    "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## GenomicRanges      "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## geometry           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ggplot2            "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## gh                 "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## git2r              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## glue               "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## gower              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## graphics           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## grDevices          "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## grid               "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## gridExtra          "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## gtable             "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## haven              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## highr              "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## HistData           "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## hms                "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## htmltools          "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## htmlwidgets        "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## httpuv             "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## httr               "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## igraph             "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"

```

```

## import "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ini "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## inum "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ipred "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## IRanges "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## iterators "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## jsonlite "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## kernlab "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## KernSmooth "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## kkn n "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## klaR "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## knitr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## labeling "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## labelled "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Lahman "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## lambda.r "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## later "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## lattice "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## lava "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## lazyeval "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## libcoin "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## lmtest "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## lubridate "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## magic "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## magrittr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## markdown "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## MASS "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Matrix "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## matrixStats "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## mboost "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## memoise "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## methods "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## mgcv "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## mime "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## miniUI "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## mlbench "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ModelMetrics "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## modelr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## monmlp "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## munsell "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## mvtnorm "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## naivebayes "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## nlme "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## nnet "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## nnls "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## numDeriv "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## odbc "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## openssl "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## optimx "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## packrat "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## parallel "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## partykit "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## pdftools "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## pillar "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"

```

```

## pkgbuild "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## pkgconfig "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## pkgload "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## PKI "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## plogr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## pls "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## plyr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## praise "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## prettyunits "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## processx "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## prodlim "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## progress "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## promises "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ps "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## purrr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## quadprog "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## quantmod "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## questionr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## r2d3 "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## R6 "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## randomForest "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## ranger "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rappdirs "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## raster "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Rborist "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rcmdcheck "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RColorBrewer "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Rcpp "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RcppArmadillo "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RcppEigen "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RcppRoll "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RCurl "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## readr "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## readxl "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## recipes "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rematch "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## remotes "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## reprex "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## reshape2 "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RJSONIO "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rlang "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rmarkdown "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## robustbase "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rpart "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rprojroot "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## Rsamtools "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rsconnect "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RSNNS "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## RSQLite "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rstudioapi "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rtracklayer "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## rvest "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## S4Vectors "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## scales "/Library/Frameworks/R.framework/Versions/3.5/Resources/library"

```

## selectr	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## sessioninfo	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## sfsmisc	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## shiny	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## snow	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## sourcetools	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## sp	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## sparklyr	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## SparseM	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## spatial	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## spData	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## splines	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## SQUAREM	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## stabs	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## stats	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## stats4	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## stringi	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## stringr	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## SummarizedExperiment	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## survival	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tcltk	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## testthat	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tibble	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tidyr	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tidyselect	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tidyverse	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## timeDate	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tinytex	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tools	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## tseries	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## TTR	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## urca	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## uroot	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## usethis	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## utf8	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## utils	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## viridisLite	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## whisker	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## withr	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## wsrf	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## xfun	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## XML	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## xml2	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## xopen	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## xtable	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## xts	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## XVector	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## yaml	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## zlibbioc	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
## zoo	"/Library/Frameworks/R.framework/Versions/3.5/Resources/library"
##	Version Priority
## abind	"1.4-5" NA
## annotate	"1.60.0" NA
## AnnotationDbi	"1.44.0" NA

## assertthat	"0.2.0"	NA
## backports	"1.1.2"	NA
## base	"3.5.1"	"base"
## base64enc	"0.1-3"	NA
## BH	"1.66.0-1"	NA
## bindr	"0.1.1"	NA
## bindrcpp	"0.2.2"	NA
## Biobase	"2.42.0"	NA
## BiocGenerics	"0.28.0"	NA
## BiocInstaller	"1.30.0"	NA
## BiocManager	"1.30.4"	NA
## BiocParallel	"1.16.2"	NA
## BiocVersion	"3.8.0"	NA
## biomaRt	"2.38.0"	NA
## Biostrings	"2.50.1"	NA
## bit	"1.1-14"	NA
## bit64	"0.9-7"	NA
## bitops	"1.0-6"	NA
## blob	"1.1.1"	NA
## boot	"1.3-20"	"recommended"
## broom	"0.5.1"	NA
## callr	"3.0.0"	NA
## caret	"6.0-81"	NA
## caTools	"1.17.1.1"	NA
## cellranger	"1.1.0"	NA
## class	"7.3-14"	"recommended"
## classInt	"0.2-3"	NA
## cli	"1.0.1"	NA
## clipr	"0.4.1"	NA
## clisymbols	"1.2.0"	NA
## cluster	"2.0.7-1"	"recommended"
## codetools	"0.2-15"	"recommended"
## colorspace	"1.3-2"	NA
## combinat	"0.0-8"	NA
## compiler	"3.5.1"	"base"
## config	"0.3"	NA
## crayon	"1.3.4"	NA
## curl	"3.2"	NA
## CVST	"0.2-2"	NA
## data.table	"1.11.8"	NA
## datasets	"3.5.1"	"base"
## DBI	"1.0.0"	NA
## dbplyr	"1.2.2"	NA
## ddalpha	"1.3.4"	NA
## DelayedArray	"0.8.0"	NA
## DEoptimR	"1.0-8"	NA
## desc	"1.2.0"	NA
## devtools	"2.0.1"	NA
## dichromat	"2.0-0"	NA
## digest	"0.6.18"	NA
## dimRed	"0.2.2"	NA
## dplyr	"0.7.8"	NA
## DRR	"0.0.3"	NA
## dslabs	"0.5.1"	NA

## e1071	"1.7-0.1"	NA
## ellipsis	"0.1.0"	NA
## evaluate	"0.12"	NA
## fansi	"0.4.0"	NA
## fastAdaboost	"1.0.0"	NA
## forcats	"0.3.0"	NA
## foreach	"1.4.4"	NA
## forecast	"8.4"	NA
## foreign	"0.8-71"	"recommended"
## forge	"0.2.0"	NA
## formatR	"1.5"	NA
## Formula	"1.2-3"	NA
## fracdiff	"1.4-2"	NA
## fs	"1.2.6"	NA
## futile.logger	"1.4.3"	NA
## futile.options	"1.0.1"	NA
## gam	"1.16"	NA
## gbm	"2.1.4"	NA
## genefilter	"1.62.0"	NA
## generics	"0.0.2"	NA
## GenomeInfoDb	"1.18.1"	NA
## GenomeInfoDbData	"1.2.0"	NA
## GenomicAlignments	"1.18.0"	NA
## GenomicFeatures	"1.34.1"	NA
## GenomicRanges	"1.34.0"	NA
## geometry	"0.3-6"	NA
## ggplot2	"3.1.0"	NA
## gh	"1.0.1"	NA
## git2r	"0.23.0"	NA
## glue	"1.3.0"	NA
## gower	"0.1.2"	NA
## graphics	"3.5.1"	"base"
## grDevices	"3.5.1"	"base"
## grid	"3.5.1"	"base"
## gridExtra	"2.3"	NA
## gtable	"0.2.0"	NA
## haven	"2.0.0"	NA
## highr	"0.7"	NA
## HistData	"0.8-4"	NA
## hms	"0.4.2"	NA
## htmltools	"0.3.6"	NA
## htmlwidgets	"1.3"	NA
## httpuv	"1.4.5"	NA
## httr	"1.3.1"	NA
## igraph	"1.2.2"	NA
## import	"1.1.0"	NA
## ini	"0.3.1"	NA
## inum	"1.0-0"	NA
## ipred	"0.9-8"	NA
## IRanges	"2.16.0"	NA
## iterators	"1.0.10"	NA
## jsonlite	"1.5"	NA
## kernlab	"0.9-27"	NA
## KernSmooth	"2.23-15"	"recommended"

## kkn	"1.3.1"	NA
## klaR	"0.6-14"	NA
## knitr	"1.20"	NA
## labeling	"0.3"	NA
## labelled	"2.0.1"	NA
## Lahman	"6.0-0"	NA
## lambda.r	"1.2.3"	NA
## later	"0.7.5"	NA
## lattice	"0.20-38"	"recommended"
## lava	"1.6.4"	NA
## lazyeval	"0.2.1"	NA
## libcoin	"1.0-2"	NA
## lmtest	"0.9-36"	NA
## lubridate	"1.7.4"	NA
## magic	"1.5-9"	NA
## magrittr	"1.5"	NA
## markdown	"0.8"	NA
## MASS	"7.3-51.1"	"recommended"
## Matrix	"1.2-15"	"recommended"
## matrixStats	"0.54.0"	NA
## mboost	"2.9-1"	NA
## memoise	"1.1.0"	NA
## methods	"3.5.1"	"base"
## mgcv	"1.8-26"	"recommended"
## mime	"0.6"	NA
## miniUI	"0.1.1.1"	NA
## mlbench	"2.1-1"	NA
## ModelMetrics	"1.2.2"	NA
## modelr	"0.1.2"	NA
## monmlp	"1.1.5"	NA
## munsell	"0.5.0"	NA
## mvtnorm	"1.0-8"	NA
## naivebayes	"0.9.2"	NA
## nlme	"3.1-137"	"recommended"
## nnet	"7.3-12"	"recommended"
## nnls	"1.4"	NA
## numDeriv	"2016.8-1"	NA
## odbc	"1.1.6"	NA
## openssl	"1.1"	NA
## optimx	"2018-7.10"	NA
## packrat	"0.5.0"	NA
## parallel	"3.5.1"	"base"
## partykit	"1.2-2"	NA
## pdftools	"1.8"	NA
## pillar	"1.3.0"	NA
## pkgbuild	"1.0.2"	NA
## pkgconfig	"2.0.2"	NA
## pkgload	"1.0.2"	NA
## PKI	"0.1-5.1"	NA
## plogr	"0.2.0"	NA
## pls	"2.7-0"	NA
## plyr	"1.8.4"	NA
## praise	"1.0.0"	NA
## prettyunits	"1.0.2"	NA

## processx	"3.2.1"	NA
## prodlim	"2018.04.18"	NA
## progress	"1.2.0"	NA
## promises	"1.0.1"	NA
## ps	"1.2.1"	NA
## purrr	"0.2.5"	NA
## quadprog	"1.5-5"	NA
## quantmod	"0.4-13"	NA
## questionr	"0.7.0"	NA
## r2d3	"0.2.3"	NA
## R6	"2.3.0"	NA
## randomForest	"4.6-14"	NA
## ranger	"0.10.1"	NA
## rappdirs	"0.3.1"	NA
## raster	"2.8-4"	NA
## Rborist	"0.1-8"	NA
## rcmdcheck	"1.3.2"	NA
## RColorBrewer	"1.1-2"	NA
## Rcpp	"1.0.0"	NA
## RcppArmadillo	"0.9.200.5.0"	NA
## RcppEigen	"0.3.3.5.0"	NA
## RcppRoll	"0.3.0"	NA
## RCurl	"1.95-4.11"	NA
## readr	"1.2.1"	NA
## readxl	"1.1.0"	NA
## recipes	"0.1.4"	NA
## rematch	"1.0.1"	NA
## remotes	"2.0.2"	NA
## reprex	"0.2.1"	NA
## reshape2	"1.4.3"	NA
## RJSONIO	"1.3-1.1"	NA
## rlang	"0.3.1"	NA
## rmarkdown	"1.10"	NA
## robustbase	"0.93-3"	NA
## rpart	"4.1-13"	"recommended"
## rprojroot	"1.3-2"	NA
## Rsamtools	"1.34.0"	NA
## rsconnect	"0.8.13"	NA
## RSNNS	"0.4-11"	NA
## RSQLite	"2.1.1"	NA
## rstudioapi	"0.8"	NA
## rtracklayer	"1.42.1"	NA
## rvest	"0.3.2"	NA
## S4Vectors	"0.20.1"	NA
## scales	"1.0.0"	NA
## selectr	"0.4-1"	NA
## sessioninfo	"1.1.1"	NA
## sfsmisc	"1.1-3"	NA
## shiny	"1.2.0"	NA
## snow	"0.4-3"	NA
## sourcetools	"0.1.7"	NA
## sp	"1.3-1"	NA
## sparklyr	"1.0.0"	NA
## SparseM	"1.77"	NA

