

Report - MovieLens Recommender System Capstone Project

Nitesh Kumar Gupta - Harvard Data Science Professional

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1 Executive Summary

The purpose for this project is to create a movie recommender system using MovieLens dataset provided as bootstrap code to load data.

The version of movielens dataset received after execution of bootstrap code provided within requirement contains approximately 10 Millions of movies ratings which is divided in approximately 9 Million records for training and 1 Million records for validation. Looking at dataset it can be concluded that it is a small subset of a much larger and famous dataset with several millions of ratings. Into the training dataset there are approximately **70,000 users** and **11,000 different movies** divided in 20 genres such as Sci-Fi, Romance, Action, Adventure, Horror, Drama, Thriller and more.

As per requirement, the recommender systems built on this dataset has been evaluated and chosen based on the RMSE - Root Mean Squared Error value. A model with RMSE value lower than **0.87750** is concluded model as a good fit for purpose. The mathematical expression used to calculate RMSE is as per below:

$$\text{RMSE} = \sqrt{\frac{1}{n} \sum_{t=1}^n e_t^2}$$

Below is a programmatic representation of above expression in a form of R programming Function which has been used across this project to calculate RMSE value for different models.

Based on the outcomes of exploratory data analysis and different model evaluation, the **Regularized Movie + User + Genre Model** is capable to reach a RMSE of **0.8627121**, which is really good.

2 Exploratory Data Analysis

2.1 Inital data Exploration

The 10 Million records are divided into two dataset namely **edx** for model training purpose and **validation** for the model validation phase.

The **edx** training dataset contains approximately 9 Million of rows having approximately 70,000 distinct users and 11,000 distinct movies with rating score between 0.5 and 5. There is no missing values (0 or NA).

edx dataset

Users	Movies
69878	10677

Missing Values in both dataset

	x
userId	0
movieId	0
rating	0
timestamp	0
title	0
genres	0

The MovieLens dataset have six features/variables/columns in both edx and validation datasets:

- **userId** <integer> that contains the unique identification number for each user.
- **movieId** <numeric> that contains the unique identification number for each movie.

- **rating** <numeric> that contains the rating of one movie by one user. Ratings are made on a 5-Star scale with half-star increments.
- **timestamp** <integer> that contains the timestamp for one specific rating provided by one user.
- **title** <character> that contains the title of each movie including the year of the release.
- **genres** <character> that contains a list of pipe-separated of genre of each movie.

First 6 Rows of edx dataset

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

2.2 Dataset Pre-Processing and Feature Engineering

Looking at first six sample rows of training dataset, we can clearly notice that the **genres** is a list values in string format separated by pipe symbol. It's necessary to extract them in rows for more consistent, robust and precise estimate. We also observe that the **title** contains the year when the movie was released. Movie released year may be necessary factor to predict the movie rating. Finally, extracting the year and the month for each rating from **timestamp** may be beneficial as they might have correlation with movie rating.

The pre-processing phase and feature engineering is composed by four steps as mentioned below:

1. Convert **timestamp** to a human readable date format.
2. Extract the month and the year from the date.
3. Extract the movie release year for each movie from the title. Clean title by removing release year.
4. Separate each genre from the pipe-separated value. It increases the size of both datasets as separate rows will get created for each genre.

After pre-processing and feature engineering, the data, **edx** dataset looks like this with additional 5 features and in total 11 features. Similarly, same 5 new features has been added to validation dataset:

Pre-processed and feature engineered edx datadataset First six rows of edx training dataset.

userId	movieId	rating	title	genre	release	yearOfRating	monthOfRating
1	122	5	Boomerang	Comedy	1992	1996	8
1	122	5	Boomerang	Romance	1992	1996	8
1	185	5	Net, The	Action	1995	1996	8
1	185	5	Net, The	Crime	1995	1996	8
1	185	5	Net, The	Thriller	1995	1996	8
1	292	5	Outbreak	Action	1995	1996	8

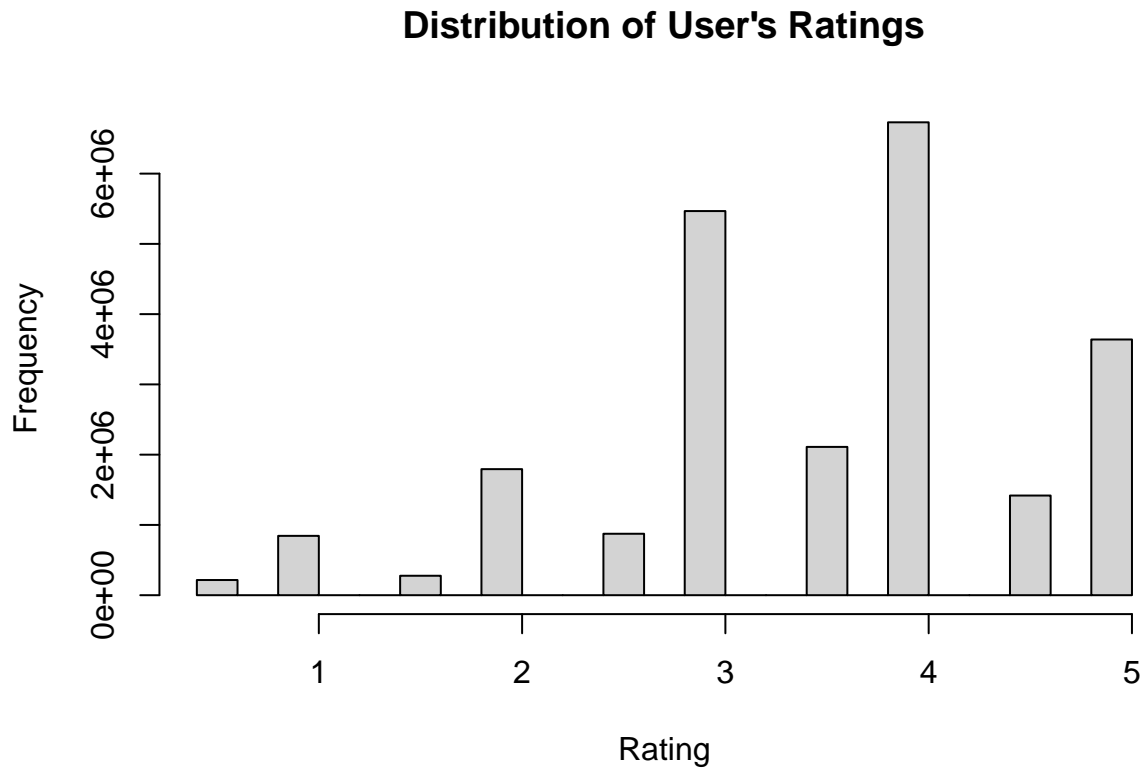
Pre-processed and feature engineered validation datadataset First six rows of validation dataset.

userId	movieId	rating	title	genre	release	yearOfRating	monthOfRating
1	231	5	Dumb & Dumber	Comedy	1994	1996	8
1	480	5	Jurassic Park	Action	1993	1996	8
1	480	5	Jurassic Park	Adventure	1993	1996	8
1	480	5	Jurassic Park	Sci-Fi	1993	1996	8
1	480	5	Jurassic Park	Thriller	1993	1996	8
1	586	5	Home Alone	Children	1990	1996	8

2.3 Rating Distribution

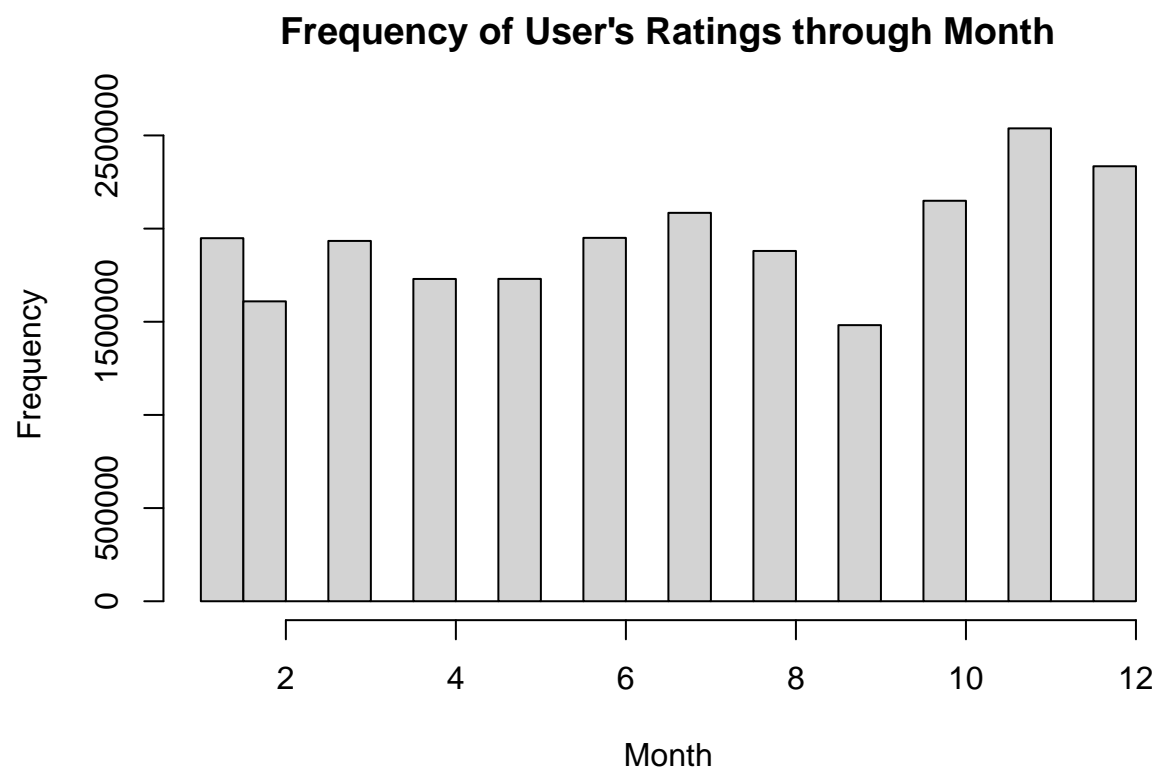
Overview of Rating Distribution

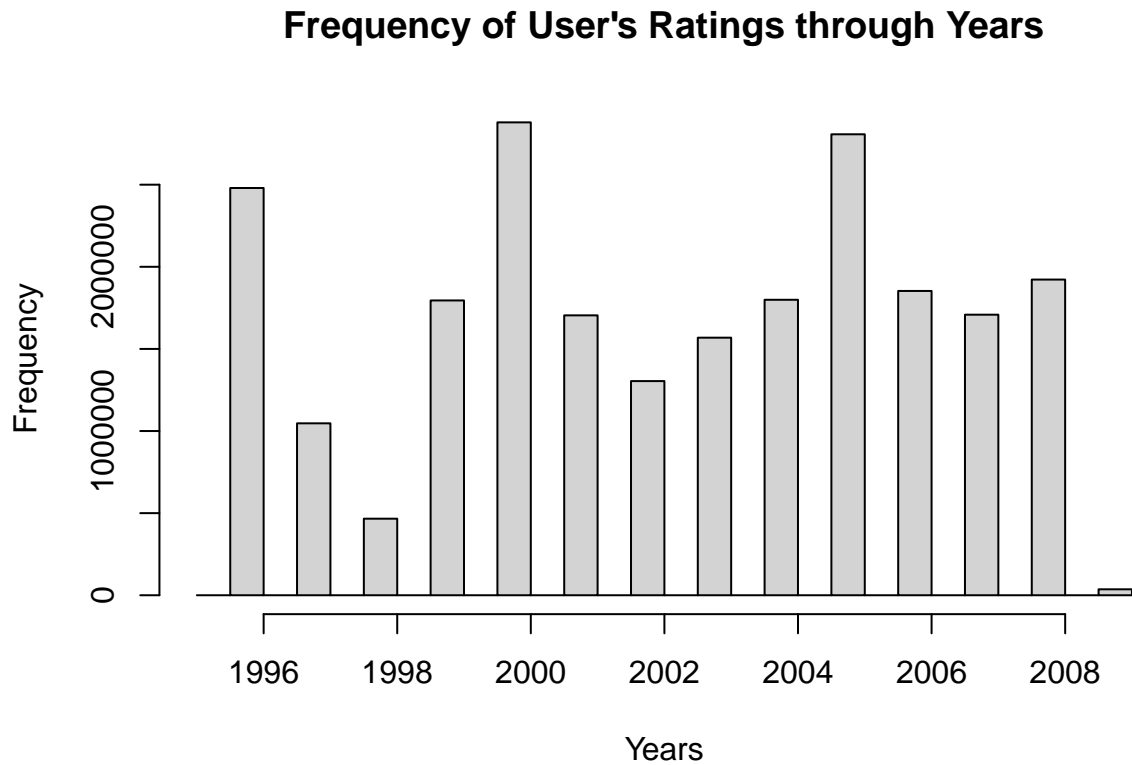
Below graph depicts movie rating distribution on a scale of 0 to 5 star with an increment of 0.5 (half) star. It can be clearly seen that there is no zero star rating. In addition, whole number stars i.e. 1,2,3,4, and 5 are more common as compared to non-whole number stars such as 0.5,1.5,2.5,3.5, and 4.5.



Overview of Rating Frequency through Months and Years

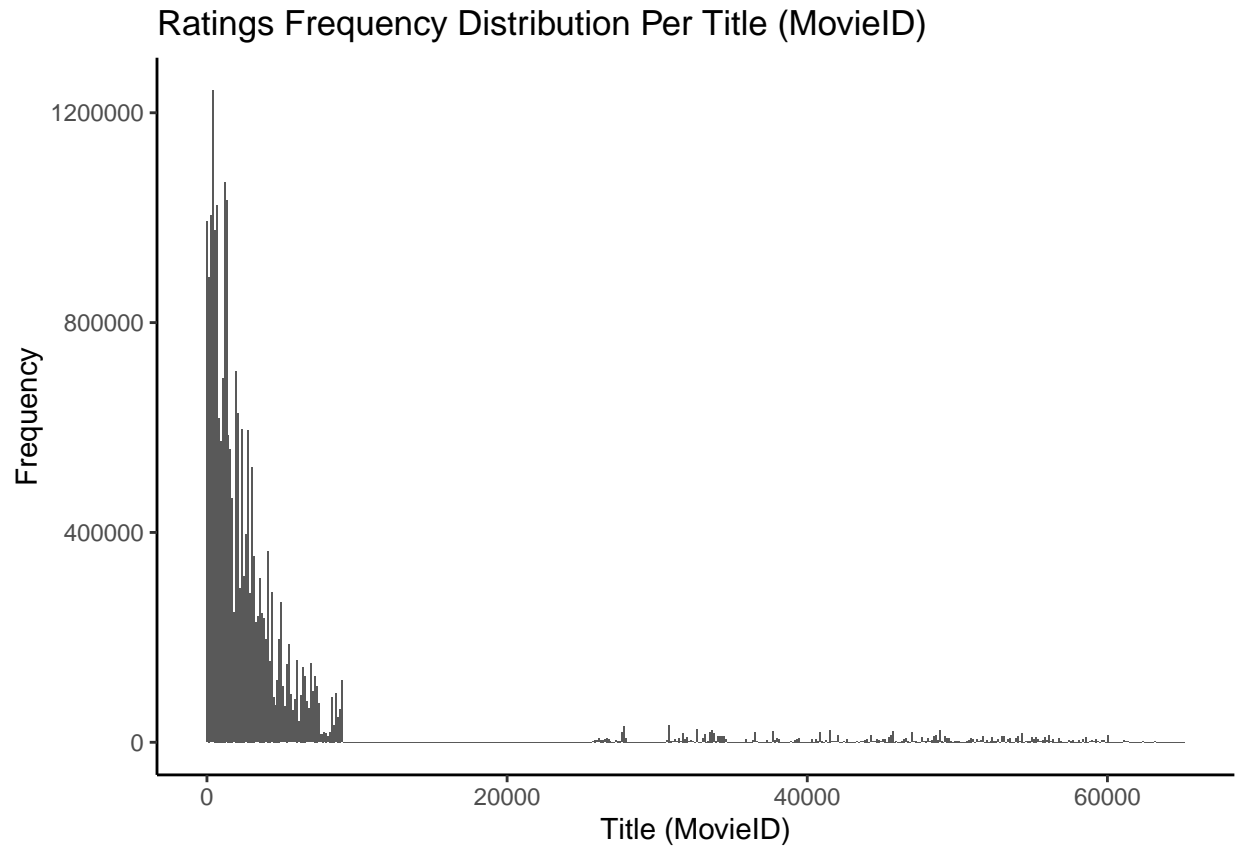
Below bar graphs shows movie rating frequency distribution through year months and years. It can be clearly seen that November month has accounted for highest number of ratings followed by December where as least number of rating has been received during the month of September. Year 2000 accounted for largest number of rating followed by 2005 where as 1998 recorded lowest number of ratings.





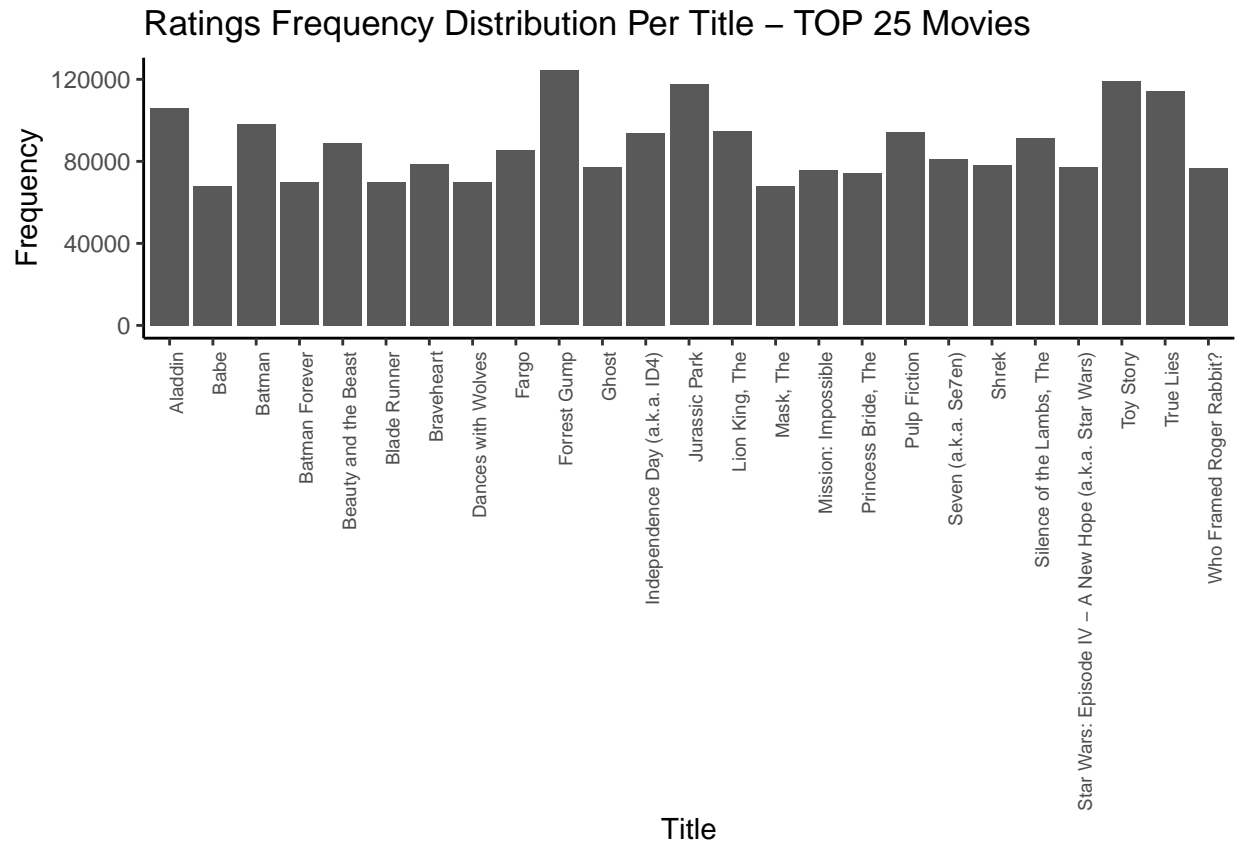
2.3.1 Numbers of Ratings per Movie

Below histogram graph shows numbers of rating per movie between year 1996 and 2008. After looking at graph it can be clearly seen that movie ids between 1000 and 2500 has not been rated at all. In addition, majority of rating has been received for movies with IDs between 1 and 1000. Very few ratings has been recorded for movies having movieIds greater than 2500. Overall, it can be concluded that most popular movies are those which have lowest movieIds.



