

Movielens Recommendation System

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Abstract

This is a movie recommendation system report for the Harvard-X Data Science Capstone Project.

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1 Executive Summary

The first automated recommender system was originally developed in 1993 by the University of Minnesota for Usenet article recommendations (Grouplens). MovieLens was also developed to study recommendation engines, tagging systems, and user interfaces. The Grouplens system predicted how much other users will like an article (before reading it), based on ratings from other users. Using collaborative filtering, this was one of the first algorithms to automatically make predictions on historical rating patterns. (https://en.wikipedia.org/wiki/GroupLens_Research)

This report describes a movie recommendation algorithm design using the 10M version of the MovieLens dataset. The 10M MovieLens dataset supplied consists of approximately 10 million movie ratings (this is however a small subset of the original MovieLens dataset). The movieLens dataset supplied in this report was split into a training and test set (with a 90%/10% split respectively). The training and test sets were named “edx” and “validation”.

By using the “edx” and “validation” datasets, the goal of the recommender algorithm is to predict movie ratings (from the “validation” set) by training a machine learning algorithm using the inputs from the “edx” dataset. The benchmark Root Mean Squared Error (RMSE) for the algorithm was defined as ≤ 0.8649 .

The “edx” and “validation” datasets can be summarized as follows:

edx dataset

Nr of Movies: 10677

Nr of Users: 69878

Nr of Genres: 19

validation dataset

Nr of Movies: 9809

Nr of Users: 68534

Nr of Genres: 19

The RMSE formula used in this report:

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

To achieve the benchmark RMSE, various algorithms were tested on a smaller test and training set. The algorithm yielding the best RMSE was then implemented using the validation set. Through hours of training and testing the lowest RMSE achieved was 0.7829341 on the validation set, using the Matrix factorization with Stochastic Gradient Descent algorithm.

This report consists of the following sections:

Section 2: Initial Dataset Exploration

Section 3: Feature Engineering/Data Cleansing

Section 4: Data Analysis

Section 5: Methods/Analysis

Section 6: Results

Section 7: Conclusion

Section 8: References

Section 9: Environmental Variables

2 Initial Dataset Exploration

Initial Data Exploration of the edx and validation datasets are discussed in the sections below.

2.1 Check Dataset Composition

First 5 rows of edx Dataset

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

Note: edx Dataset Columns Overview

Dataset Features/Variables/Columns

ColName	Datatype	Description
userId	integer	Unique ID for the user
movieId	numeric	Unique ID for the movie
rating	numeric	A rating between 0 and 5 for the movie
timestamp	integer	Date and time the rating was given
title	character	Movie title (not unique)
genres	character	Pipe-Separated Genres associated with the movie

Note: edx Column and Datatype Overview

2.2 Summarize Dataset Columns

edx dataset

Rows	Cols	Movies	Users	Genres
9000055	6	10677	69878	797

Note: edx Dataset Overview

validation dataset

Rows	Cols	Movies	Users	Genres
999999	6	9809	68534	773

Note: validation Dataset Overview

2.3 Check Dataset For NA's

edx dataset

	x
userId	0
movieId	0
rating	0
timestamp	0
title	0
genres	0
<i>Note:</i> Check NA's edx Dataset	

validation dataset

	x
userId	0
movieId	0
rating	0
timestamp	0
title	0
genres	0
<i>Note:</i> Check NA's validation Dataset	

This indicates that no records needs to be removed (for the accuracy and operation of the algorithm)

3 Feature Engineering/Data Cleansing

The aim of feature engineering or data cleansing is to modify (add/delete/update) existing columns in the edx and validation datasets to provide the required functionality for the machine learning algorithm

3.1 Timestamps

As identified in the exploratory data analysis section, the timestamp column in the edx/validation datasets are integers representing a UNIX timestamp. By converting this timestamp to a human-readable timestamp and assigning it to a new column (date), more analysis can be done on the date column.

```
## Observations: 9,000,055
## Variables: 6
## $ userId      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2,...
## $ movieId     <dbl> 122, 185, 292, 316, 329, 355, 356, 362, 364, 370, 377, 420,...
## $ rating      <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5,...
## $ timestamp   <int> 838985046, 838983525, 838983421, 838983392, 838983392, 8389...
## $ title       <chr> "Boomerang (1992)", "Net, The (1995)", "Outbreak (1995)", "...
## $ genres      <chr> "Comedy|Romance", "Action|Crime|Thriller", "Action|Drama|Sc...
```

```
# Convert UNIX Timestamp to Human Readable Date
edx <- mutate(edx, date = as_datetime(timestamp))
validation <- mutate(validation, date = as_datetime(timestamp))
```

The resultant summary for both datasets are as follows:

```
## Observations: 9,000,055
## Variables: 7
## $ userId      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2,...
## $ movieId     <dbl> 122, 185, 292, 316, 329, 355, 356, 362, 364, 370, 377, 420,...
## $ rating      <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5,...
## $ timestamp   <int> 838985046, 838983525, 838983421, 838983392, 838983392, 8389...
## $ title       <chr> "Boomerang (1992)", "Net, The (1995)", "Outbreak (1995)", "...
## $ genres      <chr> "Comedy|Romance", "Action|Crime|Thriller", "Action|Drama|Sc...
## $ date        <dtm> 1996-08-02 11:24:06, 1996-08-02 10:58:45, 1996-08-02 10:57...
```

```
## Observations: 999,999
## Variables: 7
## $ userId      <int> 1, 1, 1, 2, 2, 2, 3, 3, 4, 4, 4, 5, 5, 5, 5, 5, 5, 5, 5,...
## $ movieId     <dbl> 231, 480, 586, 151, 858, 1544, 590, 4995, 34, 432, 434, 85,...
## $ rating      <dbl> 5.0, 5.0, 5.0, 3.0, 2.0, 3.0, 3.5, 4.5, 5.0, 3.0, 3.0, 3.0,...
## $ timestamp   <int> 838983392, 838983653, 838984068, 868246450, 868245645, 8682...
## $ title       <chr> "Dumb & Dumber (1994)", "Jurassic Park (1993)", "Home Alone...
## $ genres      <chr> "Comedy", "Action|Adventure|Sci-Fi|Thriller", "Children|Com...
## $ date        <dtm> 1996-08-02 10:56:32, 1996-08-02 11:00:53, 1996-08-02 11:07...
```