```

## spatial                "7.3-11"      "recommended"
## spData                 "0.2.9.6"      NA
## splines                "3.5.1"       "base"
## SQUAREM               "2017.10-1"    NA
## stabs                  "0.6-3"       NA
## stats                  "3.5.1"       "base"
## stats4                 "3.5.1"       "base"
## stringi                "1.2.4"       NA
## stringr                "1.3.1"       NA
## SummarizedExperiment "1.12.0"    NA
## survival               "2.43-3"     "recommended"
## tcltk                  "3.5.1"       "base"
## testthat               "2.0.1"       NA
## tibble                 "1.4.2"       NA
## tidyr                  "0.8.2"       NA
## tidyselect             "0.2.5"       NA
## tidyverse              "1.2.1"       NA
## timeDate               "3043.102"    NA
## tinytex                "0.10"       NA
## tools                  "3.5.1"       "base"
## tseries                "0.10-46"    NA
## TTR                    "0.23-4"     NA
## urca                   "1.3-0"       NA
## uroot                  "2.0-9"       NA
## usethis                "1.4.0"       NA
## utf8                   "1.1.4"       NA
## utils                  "3.5.1"       "base"
## viridisLite            "0.3.0"       NA
## whisker                "0.3-2"       NA
## withr                  "2.1.2"       NA
## wsrfl                  "1.7.17"    NA
## xfun                   "0.4"        NA
## XML                    "3.98-1.16"   NA
## xml2                   "1.2.0"       NA
## xopen                  "1.0.0"       NA
## xtable                 "1.8-3"       NA
## xts                    "0.11-2"    NA
## XVector                "0.22.0"    NA
## yaml                   "2.2.0"       NA
## zlibbioc               "1.28.0"    NA
## zoo                    "1.8-4"       NA
##
## Depends
## abind                  "R (>= 1.5.0)"
## annotate               "R (>= 2.10), AnnotationDbi (>= 1.27.5), XML"
## AnnotationDbi          "R (>= 2.7.0), methods, utils, stats4, BiocGenerics (>= 0.23.1), Biobase (>= 1
## assertthat             NA
## backports              "R (>= 3.0.0)"
## base                   NA
## base64enc              "R (>= 2.9.0)"
## BH                     NA
## bindr                  NA
## bindrcpp               NA
## Biobase                "R (>= 2.10), BiocGenerics (>= 0.27.1), utils"
## BiocGenerics           "methods, utils, graphics, stats, parallel"

```

```

## BiocInstaller      "R (>= 3.5.0)"
## BiocManager        "R (>= 3.5.0)"
## BiocParallel       "methods"
## BiocVersion        "R (>= 3.5.0), R (< 3.6.0)"
## biomaRt            "methods"
## Biostrings         "R (>= 3.5.0), methods, BiocGenerics, S4Vectors, IRanges,\nXVector"
## bit                "R (>= 2.9.2)"
## bit64              "R (>= 3.0.1), bit (>= 1.1-12), utils, methods, stats"
## bitops             NA
## blob               NA
## boot              "R (>= 3.0.0), graphics, stats"
## broom              "R (>= 3.1)"
## callr              NA
## caret              "R (>= 2.10), lattice (>= 0.20), ggplot2"
## caTools            "R (>= 2.2.0)"
## cellranger         "R (>= 3.0.0)"
## class              "R (>= 3.0.0), stats, utils"
## classInt           "R (>= 2.2), spData (>= 0.2.6.2)"
## cli                "R (>= 2.10)"
## clipr              NA
## clisymbols         NA
## cluster            "R (>= 3.2.0)"
## codetools          "R (>= 2.1)"
## colorspace         "R (>= 2.13.0), methods"
## combinat           NA
## compiler           NA
## config             NA
## crayon             NA
## curl               "R (>= 3.0.0)"
## CVST               "kernlab,Matrix"
## data.table         "R (>= 3.1.0)"
## datasets           NA
## DBI                "R (>= 3.0.0), methods"
## dbplyr             "R (>= 3.2)"
## ddalpha            "R (>= 2.10), stats, utils, graphics, grDevices, MASS, class,\nrobase, sfsm"
## DelayedArray       "R (>= 3.4), methods, stats4, matrixStats, BiocGenerics (>= \n0.27.1), S4Vectors"
## DEoptimR           NA
## desc              "R (>= 3.1.0)"
## devtools           "R (>= 3.0.2)"
## dichromat         "R (>= 2.10), stats"
## digest            "R (>= 3.1.0)"
## dimRed             "R (>= 3.0.0), DRR"
## dplyr             "R (>= 3.1.2)"
## DRR               "kernlab, CVST, Matrix"
## dslabs            "R (>= 3.1.2)"
## e1071             NA
## ellipsis          "R (>= 3.1)"
## evaluate          "R (>= 3.0.2)"
## fansi             "R (>= 3.1.0)"
## fastAdaboost      "R (>= 3.1.2)"
## forcats           "R (>= 3.1)"
## foreach           "R (>= 2.5.0)"
## forecast          "R (>= 3.0.2),"
## foreign           "R (>= 3.0.0)"

```

```

## forge "R (>= 3.1.2)"
## formatR "R (>= 3.0.2)"
## Formula "R (>= 2.0.0), stats"
## fracdiff NA
## fs "R (>= 3.1)"
## futile.logger "R (>= 3.0.0)"
## futile.options "R (>= 2.8.0)"
## gam "stats, splines, foreach"
## gbm "R (>= 2.9.0)"
## genefilter NA
## generics "R (>= 3.1)"
## GenomeInfoDb "R (>= 3.1), methods, BiocGenerics (>= 0.13.8), S4Vectors (>=\n0.17.25), IRanges"
## GenomeInfoDbData "R (>= 3.3)"
## GenomicAlignments "R (>= 2.10), methods, BiocGenerics (>= 0.15.3), S4Vectors (>=\n0.19.11), IRanges"
## GenomicFeatures "BiocGenerics (>= 0.1.0), S4Vectors (>= 0.17.29), IRanges (>=\n2.13.23), GenomeInfoDb"
## GenomicRanges "R (>= 2.10), methods, stats4, BiocGenerics (>= 0.25.3),\nS4Vectors (>= 0.19.11)"
## geometry "R (>= 2.5.0), magic"
## ggplot2 "R (>= 3.1)"
## gh NA
## git2r "R (>= 3.1)"
## glue "R (>= 3.1)"
## gower NA
## graphics NA
## grDevices NA
## grid NA
## gridExtra NA
## gtable "R (>= 2.14)"
## haven "R (>= 3.1)"
## highr "R (>= 3.0.2)"
## HistData NA
## hms NA
## htmltools "R (>= 2.14.1)"
## htmlwidgets NA
## httpuv "R (>= 2.15.1), methods"
## httr "R (>= 3.0.0)"
## igraph "methods"
## import NA
## ini NA
## inum "R (>= 3.3.0)"
## ipred "R (>= 2.10)"
## IRanges "R (>= 3.1.0), methods, utils, stats, BiocGenerics (>= 0.25.3),\nS4Vectors (>= 0.19.11)"
## iterators "R (>= 2.5.0), utils"
## jsonlite "methods"
## kernlab "R (>= 2.10)"
## KernSmooth "R (>= 2.5.0), stats"
## kknns "R (>= 2.10)"
## klaR "R (>= 2.10.0), MASS"
## knitr "R (>= 3.1.0)"
## labeling NA
## labelled NA
## Lahman "R (>= 2.10)"
## lambda.r "R (>= 3.0.0)"
## later NA
## lattice "R (>= 3.0.0)"

```

```

## lava "R (>= 3.0)"
## lazyeval "R (>= 3.1.0)"
## libcoin "R (>= 3.4.0)"
## lmtest "R (>= 2.10.0), stats, zoo"
## lubridate "methods, R (>= 3.0.0)"
## magic "R (>= 2.10), abind"
## magrittr NA
## markdown "R (>= 2.11.1)"
## MASS "R (>= 3.1.0), grDevices, graphics, stats, utils"
## Matrix "R (>= 3.2.0)"
## matrixStats "R (>= 2.12.0)"
## mboost "R (>= 3.2.0), methods, stats, parallel, stabs (>= 0.5-0)"
## memoise NA
## methods NA
## mgcv "R (>= 2.14.0), nlme (>= 3.1-64)"
## mime NA
## miniUI NA
## mlbench "R (>= 2.10)"
## ModelMetrics "R (>= 3.2.2)"
## modelr "R (>= 3.1)"
## monmlp "optimx"
## munsell NA
## mvtnorm "R(>= 1.9.0)"
## naivebayes NA
## nlme "R (>= 3.4.0)"
## nnet "R (>= 2.14.0), stats, utils"
## nnls NA
## numDeriv "R (>= 2.11.1)"
## odbc "R (>= 3.2.0)"
## openssl NA
## optimx NA
## packrat "R (>= 3.0.0)"
## parallel NA
## partykit "R (>= 3.1.0), graphics, grid, libcoin (>= 1.0-0), mvtnorm"
## pdftools NA
## pillar NA
## pkgbuild "R (>= 3.1)"
## pkgconfig NA
## pkgload NA
## PKI "R (>= 2.9.0), base64enc"
## plogr NA
## pls "R (>= 2.10)"
## plyr "R (>= 3.1.0)"
## praise NA
## prettyunits NA
## processx NA
## prodlim "R (>= 2.9.0)"
## progress NA
## promises NA
## ps "R (>= 3.1)"
## purrr "R (>= 3.1)"
## quadprog "R (>= 2.15.0)"
## quantmod "R (>= 3.2.0), xts(>= 0.9-0), zoo, TTR(>= 0.2), methods"
## questionr "R (>= 2.10)"

```



```

## r2d3 "R (>= 3.1.2)"
## R6 "R (>= 3.0)"
## randomForest "R (>= 3.2.2), stats"
## ranger "R (>= 3.1)"
## rappdirs "R (>= 2.14), methods"
## raster "methods, sp (>= 1.2-0), R (>= 3.0.0)"
## Rborist "Rcpp (>= 0.12.2), R(>= 3.1)"
## rcmdcheck NA
## RColorBrewer "R (>= 2.0.0)"
## Rcpp "R (>= 3.0.0)"
## RcppArmadillo "R (>= 3.3.0)"
## RcppEigen "R (>= 2.15.1)"
## RcppRoll "R (>= 2.15.1)"
## RCurl "R (>= 3.0.0), methods, bitops"
## readr "R (>= 3.0.2)"
## readxl NA
## recipes "R (>= 3.1), dplyr"
## rematch NA
## remotes "R (>= 3.0.0)"
## reprex "R (>= 3.1)"
## reshape2 "R (>= 3.1)"
## RJSONIO NA
## rlang "R (>= 3.1.0)"
## rmarkdown "R (>= 3.0)"
## robustbase "R (>= 3.1.0)"
## rpart "R (>= 2.15.0), graphics, stats, grDevices"
## rprojroot "R (>= 3.0.0)"
## Rsamtools "methods, GenomeInfoDb (>= 1.1.3), GenomicRanges (>= 1.31.8),\nBiostrings (>= 2
## rsconnect "R (>= 3.0.0)"
## RSNNS "R (>= 2.10.0), methods, Rcpp (>= 0.8.5)"
## RSQLite "R (>= 3.1.0)"
## rstudioapi NA
## rtracklayer "R (>= 3.3), methods, GenomicRanges (>= 1.31.8)"
## rvest "R (>= 3.0.1), xml2"
## S4Vectors "R (>= 3.3.0), methods, utils, stats, stats4, BiocGenerics (>=\n0.23.3)"
## scales "R (>= 3.1)"
## selectr "R (>= 3.0)"
## sessioninfo NA
## sfsmisc "R (>= 3.2.0)"
## shiny "R (>= 3.0.2), methods"
## snow "R (>= 2.13.1), utils"
## sourcetools "R (>= 3.0.2)"
## sp "R (>= 3.0.0), methods"
## sparklyr "R (>= 3.2)"
## SparseM "R (>= 2.15), methods"
## spatial "R (>= 3.0.0), graphics, stats, utils"
## spData "R (>= 3.3.0)"
## splines NA
## SQUAREM "R (>= 3.0)"
## stabs "R (>= 2.14.0), methods, stats, parallel"
## stats NA
## stats4 NA
## stringi "R (>= 2.14)"
## stringr "R (>= 3.1)"

```