2.3.2 Top Rated Movies

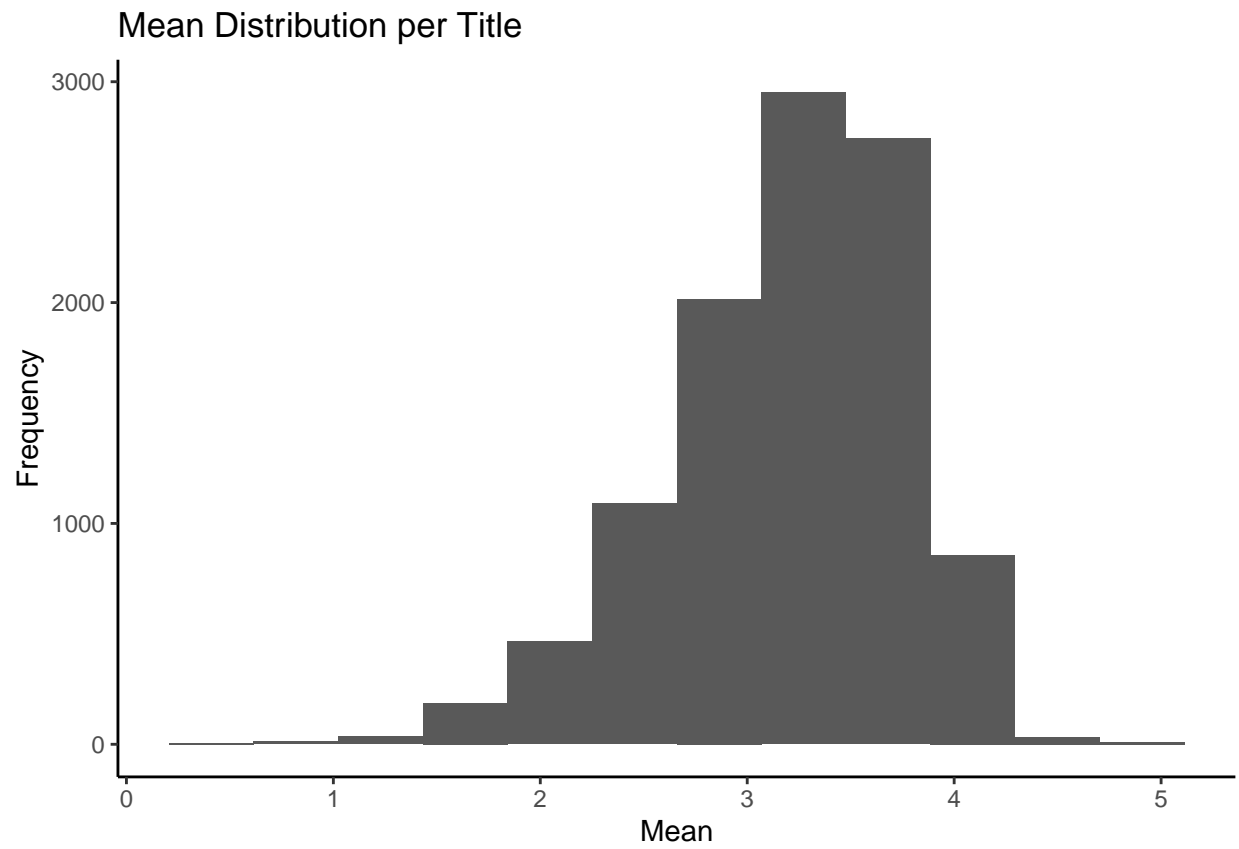
Below bar graph shows top 25 movies with total number of ratings received. It can be clearly seen that Forrest Gump has received highest number of rating where as movies like Babe, The Mask, and Batman Forever stood at the end of top 25 movie list.



title	count
Forrest Gump	124316
Toy Story	118950
Jurassic Park	117440
True Lies	114115
Aladdin	105865
Batman	98340
Lion King, The	94605
Pulp Fiction	94086
Independence Day (a.k.a. ID4)	93796
Silence of the Lambs, The	91146
Beauty and the Beast	89145
Fargo	85580
Seven (a.k.a. Se7en)	81244
Braveheart	78636
Shrek	78378
Ghost	77440
Star Wars: Episode IV - A New Hope (a.k.a. Star Wars)	77016
Who Framed Roger Rabbit?	76825
Mission: Impossible	75968
Princess Bride, The	74045
Dances with Wolves	70101
Blade Runner	69785
Batman Forever	69656
Mask, The	68172
Babe	68124

2.3.3 Mean Distribution per Title (Movie ID)

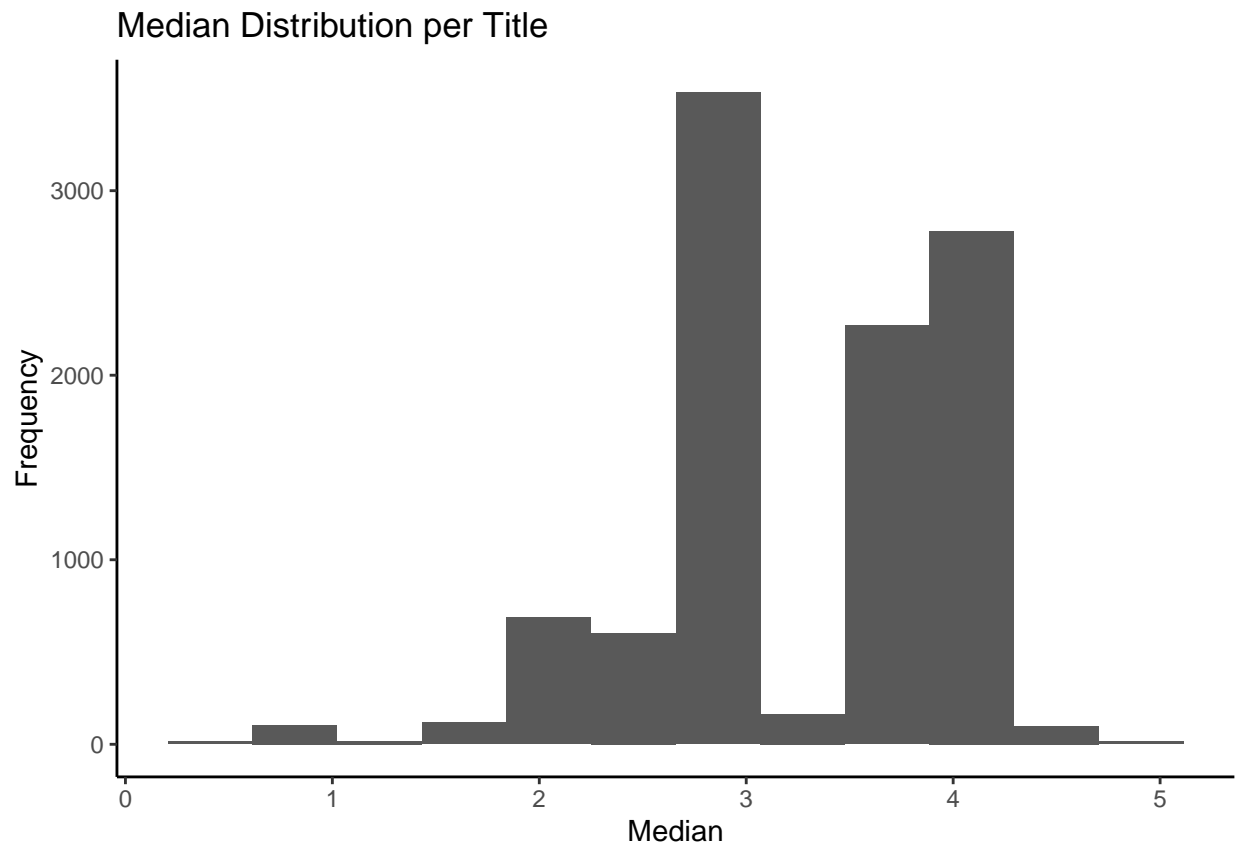
Below histogram and table shows rating mean distribution per movie title. It can be clearly seen that there are few movies such as The Blue Light, Sun Alley, and few more which has recorded 5 star rating. However, 3 star rating appears to be recorded for highest number. 0.5 (half) star and 5 star has been given to very few movies.



title	mean
Blue Light, The (Das Blaue Licht)	5.000000
Fighting Elegy (Kenka erejii)	5.000000
Hellhounds on My Trail	5.000000
Satan's Tango (SÄtÄntangÄ ³)	5.000000
Shadows of Forgotten Ancestors	5.000000
Sun Alley (Sonnenallee)	5.000000
Constantine's Sword	4.750000
Human Condition II, The (Ningen no joken II)	4.750000
Human Condition III, The (Ningen no joken III)	4.750000
Who's Singin' Over There? (a.k.a. Who Sings Over There) (Ko to tamo peva)	4.750000
Class, The (Entre les Murs)	4.666667
I'm Starting From Three (Ricomincio da Tre)	4.666667
Bad Blood (Mauvais sang)	4.500000
Demon Lover Diary	4.500000
End of Summer, The (Kohayagawa-ke no aki)	4.500000
Kansas City Confidential	4.500000
Ladrones	4.500000
Life of Oharu, The (Saikaku ichidai onna)	4.500000
Man Named Pearl, A	4.500000
Mickey	4.500000
Please Vote for Me	4.500000
Power of Nightmares: The Rise of the Politics of Fear, The	4.500000
Testament of Orpheus, The (Testament d'OrphÄe)	4.500000
Tokyo!	4.500000
Valerie and Her Week of Wonders (Valerie a tÄ½den divu)	4.500000

2.3.4 Median Distribution per Title (Movie ID)

Below graph and table shows median distribution per movie title. Similar to our previous findings, very few movies like The Blue Light, Sun Alley, and few more has got highest median value of 5. Majority of movies, above frequency 3000, has received 3 star rating. 4 and 4.5 star remains second popular rating.



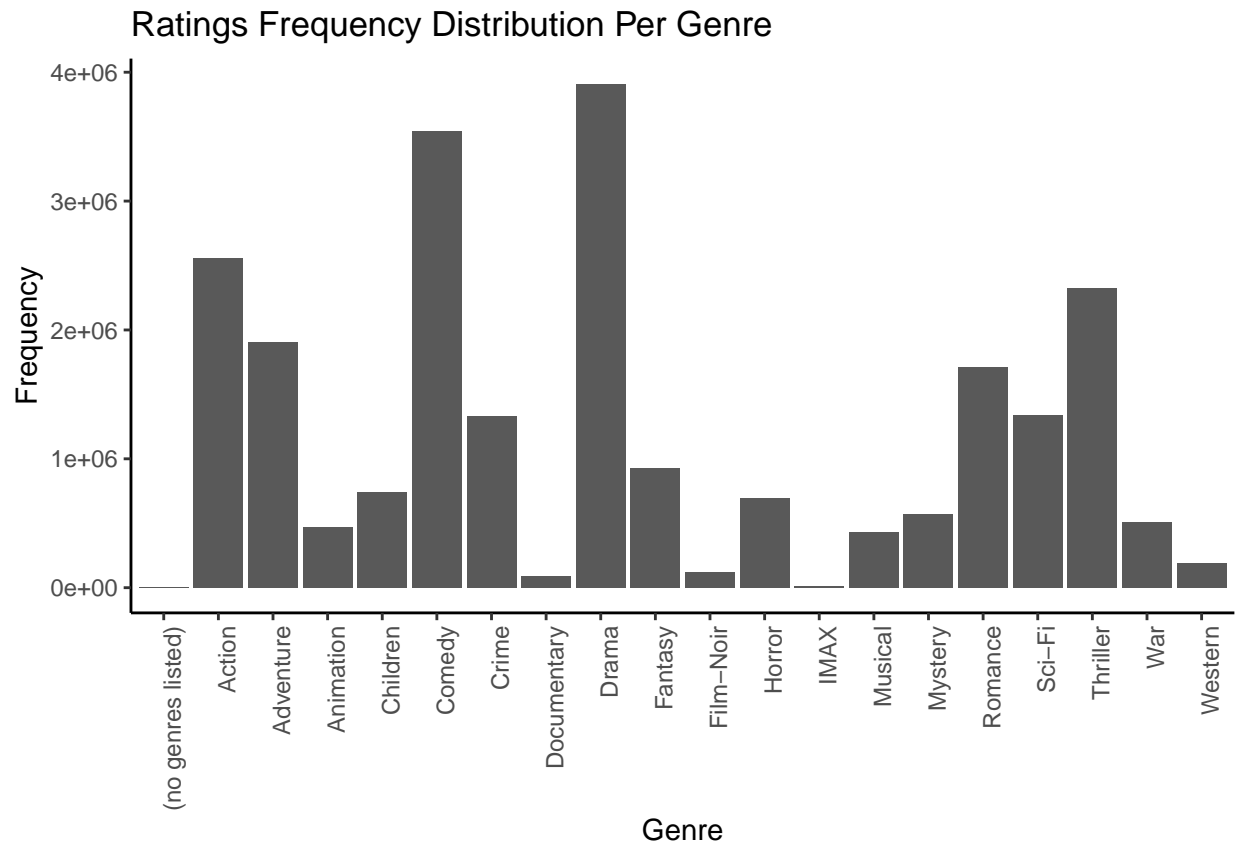
title	median
Blue Light, The (Das Blaue Licht)	5.00
Class, The (Entre les Murs)	5.00
Fighting Elegy (Kenka erejii)	5.00
Godfather, The	5.00
Hellhounds on My Trail	5.00
Kids of Survival	5.00
Satan's Tango (SÄtÄntangÄ ³)	5.00
Shadows of Forgotten Ancestors	5.00
Shawshank Redemption, The	5.00
Sun Alley (Sonnenallee)	5.00
Who's Singin' Over There? (a.k.a. Who Sings Over There) (Ko to tamo peva)	5.00
World of Apu, The (Apu Sansar)	5.00
Constantine's Sword	4.75
Human Condition II, The (Ningen no joken II)	4.75
Human Condition III, The (Ningen no joken III)	4.75
400 Blows, The (Les Quatre cents coups)	4.50
49 Up	4.50
Amelie (Fabuleux destin d'AmÄlie Poulain, Le)	4.50
American Beauty	4.50
Andrei Rublev (Andrey Rublyov)	4.50
Bad Blood (Mauvais sang)	4.50
Best of Youth, The (La Meglio gioventÄ ¹)	4.50
Cabeza de Vaca	4.50
Casablanca	4.50
Celebration, The (Festen)	4.50

2.4 Genre Analysis

2.4.1 Rating Distribution per Genre

Overview of Rating distribution over Genre

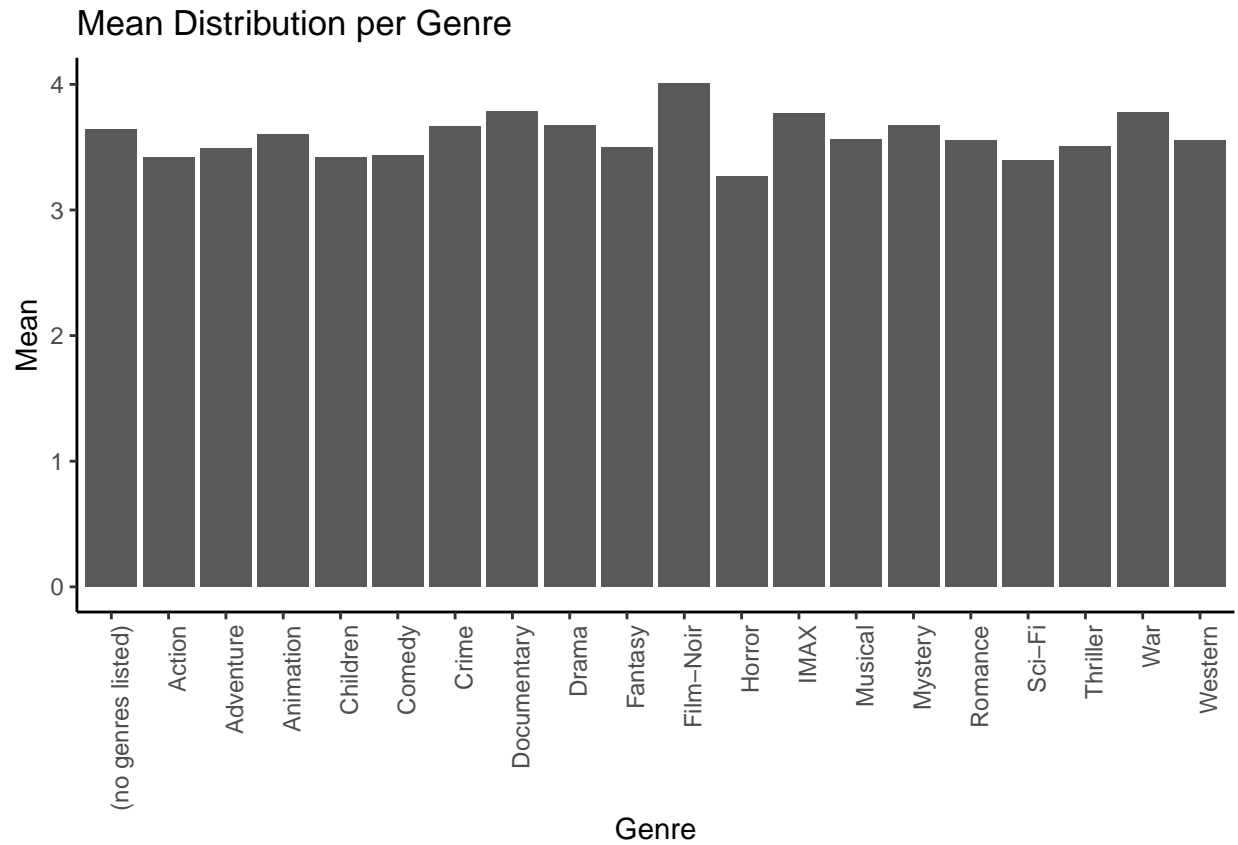
Below bar graph shows rating distribution over genre. Genre Drama and Comedy seems to be remain most and second most popular in terms of rating where as least rating has been recorded for genre type IMAX. Documentary remains second last in terms of receiving ratings. Another thing to be noted here is that 7 movies does not have genre.



genre	count
Drama	3910127
Comedy	3540930
Action	2560545
Thriller	2325899
Adventure	1908892
Romance	1712100
Sci-Fi	1341183
Crime	1327715
Fantasy	925637
Children	737994
Horror	691485
Mystery	568332
War	511147
Animation	467168
Musical	433080
Western	189394
Film-Noir	118541
Documentary	93066
IMAX	8181
(no genres listed)	7

2.4.2 Mean Distribution per Genre

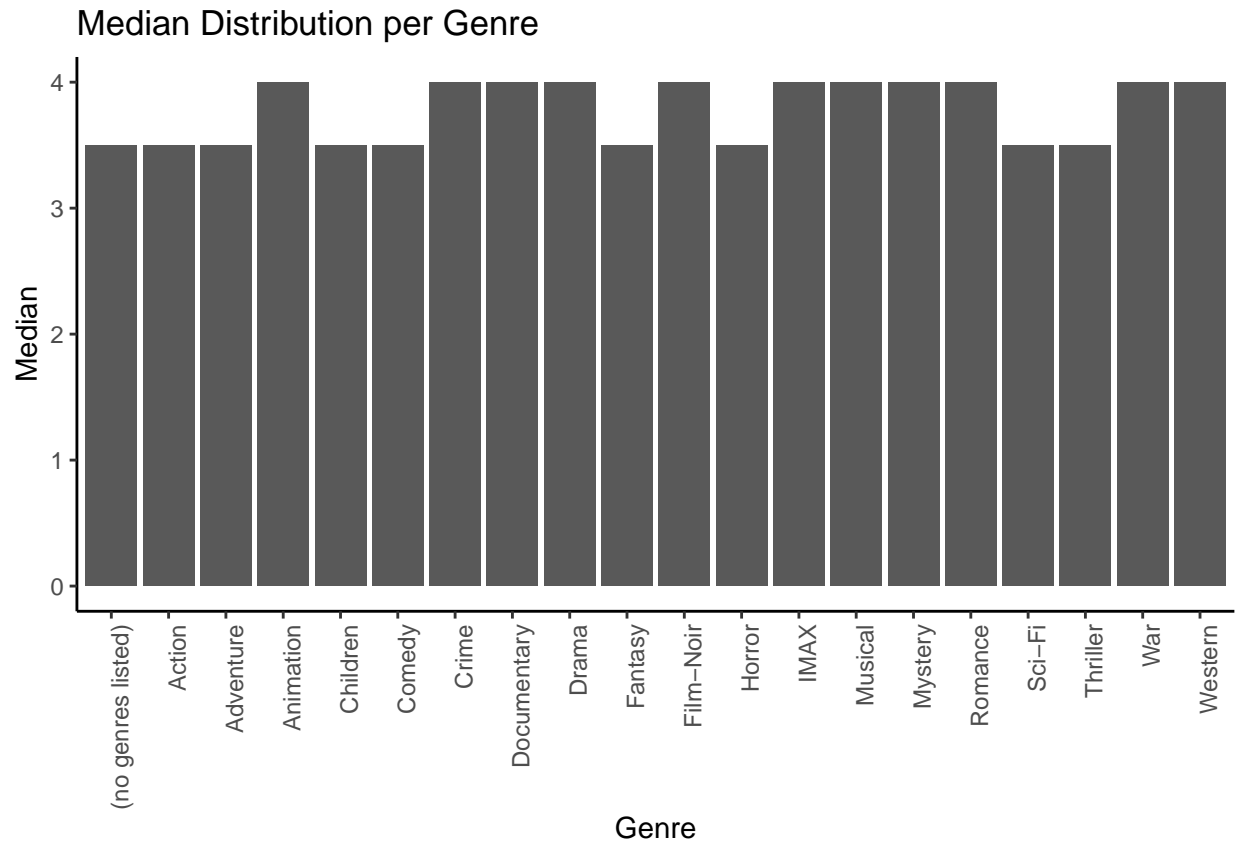
Below bar graph shows rating mean distribution per genre and it can be clearly seen that mean remains consistent around 3.5 with slight variance.



genre	mean
Film-Noir	4.011625
Documentary	3.783487
War	3.780813
IMAX	3.767693
Mystery	3.677001
Drama	3.673131
Crime	3.665925
(no genres listed)	3.642857
Animation	3.600644
Musical	3.563305
Western	3.555918
Romance	3.553813
Thriller	3.507676
Fantasy	3.501946
Adventure	3.493544
Comedy	3.436908
Action	3.421405
Children	3.418715
Sci-Fi	3.395743
Horror	3.269815

2.4.3 Median Distribution per Genre

Below bar graph shows rating median distribution per genre. Similar to mean, median remain consistence between 4 and 3.5 star rating.



genre	median
Animation	4.0
Crime	4.0
Documentary	4.0
Drama	4.0
Film-Noir	4.0
IMAX	4.0
Musical	4.0
Mystery	4.0
Romance	4.0
War	4.0
Western	4.0
(no genres listed)	3.5
Action	3.5
Adventure	3.5
Children	3.5
Comedy	3.5
Fantasy	3.5
Horror	3.5
Sci-Fi	3.5
Thriller	3.5

3 Analysis - Model Building and Evaluation

3.1 Naive Baseline Model

The simplest model that someone can build, is a Naive Model which ALWAYS predict the mean value. In this case, the mean is approximately equal to 3.5.

```
## [1] "The mean is: 3.52701897954609"
```

3.1.1 Naive Mean-Baseline Model

The formula used is:

$$Y_{u,i} = \hat{\mu} + \varepsilon_{u,i}$$

With $\hat{\mu}$ is the mean and $\varepsilon_{i,u}$ is the independent errors sampled from the same distribution centered at 0.