3.2 Extracting Year and Month of Rating

From the new converted timestamp column (date), the year and month of rating can be extracted for data analysis and algorithm feature addition.

```
# Extract the year and month of rate in both dataset
```

```
edx$yearOfRate <- format(edx$date, "%Y")
edx$monthOfRate <- format(edx$date, "%m")

validation$yearOfRate <- format(validation$date, "%Y")
validation$monthOfRate <- format(validation$date, "%m")
```

```
## Observations: 9,000,055
## Variables: 9
## $ userId      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ...
## $ movieId     <dbl> 122, 185, 292, 316, 329, 355, 356, 362, 364, 370, 377, 42...
## $ rating      <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, ...
## $ timestamp   <int> 838985046, 838983525, 838983421, 838983392, 838983392, 83...
## $ title       <chr> "Boomerang (1992)", "Net, The (1995)", "Outbreak (1995)",...
## $ genres      <chr> "Comedy|Romance", "Action|Crime|Thriller", "Action|Drama|...
## $ date        <dtm> 1996-08-02 11:24:06, 1996-08-02 10:58:45, 1996-08-02 10:...
## $ yearOfRate  <chr> "1996", "1996", "1996", "1996", "1996", "1996", "1996", "...
## $ monthOfRate <chr> "08", "08", "08", "08", "08", "08", "08", "08", "08", "08..."
```

3.3 Extracting the Year of Release for Each Movie

The release year for each movie is currently contained in the the title of the movie. By splitting the year from the movie title, further data analysis can be performed.

```
# Extract the year and month of rate 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]),
  as.integer(release))) %>% 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]),
  as.integer(release))) %>% mutate(title = if_else(is.na(titleTemp),
  title, titleTemp)) %>% select(-titleTemp)
```

```
## Observations: 9,000,055
## Variables: 10
## $ userId      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ...
## $ movieId     <dbl> 122, 185, 292, 316, 329, 355, 356, 362, 364, 370, 377, 42...
```

```
## $ rating      <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, ...
## $ timestamp   <int> 838985046, 838983525, 838983421, 838983392, 838983392, 83...
## $ title       <chr> "Boomerang", "Net, The", "Outbreak", "Stargate", "Star Tr...
## $ release     <int> 1992, 1995, 1995, 1994, 1994, 1994, 1994, 1994, 1994, 199...
## $ genres      <chr> "Comedy|Romance", "Action|Crime|Thriller", "Action|Drama|...
## $ date        <dtm> 1996-08-02 11:24:06, 1996-08-02 10:58:45, 1996-08-02 10:...
## $ yearOfRate  <chr> "1996", "1996", "1996", "1996", "1996", "1996", "1996", "...
## $ monthOfRate <chr> "08", "08", "08", "08", "08", "08", "08", "08", "08", "08..."
```

3.4 Genres

As identified in the exploratory data analysis section, the genres listed per movie is pipe-separated. This means that a movie can be classified under a combination of genres. Genres will be split up for data analysis portions only.

3.5 Datatype Conversion

To ensure the datatypes of the columns to be used in the machine learning algorithm matches the requirements, the following conversions were done.

```
# Convert the columns into the desired data type

edx$yearOfRate <- as.numeric(edx$yearOfRate)
edx$monthOfRate <- as.numeric(edx$monthOfRate)
edx$release <- as.numeric(edx$release)
validation$yearOfRate <- as.numeric(validation$yearOfRate)
validation$monthOfRate <- as.numeric(validation$monthOfRate)
validation$release <- as.numeric(validation$release)
```

3.6 Variable Cleanup

To optimize memory and storage space on the computer of datasets, unused columns were removed.

```
# Remove unnecessary columns on edx and validation dataset

edx <- edx %>% select(userId, movieId, rating, title, genres,
  release, yearOfRate, monthOfRate)
validation <- validation %>% select(userId, movieId, rating,
  title, genres, release, yearOfRate, monthOfRate)
```