```

## SummarizedExperiment "R (>= 3.2), methods, GenomicRanges (>= 1.33.6), Biobase,\nDelayedArray (>= 0.3
## survival "R (>= 2.13.0)"
## tcltk NA
## testthat "R (>= 3.1)"
## tibble "R (>= 3.1.0)"
## tidyr "R (>= 3.1)"
## tidyselect "R (>= 3.1)"
## tidyverse NA
## timeDate "R (>= 2.15.1), graphics, utils, stats, methods"
## tinytex NA
## tools NA
## tseries "R (>= 2.10.0)"
## TTR NA
## urca "R (>= 2.0.0), methods"
## uroot "R (>= 3.0.0), stats"
## usethis "R (>= 3.1)"
## utf8 "R (>= 2.10)"
## utils NA
## viridisLite "R (>= 2.10)"
## whisker NA
## withr "R (>= 3.0.2)"
## wsrf "parallel, R (>= 3.3.0), Rcpp (>= 0.10.2), stats"
## xfun NA
## XML "R (>= 2.13.0), methods, utils"
## xml2 "R (>= 3.1.0)"
## xopen "R (>= 3.1)"
## xtable "R (>= 2.10.0)"
## xts "zoo (>= 1.7-12)"
## XVector "R (>= 2.8.0), methods, BiocGenerics (>= 0.19.2), S4Vectors (>=\n0.19.15), IRan
## yaml NA
## zlibbioc NA
## zoo "R (>= 3.1.0), stats"
## Imports
## abind "methods, utils"
## annotate "Biobase, DBI, xtable, graphics, utils, stats, methods,\nBiocGenerics (>= 0.13.
## AnnotationDbi "DBI, RSQLite, S4Vectors (>= 0.9.25)"
## assertthat "tools"
## backports "utils"
## base NA
## base64enc NA
## BH NA
## bindr NA
## bindrcpp "bindr (>= 0.1.1), Rcpp (>= 0.12.16)"
## Biobase "methods"
## BiocGenerics "methods, utils, graphics, stats, parallel"
## BiocInstaller NA
## BiocManager "utils"
## BiocParallel "stats, utils, futile.logger, parallel, snow"
## BiocVersion NA
## biomaRt "utils, XML, RCurl, AnnotationDbi, progress, stringr, http"
## Biostrings "graphics, methods, stats, utils"
## bit NA
## bit64 NA
## bitops NA

```

```

## blob "methods, prettyunits"
## boot NA
## broom "backports, dplyr, generics (>= 0.0.2), methods, nlme, purrr,\nreshape2, stringr"
## callr "base64enc, processx (>= 3.2.0), R6, utils"
## caret "foreach, methods, plyr, ModelMetrics (>= 1.1.0), nlme,\nreshape2, stats, statsmodels"
## caTools "bitops"
## cellranger "rematch, tibble"
## class "MASS"
## classInt "grDevices, stats, graphics, e1071, class"
## cli "assertthat, crayon (>= 1.3.4), methods, utils"
## clipr "utils"
## clisymbols NA
## cluster "graphics, grDevices, stats, utils"
## codetools NA
## colorspace "graphics, grDevices"
## combinat NA
## compiler NA
## config "yaml (>= 2.1.13)"
## crayon "grDevices, methods, utils"
## curl NA
## CVST NA
## data.table "methods"
## datasets NA
## DBI NA
## dbplyr "assertthat (>= 0.2.0), DBI (>= 0.7), dplyr (>= 0.7.4), glue\n(>= 1.2.0), methods"
## ddalpha "Rcpp (>= 0.11.0)"
## DelayedArray "stats"
## DEoptimR "stats"
## desc "assertthat, utils, R6, crayon, rprojroot"
## devtools "callr, cli, digest, git2r (>= 0.23.0), httr (>= 0.4),\njsonlite, memoise (>= 1.3.0)"
## dichromat NA
## digest NA
## dimRed "magrittr, methods"
## dplyr "assertthat (>= 0.2.0), bindrcpp (>= 0.2.0.9000), glue (>= 1.1.1), magrittr (>= 2.0.0)"
## DRR "stats, methods"
## dslabs "ggplot2"
## e1071 "graphics, grDevices, class, stats, methods, utils"
## ellipsis NA
## evaluate "methods"
## fansi NA
## fastAdaboost "Rcpp, rpart"
## forcats "magrittr, rlang, tibble"
## foreach "codetools, utils, iterators"
## forecast "colorspace, fracdiff, ggplot2 (>= 2.2.1), graphics, lmtest,\nmagrittr, nnet, plotly"
## foreign "methods, utils, stats"
## forge "rlang (>= 0.3.1), magrittr"
## formatR NA
## Formula NA
## fracdiff NA
## fs "methods, Rcpp"
## futile.logger "utils, lambda.r (>= 1.1.0), futile.options"
## futile.options NA
## gam NA
## gbm "gridExtra, lattice, parallel, survival"

```

```

## genefilter      "S4Vectors (>= 0.9.42), AnnotationDbi, annotate, Biobase,\ngraphics, methods, s
## generics        "methods"
## GenomeInfoDb    "stats, stats4, utils, RCurl, GenomeInfoDbData"
## GenomeInfoDbData NA
## GenomicAlignments "methods, utils, stats, BiocGenerics, S4Vectors, IRanges,\nGenomicRanges, Biost
## GenomicFeatures  "methods, utils, stats, tools, DBI, RSQLite (>= 2.0), RCurl,\nXVector (>= 0.19.
## GenomicRanges    "utils, stats, XVector (>= 0.19.8)"
## geometry        NA
## ggplot2          "digest, grid, gtable (>= 0.1.1), lazyeval, MASS, mgcv, plyr\n(>= 1.7.1), reshap
## gh               "ini, jsonlite, httr"
## git2r            "graphics, utils"
## glue             "methods"
## gower            NA
## graphics         "grDevices"
## grDevices        NA
## grid             "grDevices, utils"
## gridExtra        "gtable, grid, grDevices, graphics, utils"
## gtable           "grid"
## haven            "forcats (>= 0.2.0), hms, Rcpp (>= 0.11.4), readr (>= 0.1.0),\ntibble"
## highr            NA
## HistData         NA
## hms              "methods, pkgconfig, rlang"
## htmltools        "utils, digest, Rcpp"
## htmlwidgets      "grDevices, htmltools (>= 0.3), jsonlite (>= 0.9.16), yaml"
## httpuv           "Rcpp (>= 0.11.0), utils, promises, later (>= 0.7.3)"
## httr             "jsonlite, mime, curl (>= 0.9.1), openssl (>= 0.8), R6"
## igraph           "graphics, grDevices, magrittr, Matrix, pkgconfig (>= 2.0.0),\nstats, utils"
## import           NA
## ini              NA
## inum             "stats, libcoin (>= 1.0-0)"
## ipred            "rpart (>= 3.1-8), MASS, survival, nnet, class, prodlim"
## IRanges          "stats4"
## iterators        NA
## jsonlite         NA
## kernlab          "methods, stats, grDevices, graphics"
## KernSmooth       NA
## kkn              "igraph (>= 1.0), Matrix, stats, graphics"
## klaR             "combinat, questionr, grDevices, stats, utils, graphics"
## knitr            "evaluate (>= 0.10), highr, markdown, stringr (>= 0.6), yaml,\nmethods, tools"
## labeling         NA
## labelled         "haven (>= 2.0.0), dplyr, stats"
## Lahman           "dplyr"
## lambda.r         "formatR"
## later            "Rcpp (>= 0.12.9), rlang"
## lattice          "grid, grDevices, graphics, stats, utils"
## lava             "grDevices, graphics, methods, numDeriv, stats, survival,\nSQUAREM, utils"
## lazyeval         NA
## libcoin          "stats, mvtnorm"
## lmtest           "graphics"
## lubridate        "stringr, Rcpp (>= 0.12.13),"
## magic            NA
## magrittr         NA
## markdown         "utils, mime (>= 0.3)"
## MASS             "methods"

```

```

## Matrix "methods, graphics, grid, stats, utils, lattice"
## matrixStats NA
## mboost "Matrix, survival, splines, lattice, nnls, quadprog, utils,\ngraphics, grDevices"
## memoise "digest (>= 0.6.3)"
## methods "utils, stats"
## mgcv "methods, stats, graphics, Matrix"
## mime "tools"
## miniUI "shiny (>= 0.13), htmltools (>= 0.3), utils"
## mlbench NA
## ModelMetrics "Rcpp, data.table"
## modelr "broom, dplyr, magrittr, purrr (>= 0.2.2), tibble, tidyr (>= 0.8.0), rlang (>= 0.2.0)"
## monmlp NA
## munsell "colorspace, methods"
## mvtnorm "stats, methods"
## naivebayes NA
## nlme "graphics, stats, utils, lattice"
## nnet NA
## nnls NA
## numDeriv NA
## odbc "DBI (>= 1.0.0), methods, Rcpp (>= 0.12.11), blob (>= 1.1.0),\nbit64, hms"
## openssl NA
## optimx "numDeriv"
## packrat "tools, utils"
## parallel "tools, compiler"
## partykit "grDevices, stats, utils, survival, Formula (>= 1.2-1), inum\n(>= 1.0-0), rpart"
## pdftools "Rcpp (>= 0.12.12)"
## pillar "cli (>= 1.0.0), crayon (>= 1.3.4), fansi, methods, rlang (>= 0.2.0), utf8 (>= 0.2.0)"
## pkgbuild "callr (>= 2.0.0), cli, crayon, desc, prettyunits, R6,\nprojroot, withr (>= 2.0.0)"
## pkgconfig "utils"
## pkgload "desc, methods, pkgbuild, rlang, rprojroot, rstudioapi, utils,\nwithr"
## PKI NA
## plogr NA
## pls "grDevices, graphics, methods, stats"
## plyr "Rcpp (>= 0.11.0)"
## praise NA
## prettyunits "magrittr, assertthat, methods"
## processx "ps, R6, utils"
## prodlim "Rcpp (>= 0.11.5), stats, graphics, survival, KernSmooth, lava"
## progress "hms, prettyunits, R6, crayon"
## promises "R6, Rcpp, later, rlang, stats, magrittr"
## ps "utils"
## purrr "magrittr (>= 1.5), rlang (>= 0.1), tibble"
## quadprog NA
## quantmod "curl"
## questionr "shiny (>= 1.0.5), miniUI, rstudioapi, highr, classInt,\nhtmltools, graphics, survival"
## r2d3 "htmlwidgets (>= 1.2), htmltools, jsonlite, rstudioapi"
## R6 NA
## randomForest NA
## ranger "Rcpp (>= 0.11.2), Matrix"
## rappdirs NA
## raster "Rcpp"
## Rborist NA
## rcmdcheck "callr (>= 2.0.0), cli, crayon, desc (>= 1.2.0), digest,\nnpkgbuild, prettyunits"
## RColorBrewer NA

```

```

## Rcpp "methods, utils"
## RcppArmadillo "Rcpp (>= 0.11.0), stats, utils, methods"
## RcppEigen "Matrix (>= 1.1-0), Rcpp (>= 0.11.0), stats, utils"
## RcppRoll "Rcpp"
## RCurl NA
## readr "Rcpp (>= 0.12.0.5), tibble, hms (>= 0.4.1), R6, clipr"
## readxl "cellranger, Rcpp (>= 0.12.12), tibble (>= 1.1)"
## recipes "generics, gower, ipred, lubridate, magrittr, Matrix, purrr (>=\n0.2.3), RcppRo
## rematch NA
## remotes "methods, utils"
## reprex "callr (>= 2.0.0), clipr (>= 0.4.0), fs, rlang, rmarkdown,\nntools, utils, whisk
## reshape2 "plyr (>= 1.8.1), Rcpp, stringr"
## RJSONIO "methods"
## rlang NA
## rmarkdown "tools, utils, knitr (>= 1.18), yaml (>= 2.1.5), htmltools (>=\n0.3.5), evaluat
## robustbase "stats, graphics, utils, methods, DEoptimR"
## rpart NA
## rprojroot "backports"
## Rsamtools "utils, BiocGenerics (>= 0.25.1), S4Vectors (>= 0.17.25),\nIRanges (>= 2.13.12)
## rsconnect "openssl, RCurl, jsonlite, packrat (>= 0.4.8-1), yaml (>=\n2.1.5), rstudioapi (
## RSNNS NA
## RSQLite "bit64, blob (>= 1.1.1), DBI (>= 1.0.0), memoise, methods,\nnpkgconfig, Rcpp (>=
## rstudioapi NA
## rtracklayer "XML (>= 1.98-0), BiocGenerics (>= 0.25.1), S4Vectors (>=\n0.19.22), IRanges (>
## rvest "httr (>= 0.5), selectr, magrittr"
## S4Vectors NA
## scales "labeling, munsell (>= 0.5), R6, RColorBrewer, Rcpp,\nviridisLite"
## selectr "methods, stringr, R6"
## sessioninfo "cli, tools, utils, withr"
## sfsmisc "grDevices, methods, utils, stats"
## shiny "utils, grDevices, httpuv (>= 1.4.4), mime (>= 0.3), jsonlite\n(>= 0.9.16), xtal
## snow NA
## sourcetools NA
## sp "utils, stats, graphics, grDevices, lattice, grid"
## sparklyr "assertthat, base64enc, config (>= 0.2), DBI (>= 0.6-1), dplyr\n(>= 0.7.2), dbplyr
## SparseM "graphics, stats, utils"
## spatial NA
## spData NA
## splines "graphics, stats"
## SQUAREM NA
## stabs "graphics, grDevices, utils"
## stats "utils, grDevices, graphics"
## stats4 "graphics, methods, stats"
## stringi "tools, utils, stats"
## stringr "glue (>= 1.2.0), magrittr, stringi (>= 1.1.7)"
## SummarizedExperiment "utils, stats, tools, Matrix, BiocGenerics (>= 0.15.3),\nS4Vectors (>= 0.17.25)
## survival "graphics, Matrix, methods, splines, stats, utils"
## tcltk "utils"
## testthat "cli, crayon, digest, magrittr, methods, praise, R6 (>= 2.2.0),\nrlang, withr (
## tibble "cli, crayon, methods, pillar (>= 1.1.0), rlang, utils"
## tidyr "dplyr (>= 0.7.0), glue, magrittr, purrr, Rcpp, rlang, stringi,\ntibble, tidyse
## tidyselect "glue (>= 1.3.0), purrr, rlang (>= 0.2.2), Rcpp (>= 0.12.0)"
## tidyverse "broom (>= 0.4.2), cli (>= 1.0.0), crayon (>= 1.3.4), dplyr (>=\n0.7.4), dbplyr
## timeDate NA

```