The RMSE on the **validation** dataset is **1.052**. It is very far from the target RMSE (below 0.87) which indicates poor performance for the model.

3.2 Movie-Based Model, a Content-based Approach

Taking content into account is first approach towards Non-Naive model. In this case, considering co-relation between higher and lower movie rating will result in better performance than Naive model.

The formula used is:

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

With $\hat{\mu}$ is the mean and $\varepsilon_{i,u}$ is the independent errors sampled from the same distribution centered at 0. The b_m is a measure for the popularity of movie m , i.e. the bias of movie m .

The RMSE on the **validation** dataset is **0.941**. It better than the Naive Mean-Baseline Model, but it is also very far from the target RMSE (below 0.87) which indicates poor performance model considering expectation of below 0.87 RMSE.

3.3 Movie + User Model, a User-based approach

The second Non-Naive Model consider that the users have different tastes and rate differently.

The formula used is:

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

With $\hat{\mu}$ is the mean and $\varepsilon_{i,u}$ is the independent errors sampled from the same distribution centered at 0. The b_m is a measure for the popularity of movie m , i.e. the bias of movie m . The b_u is a measure for the mildness of user u , i.e. the bias of user u .

The RMSE on the **validation** dataset is **0.8633** and very close to expected RMSE of 0.87. The Movie + User Based Model reaches the desired performance; however, regularization techniques may improve the performance with little margin. We will see result of regularization techniques in later paragraphs.

3.4 Movie + User + Genre Model, the Genre Popularity

The formula used is:

$$Y_{u,i} = \hat{\mu} + b_m + b_u + b_{u,g} + \epsilon_{u,i}$$

With $\hat{\mu}$ is the mean and $\epsilon_{i,u}$ is the independent errors sampled from the same distribution centered at 0. The b_m is a measure for the popularity of movie m , i.e. the bias of movie m . The b_u is a measure for the mildness of user u , i.e. the bias of user u . The $b_{u,g}$ is a measure for how much a user u likes the genre g .

The RMSE on the **validation** dataset is **0.8632** and this is very good result slightly better than Movie + User based model. The Movie + User + Genre Based Model reaches the desired performance but adding the **genre** predictor, doesn't improve significantly the model's performance. Applying the regularization techniques, can improve the performance just a little which we are going to explore in next section.

3.5 Regularization

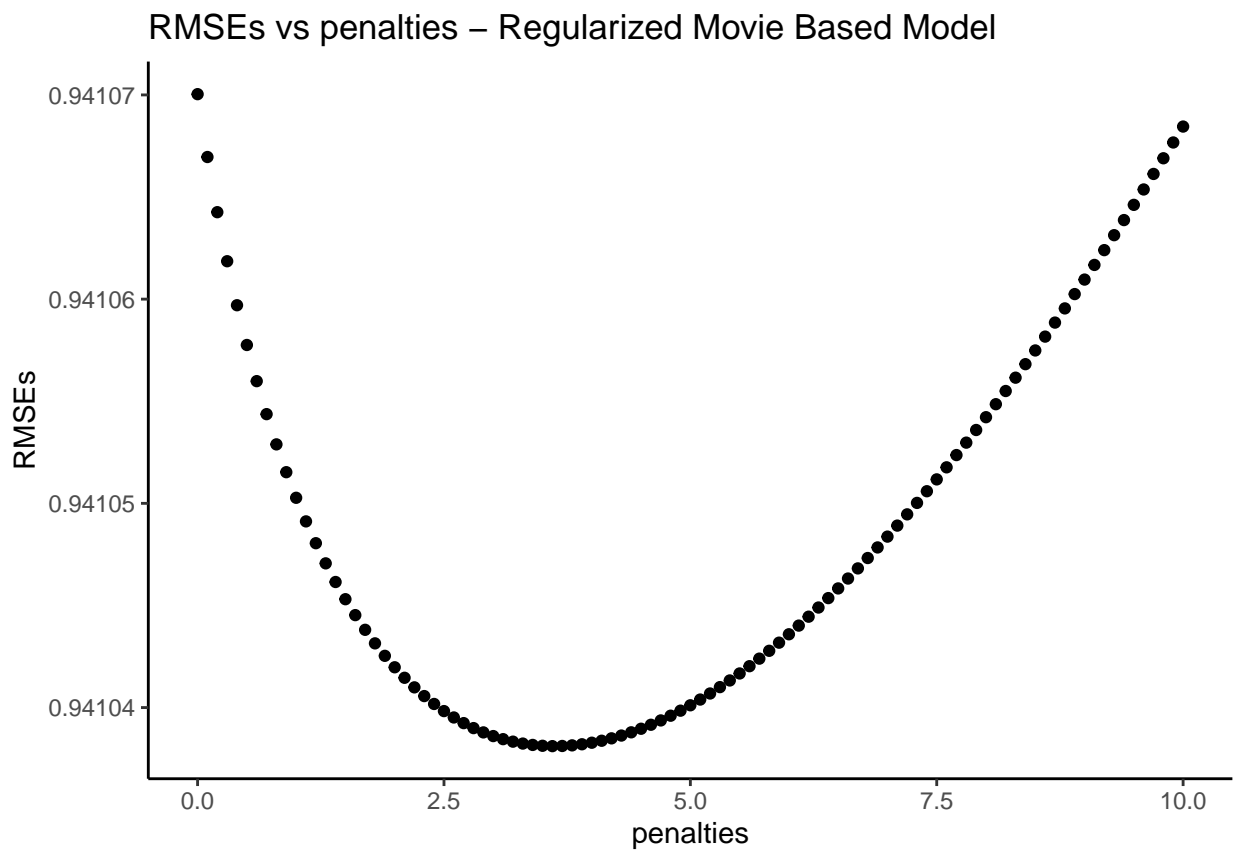
The regularization method allows us to add a penalty λ (lambda) to penalizes movies with large estimates from a small sample size. In order to optimize b_m , we can use below equation:

$$\frac{1}{N} \sum_{u,i} (y_{u,i} - \mu - b_i)^2 + \lambda \sum_i b_i^2$$

which can be further reduced to this equation:

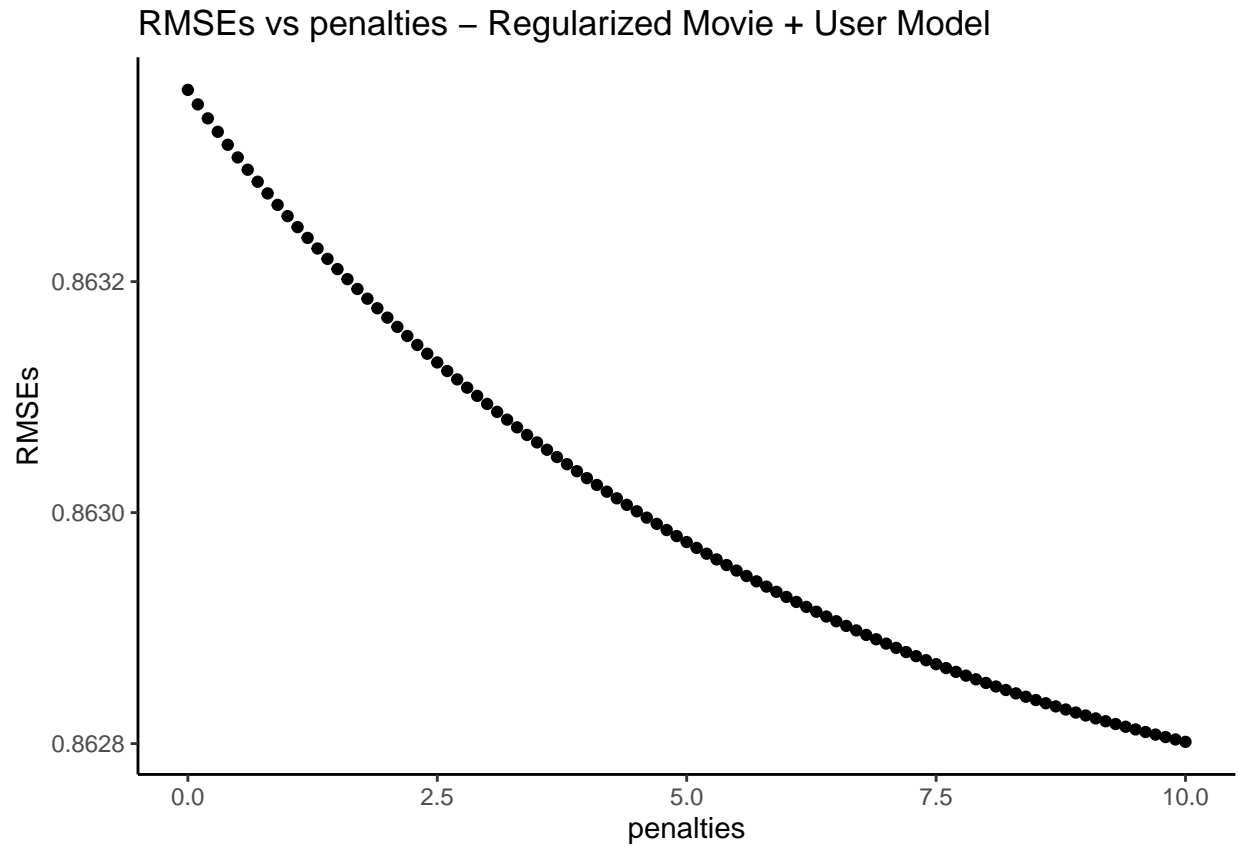
$$\hat{b}_i(\lambda) = \frac{1}{\lambda + n_i} \sum_{u=1}^{n_i} (Y_{u,i} - \hat{\mu})$$

3.5.1 Regularized Movie-Based Model



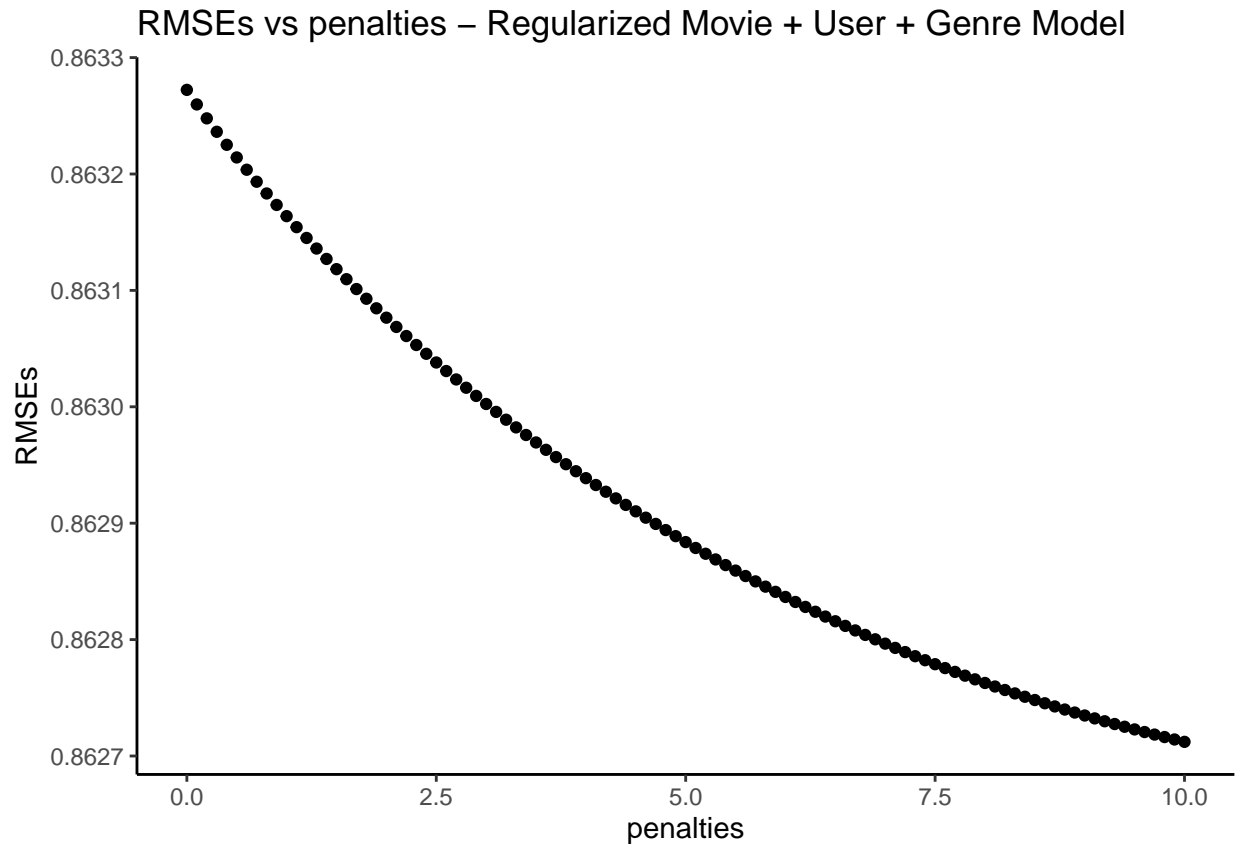
The RMSE on the `validation` dataset is **0.9410** and this is very far from desired RMSE of **0.87**. The Regularized Movie + User Based Model does not reaches the desired performance.

3.5.2 Regularized Movie + User Model



The RMSE on the **validation** dataset is **0.8628** and reaches the desired RMSE value. However, Regularized Movie + User Based Model improves by just a little as compared to the result of the Non-Regularized Movie + User Model which is **0.8633**.

3.5.3 Regularized Movie + User + Genre Model



The RMSE on the **validation** dataset is **0.8627** which is the best result among all models we have created so far. Although the Regularized Movie + User + Genre Based Model improves RMSE score by just a little as compared to the result of the Non-Regularized Movie + User + Genre Based Model RMSE score of **0.8632**, it performs better than all other models.

4 Results

Below table list all models built during this project using training **edx** dataset and validated on the **validation** dataset.

model	RMSE
Naive Mean - Baseline Model	1.0525579
Movie - Based Model	0.9410700
Movie + User Based Model	0.8633660
Movie + User + Genre Based Model	0.8632723
Regularized Movie - Based Model	0.9410381
Regularized Movie + User Based Model	0.8628015
Regularized Movie + User + Genre Based Model	0.8627121

5 Conclusion

Overall, **movieId** and **userId** contributes more than the **genre** predictor. Although desired performance can be achieved without applying regularization techniques, consider applying regularization technique will be a

good idea as it improves overall performance and reaches best RMSE score of **0.8627** which is best among all other trained models.

6 Appendix

6.1 1a - Initial Code provided by edX and code for MovieLens training and validation dataset preparation

```
#####
# Create edx set, validation set (final hold-out test set)
#####

# Note: this process could take a couple of minutes

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")
if(!require(data.table)) install.packages("data.table", repos = "http://cran.us.r-project.org")

library(tidyverse)
library(caret)
library(data.table)

# MovieLens 10M dataset:
# https://grouplens.org/datasets/movielens/10m/
# http://files.grouplens.org/datasets/movielens/ml-10m.zip

dl <- tempfile()
download.file("http://files.grouplens.org/datasets/movielens/ml-10m.zip", dl)

ratings <- fread(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")

# if using R 3.6 or earlier:
# movies <- as.data.frame(movies) %>% mutate(movieId = as.numeric(levels(movieId))[movieId],
#                                           title = as.character(title),
#                                           genres = as.character(genres))
# if using R 4.0 or later:
movies <- as.data.frame(movies) %>% mutate(movieId = as.numeric(movieId),
                                           title = as.character(title),
                                           genres = as.character(genres))

movielens <- left_join(ratings, movies, by = "movieId")

# Validation set will be 10% of MovieLens data
set.seed(1, sample.kind="Rounding") # if using R 3.5 or earlier, use `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 set
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)
```

6.2 1b - Code for MovieLens data analysis

```
#####
# MovieLens feature engineering and data analysis
#####

# Install all needed libraries if it is not present
if(!require(tidyverse)) install.packages("tidyverse")
if(!require(kableExtra)) install.packages("kableExtra")
if(!require(tidyr)) install.packages("tidyr")
if(!require(tidyverse)) install.packages("tidyverse")
if(!require(stringr)) install.packages("stringr")
if(!require(forcats)) install.packages("forcats")
if(!require(ggplot2)) install.packages("ggplot2")

# Loading all needed libraries
library(dplyr)
library(tidyverse)
library(kableExtra)
library(tidyr)
library(stringr)
library(forcats)
library(ggplot2)

# The general RMSE function that will be used to evaluate overall performance of models:
RMSE <- function(true_ratings = NULL, predicted_ratings = NULL) {
  sqrt(mean((true_ratings - predicted_ratings)^2))
}

# MovieLens data preparation work including feature engineering and data type correction
# Convert timestamp to a human readable date format in both training and validation dataset
edx$formated_timestamp <- as.POSIXct(edx$timestamp, origin="1970-01-01")
validation$formated_timestamp <- as.POSIXct(validation$timestamp, origin="1970-01-01")

# Extract the year and month of rating in both dataset
edx$yearOfRating <- format(edx$formated_timestamp,"%Y")
edx$monthOfRating <- format(edx$formated_timestamp,"%m")
validation$yearOfRating <- format(validation$formated_timestamp,"%Y")
validation$monthOfRating <- format(validation$formated_timestamp,"%m")

# Extract the year of release for each movie in both dataset
# edx dataset
edx <- edx %>%
  mutate(title = str_trim(title)) %>%
  extract(title, c("titleTemp", "release"), regex = "^(.*) \\((([0-9 \\-]*)\\))$", remove = F) %>%
  mutate(release = if_else(str_length(release) > 4, as.integer(str_split(release, "-", simplify = T)[1]
```

```

mutate(title = if_else(is.na(titleTemp), title, titleTemp)) %>%
select(-titleTemp)

# validation dataset
validation <- validation %>%
  mutate(title = str_trim(title)) %>%
  extract(title, c("titleTemp", "release"), regex = "^(.*) \\((([0-9 \\-]*)\\))$", remove = F) %>%
  mutate(release = if_else(str_length(release) > 4, as.integer(str_split(release, "-", simplify = T)[1]),
    mutate(title = if_else(is.na(titleTemp), title, titleTemp)) %>%
  select(-titleTemp)

# Extract the genre in edx datasets and label missing genre in case any to include them in summary
# Error in separate_rows(genre, sep = "\\|") : object 'genre' not found, thus need to first convert it
edx <- edx %>%
  mutate(genre = fct_explicit_na(genres, na_level = "(missing)")) %>%
  mutate(genre = as.character(genre)) %>%
  separate_rows(genre, sep = "\\|")

# Extract the genre in validation datasets
validation <- validation %>%
  mutate(genre = fct_explicit_na(genres, na_level = "(missing)")) %>%
  mutate(genre = as.character(genre)) %>%
  separate_rows(genre, sep = "\\|")

# remove unnecessary columns on both dataset
edx <- edx %>% select(userId, movieId, rating, title, genre, release, yearOfRating, monthOfRating)
validation <- validation %>% select(userId, movieId, rating, title, genre, release, yearOfRating, monthOfRating)

# Convert newly added features into numeric data type for calculation precision
edx$yearOfRating <- as.numeric(edx$yearOfRating)
edx$monthOfRating <- as.numeric(edx$monthOfRating)
edx$release <- as.numeric(edx$release)
validation$yearOfRating <- as.numeric(validation$yearOfRating)
validation$monthOfRating <- as.numeric(validation$monthOfRating)
validation$release <- as.numeric(validation$release)

# Models exploration

# Average by all movies rating
mu_hat <- mean(edx$rating)

# RMSE on the validation set
mean_model_rmse <- RMSE(validation$rating, mu_hat) #1.052 root mean square error

# Since we are going to explore other various methods/models,
# I need a variable to cache RMSE result of each for future reference.
results <- data.frame(model="Naive Mean - Baseline Model", RMSE=mean_model_rmse)