3.7 Pre-processing Results

The resultant dataset after pre-processing as as follows:

```
# Pre-processing results
glimpse(edx)

## Observations: 9,000,055
## Variables: 8
## $ userId      <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ...
```



```
## $ movieId      <dbl> 122, 185, 292, 316, 329, 355, 356, 362, 364, 370, 377, 42...
## $ rating       <dbl> 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, ...
## $ title        <chr> "Boomerang", "Net, The", "Outbreak", "Stargate", "Star Tr...
## $ genres       <chr> "Comedy|Romance", "Action|Crime|Thriller", "Action|Drama|...
## $ release      <dbl> 1992, 1995, 1995, 1994, 1994, 1994, 1994, 1994, 1994, 199...
## $ yearOfRate   <dbl> 1996, 1996, 1996, 1996, 1996, 1996, 1996, 1996, 1996, 199...
## $ monthOfRate  <dbl> 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, ...
```

```
glimpse(validation)
```

```
## Observations: 999,999
## Variables: 8
## $ userId       <int> 1, 1, 1, 2, 2, 2, 3, 3, 4, 4, 4, 5, 5, 5, 5, 5, 5, 5, ...
## $ movieId      <dbl> 231, 480, 586, 151, 858, 1544, 590, 4995, 34, 432, 434, 8...
## $ rating       <dbl> 5.0, 5.0, 5.0, 3.0, 2.0, 3.0, 3.5, 4.5, 5.0, 3.0, 3.0, 3....
## $ title        <chr> "Dumb & Dumber", "Jurassic Park", "Home Alone", "Rob Roy"...
## $ genres       <chr> "Comedy", "Action|Adventure|Sci-Fi|Thriller", "Children|C...
## $ release      <dbl> 1994, 1993, 1990, 1995, 1972, 1997, 1990, 2001, 1995, 199...
## $ yearOfRate   <dbl> 1996, 1996, 1996, 1997, 1997, 1997, 2006, 2005, 1996, 199...
## $ monthOfRate  <dbl> 8, 8, 8, 7, 7, 7, 1, 12, 10, 10, 10, 3, 3, 3, 3, 3, 3, 3,...
```

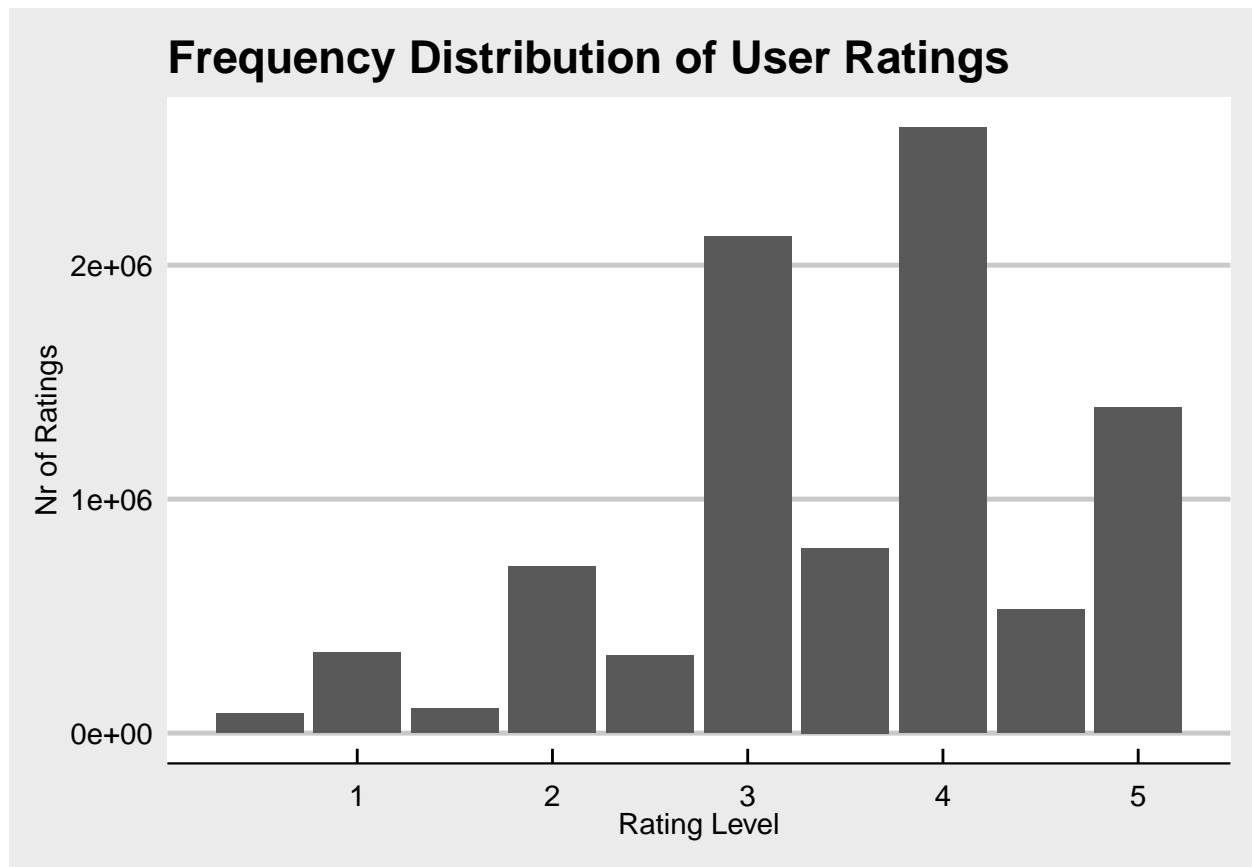
4 Data Analysis

The aim of the data analysis was to obtain a better picture on the type of data available in the dataset. Some useful insights were gained on the rating patterns, movie popularity, genre popularity and general statistical distributions.