```

## tinytex          "xfun (>= 0.3)"
## tools            NA
## tseries          "graphics, stats, utils, quadprog, zoo, quantmod (>= 0.4-9)"
## TTR              "xts (>= 0.10-0), zoo, curl"
## urca             "nlme, graphics, stats"
## uroot            NA
## usethis           "clipr (>= 0.3.0), clisymbols, crayon, curl (>= 2.7), desc, fs\n(>= 1.2.0), gh,
## utf8             NA
## utils            NA
## viridisLite      NA
## whisker          NA
## withr            "stats, graphics, grDevices"
## wsrf             NA
## xfun             "tools"
## XML              NA
## xml2             "Rcpp"
## xopen            "processx"
## xtable           "stats, utils"
## xts              "methods"
## XVector          "methods, utils, zlibbioc, BiocGenerics, S4Vectors, IRanges"
## yaml            NA
## zlibbioc         NA
## zoo              "utils, graphics, grDevices, lattice (>= 0.20-27)"
##                 LinkingTo
## abind            NA
## annotate          NA
## AnnotationDbi     NA
## assertthat        NA
## backports         NA
## base             NA
## base64enc         NA
## BH               NA
## bindr            NA
## bindrcpp          "plogr, Rcpp"
## Biobase           NA
## BiocGenerics      NA
## BiocInstaller     NA
## BiocManager       NA
## BiocParallel      "BH"
## BiocVersion       NA
## biomaRt           NA
## Biostrings        "S4Vectors, IRanges, XVector (>= 0.21.4)"
## bit              NA
## bit64            NA
## bitops           NA
## blob             NA
## boot             NA
## broom            NA
## callr            NA
## caret            NA
## caTools          NA
## cellranger       NA
## class            NA
## classInt         NA

```

## cli	NA
## clipr	NA
## clisymbols	NA
## cluster	NA
## codetools	NA
## colorspace	NA
## combinat	NA
## compiler	NA
## config	NA
## crayon	NA
## curl	NA
## CVST	NA
## data.table	NA
## datasets	NA
## DBI	NA
## dbplyr	NA
## ddalpha	"BH, Rcpp"
## DelayedArray	"S4Vectors"
## DEoptimR	NA
## desc	NA
## devtools	NA
## dichromat	NA
## digest	NA
## dimRed	NA
## dplyr	"BH (>= 1.58.0-1), bindrcpp (>= 0.2.0.9000), plogr (>=\n0.1.10), Rcpp (>= 0.12.0)"
## DRR	NA
## dslabs	NA
## e1071	NA
## ellipsis	NA
## evaluate	NA
## fansi	NA
## fastAdaboost	"Rcpp (>= 0.12.0)"
## forcats	NA
## foreach	NA
## forecast	"Rcpp (>= 0.11.0), RcppArmadillo (>= 0.2.35)"
## foreign	NA
## forge	NA
## formatR	NA
## Formula	NA
## fracdiff	NA
## fs	"Rcpp"
## futile.logger	NA
## futile.options	NA
## gam	NA
## gbm	NA
## genefilter	NA
## generics	NA
## GenomeInfoDb	NA
## GenomeInfoDbData	NA
## GenomicAlignments	"S4Vectors, IRanges"
## GenomicFeatures	NA
## GenomicRanges	"S4Vectors, IRanges"
## geometry	NA
## ggplot2	NA

## gh	NA
## git2r	NA
## glue	NA
## gower	NA
## graphics	NA
## grDevices	NA
## grid	NA
## gridExtra	NA
## gtable	NA
## haven	"Rcpp"
## highr	NA
## HistData	NA
## hms	NA
## htmltools	"Rcpp"
## htmlwidgets	NA
## httpuv	"Rcpp, BH, later"
## httr	NA
## igraph	NA
## import	NA
## ini	NA
## inum	NA
## ipred	NA
## IRanges	"S4Vectors"
## iterators	NA
## jsonlite	NA
## kernlab	NA
## KernSmooth	NA
## kkn	NA
## klaR	NA
## knitr	NA
## labeling	NA
## labelled	NA
## Lahman	NA
## lambda.r	NA
## later	"Rcpp, BH"
## lattice	NA
## lava	NA
## lazyeval	NA
## libcoin	"mvtnorm"
## lmttest	NA
## lubridate	"Rcpp,"
## magic	NA
## magrittr	NA
## markdown	NA
## MASS	NA
## Matrix	NA
## matrixStats	NA
## mboost	NA
## memoise	NA
## methods	NA
## mgcv	NA
## mime	NA
## miniUI	NA
## mlbench	NA

## ModelMetrics	"Rcpp"
## modelr	NA
## monmlp	NA
## munsell	NA
## mvtnorm	NA
## naivebayes	NA
## nlme	NA
## nnet	NA
## nnls	NA
## numDeriv	NA
## odbc	"Rcpp, BH"
## openssl	NA
## optimx	NA
## packrat	NA
## parallel	NA
## partykit	NA
## pdftools	"Rcpp"
## pillar	NA
## pkgbuild	NA
## pkgconfig	NA
## pkgload	NA
## PKI	NA
## plogr	NA
## pls	NA
## plyr	"Rcpp"
## praise	NA
## prettyunits	NA
## processx	NA
## prodlim	"Rcpp"
## progress	NA
## promises	"later, Rcpp"
## ps	NA
## purrr	NA
## quadprog	NA
## quantmod	NA
## questionr	NA
## r2d3	NA
## R6	NA
## randomForest	NA
## ranger	"Rcpp, RcppEigen"
## rappdirs	NA
## raster	"Rcpp"
## Rborist	"Rcpp, RcppArmadillo"
## rcmdcheck	NA
## RColorBrewer	NA
## Rcpp	NA
## RcppArmadillo	"Rcpp"
## RcppEigen	"Rcpp"
## RcppRoll	"Rcpp"
## RCurl	NA
## readr	"Rcpp, BH"
## readxl	"Rcpp"
## recipes	NA
## rematch	NA

## remotes	NA
## reprex	NA
## reshape2	"Rcpp"
## RJSONIO	NA
## rlang	NA
## rmarkdown	NA
## robustbase	NA
## rpart	NA
## rprojroot	NA
## Rsamtools	"S4Vectors, IRanges, XVector, Biostrings"
## rsconnect	NA
## RSNNS	"Rcpp"
## RSQLite	"BH, plogr (>= 0.2.0), Rcpp"
## rstudioapi	NA
## rtracklayer	"S4Vectors, IRanges, XVector"
## rvest	NA
## S4Vectors	NA
## scales	"Rcpp"
## selectr	NA
## sessioninfo	NA
## sfsmisc	NA
## shiny	NA
## snow	NA
## sourcetools	NA
## sp	NA
## sparklyr	NA
## SparseM	NA
## spatial	NA
## spData	NA
## splines	NA
## SQUAREM	NA
## stabs	NA
## stats	NA
## stats4	NA
## stringi	NA
## stringr	NA
## SummarizedExperiment	NA
## survival	NA
## tcltk	NA
## testthat	NA
## tibble	NA
## tidyr	"Rcpp"
## tidyselect	"Rcpp (>= 0.12.0),"
## tidyverse	NA
## timeDate	NA
## tinytex	NA
## tools	NA
## tseries	NA
## TTR	"xts"
## urca	NA
## uroot	NA
## usethis	NA
## utf8	NA
## utils	NA

```

## viridisLite      NA
## whisker          NA
## withr            NA
## wsrf             "Rcpp"
## xfun             NA
## XML              NA
## xml2             "Rcpp (>= 0.12.12)"
## xopen            NA
## xtable           NA
## xts              "zoo"
## XVector          "S4Vectors, IRanges"
## yaml            NA
## zlibbioc         NA
## zoo              NA
##                 Suggests
## abind            NA
## annotate         "hgu95av2.db, genefilter, Biostrings (>= 2.25.10), IRanges,\nrae230a.db, rae230a.db"
## AnnotationDbi    "hgu95av2.db, GO.db, org.Sc.sgd.db, org.At.tair.db, KEGG.db,\nRUnit, TxDb.Hsapiens.UCEPChromASSEMBLY"
## assertthat       "testthat"
## backports        NA
## base             "methods"
## base64enc        NA
## BH               NA
## bindr            "testthat"
## bindrcpp         "testthat"
## Biobase          "tools, tkWidgets, ALL, RUnit, golubEssets"
## BiocGenerics     "Biobase, S4Vectors, IRanges, GenomicRanges, Rsamtools,\nAnnotationDbi, oligo"
## BiocInstaller    "remotes, RUnit, BiocGenerics"
## BiocManager      "BiocStyle, BiocVersion, remotes, testthat, knitr, withr"
## BiocParallel     "BiocGenerics, tools, foreach, BatchJobs, BBmisc, doParallel,\nRmpi, GenomicRanges"
## BiocVersion      NA
## biomaRt          "annotate, BiocStyle, knitr, rmarkdown, testthat"
## Biostrings       "BSgenome (>= 1.13.14), BSgenome.Celegans.UCSC.ce2 (>=\n1.3.11), BSgenome.Dmelanogaster.UCSC.dm3"
## bit              NA
## bit64            NA
## bitops           NA
## blob             "covr, pillar (>= 1.2.1), testthat"
## boot             "MASS, survival"
## broom            "AER, akima, AUC, bbmle, betareg, biglm, binGroup, boot, brms,\nmbterm, car, caracas"
## callr            "covr, crayon, ps, testthat, withr"
## caret            "BradleyTerry2, e1071, earth (>= 2.2-3), fastICA, gam (>=\n1.15), ipred, kernlab"
## caTools          "MASS, rpart"
## cellranger       "covr, testthat (>= 1.0.0), knitr, rmarkdown"
## class            NA
## classInt         NA
## cli              "covr, fansi, mockery, testthat, webshot, withr"
## clipr            "rstudioapi (>= 0.5), testthat, covr"
## clisymbols       "testthat"
## cluster          "MASS, Matrix"
## codetools        NA
## colorspace       "datasets, stats, utils, KernSmooth, MASS, kernlab, mvtnorm,\nvcd, dichromat, tcltk"
## combinat         NA
## compiler         NA
## config           "testthat, knitr"

```

```

## crayon "mockery, rstudioapi, testthat, withr"
## curl "spelling, testthat (>= 1.0.0), knitr, jsonlite, rmarkdown,\nmagrittr, httpuv, v
## CVST NA
## data.table "bit64, curl, R.utils, knitr, xts, nanotime, zoo"
## datasets NA
## DBI "blob, covr, hms, knitr, magrittr, rprojroot, rmarkdown,\nRSQLite (>= 1.1-2), t
## dbplyr "bit64, covr, knitr, Lahman (>= 5.0.0), nycflights13 (>=\n0.2.2), rmarkdown, RM
## ddalpha NA
## DelayedArray "Matrix, HDF5Array, genefilter, SummarizedExperiment, airway,\npryr, DelayedMat
## DEoptimR NA
## desc "covr, testthat, whoami, withr"
## devtools "BiocInstaller, BiocManager, bitops, covr (>= 3.2.0), crayon,\nncurl (>= 0.9), e
## dichromat NA
## digest "knitr, rmarkdown"
## dimRed "NMF, MASS, Matrix, RANN, RSpectra, Rtsne, cccd, coRanking,\nndiffusionMap, ener
## dplyr "bit64 (>= 0.9.7), callr, covr (>= 3.0.1), DBI (>= 0.7.14),\nndbplyr (>= 1.2.0),
## DRR "knitr, rmarkdown"
## dslabs NA
## e1071 "cluster, mlbench, nnet, randomForest, rpart, SparseM, xtable,\nMatrix, MASS"
## ellipsis "covr, testthat"
## evaluate "testthat, lattice, ggplot2"
## fansi "unitizer, knitr, rmarkdown"
## fastAdaboost "testthat, knitr, MASS"
## forcats "covr, ggplot2, testthat"
## foreach "randomForest"
## forecast "expsmooth, knitr, rmarkdown, rticles, testthat"
## foreign NA
## forge "testthat, covr"
## formatR "codetools, shiny, testit, rmarkdown, knitr"
## Formula NA
## fracdiff "longmemo, urca"
## fs "testthat, covr, pillar (>= 1.0.0), crayon, withr"
## futile.logger "testthat, jsonlite"
## futile.options NA
## gam "akima"
## gbm "knitr, pdp, RUnit, splines, viridis"
## genefilter "class, hgu95av2.db, tkWidgets, ALL, ROC, DESeq, pasilla,\nBiocStyle, knitr"
## generics "covr, pkgload, testthat, tibble"
## GenomeInfoDb "GenomicRanges, Rsamtools, GenomicAlignments, BSgenome,\nGenomicFeatures, BSgenome
## GenomeInfoDbData NA
## GenomicAlignments "ShortRead, rtracklayer, BSgenome, GenomicFeatures,\nRNAseqData.HNRNPC.bam.chr1
## GenomicFeatures "RMariaDB, org.Mm.eg.db, org.Hs.eg.db, BSgenome,\nBSgenome.Hsapiens.UCSC.hg19 (
## GenomicRanges "Matrix, Biobase, AnnotationDbi, annotate, Biostrings (>=\n2.25.3), SummarizedE
## geometry "testthat, rgl, R.matlab, tripack"
## ggplot2 "covr, dplyr, ggplot2movies, hexbin, Hmisc, lattice, mapproj,\nmaps, maptools, m
## gh "covr, pingr, testthat"
## git2r "getPass"
## glue "testthat, covr, magrittr, crayon, knitr, rmarkdown, DBI,\nRSQLite, R.utils, fo
## gower "testthat, knitr, rmarkdown"
## graphics NA
## grDevices "KernSmooth"
## grid "lattice"
## gridExtra "ggplot2, egg, lattice, knitr, testthat"
## gtable "testthat, covr"

```