```

```

# Average by movie
movie_avgs <- edx %>%
  group_by(movieId) %>%
  summarize(b_m = mean(rating - mu_hat))

# Predicted ratings on validation dataset
movie_model_pred <- validation %>%
  left_join(movie_avgs, by='movieId') %>%
  mutate(pred = mu_hat + b_m) %>%
  pull(pred)

movie_model_rmse<- RMSE(validation$rating, movie_model_pred) # 0.941 RMSE

# Adding movie model to the results
results <- results %>% add_row(model="Movie - Based Model", RMSE=movie_model_rmse)

# Average by user
user_avgs <- edx %>%
  left_join(movie_avgs, by='movieId') %>%
  group_by(userId) %>%
  summarize(b_u = mean(rating - mu_hat - b_m))

# Predicted ratings on validation dataset using movie and user average
movie_user_pred <- validation %>%
  left_join(movie_avgs, by='movieId') %>%
  left_join(user_avgs, by='userId') %>%
  mutate(pred = mu_hat + b_m + b_u) %>%
  pull(pred)

movie_user_model_rmse <- RMSE(validation$rating, movie_user_pred)

# Adding movie user model to the results
results <- results %>% add_row(model="Movie + User Based Model", RMSE=movie_user_model_rmse)

# Average by genre
genre_avgs <- edx %>%
  left_join(movie_avgs, by='movieId') %>%
  left_join(user_avgs, by='userId') %>%
  group_by(genre) %>%
  summarize(b_u_g = mean(rating - mu_hat - b_m - b_u))

# Predicted ratings on validation dataset using movie, user, and genre
movie_user_genre_pred <- validation %>%
  left_join(movie_avgs, by='movieId') %>%
  left_join(user_avgs, by='userId') %>%
  left_join(genre_avgs, by='genre') %>%
  mutate(pred = mu_hat + b_m + b_u + b_u_g) %>%
  pull(pred)

movie_user_genre_model_rmse <- RMSE(validation$rating, movie_user_genre_pred) # 0.863 RMSE

# Adding movie user genre model to the results
results <- results %>% add_row(model="Movie + User + Genre Based Model", RMSE=movie_user_genre_model_rmse)

```

```

# Regularization to penalize movies with large estimates from small sample size.

# Penalty table
penalties <- seq(0, 10, 0.1)

# Predicted ratings on validation dataset using different values of penalties based on movie
rmses <- sapply(penalties, function(penalty) {

  # Average by movie
  b_m <- edx %>%
    group_by(movieId) %>%
    summarize(b_m = sum(rating - mu_hat) / (n() + penalty))

  # Compute the predicted ratings on validation dataset
  predicted_ratings <- validation %>%
    left_join(b_m, by='movieId') %>%
    mutate(pred = mu_hat + b_m) %>%
    pull(pred)

  # Predict the RMSE on the validation set
  return(RMSE(validation$rating, predicted_ratings))
})

# Get the penalty value that minimize the RMSE
min_penalty <- penalties[which.min(rmses)] # 3.6

# Predict the RMSE on the validation set
regularized_movie_model_rmse <- min(rmses) # 0.941 RMSE

# Adding the regularized movie model rmse to the results
results <- results %>% add_row(model="Regularized Movie - Based Model", RMSE=regularized_movie_model_rmse)

# Predicted ratings on validation dataset using different values of penalties based on movie and user
rmses <- sapply(penalties, function(penalty) {

  # Average by movie
  b_m <- edx %>%
    group_by(movieId) %>%
    summarize(b_m = sum(rating - mu_hat) / (n() + penalty))

  # Average by user and movie
  b_u <- edx %>%
    left_join(b_m, by='movieId') %>%
    group_by(userId) %>%
    summarize(b_u = sum(rating - b_m - mu_hat) / (n() + penalty))

  # Predicted ratings on validation dataset by movie and user
  predicted_ratings <- validation %>%
    left_join(b_m, by='movieId') %>%
    left_join(b_u, by='userId') %>%
    mutate(pred = mu_hat + b_m + b_u) %>%
    pull(pred)
})

```

```

    # Predict the RMSE on the validation set
    return(RMSE(validation$rating, predicted_ratings))
  })

# Get the penalty value that minimize the RMSE
min_penalty <- penalties[which.min(rmses)] # 10

# Predict the RMSE on the validation set
regularized_movie_user_model_rmse <- min(rmses) # 0.8628

# Adding the results to the results dataset
results <- results %>% add_row(model="Regularized Movie + User Based Model", RMSE=regularized_movie_user_model_rmse)

#####
# Testing above findings with higher penalties values for movie, user, and genre
#####

penalties <- seq(0, 15, 0.1)

# Compute the predicted ratings on validation dataset using different values of penalties
rmses <- sapply(penalties, function(penalty) {

  # Average by movie
  b_m <- edx %>%
    group_by(movieId) %>%
    summarize(b_m = sum(rating - mu_hat) / (n() + penalty))

  # Average by user
  b_u <- edx %>%
    left_join(b_m, by='movieId') %>%
    group_by(userId) %>%
    summarize(b_u = sum(rating - b_m - mu_hat) / (n() + penalty))

  # Average by movie and user
  b_u_g <- edx %>%
    left_join(b_m, by='movieId') %>%
    left_join(b_u, by='userId') %>%
    group_by(genre) %>%
    summarize(b_u_g = sum(rating - b_m - mu_hat - b_u) / (n() + penalty))

  # Compute the predicted ratings on validation dataset using movie, user, and genre
  predicted_ratings <- validation %>%
    left_join(b_m, by='movieId') %>%
    left_join(b_u, by='userId') %>%
    left_join(b_u_g, by='genre') %>%
    mutate(pred = mu_hat + b_m + b_u + b_u_g) %>%
    pull(pred)

  # Predict the RMSE on the validation set
  return(RMSE(validation$rating, predicted_ratings))
})

```

```

# Get the penalties value that minimize the RMSE
min_penalty <- penalties[which.min(rmses)] # 14.8

# Predict the RMSE on the validation set
regularized_movie_user_genre_model_rmse <- min(rmses) # 0.8626 (no improvement observed on higher penal.

# Adding the regularized movie user genre RMSE to the results
results <- results %>% add_row(model="Regularized Movie + User + Genre Based Model", RMSE=regularized_m

results

```

6.3 1c - Enviroment

```

print("Operating System:")
## [1] "Operating System:"

version

##
## platform      _
## arch          x86_64-mingw32
## os            mingw32
## system        x86_64, mingw32
## status
## major         4
## minor         0.2
## year          2020
## month         06
## day           22
## svn rev       78730
## language      R
## version.string R version 4.0.2 (2020-06-22)
## nickname      Taking Off Again

print("All installed packages")
## [1] "All installed packages"

installed.packages()

##           Package           LibPath
## abind          "abind"          "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## annotate        "annotate"      "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## AnnotationDbi  "AnnotationDbi" "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## arm            "arm"            "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## askpass        "askpass"        "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## assertthat     "assertthat"     "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## backports      "backports"      "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## base           "base"           "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## base64enc      "base64enc"      "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## BH             "BH"            "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## Biobase        "Biobase"        "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## BiocGenerics   "BiocGenerics"   "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## BiocManager    "BiocManager"    "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## BiocVersion    "BiocVersion"    "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## bit            "bit"            "C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## bit64          "bit64"          "C:/Users/niteshkg/Documents/R/R-4.0.2/library"

```

## bitops	"bitops"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## blob	"blob"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## boot	"boot"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## brew	"brew"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## broom	"broom"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## callr	"callr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## caret	"caret"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## caTools	"caTools"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## cellranger	"cellranger"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## data.table	"data.table"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## datasets	"datasets"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## DBI	"DBI"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## dbplyr	"dbplyr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## dslabs	"dslabs"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## e1071	"e1071"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## lubridate	"lubridate"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## magrittr	"magrittr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## markdown	"markdown"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"

## MASS	"MASS"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## Matrix	"Matrix"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## matrixStats	"matrixStats"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## mboost	"mboost"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## memoise	"memoise"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## methods	"methods"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## mgcv	"mgcv"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## mime	"mime"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## miniUI	"miniUI"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## minqa	"minqa"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## ModelMetrics	"ModelMetrics"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## modelr	"modelr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## monmlp	"monmlp"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## munsell	"munsell"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## mvtnorm	"mvtnorm"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## naivebayes	"naivebayes"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## nlme	"nlme"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## nloptr	"nloptr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## nnet	"nnet"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## nnls	"nnls"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## numDeriv	"numDeriv"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## openssl	"openssl"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## optimx	"optimx"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## parallel	"parallel"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## partykit	"partykit"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## pdftools	"pdftools"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## pillar	"pillar"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## pkgbuild	"pkgbuild"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## pkgconfig	"pkgconfig"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## pkgload	"pkgload"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## plyr	"plyr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## png	"png"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## praise	"praise"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## prettyunits	"prettyunits"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## pROC	"pROC"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## processx	"processx"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## progress	"progress"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## ps	"ps"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## purrr	"purrr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## qpdf	"qpdf"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## quadprog	"quadprog"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## questionr	"questionr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## R.cache	"R.cache"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## R.methodsS3	"R.methodsS3"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## R.oo	"R.oo"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## R.utils	"R.utils"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## R6	"R6"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## randomForest	"randomForest"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## ranger	"ranger"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rappdirs	"rappdirs"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## Rborist	"Rborist"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"

## rcmdcheck	"rcmdcheck"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## RColorBrewer	"RColorBrewer"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## Rcpp	"Rcpp"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## RcppEigen	"RcppEigen"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## RCurl	"RCurl"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## readr	"readr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## readxl	"readxl"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## recipes	"recipes"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rematch	"rematch"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rematch2	"rematch2"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## remotes	"remotes"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## reprex	"reprex"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## reshape2	"reshape2"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rex	"rex"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rlang	"rlang"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rmarkdown	"rmarkdown"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## roxygen2	"roxygen2"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rpart	"rpart"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rpart.plot	"rpart.plot"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rprojroot	"rprojroot"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## RSNNs	"RSNNs"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## RSQLite	"RSQLite"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rstudioapi	"rstudioapi"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rversions	"rversions"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## rvest	"rvest"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## S4Vectors	"S4Vectors"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## scales	"scales"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## selectr	"selectr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## sessioninfo	"sessioninfo"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## shiny	"shiny"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## SnowballC	"SnowballC"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## sourcetools	"sourcetools"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## spatial	"spatial"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## splines	"splines"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## SQUAREM	"SQUAREM"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## stats4	"stats4"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## stopwords	"stopwords"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## stringi	"stringi"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## stringr	"stringr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## styler	"styler"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## survival	"survival"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## sys	"sys"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tcltk	"tcltk"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## testthat	"testthat"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## textdata	"textdata"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tibble	"tibble"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tidyr	"tidyr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tidyselect	"tidyselect"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tidytext	"tidytext"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tidyverse	"tidyverse"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## timeDate	"timeDate"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"

## tinytex	"tinytex"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## titanic	"titanic"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tokenizers	"tokenizers"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## tools	"tools"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## translations	"translations"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## triebeard	"triebeard"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## urltools	"urltools"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## usethis	"usethis"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## utf8	"utf8"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## utils	"utils"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## vctrs	"vctrs"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## VGAM	"VGAM"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## viridis	"viridis"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## viridisLite	"viridisLite"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## webshot	"webshot"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## whisker	"whisker"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## withr	"withr"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## wsrf	"wsrf"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## xfun	"xfun"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## XML	"XML"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## xml2	"xml2"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## xopen	"xopen"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## xtable	"xtable"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
## yaml	"yaml"	"C:/Users/niteshkg/Documents/R/R-4.0.2/library"
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## abind	"1.4-5"	NA
## annotate	"1.66.0"	NA
## AnnotationDbi	"1.50.3"	NA
## arm	"1.11-2"	NA
## askpass	"1.1"	NA
## assertthat	"0.2.1"	NA
## backports	"1.1.9"	NA
## base	"4.0.2"	"base"
## base64enc	"0.1-3"	NA
## BH	"1.72.0-3"	NA
## Biobase	"2.48.0"	NA
## BiocGenerics	"0.34.0"	NA
## BiocManager	"1.30.10"	NA
## BiocVersion	"3.11.1"	NA
## bit	"4.0.4"	NA
## bit64	"4.0.5"	NA
## bitops	"1.0-6"	NA
## blob	"1.2.1"	NA
## boot	"1.3-25"	"recommended"
## brew	"1.0-6"	NA
## broom	"0.7.2"	NA
## callr	"3.5.1"	NA
## caret	"6.0-86"	NA
## caTools	"1.18.0"	NA
## cellranger	"1.1.0"	NA
## checkmate	"2.0.0"	NA
## class	"7.3-17"	"recommended"
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## cli	"2.1.0"	NA

## clipr	"0.7.1"	NA
## cluster	"2.1.0"	"recommended"
## coda	"0.19-4"	NA
## codetools	"0.2-16"	"recommended"
## colorspace	"1.4-1"	NA
## combinat	"0.0-8"	NA
## commonmark	"1.7"	NA
## compiler	"4.0.2"	"base"
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## cpp11	"0.2.3"	NA
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## crosstalk	"1.1.0.1"	NA
## curl	"4.3"	NA
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## datasets	"4.0.2"	"base"
## DBI	"1.1.0"	NA
## dbplyr	"1.4.4"	NA
## desc	"1.2.0"	NA
## devtools	"2.3.2"	NA
## digest	"0.6.27"	NA
## dplyr	"1.0.2"	NA
## dslabs	"0.7.3"	NA
## DT	"0.16"	NA
## e1071	"1.7-4"	NA
## ellipsis	"0.3.1"	NA
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## farver	"2.0.3"	NA
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## fastmap	"1.0.1"	NA
## forcats	"0.5.0"	NA
## foreach	"1.5.1"	NA
## foreign	"0.8-80"	"recommended"
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## fs	"1.5.0"	NA
## gam	"1.20"	NA
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## generics	"0.0.2"	NA
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## glue	"1.4.2"	NA
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## grid	"4.0.2"	"base"
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## gtable	"0.3.0"	NA
## gutenbergr	"0.2.0"	NA
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## htmlwidgets	"1.5.2"	NA
## httpuv	"1.5.4"	NA
## httr	"1.4.2"	NA
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## igraph	"1.2.6"	NA
## import	"1.2.0"	NA
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## ipred	"0.9-9"	NA
## IRanges	"2.22.2"	NA
## isoband	"0.2.2"	NA
## ISOcodes	"2020.03.16"	NA
## iterators	"1.0.13"	NA
## janeaustenr	"0.1.5"	NA
## jpeg	"0.1-8.1"	NA
## jsonlite	"1.7.1"	NA
## kableExtra	"1.3.1"	NA
## kernlab	"0.9-29"	NA
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## knitrLatex	"0.9.0"	NA
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## lava	"1.6.8"	NA
## lazyeval	"0.2.2"	NA
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## lifecycle	"0.2.0"	NA
## lme4	"1.1-25"	NA
## LogicReg	"1.6.2"	NA
## lubridate	"1.7.9"	NA
## magrittr	"1.5"	NA
## markdown	"1.1"	NA
## MASS	"7.3-53"	"recommended"
## Matrix	"1.2-18"	"recommended"
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## mboost	"2.9-3"	NA
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## miniUI	"0.1.1.1"	NA
## minqa	"1.2.4"	NA
## ModelMetrics	"1.2.2.2"	NA
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## monmlp	"1.1.5"	NA

## munsell	"0.5.0"	NA
## mvtnorm	"1.1-1"	NA
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## nlme	"3.1-148"	"recommended"
## nloptr	"1.2.2.2"	NA
## nnet	"7.3-14"	"recommended"
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## numDeriv	"2016.8-1.1"	NA
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## optimx	"2020-4.2"	NA
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## pillar	"1.4.6"	NA
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## png	"0.1-7"	NA
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## pROC	"1.16.2"	NA
## processx	"3.4.4"	NA
## prodlim	"2019.11.13"	NA
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## ps	"1.4.0"	NA
## purrr	"0.3.4"	NA
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## quadprog	"1.5-8"	NA
## questionr	"0.7.3"	NA
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## R.methodsS3	"1.8.1"	NA
## R.oo	"1.24.0"	NA
## R.utils	"2.10.1"	NA
## R6	"2.4.1"	NA
## randomForest	"4.6-14"	NA
## ranger	"0.12.1"	NA
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## reshape2	"1.4.4"	NA

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## RSNNS	"0.4-12"	NA
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## rstudioapi	"0.11"	NA
## rversions	"2.0.2"	NA
## rvest	"0.3.6"	NA
## S4Vectors	"0.26.1"	NA
## scales	"1.1.1"	NA
## selectr	"0.4-2"	NA
## sessioninfo	"1.1.1"	NA
## shiny	"1.5.0"	NA
## SnowballC	"0.7.0"	NA
## sourcetools	"0.1.7"	NA
## spatial	"7.3-12"	"recommended"
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## SQUAREM	"2020.5"	NA
## stabs	"0.6-3"	NA
## statmod	"1.4.35"	NA
## stats	"4.0.2"	"base"
## stats4	"4.0.2"	"base"
## stopwords	"2.0"	NA
## stringi	"1.5.3"	NA
## stringr	"1.4.0"	NA
## styler	"1.3.2"	NA
## survival	"3.1-12"	"recommended"
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## tcltk	"4.0.2"	"base"
## testthat	"2.3.2"	NA
## textdata	"0.4.1"	NA
## tibble	"3.0.3"	NA
## tidyr	"1.1.2"	NA
## tidyselect	"1.1.0"	NA
## tidytext	"0.2.6"	NA
## tidyverse	"1.3.0"	NA
## timeDate	"3043.102"	NA
## tinytex	"0.26"	NA
## titanic	"0.1.0"	NA
## tokenizers	"0.2.1"	NA
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## translations	"4.0.2"	NA
## triebeard	"0.3.0"	NA
## urltools	"1.7.3"	NA
## usethis	"1.6.3"	NA
## utf8	"1.1.4"	NA
## utils	"4.0.2"	"base"
## vctrs	"0.3.4"	NA
## VGAM	"1.1-4"	NA
## viridis	"0.5.1"	NA


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## viridisLite      "0.3.0"      NA
## webshot          "0.5.2"      NA
## whisker          "0.4"        NA
## withr            "2.3.0"      NA
## wsrfl            "1.7.17"     NA
## xfun             "0.18"       NA
## XML              "3.99-0.5"   NA
## xml2             "1.3.2"      NA
## xopen            "1.0.0"      NA
## xtable           "1.8-4"      NA
## yaml             "2.2.1"      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 (>= 0.29.2), Biobase (>= 1.17.0),
## arm               "R (>= 3.1.0), MASS, Matrix (>= 1.0), stats, lme4 (>= 1.0)"
## askpass           NA
## assertthat        NA
## backports         "R (>= 3.0.0)"
## base              NA
## base64enc         "R (>= 2.9.0)"
## BH                NA
## Biobase            "R (>= 2.10), BiocGenerics (>= 0.27.1), utils"
## BiocGenerics      "R (>= 3.6.0), methods, utils, graphics, stats, parallel"
## BiocManager       NA
## BiocVersion        "R (>= 4.0.0)"
## bit               "R (>= 2.9.2)"
## bit64             "R (>= 3.0.1), bit (>= 4.0.0), utils, methods, stats"
## bitops            NA
## blob              NA
## boot              "R (>= 3.0.0), graphics, stats"
## brew              NA
## broom             "R (>= 3.1)"
## callr             NA
## caret             "R (>= 3.2.0), lattice (>= 0.20), ggplot2"
## caTools           "R (>= 3.6.0)"
## cellranger        "R (>= 3.0.0)"
## checkmate         "R (>= 3.0.0)"
## class             "R (>= 3.0.0), stats, utils"
## classInt          "R (>= 2.2)"
## cli               "R (>= 2.10)"
## clipr             NA
## cluster           "R (>= 3.3.0)"
## coda              "R (>= 2.14.0)"
## codetools         "R (>= 2.1)"
## colorspace        "R (>= 3.0.0), methods"
## combinat          NA
## commonmark        NA
## compiler          NA
## covr              "R (>= 3.1.0), methods"
## cpp11             NA
## crayon            NA
## crosstalk         NA
## curl              "R (>= 3.0.0)"

```