4.1 Distributions

User Rating Distribution

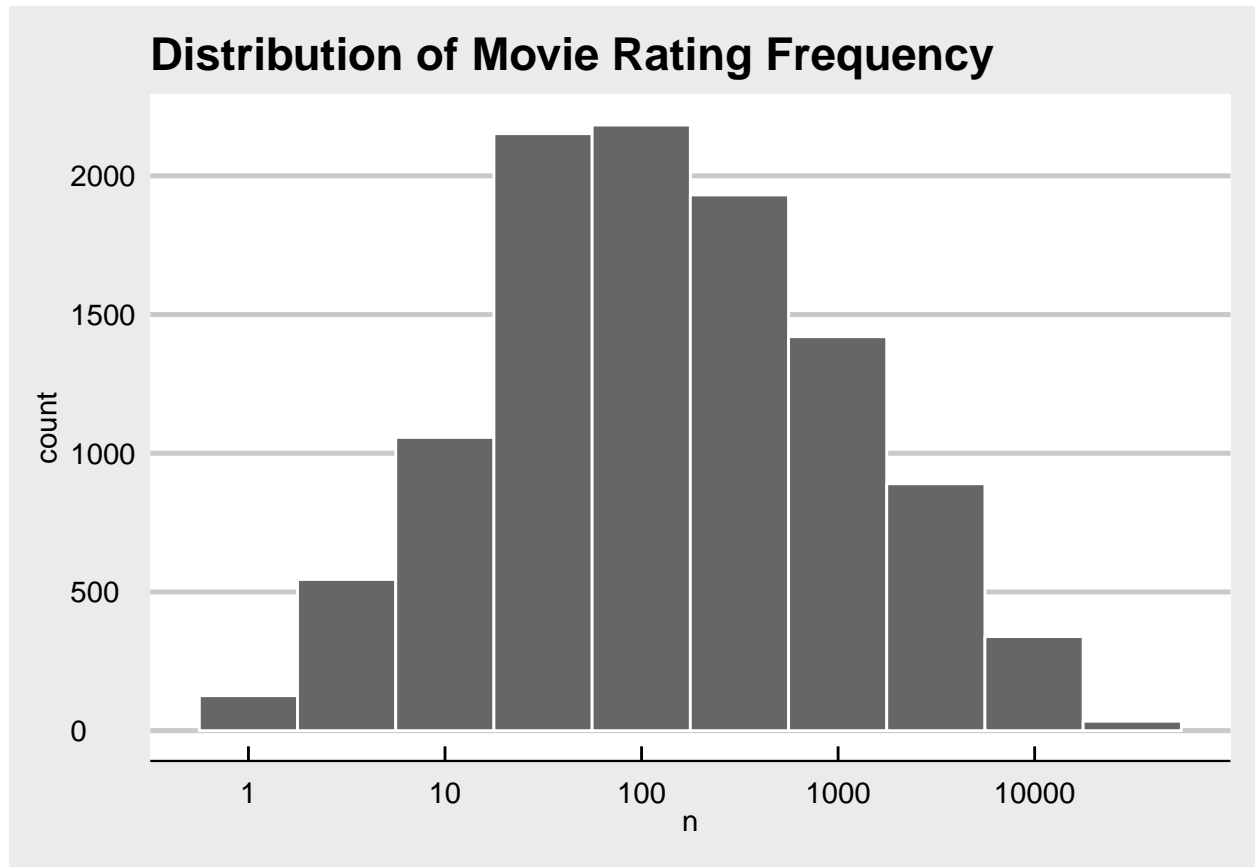
From the graph below, most of the ratings done by users are 3 and above.



rating	ratings_distribution_sum
4.0	2588430
3.0	2121240
5.0	1390114
3.5	791624
2.0	711422
4.5	526736
1.0	345679
2.5	333010
1.5	106426
0.5	85374

Note: Nr of Ratings per Rating Category

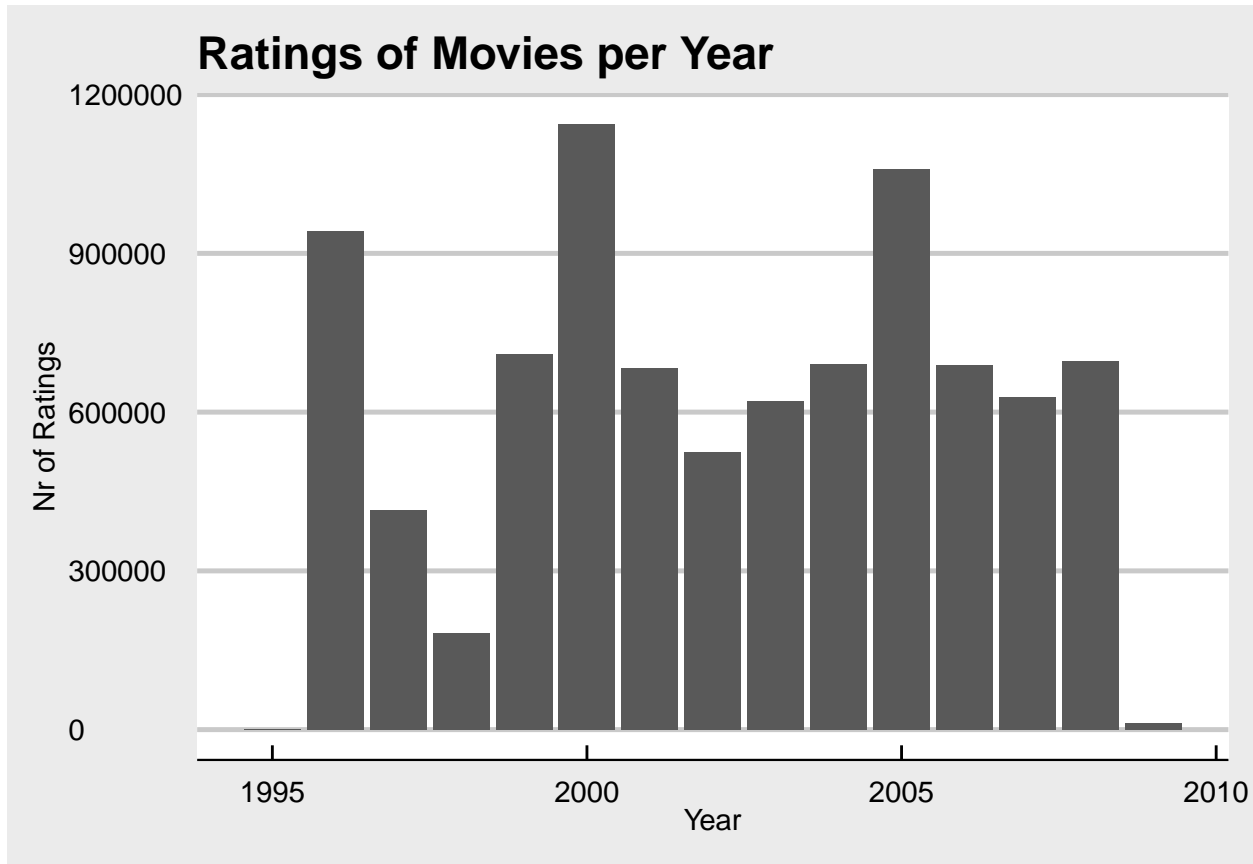
Movie Rating Frequency Distribution
The movie rating distribution is shown below:



4.2 Movie Ratings

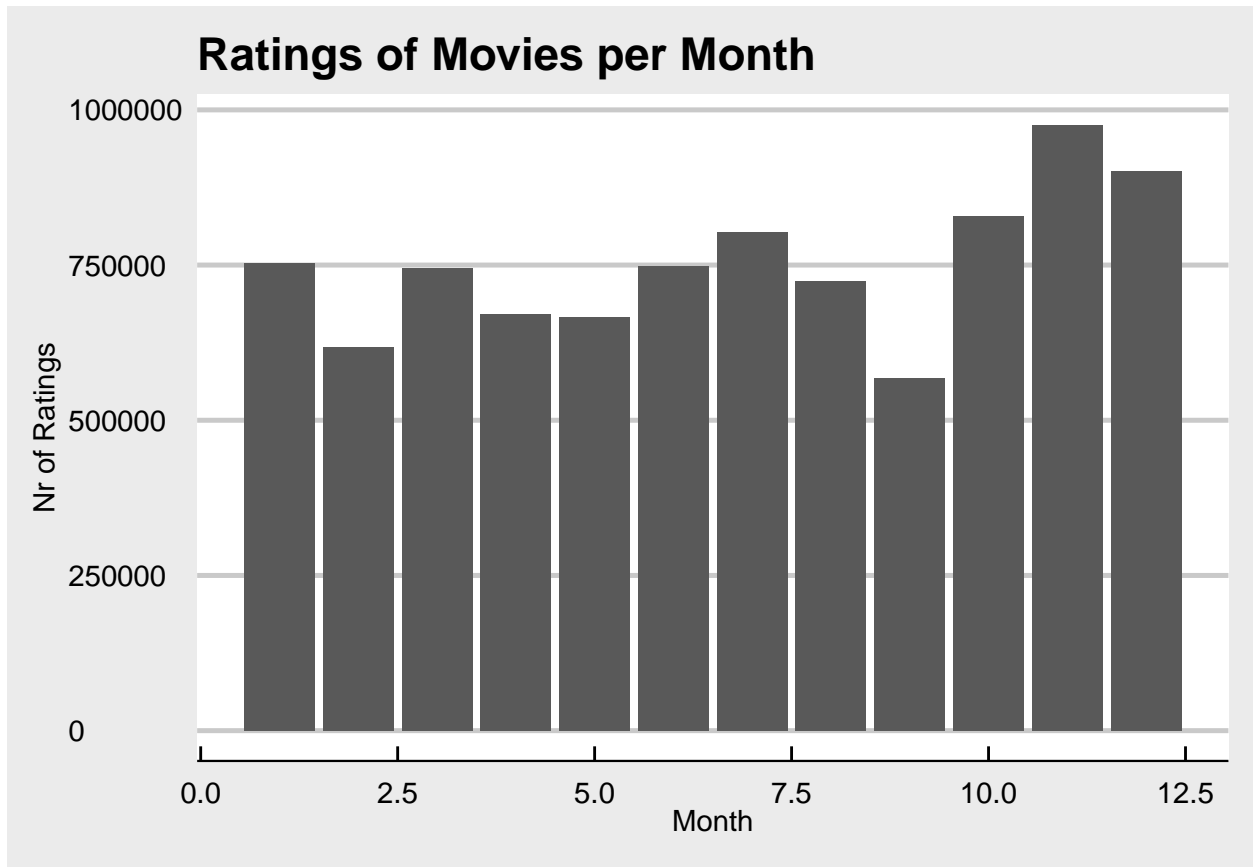
Movies Rated Per Year

From the graph below, most movies were rated in 2000.