```

## haven "covr, fs, knitr, rmarkdown, testthat"
## highr "knitr, testit"
## HistData "gtools, KernSmooth, maps, ggplot2, scales, proto, grid,\nreshape, plyr, lattice"
## hms "crayon, lubridate, pillar (>= 1.1.0), testthat"
## htmltools "markdown, testthat"
## htmlwidgets "knitr (>= 1.8)"
## httpuv "testthat, callr"
## httr "httpuv, jpeg, knitr, png, testthat (>= 0.8.0), readr, xml2,\nrmarkdown, covr"
## igraph "ape, digest, graph, igraphdata, rgl, scales, stats4, tcltk,\ntestthat"
## import "knitr"
## ini "testthat"
## inum NA
## ipred "mvtnorm, mlbench, TH.data"
## IRanges "XVector, GenomicRanges, Rsamtools, GenomicAlignments,\nGenomicFeatures, BSgenome"
## iterators "RUnit, foreach"
## jsonlite "httr, curl, plyr, testthat, knitr, rmarkdown, R.rsp, sp"
## kernlab NA
## KernSmooth "MASS"
## kknn NA
## klaR "scatterplot3d (>= 0.3-22), som, mlbench, rpart, e1071"
## knitr "formatR, testit, digest, rgl (>= 0.95.1201), codetools,\nrmarkdown, htmlwidgets"
## labeling NA
## labelled "testthat, knitr, rmarkdown, questionr"
## Lahman "lattice, ggplot2, googleVis, data.table, vcd, reshape2,\ntidyr, zipcode"
## lambda.r "testit"
## later "knitr, rmarkdown, testthat"
## lattice "KernSmooth, MASS, latticeExtra"
## lava "KernSmooth, Matrix, Rgraphviz, ascii, data.table, ellipse,\nfields, foreach, g"
## lazyeval "knitr, rmarkdown (>= 0.2.65), testthat, covr"
## libcoin "coin"
## lmtest "car, strucchange, sandwich, dynlm, stats4, survival, AER"
## lubridate "testthat, knitr, covr"
## magic NA
## magrittr "testthat, knitr"
## markdown "knitr, RCurl"
## MASS "lattice, nlme, nnet, survival"
## Matrix "expm, MASS"
## matrixStats "base64enc, ggplot2, knitr, microbenchmark, R.devices, R.rsp"
## mboost "TH.data, MASS, fields, BayesX, gbm, mlbench, RColorBrewer,\nrpart (>= 4.0-3), r"
## memoise "testthat, aws.s3, httr, covr"
## methods "codetools"
## mgcv "splines, parallel, survival, MASS"
## mime NA
## miniUI NA
## mlbench "lattice"
## ModelMetrics "testthat"
## modelr "compiler, covr, ggplot2, testthat"
## monmlp NA
## munsell "ggplot2, testthat"
## mvtnorm NA
## naivebayes NA
## nlme "Hmisc, MASS"
## nnet "MASS"
## nnls NA

```

```

## numDeriv      NA
## odbc          "tibble, DBItest, testthat, covr, magrittr"
## openssl       "testthat, digest, knitr, rmarkdown, jsonlite, jose"
## optimx        "knitr, rmarkdown, setRNG, BB, ucminf, minqa, dfoptim,\nlbfgsb3, lbfgs, subplex"
## packrat       "testthat (>= 0.7), devtools, httr, knitr, rmarkdown"
## parallel      "methods"
## partykit      "XML, pmml, rJava, sandwich, strucchange, vcd, AER, mlbench,\nTH.data (>= 1.0-3"
## pdftools      "jpeg, png, webp, testthat"
## pillar        "knitr (>= 1.19), lubridate, testthat (>= 2.0.0), withr"
## pkgbuild      "Rcpp, testthat, covr"
## pkgconfig     "covr, testthat, disposables (>= 1.0.3)"
## pkgload       "bitops, covr, Rcpp, testthat"
## PKI           NA
## plogr         "Rcpp"
## pls           "MASS, parallel, Rmpi, testthat, RUnit"
## plyr          "abind, testthat, tcltk, foreach, doParallel, itertools,\niterators, covr"
## praise        "testthat"
## prettyunits   "testthat"
## processx      "callr, covr, crayon, debugme, parallel, testthat, withr"
## prodlim       NA
## progress      "Rcpp, testthat, withr"
## promises      "testthat, future, knitr, rmarkdown"
## ps            "callr, covr, curl, pingr, processx (>= 3.1.0), R6, rlang,\ntestthat, tibble"
## purrr         "covr, dplyr (>= 0.7.5), knitr, rmarkdown, testthat"
## quadprog      NA
## quantmod      "DBI,RMySQL,SQLite,timeSeries,XML,downloader,jsonlite(>= 1.1)"
## questionr     "memisc, testthat, roxygen2, dplyr, tidyr, janitor, forcats,\nknitr"
## r2d3          "knitr, rmarkdown, shiny, shinytest, testthat, webshot"
## R6            "knitr, microbenchmark, pryr, testthat, ggplot2, scales"
## randomForest  "RColorBrewer, MASS"
## ranger        "survival, testthat"
## rappdirs      "testthat, roxygen2"
## raster        "rgdal (>= 0.9-1), rgeos (>= 0.3-8), ncdf4, igraph, tcltk,\nparallel, rasterVis"
## Rborist        "testthat, knitr, rmarkdown"
## rcmdcheck     "covr, knitr, mockery, rmarkdown, testthat"
## RColorBrewer  NA
## Rcpp          "RUnit, inline, rbenchmark, knitr, rmarkdown, pinp, pkgKitten\n(>= 0.1.2)"
## RcppArmadillo "RUnit, Matrix, pkgKitten, reticulate, rmarkdown, knitr, pinp,\nslam"
## RcppEigen     "inline, RUnit, pkgKitten, microbenchmark"
## RcppRoll      "zoo, testthat"
## RCurl         "Rcompression, XML"
## readr         "curl, testthat, knitr, rmarkdown, stringi, covr, spelling"
## readxl        "covr, knitr, rmarkdown, rprojroot (>= 1.1), testthat"
## recipes       "covr, ddalpaha, dimRed (>= 0.2.2), fastICA, ggplot2, igraph,\nkernlab, knitr, NA"
## rematch      "covr, testthat"
## remotes       "curl, covr, git2r (>= 0.23.0), knitr, mockery, pkgbuild (>=\n1.0.1), pingr, rm"
## reprex        "covr, devtools, fortunes, knitr, miniUI, rprojroot,\nrstudioapi, shiny, styler"
## reshape2     "covr, lattice, testthat (>= 0.8.0)"
## RJSONIO       NA
## rlang         "crayon, magrittr, methods, pillar, testthat (>= 2.0.0), covr"
## rmarkdown     "shiny (>= 0.11), tufte, testthat, digest, dygraphs, tibble"
## robustbase    "grid, MASS, lattice, boot, cluster, Matrix, robust,\nfit.models, MPV, xtable, g"
## rpart         "survival"
## rprojroot     "testthat, mockr, knitr, withr, rmarkdown"

```

```

## Rsamtools "GenomicAlignments, ShortRead (>= 1.19.10), GenomicFeatures,\nTxDb.Dmelanogaster"
## rsconnect "knitr, testthat, rmarkdown (>= 1.1), plumber (>= 0.3.2),\nreticulate, shiny, s
## RSNNs "scatterplot3d,NeuralNetTools"
## RSQLite "DBItest, knitr, rmarkdown, testthat"
## rstudioapi "testthat, knitr, rmarkdown"
## rtracklayer "BSgenome (>= 1.33.4), humanStemCell, microRNA (>= 1.1.1),\ngenefilter, limma, c
## rvest "testthat, knitr, png, stringi (>= 0.3.1), rmarkdown, covr"
## S4Vectors "IRanges, GenomicRanges, SummarizedExperiment, Matrix,\nDelayedArray, ShortRead
## scales "dichromat, bit64, covr, hms, testthat (>= 2.0)"
## selectr "testthat, XML, xml2"
## sessioninfo "callr, covr, mockery, testthat"
## sfsmisc "datasets, tcltk, cluster, lattice, MASS, Matrix, nlme, lokern"
## shiny "datasets, Cairo (>= 1.5-5), testthat, knitr (>= 1.6),\nmarkdown, rmarkdown, gg
## snow "Rmpi,rlecuyer,nws"
## sourcetools "testthat"
## sp "RColorBrewer, rgdal (>= 0.8-7), rgeos (>= 0.3-13), gstat,\nmaptools, deldir"
## sparklyr "broom, ggplot2, glmnet, janeaustenr, Lahman, mlbench, nnet,\nnycflights13, R6,
## SparseM NA
## spatial "MASS"
## spData "foreign, maptools, raster, rgdal, sf, sp, spDataLarge (>=\n0.2.7.3), spdep"
## splines "Matrix, methods"
## SQUAREM "setRNG"
## stabs "glmnet, lars, mboost (> 2.3-0), gamboostLSS (>= 1.2-0), QUIC,\nTH.data, hdi, t
## stats "MASS, Matrix, SuppDists, methods, stats4"
## stats4 NA
## stringi NA
## stringr "covr, htmltools, htmlwidgets, knitr, rmarkdown, testthat"
## SummarizedExperiment "annotate, AnnotationDbi, hgu95av2.db, GenomicFeatures,\nTxDb.Hsapiens.UCSC.hg1
## survival NA
## tcltk NA
## testthat "covr, devtools, knitr, rmarkdown, usethis, xml2"
## tibble "covr, dplyr, import, knitr (>= 1.5.32), microbenchmark,\nmockr, nycflights13,
## tidyr "covr, gapminder, knitr, rmarkdown, testthat"
## tidyselect "covr, dplyr, testthat"
## tidyverse "feather (>= 0.3.1), knitr (>= 1.17), rmarkdown (>= 1.7.4)"
## timeDate "date, RUnit"
## tinytex "testit, rstudioapi"
## tools "codetools, methods, xml2, curl"
## tseries NA
## TTR "RUnit"
## urca NA
## uroot NA
## usethis "covr, knitr, magick, rmarkdown, roxygen2, spelling (>= 1.2),\nstyler (>= 1.0.2)
## utf8 "knitr, rmarkdown, testthat"
## utils "methods, xml2, commonmark"
## viridisLite "hexbin (>= 1.27.0), ggplot2 (>= 1.0.1), testthat, covr"
## whisker "markdown"
## withr "testthat, covr, lattice, DBI, RSQLite, methods, knitr,\nrmmarkdown"
## wsrfr "knitr (>= 1.5), party (>= 1.0.7), randomForest (>= 4.6.7),\nrattle.data (>= 1.0
## xfun "testit, parallel, rstudioapi, tinytex, mime, markdown, knitr,\nhtmltools, base
## XML "bitops, RCurl"
## xml2 "testthat, curl, covr, knitr, rmarkdown, magrittr, httr"
## xopen "ps, testthat"
## xtable "knitr, spdep, splm, sphet, plm, zoo, survival"

```