```

## data.table      "R (>= 3.1.0)"
## datasets        NA
## DBI              "methods, R (>= 3.0.0)"
## dbplyr           "R (>= 3.1)"
## desc            "R (>= 3.1.0)"
## devtools        "R (>= 3.0.2), usethis (>= 1.6.3)"
## digest          "R (>= 3.3.0)"
## dplyr           "R (>= 3.2.0)"
## dslabs          "R (>= 3.1.2)"
## DT              NA
## e1071            NA
## ellipsis        "R (>= 3.2)"
## evaluate        "R (>= 3.0.2)"
## fansi           "R (>= 3.1.0)"
## farver          NA
## fastAdaboost    "R (>= 3.1.2)"
## fastmap         NA
## forcats         "R (>= 3.2)"
## foreach         "R (>= 2.5.0)"
## foreign         "R (>= 4.0.0)"
## Formula         "R (>= 2.0.0), stats"
## fs              "R (>= 3.1)"
## gam             "R (>= 3.5.0),stats, splines, foreach"
## gbm             "R (>= 2.9.0)"
## genefilter      NA
## generics        "R (>= 3.1)"
## ggplot2         "R (>= 3.2)"
## gh              NA
## git2r           "R (>= 3.1)"
## glue            "R (>= 3.2)"
## gower           NA
## graphics        NA
## grDevices       NA
## grid            NA
## gridExtra       NA
## gtable          "R (>= 3.0)"
## gutenbergr      "R (>= 2.10)"
## haven           "R (>= 3.2)"
## highr           "R (>= 3.2.3)"
## HistData        NA
## Hmisc           "lattice, survival (>= 3.1-6), Formula, ggplot2 (>= 2.2)"
## hms             NA
## htmlTable       NA
## htmltools       "R (>= 2.14.1)"
## htmlwidgets     NA
## httpuv          "R (>= 2.15.1)"
## httr            "R (>= 3.2)"
## hunspell        "R (>= 3.0.2)"
## 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 (>= 0.25.14)"

```

```

## isoband      NA
## ISOcodes     "R (>= 3.5.0)"
## iterators    "R (>= 2.5.0), utils"
## janeaustenr  "R (>= 3.1.2)"
## jpeg         "R (>= 2.9.0)"
## jsonlite     "methods"
## kableExtra   "R (>= 3.1.0)"
## kernlab      "R (>= 2.10)"
## KernSmooth   "R (>= 2.5.0), stats"
## kknn         "R (>= 2.10)"
## klaR         "R (>= 2.10.0), MASS"
## knitrLatex   "R (>= 3.2.0)"
## knitr        "R (>= 3.2.3)"
## labeling     NA
## labelled     NA
## Lahman       "R (>= 3.5.0)"
## later        NA
## lattice      "R (>= 3.0.0)"
## latticeExtra "R (>= 3.6.0), lattice"
## lava         "R (>= 3.5)"
## lazyeval     "R (>= 3.1.0)"
## libcoin      "R (>= 3.4.0)"
## lifecycle    "R (>= 3.2)"
## lme4         "R (>= 3.2.0), Matrix (>= 1.2-1), methods, stats"
## LogicReg     "R (>= 2.10), survival"
## lubridate    "methods, R (>= 3.2)"
## 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, stats (>= 0.5-0)"
## memoise      NA
## methods      NA
## mgcv         "R (>= 2.14.0), nlme (>= 3.1-64)"
## mime         NA
## miniUI       NA
## minqa        NA
## ModelMetrics "R (>= 3.2.2)"
## modelr       "R (>= 3.2)"
## monmlp       "optimx"
## munsell      NA
## mvtnorm      "R(>= 3.5.0)"
## naivebayes   NA
## nlme         "R (>= 3.4.0)"
## nloptr       NA
## nnet         "R (>= 3.0.0), stats, utils"
## nnls        NA
## numDeriv     "R (>= 2.11.1)"
## openssl      NA
## optimx       NA
## parallel     NA
## partykit     "R (>= 3.5.0), graphics, grid, libcoin (>= 1.0-0), mvtnorm"
## pdftools     NA

```

```

## pillar          NA
## pkgbuild        "R (>= 3.1)"
## pkgconfig       NA
## pkgload         NA
## plogr           NA
## plyr            "R (>= 3.1.0)"
## png             "R (>= 2.9.0)"
## praise         NA
## prettyunits     NA
## pROC            "R (>= 2.14)"
## processx       NA
## prodlim        "R (>= 2.9.0)"
## progress       NA
## promises       NA
## ps             "R (>= 3.1)"
## purrr          "R (>= 3.2)"
## qpdf           NA
## quadprog       "R (>= 3.1.0)"
## questionr      "R (>= 3.5.0)"
## R.cache        "R (>= 2.14.0)"
## R.methodsS3    "R (>= 2.13.0)"
## R.oo           "R (>= 2.13.0), R.methodsS3 (>= 1.8.0)"
## R.utils        "R (>= 2.14.0), R.oo (>= 1.23.0)"
## R6             "R (>= 3.0)"
## randomForest   "R (>= 3.2.2), stats"
## ranger         "R (>= 3.1)"
## rappdirs       "R (>= 2.14), methods"
## Rborist        "R(>= 3.3)"
## rcmdcheck      NA
## RColorBrewer   "R (>= 2.0.0)"
## Rcpp           NA
## RcppEigen      "R (>= 2.15.1)"
## RCurl          "R (>= 3.4.0), methods"
## readr          "R (>= 3.1)"
## readxl         NA
## recipes        "R (>= 3.1), dplyr"
## rematch        NA
## rematch2       NA
## remotes        "R (>= 3.0.0)"
## reprex         "R (>= 3.1)"
## reshape2       "R (>= 3.1)"
## rex            NA
## rlang          "R (>= 3.2.0)"
## rmarkdown      "R (>= 3.0)"
## roxygen2       "R (>= 3.2)"
## rpart          "R (>= 2.15.0), graphics, stats, grDevices"
## rpart.plot     "R (>= 3.4.0), rpart (>= 4.1-15)"
## rprojroot      "R (>= 3.0.0)"
## RSNNS          "R (>= 2.10.0), methods, Rcpp (>= 0.8.5)"
## RSQLite        "R (>= 3.1.0)"
## rstudioapi     NA
## rversions      NA
## rvest          "R (>= 3.2), xml2"
## S4Vectors      "R (>= 3.3.0), methods, utils, stats, stats4, BiocGenerics (>= \n0.31.1)"

```

```

## scales          "R (>= 3.2)"
## selectr         "R (>= 3.0)"
## sessioninfo     NA
## shiny           "R (>= 3.0.2), methods"
## SnowballC       NA
## sourcetools      "R (>= 3.0.2)"
## spatial          "R (>= 3.0.0), graphics, stats, utils"
## splines          NA
## SQUAREM          "R (>= 3.0)"
## stabs            "R (>= 2.14.0), methods, stats, parallel"
## statmod          "R (>= 3.0.0)"
## stats            NA
## stats4           NA
## stopwords        "R (>= 2.10)"
## stringi          "R (>= 2.14)"
## stringr          "R (>= 3.1)"
## styler           NA
## survival         "R (>= 3.4.0)"
## sys              NA
## tcltk            NA
## testthat         "R (>= 3.1)"
## textdata         NA
## tibble           "R (>= 3.1.0)"
## tidyr            "R (>= 3.1)"
## tidyselect       "R (>= 3.2)"
## tidytext         "R (>= 2.10)"
## tidyverse        "R (>= 3.2)"
## timeDate         "R (>= 2.15.1), graphics, utils, stats, methods"
## tinytex          NA
## titanic          "R (>= 3.1.2)"
## tokenizers       "R (>= 3.1.3)"
## tools            NA
## translations     NA
## triebeard        NA
## urltools         "R (>= 2.10)"
## usethis          "R (>= 3.2)"
## utf8             "R (>= 2.10)"
## utils            NA
## vctrs            "R (>= 3.2)"
## VGAM             "R (>= 3.4.0), methods, stats, stats4, splines"
## viridis          "R (>= 2.10), viridisLite (>= 0.3.0)"
## viridisLite      "R (>= 2.10)"
## webshot          "R (>= 3.0)"
## whisker          NA
## withr            "R (>= 3.2.0)"
## wsrfl            "parallel, R (>= 3.3.0), Rcpp (>= 0.10.2), stats"
## xfun             NA
## XML              "R (>= 4.0.0), methods, utils"
## xml2             "R (>= 3.1.0)"
## xopen            "R (>= 3.1)"
## xtable           "R (>= 2.10.0)"
## yaml             NA
## Imports
## abind            "methods, utils"

```

```

## annotate      "Biobase, DBI, xtable, graphics, utils, stats, methods,\nBiocGenerics (>= 0.13.8), RCu
## AnnotationDbi "DBI, RSQLite, S4Vectors (>= 0.9.25)"
## arm           "abind, coda, graphics, grDevices, Hmisc, methods, nlme, utils"
## askpass       "sys (>= 2.1)"
## assertthat    "tools"
## backports     "utils"
## base          NA
## base64enc     NA
## BH            NA
## Biobase       "methods"
## BiocGenerics  "methods, utils, graphics, stats, parallel"
## BiocManager   "utils"
## BiocVersion   NA
## bit           NA
## bit64         NA
## bitops        NA
## blob          "methods, rlang, vctrs (>= 0.2.1)"
## boot          NA
## brew          NA
## broom         "backports, dplyr (>= 1.0.0), ellipsis, generics (>= 0.0.2),\nnglue, methods, purrr, r
## callr         "processx (>= 3.4.4), R6, utils"
## caret         "foreach, methods, plyr, ModelMetrics (>= 1.2.2.2), nlme,\nreshape2, stats, stats4, ut
## caTools       "bitops"
## cellranger    "rematch, tibble"
## checkmate     "backports (>= 1.1.0), utils"
## class         "MASS"
## classInt      "grDevices, stats, graphics, e1071, class, KernSmooth"
## cli           "assertthat, crayon (>= 1.3.4), glue, methods, utils, fansi"
## clipr         "utils"
## cluster       "graphics, grDevices, stats, utils"
## coda          "lattice"
## codetools     NA
## colorspace    "graphics, grDevices, stats"
## combinat      NA
## commonmark    NA
## compiler      NA
## covr          "digest, stats, utils, jsonlite, rex, httr, crayon, withr (>=\n1.0.2), yaml"
## cpp11         NA
## crayon        "grDevices, methods, utils"
## crosstalk     "htmltools (>= 0.3.6), jsonlite, lazyeval, R6"
## curl          NA
## data.table    "methods"
## datasets      NA
## DBI           NA
## dbplyr        "assertthat (>= 0.2.0), DBI (>= 1.0.0), dplyr (>= 0.8.0), glue\n(>= 1.2.0), lifecycle,
## desc          "assertthat, utils, R6, crayon, rprojroot"
## devtools      "callr (>= 3.4.4), cli (>= 2.0.2), covr (>= 3.5.1), desc (>=\n1.2.0), DT (>= 0.15), el
## digest        "utils"
## dplyr         "ellipsis, generics, glue (>= 1.3.2), lifecycle (>= 0.2.0),\nmagrittr (>= 1.5), method
## dslabs        "ggplot2"
## DT            "htmltools (>= 0.3.6), htmlwidgets (>= 1.3), jsonlite (>=\n0.9.16), magrittr, crosstall
## e1071         "graphics, grDevices, class, stats, methods, utils"
## ellipsis      "rlang (>= 0.3.0)"
## evaluate      "methods"

```

```

## fansi                NA
## farver                NA
## fastAdaboost          "Rcpp, rpart"
## fastmap               NA
## forcats               "ellipsis, magrittr, rlang, tibble"
## foreach               "codetools, utils, iterators"
## foreign               "methods, utils, stats"
## Formula               NA
## fs                    "methods"
## gam                   NA
## gbm                   "lattice, parallel, survival"
## genefilter            "BiocGenerics (>= 0.31.2), AnnotationDbi, annotate, Biobase,\ngraphics, methods, stats"
## generics              "methods"
## ggplot2               "digest, glue, grDevices, grid, gtable (>= 0.1.1), isoband,\nMASS, mgcv, rlang (>= 0.3"
## gh                    "cli, ini, jsonlite, httr (>= 1.2)"
## git2r                 "graphics, utils"
## glue                  "methods"
## gower                 NA
## graphics              "grDevices"
## grDevices             NA
## grid                  "grDevices, utils"
## gridExtra             "gtable, grid, grDevices, graphics, utils"
## gtable                "grid"
## gutenbergr            "dplyr, readr, purrr, urltools, stringr, lazyeval"
## haven                 "forcats (>= 0.2.0), hms, methods, Rcpp (>= 0.11.4), readr (>=\n0.1.0), rlang (>= 0.4.0"
## highr                 NA
## HistData              NA
## Hmisc                 "methods, latticeExtra, cluster, rpart, nnet, foreign, gtable,\ngrid, gridExtra, data."
## hms                   "methods, pkgconfig, rlang, vctrs (>= 0.2.1)"
## htmlTable             "stringr, knitr (>= 1.6), magrittr (>= 1.5), methods,\nnccheckmate, htmlwidgets, htmltools"
## htmltools             "utils, digest, grDevices, base64enc, rlang"
## htmlwidgets           "grDevices, htmltools (>= 0.3), jsonlite (>= 0.9.16), yaml"
## httpuv                "Rcpp (>= 0.11.0), utils, R6, promises, later (>= 0.8.0)"
## httr                  "curl (>= 3.0.0), jsonlite, mime, openssl (>= 0.8), R6"
## hunspell              "Rcpp, digest"
## 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"
## isoband               "grid, utils"
## ISOcodes              NA
## iterators             NA
## janeaustenr           NA
## jpeg                  NA
## jsonlite              NA
## kableExtra            "knitr (>= 1.16), magrittr, stringr (>= 1.0), xml2 (>= 1.1.1),\nrrvest, rmarkdown (>= 1"
## kernlab               "methods, stats, grDevices, graphics"
## KernSmooth            NA
## kknk                  "igraph (>= 1.0), Matrix, stats, graphics"
## klaR                  "combinat, questionr, grDevices, stats, utils, graphics"
## knitLatex             "knitr (>= 1.10.5)"
## knitr                 "evaluate (>= 0.10), highr, markdown, stringr (>= 0.6), yaml\n(>= 2.1.19), methods, xfr

```

```

## labeling      "stats, graphics"
## labelled      "haven (>= 2.3.1), dplyr, lifecycle, rlang, vctrs, pillar,\ntidyr"
## Lahman        "dplyr"
## later         "Rcpp (>= 0.12.9), rlang"
## lattice       "grid, grDevices, graphics, stats, utils"
## latticeExtra  "grid, stats, utils, grDevices, png, jpeg, RColorBrewer"
## lava          "grDevices, graphics, methods, numDeriv, stats, survival,\nSQUAREM, utils"
## lazyeval      NA
## libcoin       "stats, mvtnorm"
## lifecycle     "glue, rlang (>= 0.4.0)"
## lme4          "graphics, grid, splines, utils, parallel, MASS, lattice, boot,\nnlme (>= 3.1-123), mi
## LogicReg      "stats, graphics, utils, grDevices"
## lubridate     "generics, Rcpp (>= 0.12.13)"
## magrittr      NA
## markdown      "utils, xfun, mime (>= 0.3)"
## MASS          "methods"
## Matrix        "methods, graphics, grid, stats, utils, lattice"
## matrixStats   NA
## mboost        "Matrix, survival, splines, lattice, nnls, quadprog, utils,\ngraphics, grDevices, part
## memoise       "digest (>= 0.6.3)"
## methods       "utils, stats"
## mgcv          "methods, stats, graphics, Matrix, splines, utils"
## mime          "tools"
## miniUI        "shiny (>= 0.13), htmltools (>= 0.3), utils"
## minqa         "Rcpp (>= 0.9.10)"
## ModelMetrics  "Rcpp, data.table"
## modelr        "broom, magrittr, purrr (>= 0.2.2), rlang (>= 0.2.0), tibble,\ntidyr (>= 0.8.0), tidys
## monmlp        NA
## munsell       "colorspace, methods"
## mvtnorm       "stats, methods"
## naivebayes    NA
## nlme          "graphics, stats, utils, lattice"
## nloptr        NA
## nnet          NA
## nnls          NA
## numDeriv      NA
## openssl       "askpass"
## optimx        "numDeriv"
## parallel      "tools, compiler"
## partykit      "grDevices, stats, utils, survival, Formula (>= 1.2-1), inum\n(>= 1.0-0), rpart (>= 4.
## pdftools      "Rcpp (>= 0.12.12), qpdf"
## pillar        "cli, crayon (>= 1.3.4), ellipsis, fansi, lifecycle, rlang (>= 1.0.3), utf8 (>= 1.1.0)
## pkgbuild      "callr (>= 3.2.0), cli, crayon, desc, prettyunits, R6,\nrprojroot, withr (>= 2.1.2)"
## pkgconfig     "utils"
## pkgload       "cli, crayon, desc, methods, pkgbuild, rlang, rprojroot,\nrstudioapi, utils, withr"
## plogr         NA
## plyr          "Rcpp (>= 0.11.0)"
## png           NA
## praise        NA
## prettyunits   NA
## pROC          "methods, plyr, Rcpp (>= 0.11.1)"
## processx      "ps (>= 1.2.0), R6, utils"
## prodlim       "Rcpp (>= 0.11.5), stats, grDevices, graphics, survival,\nKernSmooth, lava"
## progress      "hms, prettyunits, R6, crayon"

```



```

## promises      "R6, Rcpp, later, rlang, stats, magrittr"
## ps            "utils"
## purrr         "magrittr (>= 1.5), rlang (>= 0.3.1)"
## qpdf          "Rcpp, askpass, curl"
## quadprog      NA
## questionr     "shiny (>= 1.0.5), miniUI, rstudioapi, highr, styler, classInt,\nhtmltools, graphics, "
## R.cache       "utils, R.methodsS3 (>= 1.7.1), R.oo (>= 1.23.0), R.utils (>=\n2.8.0), digest (>= 0.6."
## R.methodsS3   "utils"
## R.oo          "methods, utils"
## R.utils       "methods, utils, tools, R.methodsS3 (>= 1.8.0)"
## R6            NA
## randomForest  NA
## ranger        "Rcpp (>= 0.11.2), Matrix"
## rappdirs      NA
## Rborist        "Rcpp (>= 0.12.2), data.table (>= 1.9.8), digest"
## rcmdcheck      "callr (>= 3.1.1.9000), cli (>= 1.1.0), crayon, desc (>=\n1.2.0), digest, pkgbuild, pr
## RColorBrewer   NA
## Rcpp           "methods, utils"
## RcppEigen      "Matrix (>= 1.1-0), Rcpp (>= 0.11.0), stats, utils"
## RCurl          "bitops"
## readr          "Rcpp (>= 0.12.0.5), tibble, hms (>= 0.4.1), R6, clipr, crayon,\nmethods"
## readxl         "cellranger, Rcpp (>= 0.12.18), tibble (>= 1.3.1), utils"
## recipes        "generics, glue, gower, ipred, lifecycle, lubridate, magrittr,\nMatrix, purrr (>= 0.2.
## rematch        NA
## rematch2       "tibble"
## remotes        "methods, stats, tools, utils"
## reprex         "callr (>= 2.0.0), clipr (>= 0.4.0), fs, rlang, rmarkdown,\nutils, whisker, withr"
## reshape2       "plyr (>= 1.8.1), Rcpp, stringr"
## rex            "lazyeval"
## rlang          NA
## rmarkdown      "tools, utils, knitr (>= 1.22), yaml (>= 2.1.19), htmltools (>=\n0.3.5), evaluate (>=
## roxygen2        "brew, commonmark, desc (>= 1.2.0), digest, knitr, methods,\npkgload (>= 1.0.2), purrr
## rpart          NA
## rpart.plot      NA
## rprojroot       "backports"
## RSNNS          NA
## RSQLite         "bit64, blob (>= 1.2.0), DBI (>= 1.1.0), memoise, methods,\npkgconfig, Rcpp (>= 0.12.7
## rstudioapi      NA
## rversions       "curl, utils, xml2 (>= 1.0.0)"
## rvest          "httr (>= 0.5), magrittr, selectr"
## S4Vectors       NA
## scales         "farver (>= 2.0.3), labeling, lifecycle, munsell (>= 0.5), R6,\nRColorBrewer, viridisL
## selectr         "methods, stringr, R6"
## sessioninfo     "cli, tools, utils, withr"
## shiny          "utils, grDevices, httpuv (>= 1.5.2), mime (>= 0.3), jsonlite\n(>= 0.9.16), xtable, di
## SnowballC       NA
## sourcetools     NA
## spatial         NA
## splines         "graphics, stats"
## SQUAREM        NA
## stabs           "graphics, grDevices, utils"
## statmod         "stats, graphics"
## stats          "utils, grDevices, graphics"
## stats4          "graphics, methods, stats"

```