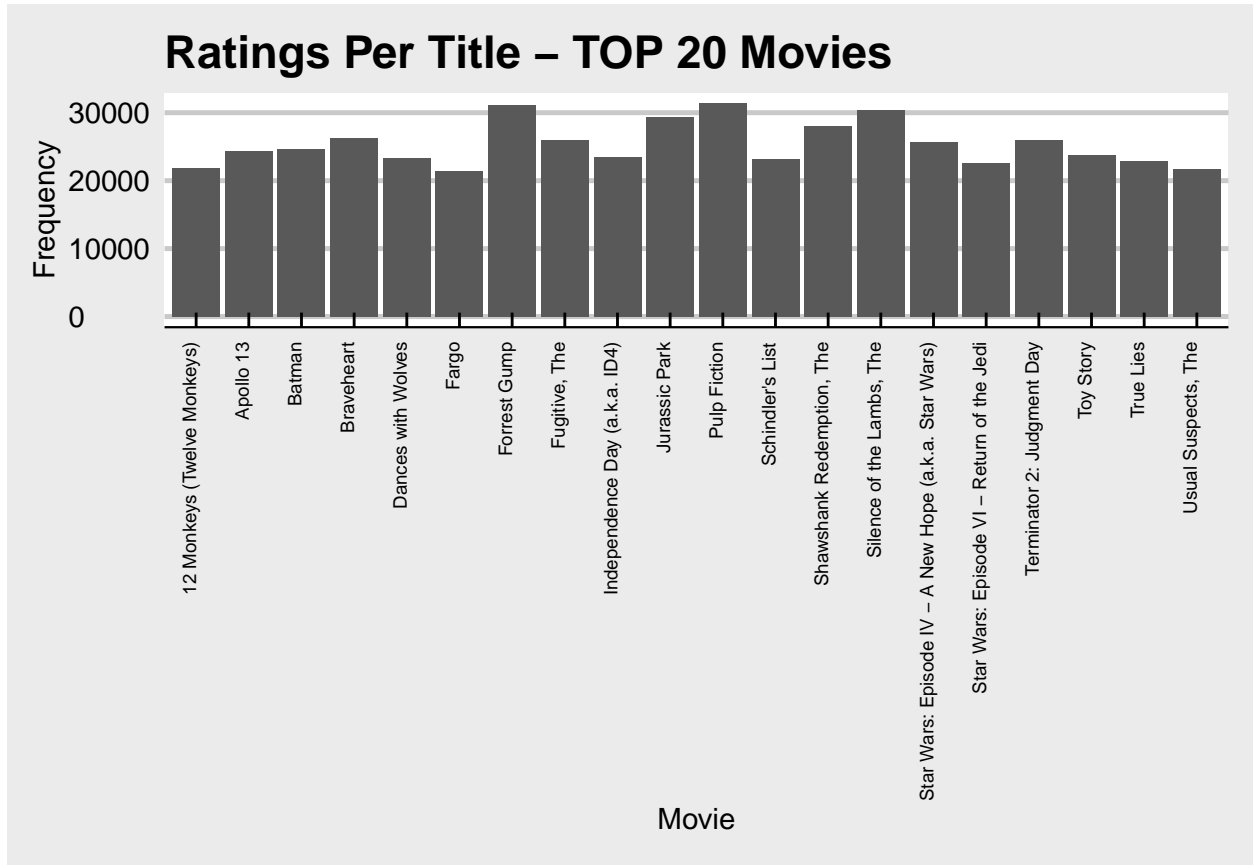
Movies Rated Per Month

From the graph below, most movies were rated in November.



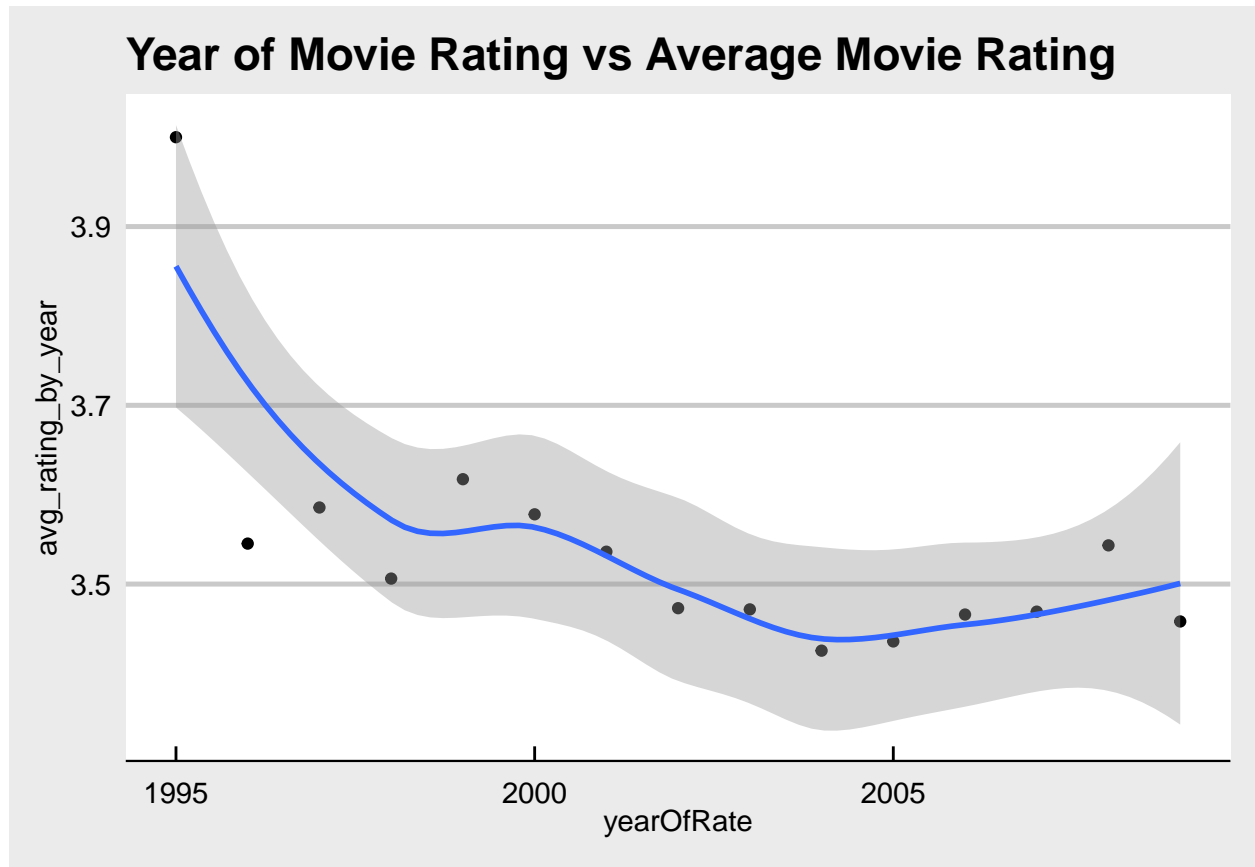
Top 20 Rated Movies

From the graph below, Forrest Gump was rated the most.