```

## xts "timeSeries, timeDate, tseries, chron, fts, tis, RUnit"
## XVector "Biostrings, drosophila2probe, RUnit"
## yaml "RUnit"
## zlibbioc NA
## zoo "coda, chron, DAAG, fts, ggplot2, mondate, scales,\nstrucchange, timeDate, time"
## Enhances
## abind NA
## annotate NA
## AnnotationDbi NA
## assertthat NA
## backports NA
## base NA
## base64enc "png"
## BH NA
## bindr NA
## bindrcpp NA
## Biobase NA
## BiocGenerics NA
## BiocInstaller NA
## BiocManager NA
## BiocParallel NA
## BiocVersion NA
## biomaRt NA
## Biostrings "Rmpi"
## bit NA
## bit64 NA
## bitops NA
## blob NA
## boot NA
## broom NA
## callr NA
## caret NA
## caTools NA
## cellranger NA
## class NA
## classInt NA
## cli NA
## clipr NA
## clisymbols NA
## cluster NA
## codetools NA
## colorspace NA
## combinat NA
## compiler NA
## config NA
## crayon NA
## curl NA
## CVST NA
## data.table NA
## datasets NA
## DBI NA
## dbplyr NA
## ddalpna NA
## DelayedArray NA

```

```

## DEoptimR          "robustbase"
## desc              NA
## devtools          NA
## dichromat         NA
## digest            NA
## dimRed            NA
## dplyr             NA
## DRR               NA
## dslabs            NA
## e1071             NA
## ellipsis          NA
## evaluate          NA
## fansi            NA
## fastAdaboost      NA
## forcats           NA
## foreach           "compiler, doMC, RUnit, doParallel"
## forecast          NA
## foreign           NA
## forge             NA
## formatR           NA
## Formula           NA
## fracdiff          NA
## fs                NA
## futile.logger     NA
## futile.options    NA
## gam               NA
## gbm               NA
## genefilter        NA
## generics          NA
## GenomeInfoDb      NA
## GenomeInfoDbData  NA
## GenomicAlignments NA
## GenomicFeatures   NA
## GenomicRanges     NA
## geometry          NA
## ggplot2           "sp"
## gh                NA
## git2r             NA
## glue              NA
## gower             NA
## graphics          NA
## grDevices         NA
## grid              NA
## gridExtra         NA
## gtable            NA
## haven             NA
## highr             NA
## HistData          NA
## hms               NA
## htmltools         "knitr"
## htmlwidgets       "shiny (>= 1.1)"
## httpuv            NA
## httr              NA
## igraph            NA

```

## import	NA
## ini	NA
## inum	NA
## ipred	NA
## IRanges	NA
## iterators	NA
## jsonlite	NA
## kernlab	NA
## KernSmooth	NA
## kkn	NA
## klaR	NA
## knitr	NA
## labeling	NA
## labelled	"memisc"
## Lahman	NA
## lambda.r	NA
## later	NA
## lattice	"chron"
## lava	NA
## lazyeval	NA
## libcoin	NA
## lmtest	NA
## lubridate	"chron, fts, timeSeries, timeDate, tis, tseries, xts, zoo"
## magic	NA
## magrittr	NA
## markdown	NA
## MASS	NA
## Matrix	"MatrixModels, graph, SparseM, sfsmisc"
## matrixStats	NA
## mboost	NA
## memoise	NA
## methods	NA
## mgcv	NA
## mime	NA
## miniUI	NA
## mlbench	NA
## ModelMetrics	NA
## modelr	NA
## monmlp	NA
## munsell	NA
## mvtnorm	NA
## naivebayes	NA
## nlme	NA
## nnet	NA
## nnls	NA
## numDeriv	NA
## odbc	NA
## openssl	NA
## optimx	NA
## packrat	NA
## parallel	"snow, nws, Rmpi"
## partykit	NA
## pdftools	NA
## pillar	NA

## pkgbuild	NA
## pkgconfig	NA
## pkgload	NA
## PKI	"gmp"
## plogr	NA
## pls	NA
## plyr	NA
## praise	NA
## prettyunits	NA
## processx	NA
## prodlim	NA
## progress	NA
## promises	NA
## ps	NA
## purrr	NA
## quadprog	NA
## quantmod	NA
## questionr	NA
## r2d3	NA
## R6	NA
## randomForest	NA
## ranger	NA
## rappdirs	NA
## raster	NA
## Rborist	"forestFloor"
## rcmdcheck	NA
## RColorBrewer	NA
## Rcpp	NA
## RcppArmadillo	NA
## RcppEigen	NA
## RcppRoll	NA
## RCurl	NA
## readr	NA
## readxl	NA
## recipes	NA
## rematch	NA
## remotes	NA
## reprex	NA
## reshape2	NA
## RJSONIO	NA
## rlang	NA
## rmarkdown	NA
## robustbase	NA
## rpart	NA
## rprojroot	NA
## Rsamtools	NA
## rsconnect	NA
## RSNNS	NA
## RSQLite	NA
## rstudioapi	NA
## rtracklayer	NA
## rvest	NA
## S4Vectors	NA
## scales	NA

## selectr	NA
## sessioninfo	NA
## sfsmisc	"mgcv, rpart, nor1mix, polycor, sm, tikzDevice"
## shiny	NA
## snow	NA
## sourcetools	NA
## sp	NA
## sparklyr	NA
## SparseM	NA
## spatial	NA
## spData	NA
## splines	NA
## SQUAREM	NA
## stabs	NA
## stats	NA
## stats4	NA
## stringi	NA
## stringr	NA
## SummarizedExperiment	NA
## survival	NA
## tcltk	NA
## testthat	NA
## tibble	NA
## tidyr	NA
## tidyselect	NA
## tidyverse	NA
## timeDate	NA
## tinytex	NA
## tools	NA
## tseries	NA
## TTR	"quantmod"
## urca	NA
## uroot	NA
## usethis	NA
## utf8	NA
## utils	NA
## viridisLite	NA
## whisker	NA
## withr	NA
## wsrfr	NA
## xfun	NA
## XML	NA
## xml2	NA
## xopen	NA
## xtable	NA
## xts	NA
## XVector	NA
## yaml	NA
## zlibbioc	NA
## zoo	NA
##	License
## abind	"LGPL (>= 2)"
## annotate	"Artistic-2.0"
## AnnotationDbi	"Artistic-2.0"

## assertthat	"GPL-3"
## backports	"GPL-2"
## base	"Part of R 3.5.1"
## base64enc	"GPL-2 GPL-3"
## BH	"BSL-1.0"
## bindr	"MIT + file LICENSE"
## bindrcpp	"MIT + file LICENSE"
## Biobase	"Artistic-2.0"
## BiocGenerics	"Artistic-2.0"
## BiocInstaller	"Artistic-2.0"
## BiocManager	"Artistic-2.0"
## BiocParallel	"GPL-2 GPL-3"
## BiocVersion	"Artistic-2.0"
## biomaRt	"Artistic-2.0"
## Biostrings	"Artistic-2.0"
## bit	"GPL-2"
## bit64	"GPL-2"
## bitops	"GPL (>= 2)"
## blob	"GPL-3"
## boot	"Unlimited"
## broom	"MIT + file LICENSE"
## callr	"MIT + file LICENSE"
## caret	"GPL (>= 2)"
## caTools	"GPL-3"
## cellranger	"MIT + file LICENSE"
## class	"GPL-2 GPL-3"
## classInt	"GPL (>= 2)"
## cli	"MIT + file LICENSE"
## clipr	"GPL-3"
## clisymbols	"MIT + file LICENSE"
## cluster	"GPL (>= 2)"
## codetools	"GPL"
## colorspace	"BSD_3_clause + file LICENSE"
## combinat	"GPL-2"
## compiler	"Part of R 3.5.1"
## config	"GPL-3"
## crayon	"MIT + file LICENSE"
## curl	"MIT + file LICENSE"
## CVST	"GPL (>= 2.0)"
## data.table	"MPL-2.0 file LICENSE"
## datasets	"Part of R 3.5.1"
## DBI	"LGPL (>= 2)"
## dbplyr	"MIT + file LICENSE"
## ddalpha	"GPL-2"
## DelayedArray	"Artistic-2.0"
## DEoptimR	"GPL (>= 2)"
## desc	"MIT + file LICENSE"
## devtools	"GPL (>= 2)"
## dichromat	"GPL-2"
## digest	"GPL (>= 2)"
## dimRed	"GPL-3 file LICENSE"
## dplyr	"MIT + file LICENSE"
## DRR	"GPL-3 file LICENSE"
## dslabs	"Artistic-2.0"

## e1071	"GPL-2"
## ellipsis	"GPL-3"
## evaluate	"MIT + file LICENSE"
## fansi	"GPL (>= 2)"
## fastAdaboost	"MIT + file LICENSE"
## forcats	"GPL-3"
## foreach	"Apache License (== 2.0)"
## forecast	"GPL-3"
## foreign	"GPL (>= 2)"
## forge	"Apache License (>= 2.0)"
## formatR	"GPL"
## Formula	"GPL-2 GPL-3"
## fracdiff	"GPL (>= 2)"
## fs	"GPL-3"
## futile.logger	"LGPL-3"
## futile.options	"LGPL-3"
## gam	"GPL-2"
## gbm	"GPL (>= 2) file LICENSE"
## genefilter	"Artistic-2.0"
## generics	"GPL-2"
## GenomeInfoDb	"Artistic-2.0"
## GenomeInfoDbData	"Artistic-2.0"
## GenomicAlignments	"Artistic-2.0"
## GenomicFeatures	"Artistic-2.0"
## GenomicRanges	"Artistic-2.0"
## geometry	"GPL (>= 3) + file LICENSE"
## ggplot2	"GPL-2 file LICENSE"
## gh	"MIT + file LICENSE"
## git2r	"GPL-2"
## glue	"MIT + file LICENSE"
## gower	"GPL-3"
## graphics	"Part of R 3.5.1"
## grDevices	"Part of R 3.5.1"
## grid	"Part of R 3.5.1"
## gridExtra	"GPL (>= 2)"
## gtable	"GPL-2"
## haven	"MIT + file LICENSE"
## highr	"GPL"
## HistData	"GPL"
## hms	"GPL-3"
## htmltools	"GPL (>= 2)"
## htmlwidgets	"MIT + file LICENSE"
## httpuv	"GPL (>= 2) file LICENSE"
## httr	"MIT + file LICENSE"
## igraph	"GPL (>= 2)"
## import	"MIT + file LICENSE"
## ini	"GPL-3"
## inum	"GPL-2"
## ipred	"GPL (>= 2)"
## IRanges	"Artistic-2.0"
## iterators	"Apache License (== 2.0)"
## jsonlite	"MIT + file LICENSE"
## kernlab	"GPL-2"
## KernSmooth	"Unlimited"

```

## kknn "GPL (>= 2)"
## klaR "GPL-2"
## knitr "GPL"
## labeling "MIT + file LICENSE | Unlimited"
## labelled "GPL-3"
## Lahman "GPL"
## lambda.r "LGPL-3"
## later "GPL (>= 2)"
## lattice "GPL (>= 2)"
## lava "GPL-3"
## lazyeval "GPL-3"
## libcoin "GPL-2"
## lmtest "GPL-2 | GPL-3"
## lubridate "GPL (>= 2)"
## magic "GPL-2"
## magrittr "MIT + file LICENSE"
## markdown "GPL-2"
## MASS "GPL-2 | GPL-3"
## Matrix "GPL (>= 2) | file LICENSE"
## matrixStats "Artistic-2.0"
## mboost "GPL-2"
## memoise "MIT + file LICENSE"
## methods "Part of R 3.5.1"
## mgcv "GPL (>= 2)"
## mime "GPL"
## miniUI "GPL-3"
## mlbench "GPL-2"
## ModelMetrics "GPL (>= 2)"
## modelr "GPL-3"
## monmlp "GPL-2"
## munsell "MIT + file LICENSE"
## mvtnorm "GPL-2"
## naivebayes "GPL-2"
## nlme "GPL (>= 2) | file LICENSE"
## nnet "GPL-2 | GPL-3"
## nnls "GPL (>= 2)"
## numDeriv "GPL-2"
## odbc "MIT + file LICENSE"
## openssl "MIT + file LICENSE"
## optimx "GPL-2"
## packrat "GPL-2"
## parallel "Part of R 3.5.1"
## partykit "GPL-2 | GPL-3"
## pdftools "MIT + file LICENSE"
## pillar "GPL-3"
## pkgbuild "GPL-3"
## pkgconfig "MIT + file LICENSE"
## pkgload "GPL-3"
## PKI "GPL-2 | GPL-3 | file LICENSE"
## plogr "MIT + file LICENSE"
## pls "GPL-2"
## plyr "MIT + file LICENSE"
## praise "MIT + file LICENSE"
## prettyunits "MIT + file LICENSE"

```