```

## stopwords      "ISOcodes, usethis, desc"
## stringi        "tools, utils, stats"
## stringr        "glue (>= 1.2.0), magrittr, stringi (>= 1.1.7)"
## styler         "backports (>= 1.1.0), cli (>= 1.1.0), magrittr (>= 1.0.1), \npurrr (>= 0.2.3), R.cache
## survival       "graphics, Matrix, methods, splines, stats, utils"
## sys            NA
## tcltk          "utils"
## testthat       "cli, crayon (>= 1.3.4), digest, ellipsis, evaluate, magrittr, \nmetho
## textdata       "fs, readr, tibble, rappdirs"
## tibble         "cli, crayon (>= 1.3.4), ellipsis (>= 0.2.0), fansi (>= 0.4.0), \nlifecycle (>= 0.2.0),
## tidyr          "dplyr (>= 0.8.2), ellipsis (>= 0.1.0), glue, magrittr, purrr, \nrlang, tibble (>= 2.1.
## tidyselect     "ellipsis, glue (>= 1.3.0), purrr (>= 0.3.2), rlang (>= 0.4.6), \nvctrs (>= 0.2.2)"
## tidytext       "rlang, tibble, dplyr, stringr, hunspell, generics, Matrix, \ntokenizers, janeaustenr, p
## tidyverse      "broom (>= 0.5.2), cli (>= 1.1.0), crayon (>= 1.3.4), dbplyr\n(>= 1.4.2), dplyr (>= 0.
## timeDate       NA
## tinytex        "xfun (>= 0.5)"
## titanic        NA
## tokenizers     "stringi (>= 1.0.1), Rcpp (>= 0.12.3), SnowballC (>= 0.5.1)"
## tools          NA
## translations   NA
## triebeard      "Rcpp"
## urltools       "Rcpp, methods, triebeard"
## usethis        "clipr (>= 0.3.0), cli, crayon, curl (>= 2.7), desc, fs (>= \n1.3.0), gh (>= 1.1.0), gi
## utf8           NA
## utils          NA
## vctrs          "ellipsis (>= 0.2.0), digest, glue, rlang (>= 0.4.7)"
## VGAM           NA
## viridis        "stats, ggplot2 (>= 1.0.1), gridExtra"
## viridisLite    NA
## webshot        "magrittr, jsonlite, callr"
## whisker        NA
## withr          "graphics, grDevices, stats"
## wsrp          NA
## xfun           "stats, tools"
## XML            NA
## xml2           "methods"
## xopen          "processx"
## xtable         "stats, utils"
## yaml          NA
##               LinkingTo
## abind          NA
## annotate       NA
## AnnotationDbi  NA
## arm            NA
## askpass        NA
## assertthat     NA
## backports      NA
## base           NA
## base64enc      NA
## BH             NA
## Biobase        NA
## BiocGenerics   NA
## BiocManager    NA
## BiocVersion    NA

```

```

## bit                NA
## bit64              NA
## bitops             NA
## blob              NA
## boot              NA
## brew              NA
## broom             NA
## callr             NA
## caret             NA
## caTools           NA
## cellranger        NA
## checkmate         NA
## class             NA
## classInt          NA
## cli               NA
## clipr             NA
## cluster           NA
## coda              NA
## codetools         NA
## colorspace        NA
## combinat          NA
## commonmark        NA
## compiler          NA
## covr              NA
## cpp11             NA
## crayon            NA
## crosstalk         NA
## curl              NA
## data.table        NA
## datasets          NA
## DBI               NA
## dbplyr            NA
## desc              NA
## devtools          NA
## digest            NA
## dplyr             NA
## dslabs            NA
## DT                NA
## e1071             NA
## ellipsis          NA
## evaluate          NA
## fansi             NA
## farver            NA
## fastAdaboost      "Rcpp (>= 0.12.0)"
## fastmap           NA
## forcats           NA
## foreach           NA
## foreign           NA
## Formula           NA
## fs                NA
## gam               NA
## gbm               NA
## genefilter        NA
## generics          NA

```

```

## ggplot2      NA
## gh           NA
## git2r        NA
## glue         NA
## gower        NA
## graphics     NA
## grDevices    NA
## grid         NA
## gridExtra    NA
## gtable       NA
## gutenbergr   NA
## haven        "Rcpp"
## highr        NA
## HistData     NA
## Hmisc        NA
## hms          NA
## htmlTable    NA
## htmltools    NA
## htmlwidgets  NA
## httpuv       "Rcpp, BH, later"
## httr         NA
## hunspell     "Rcpp (>= 0.12.12)"
## igraph       NA
## import       NA
## ini          NA
## inum         NA
## ipred        NA
## IRanges      "S4Vectors"
## isoband      "testthat"
## ISOcodes     NA
## iterators    NA
## janeaustenr  NA
## jpeg         NA
## jsonlite     NA
## kableExtra   NA
## kernlab      NA
## KernSmooth   NA
## kkn          NA
## klaR         NA
## knitLatex    NA
## knitr        NA
## labeling     NA
## labelled     NA
## Lahman       NA
## later        "Rcpp, BH"
## lattice      NA
## latticeExtra NA
## lava         NA
## lazyeval     NA
## libcoin      "mvtnorm"
## lifecycle    NA
## lme4         "Rcpp (>= 0.10.5), RcppEigen"
## LogicReg     NA
## lubridate    "Rcpp"

```

```

## magrittr      NA
## markdown      NA
## MASS          NA
## Matrix        NA
## matrixStats   NA
## mboost        NA
## memoise       NA
## methods       NA
## mgcv          NA
## mime          NA
## miniUI        NA
## minqa         "Rcpp"
## ModelMetrics  "Rcpp"
## modelr        NA
## monmlp        NA
## munsell       NA
## mvtnorm       NA
## naivebayes    NA
## nlme          NA
## nloptr        NA
## nnet          NA
## nnls          NA
## numDeriv      NA
## openssl       NA
## optimx        NA
## parallel      NA
## partykit      NA
## pdftools      "Rcpp"
## pillar        NA
## pkgbuild      NA
## pkgconfig     NA
## pkgload       NA
## plogr         NA
## plyr          "Rcpp"
## png           NA
## praise        NA
## prettyunits   NA
## pROC          "Rcpp"
## processx      NA
## proclim       "Rcpp"
## progress      NA
## promises      "later, Rcpp"
## ps            NA
## purrr         NA
## qpdf          "Rcpp"
## quadprog      NA
## questionr     NA
## R.cache       NA
## R.methodsS3    NA
## R.oo          NA
## R.utils       NA
## R6            NA
## randomForest  NA
## ranger        "Rcpp, RcppEigen"

```

```

## rappdirs      NA
## Rborist       "Rcpp"
## rcmdcheck     NA
## RColorBrewer  NA
## Rcpp          NA
## RcppEigen     "Rcpp"
## RCurl         NA
## readr         "Rcpp, BH"
## readxl        "progress, Rcpp"
## recipes       NA
## rematch       NA
## rematch2      NA
## remotes       NA
## reprex        NA
## reshape2      "Rcpp"
## rex           NA
## rlang         NA
## rmarkdown     NA
## roxygen2      "Rcpp"
## rpart         NA
## rpart.plot    NA
## rprojroot     NA
## RSNNS         "Rcpp"
## RSQLite       "BH, plogr (>= 0.2.0), Rcpp"
## rstudioapi    NA
## rversions     NA
## rvest         NA
## S4Vectors     NA
## scales        NA
## selectr       NA
## sessioninfo   NA
## shiny         NA
## SnowballC     NA
## sourcetools   NA
## spatial       NA
## splines       NA
## SQUAREM       NA
## stabs         NA
## statmod       NA
## stats         NA
## stats4        NA
## stopwords     NA
## stringi       NA
## stringr       NA
## styler        NA
## survival      NA
## sys           NA
## tcltk         NA
## testthat      NA
## textdata      NA
## tibble        NA
## tidyr         "cpp11 (>= 0.2.1)"
## tidyselect    NA
## tidytext      NA

```

```

## tidyverse      NA
## timeDate       NA
## tinytex        NA
## titanic        NA
## tokenizers     "Rcpp"
## tools          NA
## translations   NA
## triebeard      "Rcpp"
## urltools       "Rcpp"
## usethis        NA
## utf8           NA
## utils          NA
## vctrs          NA
## VGAM           NA
## viridis        NA
## viridisLite    NA
## webshot        NA
## whisker        NA
## withr          NA
## wsrf           "Rcpp"
## xfun           NA
## XML            NA
## xml2           NA
## xopen          NA
## xtable         NA
## yaml           NA
##               Suggests
## abind          NA
## annotate       "hgu95av2.db, genefilter, Biostrings (>= 2.25.10), IRanges,\nrae230a.db, rae230aprobe,
## AnnotationDbi  "hgu95av2.db, GO.db, org.Sc.sgd.db, org.At.tair.db, KEGG.db,\nRUnit, TxDb.Hsapiens.UCS
## arm            NA
## askpass        "testthat"
## assertthat     "testthat, covr"
## backports      NA
## base           "methods"
## base64enc      NA
## BH             NA
## Biobase        "tools, tkWidgets, ALL, RUnit, golubEsets"
## BiocGenerics   "Biobase, S4Vectors, IRanges, GenomicRanges, DelayedArray,\nBiocstrings, Rsamtools, Anno
## BiocManager    "BiocStyle, BiocVersion, remotes, testthat, withr, curl, knitr"
## BiocVersion    NA
## bit            "testthat (>= 0.11.0), roxygen2, knitr, rmarkdown,\nmicrobenchmark, bit64 (>= 4.0.0),
## bit64          NA
## bitops         NA
## blob           "covr, crayon, pillar (>= 1.2.1), testthat"
## boot          "MASS, survival"
## brew          NA
## broom          "AER, akima, AUC, bbmle, betareg, biglm, binGroup, boot,\nbtergm, car, caret, cluster,
## callr          "cli, covr, crayon, fansi, pingr, ps, rprojroot, spelling,\ntestthat, tibble, withr (>
## caret          "BradleyTerry2, e1071, earth (>= 2.2-3), fastICA, gam (>=\n1.15), ipred, kernlab, knitr
## caTools        "MASS, rpart"
## cellranger     "covr, testthat (>= 1.0.0), knitr, rmarkdown"
## checkmate      "R6, fastmatch, data.table (>= 1.9.8), devtools, ggplot2,\nknitr, magrittr, microbench
## class          NA

```

```

## classInt      "spData (>= 0.2.6.2), units, knitr, rmarkdown"
## cli           "callr, covr, htmlwidgets, knitr, mockery, ps (>= 1.3.4.9000),\nrmarkdown, rstudioapi,
## clipr         "covr, knitr, rmarkdown, rstudioapi (>= 0.5), testthat (>=\n2.0.0)"
## cluster       "MASS, Matrix"
## coda          NA
## codetools     NA
## colorspace    "datasets, utils, KernSmooth, MASS, kernlab, mvtnorm, vcd,\ntcltk, shiny, shinyjs, ggplot2"
## combinat      NA
## commonmark    "curl, testthat, xml2"
## compiler      NA
## covr          "R6, curl, knitr, rmarkdown, htmltools, DT (>= 0.2), testthat,\nrlang, rstudioapi (>= 0.5),
## cpp11         "bench, brio, callr, cli, covr, decor, desc, ggplot2, glue,\nknitr, lobstr, mockery, ps, rmarkdown,
## crayon        "mockery, rstudioapi, testthat, withr"
## crosstalk     "shiny, ggplot2, testthat (>= 2.1.0)"
## curl          "spelling, testthat (>= 1.0.0), knitr, jsonlite, rmarkdown,\nmagrittr, httpuv (>= 1.4.0),
## data.table    "bit64, curl, R.utils, xts, nanotime, zoo, yaml, knitr,\nrmarkdown"
## datasets      NA
## DBI           "blob, covr, hms, knitr, magrittr, rmarkdown, rprojroot,\nRSQLite (>= 1.1-2), testthat (>= 1.0.0),
## dbplyr        "bit64, covr, knitr, Lahman, nycflights13, odbc, RMariaDB (>=\n1.0.2), rmarkdown, RPostgreSQL,
## desc          "covr, testthat, whoami, withr"
## devtools      "BiocManager (>= 1.30.10), curl (>= 4.3), digest (>= 0.6.25),\nfgl, fgltools, gert, gh, gitter,
## digest        "tinytest, knitr, rmarkdown, minidown"
## dplyr         "bench, broom, callr, covr, DBI, dbplyr (>= 1.4.3), knitr,\nLahman, lobstr, microbenchmark,
## dslabs        NA
## DT            "knitr (>= 1.8), rmarkdown, shiny (>= 1.2.0), testit"
## e1071         "cluster, mlbench, nnet, randomForest, rpart, SparseM, xtable,\nMatrix, MASS, slam"
## ellipsis      "covr, testthat"
## evaluate      "testthat, lattice, ggplot2"
## fansi         "unitizer, knitr, rmarkdown"
## farver        "testthat (>= 2.1.0), covr"
## fastAdaboost  "testthat, knitr, MASS"
## fastmap       "testthat (>= 2.1.1)"
## forcats       "covr, ggplot2, testthat, readr, knitr, rmarkdown, dplyr"
## foreach       "randomForest, doMC, doParallel, testthat, knitr, rmarkdown"
## foreign       NA
## Formula       NA
## fs            "testthat, covr, pillar (>= 1.0.0), tibble (>= 1.1.0), crayon,\nrmarkdown, knitr, withr"
## gam           "akima, testthat"
## gbm           "covr, gridExtra, knitr, pdp, RUnit, splines, tinytest, vip,\nviridis"
## genefilter    "class, hgu95av2.db, tkWidgets, ALL, ROC, DESeq, pasilla,\nRColorBrewer, BiocStyle, knitr,
## generics      "covr, pkgload, testthat, tibble"
## ggplot2       "covr, dplyr, ggplot2movies, hexbin, Hmisc, knitr, lattice,\nmapproj, maps, maptools, r,
## gh            "covr, keyring, pingr, testthat, withr"
## git2r         "getPass"
## glue          "testthat, covr, magrittr, crayon, knitr, rmarkdown, DBI,\nRSQLite, R.utils, forcats, r,
## gower         "tinytest (>= 0.9.3),"
## graphics      NA
## grDevices     "KernSmooth"
## grid          "lattice"
## gridExtra     "ggplot2, egg, lattice, knitr, testthat"
## gtable        "covr, testthat, knitr, rmarkdown, ggplot2, profvis"
## gutenbergr    "knitr, rmarkdown, testthat, tidytext, ggplot2, tidyr, curl"
## haven         "covr, fs, knitr, rmarkdown, testthat, pillar (>= 1.4.0), cli,\nncrayon"
## highr         "knitr, testit"

```



```

## HistData      "gtools, KernSmooth, maps, ggplot2, scales, proto, grid,\nreshape, plyr, lattice, jpeg
## Hmisc         "acepack, chron, rms, mice, tables, knitr, plotly (>= 4.5.6),\nrlang, plyr"
## hms           "crayon, lubridate, pillar (>= 1.1.0), testthat"
## htmlTable     "testthat, XML, xml2, Hmisc, reshape, rmarkdown, chron,\nlubridate, tibble, purrr, tid
## htmltools     "markdown, testthat, withr, Cairo, ragg"
## htmlwidgets   "knitr (>= 1.8), rmarkdown"
## httpuv        "testthat, callr, curl, websocket"
## httr          "covr, httpuv, jpeg, knitr, png, readr, rmarkdown, testthat\n(>= 0.8.0), xml2"
## hunspell      "spelling, testthat, pdftools, janeaustenr, wordcloud2, knitr,\nstopwords, rmarkdown"
## igraph        "ape, digest, graph, igraphdata, rgl, scales, stats4, tcltk,\ntestthat, withr"
## import        "knitr, rmarkdown, magrittr, testthat"
## ini           "testthat"
## inum          NA
## ipred         "mvtnorm, mlbench, TH.data"
## IRanges       "XVector, GenomicRanges, Rsamtools, GenomicAlignments,\nGenomicFeatures, BSgenome.Cele
## isoband       "covr, ggplot2, knitr, magick, microbenchmark, rmarkdown, sf,\ntestthat"
## ISOcodes      NA
## iterators     "RUnit, foreach"
## janeaustenr   "dplyr, testthat"
## jpeg          NA
## jsonlite      "httr, curl, plyr, testthat, knitr, rmarkdown, R.rsp, sf"
## kableExtra    "testthat, magick, formattable, sparkline"
## kernlab       NA
## KernSmooth    "MASS"
## kkn          NA
## klaR          "scatterplot3d (>= 0.3-22), som, mlbench, rpart, e1071"
## knitLatex     NA
## knitr         "formatR, testit, digest, rgl (>= 0.95.1201), codetools,\nrmarkdown, htmlwidgets (>= 0
## labeling      NA
## labelled      "testthat, knitr, rmarkdown, questionr, snakecase, utf8, covr"
## Lahman        "lattice, ggplot2, googleVis, data.table, vcd, reshape2,\ntidyr, knitr, rmarkdown, car
## later         "knitr, rmarkdown, testthat"
## lattice       "KernSmooth, MASS, latticeExtra"
## latticeExtra  "maps, mapproj, deldir, tripack, quantreg, zoo, MASS, mgcv"
## lava          "KernSmooth, Matrix, Rgraphviz, data.table, ellipse, fields,\nforeach, geepack, gof (>
## lazyeval      "knitr, rmarkdown (>= 0.2.65), testthat, covr"
## libcoin       "coin"
## lifecycle     "covr, crayon, knitr, rmarkdown, testthat (>= 2.1.0)"
## lme4          "knitr, rmarkdown, PKPDmodels, MEMSS, testthat (>= 0.8.1),\nggplot2, mlmRev, optimx (>
## LogicReg      NA
## lubridate     "covr, knitr, testthat (>= 2.1.0), vctrs (>= 0.3.0)"
## 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), randomF
## memoise       "testthat, aws.s3, httr, covr"
## methods       "codetools"
## mgcv          "parallel, survival, MASS"
## mime          NA
## miniUI        NA
## minqa         NA
## ModelMetrics  "testthat"

```

```

## modelr      "compiler, covr, ggplot2, testthat"
## monmlp      NA
## munsell     "ggplot2, testthat"
## mvtnorm     NA
## naivebayes  "knitr, Matrix"
## nlme        "Hmisc, MASS"
## nloptr      "testthat (>= 0.8.1), knitr, rmarkdown, inline (>= 0.3.14)"
## nnet        "MASS"
## nnls        NA
## numDeriv    NA
## openssl     "testthat (>= 2.1.0), digest, knitr, rmarkdown, jsonlite,\njose, sodium"
## optimx      "knitr, rmarkdown, setRNG, BB, ucminf, minqa, dfoptim,\n\nlbfgsb3c, lbfgs, subplex"
## parallel    "methods"
## partykit    "XML, pmml, rJava, sandwich, strucchange, vcd, AER, mlbench,\n\nnTH.data (>= 1.0-3), coin"
## pdftools    "jpeg, png, webp, tesseract, testthat"
## pillar      "bit64, knitr, lubridate, testthat (>= 2.0.0), withr"
## pkgbuild    "Rcpp, cpp11, testthat, covr"
## pkgconfig   "covr, testthat, disposables (>= 1.0.3)"
## pkgload     "bitops, covr, Rcpp, testthat"
## plogr       "Rcpp"
## plyr        "abind, covr, doParallel, foreach, iterators, itertools,\n\nntcltk, testthat"
## png         NA
## praise      "testthat"
## prettyunits "codetools, covr, testthat"
## pROC        "microbenchmark, tcltk, MASS, logcondens, doParallel,\n\nntestthat, vdiff, ggplot2"
## processx    "callr (>= 3.2.0), codetools, covr, crayon, curl, debugme,\n\nnparallel, testthat, withr"
## prodlim     NA
## progress    "Rcpp, testthat, withr"
## promises    "testthat, future, knitr, rmarkdown"
## ps          "callr, covr, curl, pingr, processx (>= 3.1.0), R6, rlang,\n\nntestthat, tibble"
## purrr       "covr, crayon, dplyr (>= 0.7.8), knitr, rmarkdown, testthat,\n\nntibble, tidyselect"
## qpdf        "testthat"
## quadprog    NA
## questionr   "testthat, roxygen2, dplyr, tidyr, janitor, forcats, knitr,\n\nnrmarkdown"
## R.cache     NA
## R.methodsS3 "codetools"
## R.oo        "tools"
## R.utils     "digest (>= 0.6.10)"
## R6          "knitr, microbenchmark, pryr, testthat, ggplot2, scales"
## randomForest "RColorBrewer, MASS"
## ranger      "survival, testthat"
## rappdirs    "testthat, roxygen2"
## Rborist      "testthat, knitr, rmarkdown"
## rcmdcheck    "covr, knitr, mockery, rmarkdown, testthat"
## RColorBrewer NA
## Rcpp         "tinytest, inline, rbenchmark, pkgKitten (>= 0.1.2)"
## RcppEigen    "inline, tinytest, pkgKitten, microbenchmark"
## RCurl        "XML"
## readr        "curl, testthat, knitr, rmarkdown, stringi, covr, spelling"
## readxl       "covr, knitr, rmarkdown, rprojroot (>= 1.1), testthat"
## recipes      "covr, ddalp, dimRed (>= 0.2.2), fastICA, ggplot2, igraph,\n\nnkernlab, knitr, modeldata"
## rematch      "covr, testthat"
## rematch2     "covr, testthat"
## remotes      "brew, callr, codetools, curl, covr, git2r (>= 0.23.0), knitr,\n\nnmockery, pkgbuild (>= 1.0.0)"

```