```

## processx      "MIT + file LICENSE"
## prodlim       "GPL (>= 2)"
## progress      "MIT + file LICENSE"
## promises      "MIT + file LICENSE"
## ps            "BSD_3_clause + file LICENSE"
## purrr         "GPL-3 | file LICENSE"
## quadprog      "GPL (>= 2)"
## quantmod      "GPL-3"
## questionr     "GPL (>= 2)"
## r2d3          "BSD_3_clause + file LICENSE"
## R6            "MIT + file LICENSE"
## randomForest  "GPL (>= 2)"
## ranger        "GPL-3"
## rappdirs      "MIT + file LICENSE"
## raster        "GPL (>= 3)"
## Rborist       "MPL (>= 2) | GPL (>= 2) | file LICENSE"
## rcmdcheck     "MIT + file LICENSE"
## RColorBrewer  "Apache License 2.0"
## Rcpp          "GPL (>= 2)"
## RcppArmadillo "GPL (>= 2)"
## RcppEigen     "GPL (>= 2) | file LICENSE"
## RcppRoll      "GPL (>= 2)"
## RCurl         "BSD"
## readr         "GPL (>= 2) | file LICENSE"
## readxl        "GPL-3"
## recipes       "GPL-2"
## rematch      "MIT + file LICENSE"
## remotes       "GPL (>= 2)"
## reprex       "MIT + file LICENSE"
## reshape2     "MIT + file LICENSE"
## RJSONIO      "BSD_3_clause + file LICENSE"
## rlang        "GPL-3"
## rmarkdown    "GPL-3"
## robustbase   "GPL (>= 2)"
## rpart        "GPL-2 | GPL-3"
## rprojroot    "GPL-3"
## Rsamtools    "Artistic-2.0 | file LICENSE"
## rsconnect    "GPL-2"
## RSNNS        "LGPL (>= 2) | file LICENSE"
## RSQLite      "LGPL (>= 2)"
## rstudioapi   "MIT + file LICENSE"
## rtracklayer  "Artistic-2.0 + file LICENSE"
## rvest        "GPL-3"
## S4Vectors    "Artistic-2.0"
## scales       "MIT + file LICENSE"
## selectr      "BSD_3_clause + file LICENSE"
## sessioninfo  "GPL-2"
## sfsmisc      "GPL (>= 2)"
## shiny        "GPL-3 | file LICENSE"
## snow         "GPL"
## sourcetools  "MIT + file LICENSE"
## sp           "GPL (>= 2)"
## sparklyr     "Apache License 2.0 | file LICENSE"
## SparseM      "GPL (>= 2)"

```

## spatial	"GPL-2 GPL-3"
## spData	"CC0"
## splines	"Part of R 3.5.1"
## SQUAREM	"GPL (>= 2)"
## stabs	"GPL-2"
## stats	"Part of R 3.5.1"
## stats4	"Part of R 3.5.1"
## stringi	"file LICENSE"
## stringr	"GPL-2 file LICENSE"
## SummarizedExperiment	"Artistic-2.0"
## survival	"LGPL (>= 2)"
## tcltk	"Part of R 3.5.1"
## testthat	"MIT + file LICENSE"
## tibble	"MIT + file LICENSE"
## tidyr	"MIT + file LICENSE"
## tidyselect	"GPL-3"
## tidyverse	"GPL-3 file LICENSE"
## timeDate	"GPL (>= 2)"
## tinytex	"MIT + file LICENSE"
## tools	"Part of R 3.5.1"
## tseries	"GPL-2"
## TTR	"GPL-2"
## urca	"GPL (>= 2)"
## uroot	"GPL-2"
## usethis	"GPL-3"
## utf8	"Apache License (== 2.0) file LICENSE"
## utils	"Part of R 3.5.1"
## viridisLite	"MIT + file LICENSE"
## whisker	"GPL-3"
## withr	"GPL (>= 2)"
## wsrfr	"GPL (>= 2)"
## xfun	"MIT + file LICENSE"
## XML	"BSD_2_clause + file LICENSE"
## xml2	"GPL (>= 2)"
## xopen	"MIT + file LICENSE"
## xtable	"GPL (>= 2)"
## xts	"GPL (>= 2)"
## XVector	"Artistic-2.0"
## yaml	"BSD_3_clause + file LICENSE"
## zlibbioc	"Artistic-2.0 + file LICENSE"
## zoo	"GPL-2 GPL-3"
##	License_is_FOSS License_restricts_use OS_type MD5sum
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## annotate	NA NA NA NA
## AnnotationDbi	NA NA NA NA
## assertthat	NA NA NA NA
## backports	NA NA NA NA
## base	NA NA NA NA
## base64enc	NA NA NA NA
## BH	NA NA NA NA
## bindr	NA NA NA NA
## bindrcpp	NA NA NA NA
## Biobase	NA NA NA NA
## BiocGenerics	NA NA NA NA

## BiocInstaller	NA	NA	NA	NA
## BiocManager	NA	NA	NA	NA
## BiocParallel	NA	NA	NA	NA
## BiocVersion	NA	NA	NA	NA
## biomaRt	NA	NA	NA	NA
## Biostrings	NA	NA	NA	NA
## bit	NA	NA	NA	NA
## bit64	NA	NA	NA	NA
## bitops	NA	NA	NA	NA
## blob	NA	NA	NA	NA
## boot	NA	NA	NA	NA
## broom	NA	NA	NA	NA
## callr	NA	NA	NA	NA
## caret	NA	NA	NA	NA
## caTools	NA	NA	NA	NA
## cellranger	NA	NA	NA	NA
## class	NA	NA	NA	NA
## classInt	NA	NA	NA	NA
## cli	NA	NA	NA	NA
## clipr	NA	NA	NA	NA
## clisymbols	NA	NA	NA	NA
## cluster	NA	NA	NA	NA
## codetools	NA	NA	NA	NA
## colorspace	NA	NA	NA	NA
## combinat	NA	NA	NA	NA
## compiler	NA	NA	NA	NA
## config	NA	NA	NA	NA
## crayon	NA	NA	NA	NA
## curl	NA	NA	NA	NA
## CVST	NA	NA	NA	NA
## data.table	NA	NA	NA	NA
## datasets	NA	NA	NA	NA
## DBI	NA	NA	NA	NA
## dbplyr	NA	NA	NA	NA
## ddalpha	NA	NA	NA	NA
## DelayedArray	NA	NA	NA	NA
## DEoptimR	NA	NA	NA	NA
## desc	NA	NA	NA	NA
## devtools	NA	NA	NA	NA
## dichromat	NA	NA	NA	NA
## digest	NA	NA	NA	NA
## dimRed	NA	NA	NA	NA
## dplyr	NA	NA	NA	NA
## DRR	NA	NA	NA	NA
## dslabs	NA	NA	NA	NA
## e1071	NA	NA	NA	NA
## ellipsis	NA	NA	NA	NA
## evaluate	NA	NA	NA	NA
## fansi	NA	NA	NA	NA
## fastAdaboost	NA	NA	NA	NA
## forcats	NA	NA	NA	NA
## foreach	NA	NA	NA	NA
## forecast	NA	NA	NA	NA
## foreign	NA	NA	NA	NA

## forge	NA	NA	NA	NA
## formatR	NA	NA	NA	NA
## Formula	NA	NA	NA	NA
## fracdiff	NA	NA	NA	NA
## fs	NA	NA	NA	NA
## futile.logger	NA	NA	NA	NA
## futile.options	NA	NA	NA	NA
## gam	NA	NA	NA	NA
## gbm	NA	NA	NA	NA
## genefilter	NA	NA	NA	NA
## generics	NA	NA	NA	NA
## GenomeInfoDb	NA	NA	NA	NA
## GenomeInfoDbData	NA	NA	NA	NA
## GenomicAlignments	NA	NA	NA	NA
## GenomicFeatures	NA	NA	NA	NA
## GenomicRanges	NA	NA	NA	NA
## geometry	NA	NA	NA	NA
## ggplot2	NA	NA	NA	NA
## gh	NA	NA	NA	NA
## git2r	NA	NA	NA	NA
## glue	NA	NA	NA	NA
## gower	NA	NA	NA	NA
## graphics	NA	NA	NA	NA
## grDevices	NA	NA	NA	NA
## grid	NA	NA	NA	NA
## gridExtra	NA	NA	NA	NA
## gtable	NA	NA	NA	NA
## haven	NA	NA	NA	NA
## highr	NA	NA	NA	NA
## HistData	NA	NA	NA	NA
## hms	NA	NA	NA	NA
## htmltools	NA	NA	NA	NA
## htmlwidgets	NA	NA	NA	NA
## httpuv	NA	NA	NA	NA
## httr	NA	NA	NA	NA
## igraph	NA	NA	NA	NA
## import	NA	NA	NA	NA
## ini	NA	NA	NA	NA
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## ipred	NA	NA	NA	NA
## IRanges	NA	NA	NA	NA
## iterators	NA	NA	NA	NA
## jsonlite	NA	NA	NA	NA
## kernlab	NA	NA	NA	NA
## KernSmooth	NA	NA	NA	NA
## kkn	NA	NA	NA	NA
## klaR	NA	NA	NA	NA
## knitr	NA	NA	NA	NA
## labeling	NA	NA	NA	NA
## labelled	NA	NA	NA	NA
## Lahman	NA	NA	NA	NA
## lambda.r	NA	NA	NA	NA
## later	NA	NA	NA	NA
## lattice	NA	NA	NA	NA

## lava	NA	NA	NA	NA
## lazyeval	NA	NA	NA	NA
## libcoin	NA	NA	NA	NA
## lmtest	NA	NA	NA	NA
## lubridate	NA	NA	NA	NA
## magic	NA	NA	NA	NA
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## matrixStats	NA	NA	NA	NA
## mboost	NA	NA	NA	NA
## memoise	NA	NA	NA	NA
## methods	NA	NA	NA	NA
## mgcv	NA	NA	NA	NA
## mime	NA	NA	NA	NA
## miniUI	NA	NA	NA	NA
## mlbench	NA	NA	NA	NA
## ModelMetrics	NA	NA	NA	NA
## modelr	NA	NA	NA	NA
## monmlp	NA	NA	NA	NA
## munsell	NA	NA	NA	NA
## mvtnorm	NA	NA	NA	NA
## naivebayes	NA	NA	NA	NA
## nlme	NA	NA	NA	NA
## nnet	NA	NA	NA	NA
## nnls	NA	NA	NA	NA
## numDeriv	NA	NA	NA	NA
## odbc	NA	NA	NA	NA
## openssl	NA	NA	NA	NA
## optimx	NA	NA	NA	NA
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## parallel	NA	NA	NA	NA
## partykit	NA	NA	NA	NA
## pdftools	NA	NA	NA	NA
## pillar	NA	NA	NA	NA
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## PKI	NA	NA	NA	NA
## plogr	NA	NA	NA	NA
## pls	NA	NA	NA	NA
## plyr	NA	NA	NA	NA
## praise	NA	NA	NA	NA
## prettyunits	NA	NA	NA	NA
## processx	NA	NA	NA	NA
## proclim	NA	NA	NA	NA
## progress	NA	NA	NA	NA
## promises	NA	NA	NA	NA
## ps	NA	NA	NA	NA
## purrr	NA	NA	NA	NA
## quadprog	NA	NA	NA	NA
## quantmod	NA	NA	NA	NA
## questionr	NA	NA	NA	NA

## r2d3	NA	NA	NA	NA
## R6	NA	NA	NA	NA
## randomForest	NA	NA	NA	NA
## ranger	NA	NA	NA	NA
## rappdirs	NA	NA	NA	NA
## raster	NA	NA	NA	NA
## Rborist	NA	NA	NA	NA
## rcmdcheck	NA	NA	NA	NA
## RColorBrewer	NA	NA	NA	NA
## Rcpp	NA	NA	NA	NA
## RcppArmadillo	NA	NA	NA	NA
## RcppEigen	NA	NA	NA	NA
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## RJSONIO	NA	NA	NA	NA
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## rmarkdown	NA	NA	NA	NA
## robustbase	NA	NA	NA	NA
## rpart	NA	NA	NA	NA
## rprojroot	NA	NA	NA	NA
## Rsamtools	NA	NA	NA	NA
## rsconnect	NA	NA	NA	NA
## RSNNS	NA	NA	NA	NA
## RSQLite	NA	NA	NA	NA
## rstudioapi	NA	NA	NA	NA
## rtracklayer	NA	NA	NA	NA
## rvest	NA	NA	NA	NA
## S4Vectors	NA	NA	NA	NA
## scales	NA	NA	NA	NA
## selectr	NA	NA	NA	NA
## sessioninfo	NA	NA	NA	NA
## sfsmisc	NA	NA	NA	NA
## shiny	NA	NA	NA	NA
## snow	NA	NA	NA	NA
## sourcetools	NA	NA	NA	NA
## sp	NA	NA	NA	NA
## sparklyr	NA	NA	NA	NA
## SparseM	NA	NA	NA	NA
## spatial	NA	NA	NA	NA
## spData	NA	NA	NA	NA
## splines	NA	NA	NA	NA
## SQUAREM	NA	NA	NA	NA
## stabs	NA	NA	NA	NA
## stats	NA	NA	NA	NA
## stats4	NA	NA	NA	NA
## stringi	"yes"	NA	NA	NA
## stringr	NA	NA	NA	NA

## SummarizedExperiment	NA	NA	NA	NA
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## tcltk	NA	NA	NA	NA
## testthat	NA	NA	NA	NA
## tibble	NA	NA	NA	NA
## tidyr	NA	NA	NA	NA
## tidyselect	NA	NA	NA	NA
## tidyverse	NA	NA	NA	NA
## timeDate	NA	NA	NA	NA
## tinytex	NA	NA	NA	NA
## tools	NA	NA	NA	NA
## tseries	NA	NA	NA	NA
## TTR	NA	NA	NA	NA
## urca	NA	NA	NA	NA
## uroot	NA	NA	NA	NA
## usethis	NA	NA	NA	NA
## utf8	NA	NA	NA	NA
## utils	NA	NA	NA	NA
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## whisker	NA	NA	NA	NA
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## xml2	NA	NA	NA	NA
## xopen	NA	NA	NA	NA
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## XVector	NA	NA	NA	NA
## yaml	NA	NA	NA	NA
## zlibbioc	NA	NA	NA	NA
## zoo	NA	NA	NA	NA
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## annotate	"no"	"3.5.1"		
## AnnotationDbi	"no"	"3.5.1"		
## assertthat	"no"	"3.5.0"		
## backports	"yes"	"3.5.0"		
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## base64enc	"yes"	"3.5.0"		
## BH	"no"	"3.5.0"		
## bindr	"no"	"3.5.0"		
## bindrcpp	"yes"	"3.5.0"		
## Biobase	"yes"	"3.5.1"		
## BiocGenerics	"no"	"3.5.1"		
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## BiocManager	"no"	"3.5.0"		
## BiocParallel	"yes"	"3.5.1"		
## BiocVersion	"no"	"3.5.1"		
## biomaRt	"no"	"3.5.1"		
## Biostrings	"yes"	"3.5.1"		
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## bit64	"yes"	"3.5.0"		
## bitops	"yes"	"3.5.0"		

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## broom	"no"	"3.5.1"
## callr	"no"	"3.5.0"
## caret	"yes"	"3.5.0"
## caTools	"yes"	"3.5.0"
## cellranger	"no"	"3.5.0"
## class	"yes"	"3.5.1"
## classInt	"yes"	"3.5.0"
## cli	"no"	"3.5.0"
## clipr	"no"	"3.5.0"
## clisymbols	"no"	"3.5.0"
## cluster	"yes"	"3.5.1"
## codetools	"no"	"3.5.1"
## colorspace	"yes"	"3.5.0"
## combinat	NA	"3.5.0"
## compiler	NA	"3.5.1"
## config	"no"	"3.5.0"
## crayon	"no"	"3.5.0"
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## CVST	"no"	"3.5.0"
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## DBI	"no"	"3.5.0"
## dbplyr	"no"	"3.5.1"
## ddalpha	"yes"	"3.5.0"
## DelayedArray	"yes"	"3.5.1"
## DEoptimR	"no"	"3.5.0"
## desc	"no"	"3.5.0"
## devtools	"no"	"3.5.1"
## dichromat	NA	"3.5.0"
## digest	"yes"	"3.5.0"
## dimRed	"yes"	"3.5.1"
## dplyr	"yes"	"3.5.0"
## DRR	"no"	"3.5.0"
## dslabs	"no"	"3.5.0"
## e1071	"yes"	"3.5.2"
## ellipsis	"yes"	"3.5.2"
## evaluate	"no"	"3.5.0"
## fansi	"yes"	"3.5.0"
## fastAdaboost	"yes"	"3.5.0"
## forcats	"no"	"3.5.0"
## foreach	"no"	"3.5.0"
## forecast	"yes"	"3.5.0"
## foreign	"yes"	"3.5.0"
## forge	"no"	"3.5.2"
## formatR	"no"	"3.5.0"
## Formula	"no"	"3.5.0"
## fracdiff	NA	"3.5.0"
## fs	"yes"	"3.5.0"
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## futile.options	"no"	"3.5.0"
## gam	"yes"	"3.5.0"
## gbm	"yes"	"3.5.0"

## genefilter	"yes"	"3.5.0"
## generics	"no"	"3.5.0"
## GenomeInfoDb	"no"	"3.5.1"
## GenomeInfoDbData	"no"	"3.5.1"
## GenomicAlignments	"yes"	"3.5.1"
## GenomicFeatures	"no"	"3.5.1"
## GenomicRanges	"yes"	"3.5.1"
## geometry	"yes"	"3.5.0"
## ggplot2	"no"	"3.5.0"
## gh	"no"	"3.5.0"
## git2r	"yes"	"3.5.0"
## glue	"yes"	"3.5.0"
## gower	"yes"	"3.5.0"
## graphics	"yes"	"3.5.1"
## grDevices	"yes"	"3.5.1"
## grid	"yes"	"3.5.1"
## gridExtra	"no"	"3.5.0"
## gtable	"no"	"3.5.0"
## haven	"yes"	"3.5.0"
## highr	"no"	"3.5.0"
## HistData	"no"	"3.5.0"
## hms	"no"	"3.5.0"
## htmltools	"yes"	"3.5.0"
## htmlwidgets	"no"	"3.5.0"
## httpuv	"yes"	"3.5.0"
## httr	"no"	"3.5.0"
## igraph	"yes"	"3.5.0"
## import	"no"	"3.5.0"
## ini	"no"	"3.5.0"
## inum	"no"	"3.5.0"
## ipred	"yes"	"3.5.0"
## IRanges	"yes"	"3.5.1"
## iterators	"no"	"3.5.0"
## jsonlite	"yes"	"3.5.0"
## kernlab	"yes"	"3.5.0"
## KernSmooth	"yes"	"3.5.1"
## kkn	"yes"	"3.5.0"
## klaR	"no"	"3.5.0"
## knitr	"no"	"3.5.0"
## labeling	"no"	"3.5.0"
## labelled	"no"	"3.5.0"
## Lahman	"no"	"3.5.0"
## lambda.r	"no"	"3.5.0"
## later	"yes"	"3.5.0"
## lattice	"yes"	"3.5.0"
## lava	"no"	"3.5.0"
## lazyeval	"yes"	"3.5.0"
## libcoin	"yes"	"3.5.0"
## lmttest	"yes"	"3.5.0"
## lubridate	"yes"	"3.5.0"
## magic	"no"	"3.5.0"
## magrittr	"no"	"3.5.0"
## markdown	"yes"	"3.5.0"
## MASS	"yes"	"3.5.0"

## Matrix	"yes"	"3.5.0"
## matrixStats	"yes"	"3.5.0"
## mboost	"yes"	"3.5.0"
## memoise	"no"	"3.5.0"
## methods	"yes"	"3.5.1"
## mgcv	"yes"	"3.5.0"
## mime	"yes"	"3.5.0"
## miniUI	"no"	"3.5.0"
## mlbench	NA	"3.5.0"
## ModelMetrics	"yes"	"3.5.0"
## modelr	"no"	"3.5.0"
## monmlp	"no"	"3.5.0"
## munsell	"no"	"3.5.0"
## mvtnorm	"yes"	"3.5.0"
## naivebayes	"no"	"3.5.0"
## nlme	"yes"	"3.5.1"
## nnet	"yes"	"3.5.1"
## nnls	NA	"3.5.0"
## numDeriv	"no"	"3.5.0"
## odbc	"yes"	"3.5.0"
## openssl	"yes"	"3.5.0"
## optimx	"no"	"3.5.1"
## packrat	"no"	"3.5.1"
## parallel	"yes"	"3.5.1"
## partykit	"yes"	"3.5.0"
## pdftools	"yes"	"3.5.0"
## pillar	"no"	"3.5.0"
## pkgbuild	"no"	"3.5.0"
## pkgconfig	"no"	"3.5.0"
## pkgload	"yes"	"3.5.0"
## PKI	"yes"	"3.5.0"
## plogr	"no"	"3.5.0"
## pls	"no"	"3.5.0"
## plyr	"yes"	"3.5.0"
## praise	"no"	"3.5.0"
## prettyunits	"no"	"3.5.0"
## processx	"yes"	"3.5.1"
## prodlim	"yes"	"3.5.0"
## progress	"no"	"3.5.0"
## promises	"yes"	"3.5.0"
## ps	"yes"	"3.5.0"
## purrr	"yes"	"3.5.0"
## quadprog	"yes"	"3.5.0"
## quantmod	"no"	"3.5.0"
## questionr	"no"	"3.5.0"
## r2d3	"no"	"3.5.0"
## R6	"no"	"3.5.0"
## randomForest	"yes"	"3.5.0"
## ranger	"yes"	"3.5.0"
## rappdirs	"yes"	"3.5.0"
## raster	"yes"	"3.5.0"
## Rborist	"yes"	"3.5.0"
## rcmdcheck	"no"	"3.5.0"
## RColorBrewer	"no"	"3.5.0"

## Rcpp	"yes"	"3.5.0"
## RcppArmadillo	"yes"	"3.5.0"
## RcppEigen	"yes"	"3.5.0"
## RcppRoll	"yes"	"3.5.0"
## RCurl	"yes"	"3.5.0"
## readr	"yes"	"3.5.0"
## readxl	"yes"	"3.5.0"
## recipes	"no"	"3.5.0"
## rematch	"no"	"3.5.0"
## remotes	"no"	"3.5.0"
## reprex	"no"	"3.5.0"
## reshape2	"yes"	"3.5.0"
## RJSONIO	"yes"	"3.5.0"
## rlang	"yes"	"3.5.2"
## rmarkdown	"no"	"3.5.0"
## robustbase	"yes"	"3.5.0"
## rpart	"yes"	"3.5.1"
## rprojroot	"no"	"3.5.0"
## Rsamtools	"yes"	"3.5.1"
## rsconnect	"no"	"3.5.2"
## RSNNS	"yes"	"3.5.0"
## RSQLite	"yes"	"3.5.0"
## rstudioapi	"no"	"3.5.0"
## rtracklayer	"yes"	"3.5.1"
## rvest	"no"	"3.5.0"
## S4Vectors	"yes"	"3.5.1"
## scales	"yes"	"3.5.0"
## selectr	"no"	"3.5.0"
## sessioninfo	"no"	"3.5.0"
## sfsmisc	"no"	"3.5.0"
## shiny	"no"	"3.5.0"
## snow	"no"	"3.5.0"
## sourcetools	"yes"	"3.5.0"
## sp	"yes"	"3.5.0"
## sparklyr	"no"	"3.5.2"
## SparseM	"yes"	"3.5.0"
## spatial	"yes"	"3.5.1"
## spData	"no"	"3.5.0"
## splines	"yes"	"3.5.1"
## SQUAREM	"no"	"3.5.0"
## stabs	"no"	"3.5.0"
## stats	"yes"	"3.5.1"
## stats4	NA	"3.5.1"
## stringi	"yes"	"3.5.0"
## stringr	"no"	"3.5.0"
## SummarizedExperiment	"no"	"3.5.1"
## survival	"yes"	"3.5.0"
## tcltk	"yes"	"3.5.1"
## testthat	"yes"	"3.5.0"
## tibble	"yes"	"3.5.0"
## tidyr	"yes"	"3.5.0"
## tidyselect	"yes"	"3.5.0"
## tidyverse	"no"	"3.5.0"
## timeDate	"no"	"3.5.0"

## tinytex	"no"	"3.5.2"
## tools	"yes"	"3.5.1"
## tseries	"yes"	"3.5.0"
## TTR	"yes"	"3.5.0"
## urca	"yes"	"3.5.0"
## uroot	"yes"	"3.5.0"
## usethis	"no"	"3.5.0"
## utf8	"yes"	"3.5.0"
## utils	"yes"	"3.5.1"
## viridisLite	"no"	"3.5.0"
## whisker	"no"	"3.5.0"
## withr	"no"	"3.5.0"
## wsrf	"yes"	"3.5.0"
## xfun	"no"	"3.5.0"
## XML	"yes"	"3.5.0"
## xml2	"yes"	"3.5.0"
## xopen	"no"	"3.5.0"
## xtable	"no"	"3.5.0"
## xts	"yes"	"3.5.0"
## XVector	"yes"	"3.5.1"
## yaml	"yes"	"3.5.0"
## zlibbioc	"yes"	"3.5.1"
## zoo	"yes"	"3.5.0"