```

## reprex "covr, devtools, fortunes, knitr, miniUI, rprojroot,\nrstudioapi, shiny, styler (>= 1.0.0)"
## reshape2 "covr, lattice, testthat (>= 0.8.0)"
## rex "testthat, knitr, rmarkdown, dplyr, ggplot2, magrittr, Hmisc,\nstringr, rvest, roxygen2"
## rlang "cli, covr, crayon, glue, magrittr, methods, pillar,\nrmmarkdown, testthat (>= 2.3.0), vctrs"
## rmarkdown "shiny (>= 0.11), tufte, testthat, digest, dygraphs, vctrs,\nntibble, fs, rsconnect"
## roxygen2 "covr, devtools, rmarkdown, testthat (>= 2.1.0), R.methodsS3,\nR.oo"
## rpart "survival"
## rpart.plot "earth (>= 5.1.2)"
## rprojroot "testthat, mockr, knitr, withr, rmarkdown"
## RSNNS "scatterplot3d,NeuralNetTools"
## RSQLite "DBItest (>= 1.7.0), knitr, rmarkdown, testthat"
## rstudioapi "testthat, knitr, rmarkdown, clipr"
## rversions "mockery, testthat"
## rvest "covr, knitr, png, rmarkdown, spelling, stringi (>= 0.3.1),\nntestthat"
## S4Vectors "IRanges, GenomicRanges, SummarizedExperiment, Matrix,\nDelayedArray, ShortRead, graph"
## scales "bit64, covr, dichromat, ggplot2, hms (>= 0.5.0), testthat (>=\n2.1.0)"
## selectr "testthat, XML, xml2"
## sessioninfo "callr, covr, mockery, testthat"
## shiny "datasets, Cairo (>= 1.5-5), testthat (>= 2.1.1), knitr (>=\n1.6), markdown, rmarkdown"
## SnowballC NA
## sourcetools "testthat"
## spatial "MASS"
## splines "Matrix, methods"
## SQUAREM "setRNG"
## stabs "glmnet, lars, mboost (> 2.3-0), gamboostLSS (>= 1.2-0), QUIC,\nTH.data, hdi, testthat"
## statmod "MASS, tweedie"
## stats "MASS, Matrix, SuppDists, methods, stats4"
## stats4 NA
## stopwords "covr, lintr, quanteda, spelling, testthat"
## stringi NA
## stringr "covr, htmltools, htmlwidgets, knitr, rmarkdown, testthat"
## styler "data.tree (>= 0.1.6), digest, dplyr, here, knitr, prettycode,\nrmmarkdown, rstudioapi"
## survival NA
## sys "unix (>= 1.4), spelling, testthat"
## tcltk NA
## testthat "covr, curl (>= 0.9.5), devtools, knitr, rmarkdown, usethis,\nvctrs (>= 0.1.0), xml2"
## textdata "knitr, rmarkdown, testthat (>= 2.1.0), covr"
## tibble "bench, bit64, blob, covr, dplyr, evaluate, formattable, hms,\nhtmltools, import, knitr"
## tidyr "covr, jsonlite, knitr, repurrrsive (>= 1.0.0), rmarkdown,\nreadr, testthat (>= 2.1.0)"
## tidyselect "covr, crayon, dplyr, knitr, magrittr, rmarkdown, testthat (>=\n2.3.0), tibble (>= 2.1.0)"
## tidytext "readr, tidyr, XML, tm, quanteda, knitr, rmarkdown, ggplot2,\nreshape2, wordcloud, top"
## tidyverse "covr, feather, glue, knitr, rmarkdown, testthat"
## timeDate "date, RUnit"
## tinytex "testit, rstudioapi"
## titanic "dplyr"
## tokenizers "covr, knitr, rmarkdown, stopwords (>= 0.9.0), testthat"
## tools "codetools, methods, xml2, curl, commonmark"
## translations NA
## triebeard "knitr, rmarkdown, testthat"
## urltools "testthat, knitr"
## usethis "covr, knitr, magick, pkgdown (>= 1.4.0), rmarkdown, roxygen2,\nspelling (>= 1.2), styler"
## utf8 "knitr, rmarkdown, testthat"
## utils "methods, xml2, commonmark"
## vctrs "bit64, covr, crayon, dplyr (>= 0.8.5), generics, knitr,\nnpillar (>= 1.4.4), pkgdown, r"

```

```

## VGAM                "VGAMextra, MASS, mgcv"
## viridis             "hexbin (>= 1.27.0), scales, MASS, knitr, dichromat,\ncolorspace, rasterVis, httr, map"
## viridisLite         "hexbin (>= 1.27.0), ggplot2 (>= 1.0.1), testthat, covr"
## webshot             "httpuv, knitr, rmarkdown, shiny"
## whisker             "markdown"
## withr               "covr, DBI, knitr, lattice, methods, rmarkdown, RSQLite,\ntestthat (>= 2.1.0)"
## wsrf                "knitr (>= 1.5), party (>= 1.0.7), randomForest (>= 4.6.7),\nrattle.data (>= 1.0.2), s"
## xfun                "testit, parallel, codetools, rstudioapi, tinytex, mime,\nmardown, knitr, htmltools, "
## XML                 "bitops, RCurl"
## xml2                "covr, curl, httr, knitr, magrittr, mockery, rmarkdown,\ntestthat (>= 2.1.0)"
## xopen               "ps, testthat"
## xtable              "knitr, plm, zoo, survival"
## yaml               "RUnit"
##                     Enhances
## abind               NA
## annotate            NA
## AnnotationDbi       NA
## arm                 NA
## askpass             NA
## assertthat         NA
## backports           NA
## base                NA
## base64enc           "png"
## BH                  NA
## Biobase             NA
## BiocGenerics        NA
## BiocManager         NA
## BiocVersion         NA
## bit                 NA
## bit64              NA
## bitops              NA
## blob                NA
## boot                NA
## brew                NA
## broom               NA
## callr               NA
## caret               NA
## caTools             NA
## cellranger          NA
## checkmate           NA
## class               NA
## classInt            NA
## cli                 NA
## clipr               NA
## cluster             NA
## coda                NA
## codetools           NA
## colorspace          NA
## combinat            NA
## commonmark          NA
## compiler            NA
## covr                NA
## cpp11               NA
## crayon              NA

```

## crosstalk	NA
## curl	NA
## data.table	NA
## datasets	NA
## DBI	NA
## dbplyr	NA
## desc	NA
## devtools	NA
## digest	NA
## dplyr	NA
## dslabs	NA
## DT	NA
## e1071	NA
## ellipsis	NA
## evaluate	NA
## fansi	NA
## farver	NA
## fastAdaboost	NA
## fastmap	NA
## forcats	NA
## foreach	NA
## foreign	NA
## Formula	NA
## fs	NA
## gam	NA
## gbm	NA
## genefilter	NA
## generics	NA
## ggplot2	"sp"
## gh	NA
## git2r	NA
## glue	NA
## gower	NA
## graphics	NA
## grDevices	NA
## grid	NA
## gridExtra	NA
## gtable	NA
## gutenbergr	NA
## haven	NA
## highr	NA
## HistData	NA
## Hmisc	NA
## hms	NA
## htmlTable	NA
## htmltools	"knitr"
## htmlwidgets	"shiny (>= 1.1)"
## httpuv	NA
## httr	NA
## hunspell	NA
## igraph	NA
## import	NA
## ini	NA
## inum	NA

```

## ipred          NA
## IRanges        NA
## isoband        NA
## ISOcodes       NA
## iterators      NA
## janeaustenr    NA
## jpeg           NA
## jsonlite       NA
## kableExtra     NA
## kernlab        NA
## KernSmooth     NA
## kknk           NA
## klaR           NA
## knitrLatex     NA
## knitr          NA
## labeling       NA
## labelled       "memisc"
## Lahman         NA
## later          NA
## lattice        "chron"
## latticeExtra   NA
## lava           NA
## lazyeval       NA
## libcoin        NA
## lifecycle      NA
## lme4           NA
## LogicReg       NA
## lubridate      "chron, timeDate, tis, zoo"
## 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
## minqa          NA
## ModelMetrics   NA
## modelr         NA
## monmlp         NA
## munsell        NA
## mvtnorm        NA
## naivebayes     NA
## nlme           NA
## nloptr         NA
## nnet           NA
## nnls          NA
## numDeriv       NA
## openssl        NA
## optimx         NA
## parallel       "snow, nws, Rmpi"

```

## partykit	NA
## pdftools	NA
## pillar	NA
## pkgbuild	NA
## pkgconfig	NA
## pkgload	NA
## plogr	NA
## plyr	NA
## png	NA
## praise	NA
## prettyunits	NA
## pROC	NA
## processx	NA
## prodlim	NA
## progress	NA
## promises	NA
## ps	NA
## purrr	NA
## qpdf	NA
## quadprog	NA
## questionr	NA
## R.cache	NA
## R.methodsS3	NA
## R.oo	NA
## R.utils	NA
## R6	NA
## randomForest	NA
## ranger	NA
## rappdirs	NA
## Rborist	NA
## rcmdcheck	NA
## RColorBrewer	NA
## Rcpp	NA
## RcppEigen	NA
## RCurl	NA
## readr	NA
## readxl	NA
## recipes	NA
## rematch	NA
## rematch2	NA
## remotes	NA
## reprex	NA
## reshape2	NA
## rex	NA
## rlang	NA
## rmarkdown	NA
## roxygen2	NA
## rpart	NA
## rpart.plot	NA
## rprojroot	NA
## RSNNS	NA
## RSQLite	NA
## rstudioapi	NA
## rversions	NA

## rvest	NA
## S4Vectors	NA
## scales	NA
## selectr	NA
## sessioninfo	NA
## shiny	NA
## SnowballC	NA
## sourcetools	NA
## spatial	NA
## splines	NA
## SQUAREM	NA
## stabs	NA
## statmod	NA
## stats	NA
## stats4	NA
## stopwords	NA
## stringi	NA
## stringr	NA
## styler	NA
## survival	NA
## sys	NA
## tcltk	NA
## testthat	NA
## textdata	NA
## tibble	NA
## tidyr	NA
## tidyselect	NA
## tidytext	NA
## tidyverse	NA
## timeDate	NA
## tinytex	NA
## titanic	NA
## tokenizers	NA
## tools	NA
## translations	NA
## triebeard	NA
## urltools	NA
## usethis	NA
## utf8	NA
## utils	NA
## vctrs	NA
## VGAM	"VGAMdata"
## viridis	NA
## viridisLite	NA
## webshot	NA
## whisker	NA
## withr	NA
## wsrfr	NA
## xfun	NA
## XML	NA
## xml2	NA
## xopen	NA
## xtable	NA
## yaml	NA

##	License	License_is_FOSS
## abind	"LGPL (>= 2)"	NA
## annotate	"Artistic-2.0"	NA
## AnnotationDbi	"Artistic-2.0"	NA
## arm	"GPL (> 2)"	NA
## askpass	"MIT + file LICENSE"	NA
## assertthat	"GPL-3"	NA
## backports	"GPL-2 GPL-3"	NA
## base	"Part of R 4.0.2"	NA
## base64enc	"GPL-2 GPL-3"	NA
## BH	"BSL-1.0"	NA
## Biobase	"Artistic-2.0"	NA
## BiocGenerics	"Artistic-2.0"	NA
## BiocManager	"Artistic-2.0"	NA
## BiocVersion	"Artistic-2.0"	NA
## bit	"GPL-2 GPL-3"	NA
## bit64	"GPL-2 GPL-3"	NA
## bitops	"GPL (>= 2)"	NA
## blob	"GPL-3"	NA
## boot	"Unlimited"	NA
## brew	"GPL-2"	NA
## broom	"MIT + file LICENSE"	NA
## callr	"MIT + file LICENSE"	NA
## caret	"GPL (>= 2)"	NA
## caTools	"GPL-3"	NA
## cellranger	"MIT + file LICENSE"	NA
## checkmate	"BSD_3_clause + file LICENSE"	NA
## class	"GPL-2 GPL-3"	NA
## classInt	"GPL (>= 2)"	NA
## cli	"MIT + file LICENSE"	NA
## clipr	"GPL-3"	NA
## cluster	"GPL (>= 2)"	NA
## coda	"GPL (>= 2)"	NA
## codetools	"GPL"	NA
## colorspace	"BSD_3_clause + file LICENSE"	NA
## combinat	"GPL-2"	NA
## commonmark	"BSD_2_clause + file LICENSE"	NA
## compiler	"Part of R 4.0.2"	NA
## covr	"GPL-3"	NA
## cpp11	"MIT + file LICENSE"	NA
## crayon	"MIT + file LICENSE"	NA
## crosstalk	"MIT + file LICENSE"	NA
## curl	"MIT + file LICENSE"	NA
## data.table	"MPL-2.0 file LICENSE"	NA
## datasets	"Part of R 4.0.2"	NA
## DBI	"LGPL (>= 2.1)"	NA
## dbplyr	"MIT + file LICENSE"	NA
## desc	"MIT + file LICENSE"	NA
## devtools	"GPL (>= 2)"	NA
## digest	"GPL (>= 2)"	NA
## dplyr	"MIT + file LICENSE"	NA
## dslabs	"Artistic-2.0"	NA
## DT	"GPL-3 file LICENSE"	NA
## e1071	"GPL-2 GPL-3"	NA

## ellipsis	"GPL-3"	NA
## evaluate	"MIT + file LICENSE"	NA
## fansi	"GPL (>= 2)"	NA
## farver	"MIT + file LICENSE"	NA
## fastAdaboost	"MIT + file LICENSE"	NA
## fastmap	"MIT + file LICENSE"	NA
## forcats	"GPL-3"	NA
## foreach	"Apache License (== 2.0)"	NA
## foreign	"GPL (>= 2)"	NA
## Formula	"GPL-2 GPL-3"	NA
## fs	"GPL-3"	NA
## gam	"GPL-2"	NA
## gbm	"GPL (>= 2) file LICENSE"	NA
## genefilter	"Artistic-2.0"	NA
## generics	"GPL-2"	NA
## ggplot2	"GPL-2 file LICENSE"	NA
## gh	"MIT + file LICENSE"	NA
## git2r	"GPL-2"	NA
## glue	"MIT + file LICENSE"	NA
## gower	"GPL-3"	NA
## graphics	"Part of R 4.0.2"	NA
## grDevices	"Part of R 4.0.2"	NA
## grid	"Part of R 4.0.2"	NA
## gridExtra	"GPL (>= 2)"	NA
## gtable	"GPL-2"	NA
## gutenbergr	"GPL-2"	NA
## haven	"MIT + file LICENSE"	NA
## highr	"GPL"	NA
## HistData	"GPL"	NA
## Hmisc	"GPL (>= 2)"	NA
## hms	"GPL-3"	NA
## htmlTable	"GPL (>= 3)"	NA
## htmltools	"GPL (>= 2)"	NA
## htmlwidgets	"MIT + file LICENSE"	NA
## httpuv	"GPL (>= 2) file LICENSE"	NA
## httr	"MIT + file LICENSE"	NA
## hunspell	"GPL-2 LGPL-2.1 MPL-1.1"	NA
## igraph	"GPL (>= 2)"	NA
## import	"MIT + file LICENSE"	NA
## ini	"GPL-3"	NA
## inum	"GPL-2"	NA
## ipred	"GPL (>= 2)"	NA
## IRanges	"Artistic-2.0"	NA
## isoband	"MIT + file LICENSE"	NA
## ISOcodes	"GPL-2"	NA
## iterators	"Apache License (== 2.0)"	NA
## janeaustenr	"MIT + file LICENSE"	NA
## jpeg	"GPL-2 GPL-3"	NA
## jsonlite	"MIT + file LICENSE"	NA
## kableExtra	"MIT + file LICENSE"	NA
## kernlab	"GPL-2"	NA
## KernSmooth	"Unlimited"	NA
## kkn	"GPL (>= 2)"	NA
## klaR	"GPL-2 GPL-3"	NA

## knitrLatex	"GPL-3"	NA
## knitr	"GPL"	NA
## labeling	"MIT + file LICENSE Unlimited"	NA
## labelled	"GPL-3"	NA
## Lahman	"GPL"	NA
## later	"GPL (>= 2)"	NA
## lattice	"GPL (>= 2)"	NA
## latticeExtra	"GPL (>= 2)"	NA
## lava	"GPL-3"	NA
## lazyeval	"GPL-3"	NA
## libcoin	"GPL-2"	NA
## lifecycle	"GPL-3"	NA
## lme4	"GPL (>= 2)"	NA
## LogicReg	"GPL (>= 2)"	NA
## lubridate	"GPL (>= 2)"	NA
## magrittr	"MIT + file LICENSE"	NA
## markdown	"GPL-2"	NA
## MASS	"GPL-2 GPL-3"	NA
## Matrix	"GPL (>= 2) file LICENCE"	NA
## matrixStats	"Artistic-2.0"	NA
## mboost	"GPL-2"	NA
## memoise	"MIT + file LICENSE"	NA
## methods	"Part of R 4.0.2"	NA
## mgcv	"GPL (>= 2)"	NA
## mime	"GPL"	NA
## miniUI	"GPL-3"	NA
## minqa	"GPL-2"	NA
## ModelMetrics	"GPL (>= 2)"	NA
## modelr	"GPL-3"	NA
## monmlp	"GPL-2"	NA
## munsell	"MIT + file LICENSE"	NA
## mvtnorm	"GPL-2"	NA
## naivebayes	"GPL-2"	NA
## nlme	"GPL (>= 2) file LICENCE"	NA
## nloptr	"LGPL-3"	NA
## nnet	"GPL-2 GPL-3"	NA
## nnls	"GPL (>= 2)"	NA
## numDeriv	"GPL-2"	NA
## openssl	"MIT + file LICENSE"	NA
## optimx	"GPL-2"	NA
## parallel	"Part of R 4.0.2"	NA
## partykit	"GPL-2 GPL-3"	NA
## pdftools	"MIT + file LICENSE"	NA
## pillar	"GPL-3"	NA
## pkgbuild	"GPL-3"	NA
## pkgconfig	"MIT + file LICENSE"	NA
## pkgload	"GPL-3"	NA
## plogr	"MIT + file LICENSE"	NA
## plyr	"MIT + file LICENSE"	NA
## png	"GPL-2 GPL-3"	NA
## praise	"MIT + file LICENSE"	NA
## prettyunits	"MIT + file LICENSE"	NA
## pROC	"GPL (>= 3)"	NA
## processx	"MIT + file LICENSE"	NA

## prodlim	"GPL (>= 2)"	NA
## progress	"MIT + file LICENSE"	NA
## promises	"MIT + file LICENSE"	NA
## ps	"MIT + file LICENSE"	NA
## purrr	"GPL-3 file LICENSE"	NA
## qpdf	"Apache License 2.0"	NA
## quadprog	"GPL (>= 2)"	NA
## questionr	"GPL (>= 2)"	NA
## R.cache	"LGPL (>= 2.1)"	NA
## R.methodsS3	"LGPL (>= 2.1)"	NA
## R.oo	"LGPL (>= 2.1)"	NA
## R.utils	"LGPL (>= 2.1)"	NA
## R6	"MIT + file LICENSE"	NA
## randomForest	"GPL (>= 2)"	NA
## ranger	"GPL-3"	NA
## rappdirs	"MIT + file LICENSE"	NA
## Rborist	"MPL (>= 2) GPL (>= 2) file LICENSE"	NA
## rcmdcheck	"MIT + file LICENSE"	NA
## RColorBrewer	"Apache License 2.0"	NA
## Rcpp	"GPL (>= 2)"	NA
## RcppEigen	"GPL (>= 2) file LICENSE"	NA
## RCurl	"BSD_3_clause + file LICENSE"	NA
## readr	"GPL (>= 2) file LICENSE"	NA
## readxl	"GPL-3"	NA
## recipes	"GPL-2"	NA
## rematch	"MIT + file LICENSE"	NA
## rematch2	"MIT + file LICENSE"	NA
## remotes	"GPL (>= 2)"	NA
## reprex	"MIT + file LICENSE"	NA
## reshape2	"MIT + file LICENSE"	NA
## rex	"MIT + file LICENSE"	NA
## rlang	"GPL-3"	NA
## rmarkdown	"GPL-3"	NA
## roxygen2	"GPL (>= 2)"	NA
## rpart	"GPL-2 GPL-3"	NA
## rpart.plot	"GPL-3"	NA
## rprojroot	"GPL-3"	NA
## RSNNS	"LGPL (>= 2) file LICENSE"	NA
## RSQLite	"LGPL (>= 2.1)"	NA
## rstudioapi	"MIT + file LICENSE"	NA
## rversions	"MIT + file LICENSE"	NA
## rvest	"GPL-3"	NA
## S4Vectors	"Artistic-2.0"	NA
## scales	"MIT + file LICENSE"	NA
## selectr	"BSD_3_clause + file LICENCE"	NA
## sessioninfo	"GPL-2"	NA
## shiny	"GPL-3 file LICENSE"	NA
## SnowballC	"BSD_3_clause + file LICENSE"	NA
## sourcetools	"MIT + file LICENSE"	NA
## spatial	"GPL-2 GPL-3"	NA
## splines	"Part of R 4.0.2"	NA
## SQUAREM	"GPL (>= 2)"	NA
## stabs	"GPL-2"	NA
## statmod	"GPL-2 GPL-3"	NA

## stats	"Part of R 4.0.2"	NA
## stats4	"Part of R 4.0.2"	NA
## stopwords	"MIT + file LICENSE"	NA
## stringi	"file LICENSE"	NA
## stringr	"GPL-2 file LICENSE"	NA
## styler	"GPL-3"	NA
## survival	"LGPL (>= 2)"	NA
## sys	"MIT + file LICENSE"	NA
## tcltk	"Part of R 4.0.2"	NA
## testthat	"MIT + file LICENSE"	NA
## textdata	"MIT + file LICENSE"	NA
## tibble	"MIT + file LICENSE"	NA
## tidyr	"MIT + file LICENSE"	NA
## tidyselect	"GPL-3"	NA
## tidytext	"MIT + file LICENSE"	NA
## tidyverse	"GPL-3 file LICENSE"	NA
## timeDate	"GPL (>= 2)"	NA
## tinytex	"MIT + file LICENSE"	NA
## titanic	"CC0"	NA
## tokenizers	"MIT + file LICENSE"	NA
## tools	"Part of R 4.0.2"	NA
## translations	"Part of R 4.0.2"	NA
## triebeard	"MIT + file LICENSE"	NA
## urltools	"MIT + file LICENSE"	NA
## usethis	"GPL-3"	NA
## utf8	"Apache License (== 2.0) file LICENSE"	NA
## utils	"Part of R 4.0.2"	NA
## vctrs	"GPL-3"	NA
## VGAM	"GPL-3"	NA
## viridis	"MIT + file LICENSE"	NA
## viridisLite	"MIT + file LICENSE"	NA
## webshot	"GPL-2"	NA
## whisker	"GPL-3"	NA
## withr	"GPL (>= 2)"	NA
## wsrfr	"GPL (>= 2)"	NA
## xfun	"MIT + file LICENSE"	NA
## XML	"BSD_3_clause + file LICENSE"	NA
## xml2	"GPL (>= 2)"	NA
## xopen	"MIT + file LICENSE"	NA
## xtable	"GPL (>= 2)"	NA
## yaml	"BSD_3_clause + file LICENSE"	NA
##	License_restricts_use OS_type MD5sum NeedsCompilation Built	
## abind	NA NA NA "no" "4.0.3"	
## annotate	NA NA NA "no" "4.0.0"	
## AnnotationDbi	NA NA NA "no" "4.0.2"	
## arm	NA NA NA "no" "4.0.3"	
## askpass	NA NA NA "yes" "4.0.2"	
## assertthat	NA NA NA "no" "4.0.2"	
## backports	NA NA NA "yes" "4.0.2"	
## base	NA NA NA NA "4.0.2"	
## base64enc	NA NA NA "yes" "4.0.0"	
## BH	NA NA NA "no" "4.0.0"	
## Biobase	NA NA NA "yes" "4.0.0"	
## BiocGenerics	NA NA NA "no" "4.0.0"	

## BiocManager	NA	NA	NA	"no"	"4.0.3"
## BiocVersion	NA	NA	NA	"no"	"4.0.0"
## bit	NA	NA	NA	"yes"	"4.0.3"
## bit64	NA	NA	NA	"yes"	"4.0.3"
## bitops	NA	NA	NA	"yes"	"4.0.3"
## blob	NA	NA	NA	"no"	"4.0.2"
## boot	NA	NA	NA	"no"	"4.0.2"
## brew	NA	NA	NA	NA	"4.0.0"
## broom	NA	NA	NA	"no"	"4.0.3"
## callr	NA	NA	NA	"no"	"4.0.3"
## caret	NA	NA	NA	"yes"	"4.0.2"
## caTools	NA	NA	NA	"yes"	"4.0.3"
## cellranger	NA	NA	NA	"no"	"4.0.2"
## checkmate	NA	NA	NA	"yes"	"4.0.3"
## class	NA	NA	NA	"yes"	"4.0.2"
## classInt	NA	NA	NA	"yes"	"4.0.3"
## cli	NA	NA	NA	"no"	"4.0.3"
## clipr	NA	NA	NA	"no"	"4.0.3"
## cluster	NA	NA	NA	"yes"	"4.0.2"
## coda	NA	NA	NA	"no"	"4.0.3"
## codetools	NA	NA	NA	"no"	"4.0.2"
## colorspace	NA	NA	NA	"yes"	"4.0.2"
## combinat	NA	NA	NA	NA	"4.0.3"
## commonmark	NA	NA	NA	"yes"	"4.0.2"
## compiler	NA	NA	NA	NA	"4.0.2"
## covr	NA	NA	NA	"yes"	"4.0.3"
## cpp11	NA	NA	NA	"no"	"4.0.3"
## crayon	NA	NA	NA	"no"	"4.0.2"
## crosstalk	NA	NA	NA	"no"	"4.0.2"
## curl	NA	NA	NA	"yes"	"4.0.2"
## data.table	NA	NA	NA	"yes"	"4.0.2"
## datasets	NA	NA	NA	NA	"4.0.2"
## DBI	NA	NA	NA	"no"	"4.0.2"
## dbplyr	NA	NA	NA	"no"	"4.0.2"
## desc	NA	NA	NA	"no"	"4.0.2"
## devtools	NA	NA	NA	"no"	"4.0.3"
## digest	NA	NA	NA	"yes"	"4.0.3"
## dplyr	NA	NA	NA	"yes"	"4.0.2"
## dslabs	NA	NA	NA	"no"	"4.0.2"
## DT	NA	NA	NA	"no"	"4.0.3"
## e1071	NA	NA	NA	"yes"	"4.0.3"
## ellipsis	NA	NA	NA	"yes"	"4.0.2"
## evaluate	NA	NA	NA	"no"	"4.0.2"
## fansi	NA	NA	NA	"yes"	"4.0.2"
## farver	NA	NA	NA	"yes"	"4.0.2"
## fastAdaboost	NA	NA	NA	"yes"	"4.0.3"
## fastmap	NA	NA	NA	"yes"	"4.0.3"
## forcats	NA	NA	NA	"no"	"4.0.2"
## foreach	NA	NA	NA	"no"	"4.0.3"
## foreign	NA	NA	NA	"yes"	"4.0.2"
## Formula	NA	NA	NA	"no"	"4.0.3"
## fs	NA	NA	NA	"yes"	"4.0.2"
## gam	NA	NA	NA	"yes"	"4.0.3"
## gbm	NA	NA	NA	"yes"	"4.0.3"

## genefilter	NA	NA	NA	"yes"	"4.0.0"
## generics	NA	NA	NA	"no"	"4.0.2"
## ggplot2	NA	NA	NA	"no"	"4.0.2"
## gh	NA	NA	NA	"no"	"4.0.2"
## git2r	NA	NA	NA	"yes"	"4.0.2"
## glue	NA	NA	NA	"yes"	"4.0.2"
## gower	NA	NA	NA	"yes"	"4.0.2"
## graphics	NA	NA	NA	"yes"	"4.0.2"
## grDevices	NA	NA	NA	"yes"	"4.0.2"
## grid	NA	NA	NA	"yes"	"4.0.2"
## gridExtra	NA	NA	NA	"no"	"4.0.3"
## gtable	NA	NA	NA	"no"	"4.0.2"
## gutenbergr	NA	NA	NA	"no"	"4.0.3"
## haven	NA	NA	NA	"yes"	"4.0.2"
## highr	NA	NA	NA	"no"	"4.0.2"
## HistData	NA	NA	NA	"no"	"4.0.2"
## Hmisc	NA	NA	NA	"yes"	"4.0.3"
## hms	NA	NA	NA	"no"	"4.0.2"
## htmlTable	NA	NA	NA	"no"	"4.0.3"
## htmltools	NA	NA	NA	"yes"	"4.0.2"
## htmlwidgets	NA	NA	NA	"no"	"4.0.3"
## httpuv	NA	NA	NA	"yes"	"4.0.3"
## httr	NA	NA	NA	"no"	"4.0.2"
## hunspell	NA	NA	NA	"yes"	"4.0.2"
## igraph	NA	NA	NA	"yes"	"4.0.3"
## import	NA	NA	NA	"no"	"4.0.3"
## ini	NA	NA	NA	"no"	"4.0.2"
## inum	NA	NA	NA	"no"	"4.0.3"
## ipred	NA	NA	NA	"yes"	"4.0.2"
## IRanges	NA	NA	NA	"yes"	"4.0.0"
## isoband	NA	NA	NA	"yes"	"4.0.2"
## ISOcodes	NA	NA	NA	"no"	"4.0.0"
## iterators	NA	NA	NA	"no"	"4.0.3"
## janeaustenr	NA	NA	NA	"no"	"4.0.2"
## jpeg	NA	NA	NA	"yes"	"4.0.3"
## jsonlite	NA	NA	NA	"yes"	"4.0.2"
## kableExtra	NA	NA	NA	"no"	"4.0.3"
## kernlab	NA	NA	NA	"yes"	"4.0.3"
## KernSmooth	NA	NA	NA	"yes"	"4.0.2"
## kkn	NA	NA	NA	"yes"	"4.0.3"
## klaR	NA	NA	NA	"no"	"4.0.3"
## knitrLatex	NA	NA	NA	"no"	"4.0.3"
## knitr	NA	NA	NA	"no"	"4.0.3"
## labeling	NA	NA	NA	"no"	"4.0.3"
## labelled	NA	NA	NA	"no"	"4.0.3"
## Lahman	NA	NA	NA	"no"	"4.0.2"
## later	NA	NA	NA	"yes"	"4.0.2"
## lattice	NA	NA	NA	"yes"	"4.0.2"
## latticeExtra	NA	NA	NA	"no"	"4.0.3"
## lava	NA	NA	NA	"no"	"4.0.2"
## lazyeval	NA	NA	NA	"yes"	"4.0.2"
## libcoin	NA	NA	NA	"yes"	"4.0.3"
## lifecycle	NA	NA	NA	"no"	"4.0.2"
## lme4	NA	NA	NA	"yes"	"4.0.3"

## LogicReg	NA	NA	NA	"yes"	"4.0.3"
## lubridate	NA	NA	NA	"yes"	"4.0.2"
## magrittr	NA	NA	NA	"no"	"4.0.2"
## markdown	NA	NA	NA	"yes"	"4.0.2"
## MASS	NA	NA	NA	"yes"	"4.0.3"
## Matrix	NA	NA	NA	"yes"	"4.0.2"
## matrixStats	NA	NA	NA	"yes"	"4.0.3"
## mboost	NA	NA	NA	"yes"	"4.0.3"
## memoise	NA	NA	NA	"no"	"4.0.2"
## methods	NA	NA	NA	"yes"	"4.0.2"
## mgcv	NA	NA	NA	"yes"	"4.0.3"
## mime	NA	NA	NA	"yes"	"4.0.0"
## miniUI	NA	NA	NA	"no"	"4.0.3"
## minqa	NA	NA	NA	"yes"	"4.0.3"
## ModelMetrics	NA	NA	NA	"yes"	"4.0.2"
## modelr	NA	NA	NA	"no"	"4.0.2"
## monmlp	NA	NA	NA	"no"	"4.0.3"
## munsell	NA	NA	NA	"no"	"4.0.2"
## mvtnorm	NA	NA	NA	"yes"	"4.0.3"
## naivebayes	NA	NA	NA	"no"	"4.0.3"
## nlme	NA	NA	NA	"yes"	"4.0.2"
## nloptr	NA	NA	NA	"yes"	"4.0.3"
## nnet	NA	NA	NA	"yes"	"4.0.2"
## nnls	NA	NA	NA	NA	"4.0.3"
## numDeriv	NA	NA	NA	"no"	"4.0.0"
## openssl	NA	NA	NA	"yes"	"4.0.3"
## optimx	NA	NA	NA	"no"	"4.0.3"
## parallel	NA	NA	NA	"yes"	"4.0.2"
## partykit	NA	NA	NA	"yes"	"4.0.3"
## pdftools	NA	NA	NA	"yes"	"4.0.2"
## pillar	NA	NA	NA	"no"	"4.0.2"
## pkgbuild	NA	NA	NA	"no"	"4.0.2"
## pkgconfig	NA	NA	NA	"no"	"4.0.2"
## pkgload	NA	NA	NA	"yes"	"4.0.2"
## plogr	NA	NA	NA	"no"	"4.0.3"
## plyr	NA	NA	NA	"yes"	"4.0.2"
## png	NA	NA	NA	"yes"	"4.0.3"
## praise	NA	NA	NA	"no"	"4.0.2"
## prettyunits	NA	NA	NA	"no"	"4.0.2"
## pROC	NA	NA	NA	"yes"	"4.0.2"
## processx	NA	NA	NA	"yes"	"4.0.2"
## prodlim	NA	NA	NA	"yes"	"4.0.2"
## progress	NA	NA	NA	"no"	"4.0.2"
## promises	NA	NA	NA	"yes"	"4.0.2"
## ps	NA	NA	NA	"yes"	"4.0.3"
## purrr	NA	NA	NA	"yes"	"4.0.2"
## qpdf	NA	NA	NA	"yes"	"4.0.2"
## quadprog	NA	NA	NA	"yes"	"4.0.3"
## questionr	NA	NA	NA	"no"	"4.0.3"
## R.cache	NA	NA	NA	"no"	"4.0.3"
## R.methodsS3	NA	NA	NA	"no"	"4.0.3"
## R.oo	NA	NA	NA	"no"	"4.0.3"
## R.utils	NA	NA	NA	"no"	"4.0.3"
## R6	NA	NA	NA	"no"	"4.0.2"

## randomForest	NA	NA	NA	"yes"	"4.0.2"
## ranger	NA	NA	NA	"yes"	"4.0.3"
## rappdirs	NA	NA	NA	"yes"	"4.0.2"
## Rborist	NA	NA	NA	"yes"	"4.0.3"
## rcmdcheck	NA	NA	NA	"no"	"4.0.2"
## RColorBrewer	NA	NA	NA	"no"	"4.0.0"
## Rcpp	NA	NA	NA	"yes"	"4.0.2"
## RcppEigen	NA	NA	NA	"yes"	"4.0.3"
## RCurl	NA	NA	NA	"yes"	"4.0.3"
## readr	NA	NA	NA	"yes"	"4.0.2"
## readxl	NA	NA	NA	"yes"	"4.0.2"
## recipes	NA	NA	NA	"no"	"4.0.3"
## rematch	NA	NA	NA	"no"	"4.0.2"
## rematch2	NA	NA	NA	"no"	"4.0.2"
## remotes	NA	NA	NA	"no"	"4.0.2"
## reprex	NA	NA	NA	"no"	"4.0.2"
## reshape2	NA	NA	NA	"yes"	"4.0.2"
## rex	NA	NA	NA	"no"	"4.0.2"
## rlang	NA	NA	NA	"yes"	"4.0.2"
## rmarkdown	NA	NA	NA	"no"	"4.0.3"
## roxygen2	NA	NA	NA	"yes"	"4.0.2"
## rpart	NA	NA	NA	"yes"	"4.0.2"
## rpart.plot	NA	NA	NA	"no"	"4.0.2"
## rprojroot	NA	NA	NA	"no"	"4.0.2"
## RSNNS	NA	NA	NA	"yes"	"4.0.3"
## RSQLite	NA	NA	NA	"yes"	"4.0.3"
## rstudioapi	NA	NA	NA	"no"	"4.0.2"
## rversions	NA	NA	NA	"no"	"4.0.2"
## rvest	NA	NA	NA	"no"	"4.0.2"
## S4Vectors	NA	NA	NA	"yes"	"4.0.0"
## scales	NA	NA	NA	"no"	"4.0.2"
## selectr	NA	NA	NA	"no"	"4.0.2"
## sessioninfo	NA	NA	NA	"no"	"4.0.2"
## shiny	NA	NA	NA	"no"	"4.0.3"
## SnowballC	NA	NA	NA	"yes"	"4.0.0"
## sourcetools	NA	NA	NA	"yes"	"4.0.3"
## spatial	NA	NA	NA	"yes"	"4.0.2"
## splines	NA	NA	NA	"yes"	"4.0.2"
## SQUAREM	NA	NA	NA	"no"	"4.0.3"
## stabs	NA	NA	NA	"no"	"4.0.3"
## statmod	NA	NA	NA	"yes"	"4.0.3"
## stats	NA	NA	NA	"yes"	"4.0.2"
## stats4	NA	NA	NA	NA	"4.0.2"
## stopwords	NA	NA	NA	"no"	"4.0.2"
## stringi	NA	NA	NA	"yes"	"4.0.2"
## stringr	NA	NA	NA	"no"	"4.0.2"
## styler	NA	NA	NA	"no"	"4.0.3"
## survival	NA	NA	NA	"yes"	"4.0.2"
## sys	NA	NA	NA	"yes"	"4.0.2"
## tcltk	NA	NA	NA	"yes"	"4.0.2"
## testthat	NA	NA	NA	"yes"	"4.0.2"
## textdata	NA	NA	NA	"no"	"4.0.2"
## tibble	NA	NA	NA	"yes"	"4.0.2"
## tidyr	NA	NA	NA	"yes"	"4.0.2"

## tidyselect	NA	NA	NA	"yes"	"4.0.2"
## tidytext	NA	NA	NA	"no"	"4.0.3"
## tidyverse	NA	NA	NA	"no"	"4.0.2"
## timeDate	NA	NA	NA	"no"	"4.0.2"
## tinytex	NA	NA	NA	"no"	"4.0.3"
## titanic	NA	NA	NA	"no"	"4.0.2"
## tokenizers	NA	NA	NA	"yes"	"4.0.2"
## tools	NA	NA	NA	"yes"	"4.0.2"
## translations	NA	NA	NA	NA	"4.0.2"
## triebeard	NA	NA	NA	"yes"	"4.0.2"
## urltools	NA	NA	NA	"yes"	"4.0.2"
## usethis	NA	NA	NA	"no"	"4.0.3"
## utf8	NA	NA	NA	"yes"	"4.0.2"
## utils	NA	NA	NA	"yes"	"4.0.2"
## vctrs	NA	NA	NA	"yes"	"4.0.2"
## VGAM	NA	NA	NA	"yes"	"4.0.3"
## viridis	NA	NA	NA	"no"	"4.0.3"
## viridisLite	NA	NA	NA	"no"	"4.0.2"
## webshot	NA	NA	NA	"no"	"4.0.3"
## whisker	NA	NA	NA	"no"	"4.0.2"
## withr	NA	NA	NA	"no"	"4.0.3"
## wsrfr	NA	NA	NA	"yes"	"4.0.3"
## xfun	NA	NA	NA	"yes"	"4.0.3"
## XML	NA	NA	NA	"yes"	"4.0.3"
## xml2	NA	NA	NA	"yes"	"4.0.2"
## xopen	NA	NA	NA	"no"	"4.0.2"
## xtable	NA	NA	NA	"no"	"4.0.3"
## yaml	NA	NA	NA	"yes"	"4.0.2"