Year of Rating vs Rating Relationship

The graph below indicates the average rating per year based on the year of the rating.

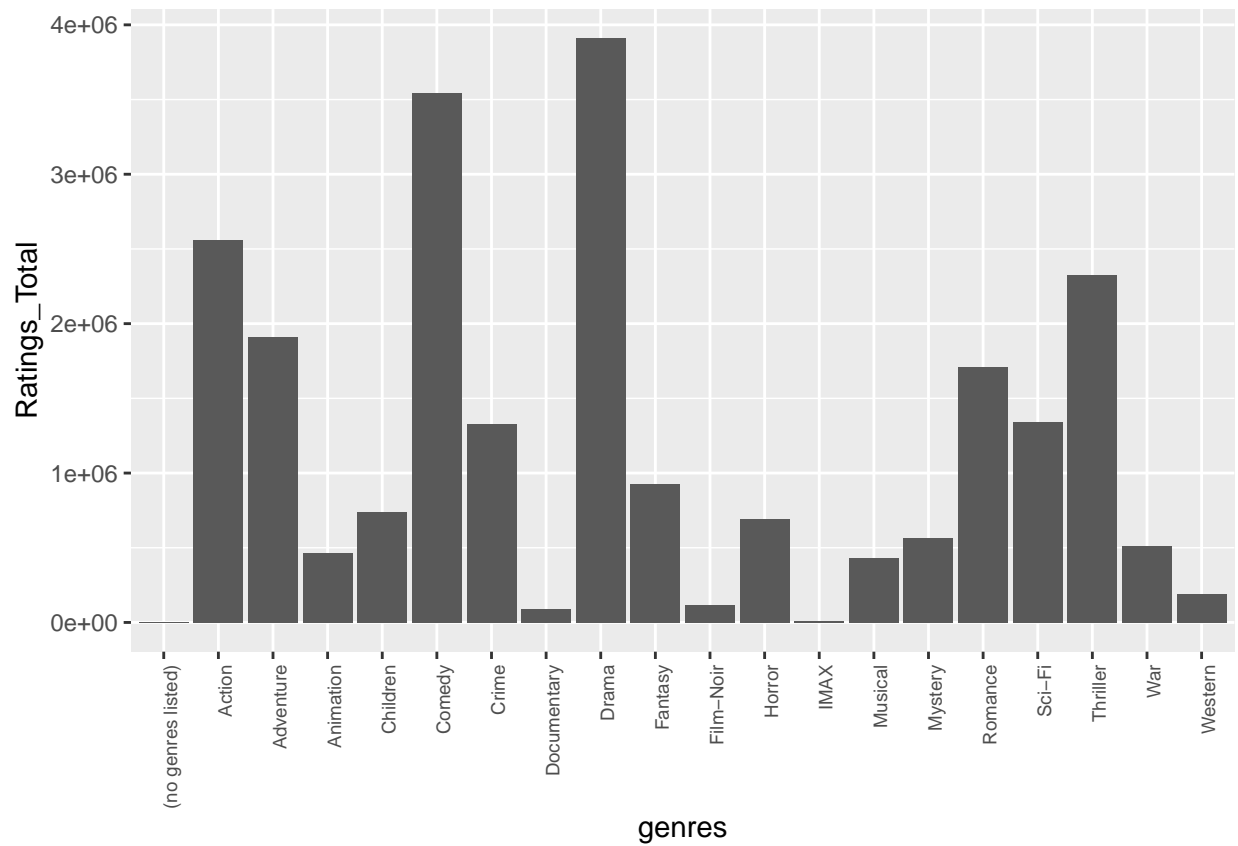


4.3 Genres

Rating Summary per Genre

The section below summarizes the ratings, users and movies per genre. As seen in the graph below, the Drama genre was rated the most times.

Graph:



NULL

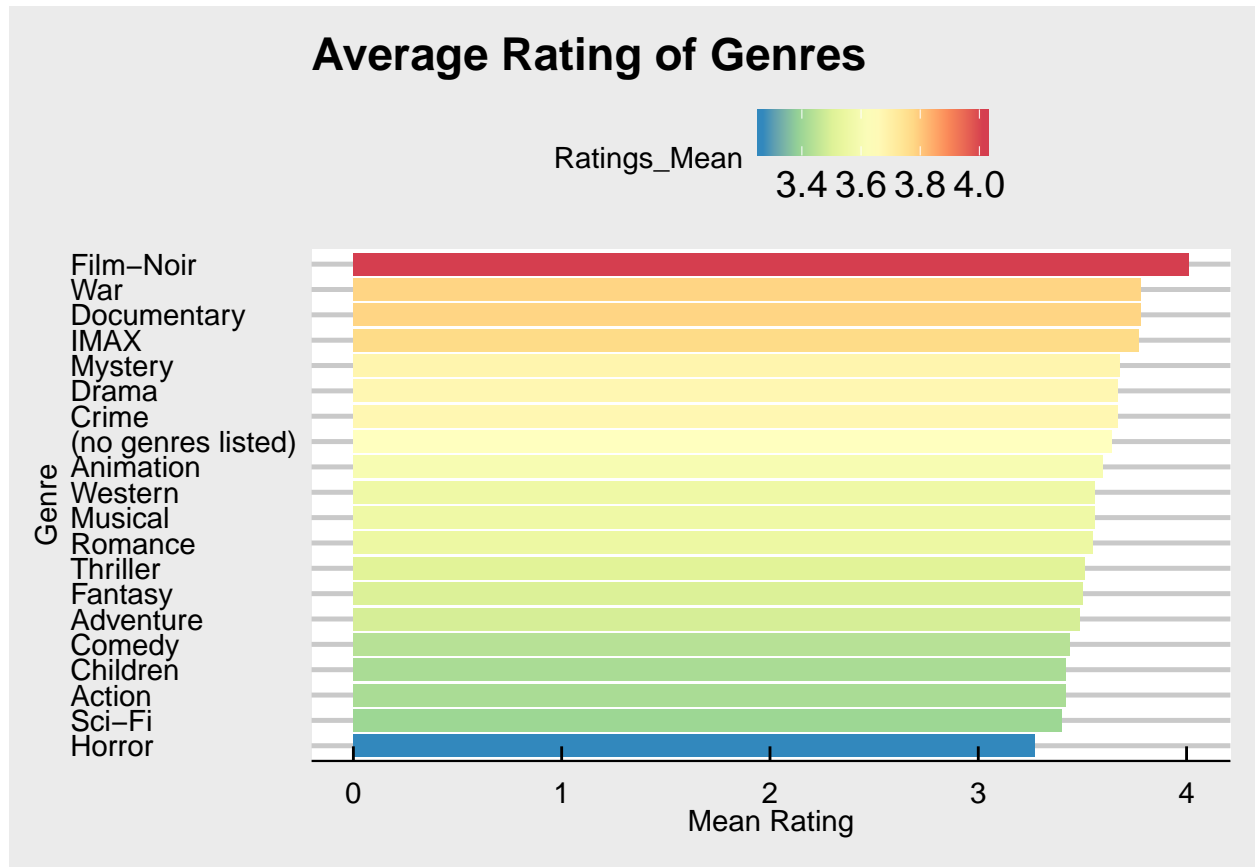
Rating's Summary:

genres	Ratings_Total	Ratings_Mean	Movies_Total	Users_Total
(no genres listed)	7	3.64	1	7
Action	2560545	3.42	1473	69607
Adventure	1908892	3.49	1025	69521
Animation	467168	3.60	286	59018
Children	737994	3.42	528	64059
Comedy	3540930	3.44	3703	69864
Crime	1327715	3.67	1117	68691
Documentary	93066	3.78	481	24295
Drama	3910127	3.67	5336	69866
Fantasy	925637	3.50	543	66833
Film-Noir	118541	4.01	148	31270
Horror	691485	3.27	1013	60695
IMAX	8181	3.77	29	6393
Musical	433080	3.56	436	58918
Mystery	568332	3.68	509	61845
Romance	1712100	3.55	1685	69530
Sci-Fi	1341183	3.40	754	68469
Thriller	2325899	3.51	1705	69567
War	511147	3.78	510	64892
Western	189394	3.56	275	47648

Note: Genre rating summary

Mean rating per Genre

The graph below indicates that the Film-Noir Genre was rated the highest mean score.



5 Methodology

This section describes the machine learning methodology followed.

5.1 RMSE Calculation

As per the project requirements, the benchmark RMSE for this project is 0.8649. The following function was created to calculate the RMSE:

```
# RMSE Function for Analysis

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

5.2 Plot Function for Predicted vs Real Ratings

A plot function was created to minimize code for handling “real vs predicted rating” plots of different models being tested:

```
# Plot function for predicted vs real ratings
Pred_Plot <- function(true_ratings = NULL, predicted_ratings = NULL,
  titlex = NULL) {
  pred_ratings <- round(predicted_ratings/0.5) * 0.5
  MF_first50_pred <- data.frame(true_ratings[1:50], predicted_ratings[1:50],
    correct_predicted = 0)
  names(MF_first50_pred) <- c("real_ratings", "predicted_ratings")
  MF_first50_pred$correct_predicted <- ifelse(MF_first50_pred$real_ratings ==
    MF_first50_pred$predicted_ratings, 1, 0)

  pmf <- ggplot(data = MF_first50_pred, aes(x = real_ratings,
    y = predicted_ratings, colour = correct_predicted)) +
    xlab("Real Ratings") + ylab("Predicted Ratings") + ggtitle(paste(titlex,
      " (Real vs Pred Ratings [50])")) + theme(plot.title = element_text(size = 12,
        color = "black", hjust = 0.5)) + geom_jitter()

  plot(pmf)
}
```

5.3 Training and Test Data Sets

Due to the size of the supplied datasets, a smaller training and test data set was created from the edx dataset to evaluate the machine learning algorithms (using a 80%/20% split with 10M records):

```
set.seed(1, sample.kind = "Rounding")

# Create smaller dataset for training and testing models
edx2 <- head(edx, 1e+06)
test_index <- createDataPartition(y = edx2$rating, times = 1,
  p = 0.2, list = FALSE)
```

```
train_set <- edx2[-test_index, ]
test_set <- edx2[test_index, ]

# Make sure userId and movieId in test set are also in train
# set
test_set <- test_set %>% semi_join(train_set, by = "movieId") %>%
  semi_join(train_set, by = "userId")

rm(test_index)
```

The final machine learning algorithm will be tested against the validation set to determine the RMSE.

5.4 Machine Learning Algorithms

To obtain the required RMSE, two of algorithms was tested, and will be described below:

5.4.1 Model 1: Netflix Inspired Algorithm

This algorithm was inspired by the course material from the Harvard-X Datascience program and the Netflix challenge of 2011.

The algorithm composition is as follows:

Naïve Baseline Model

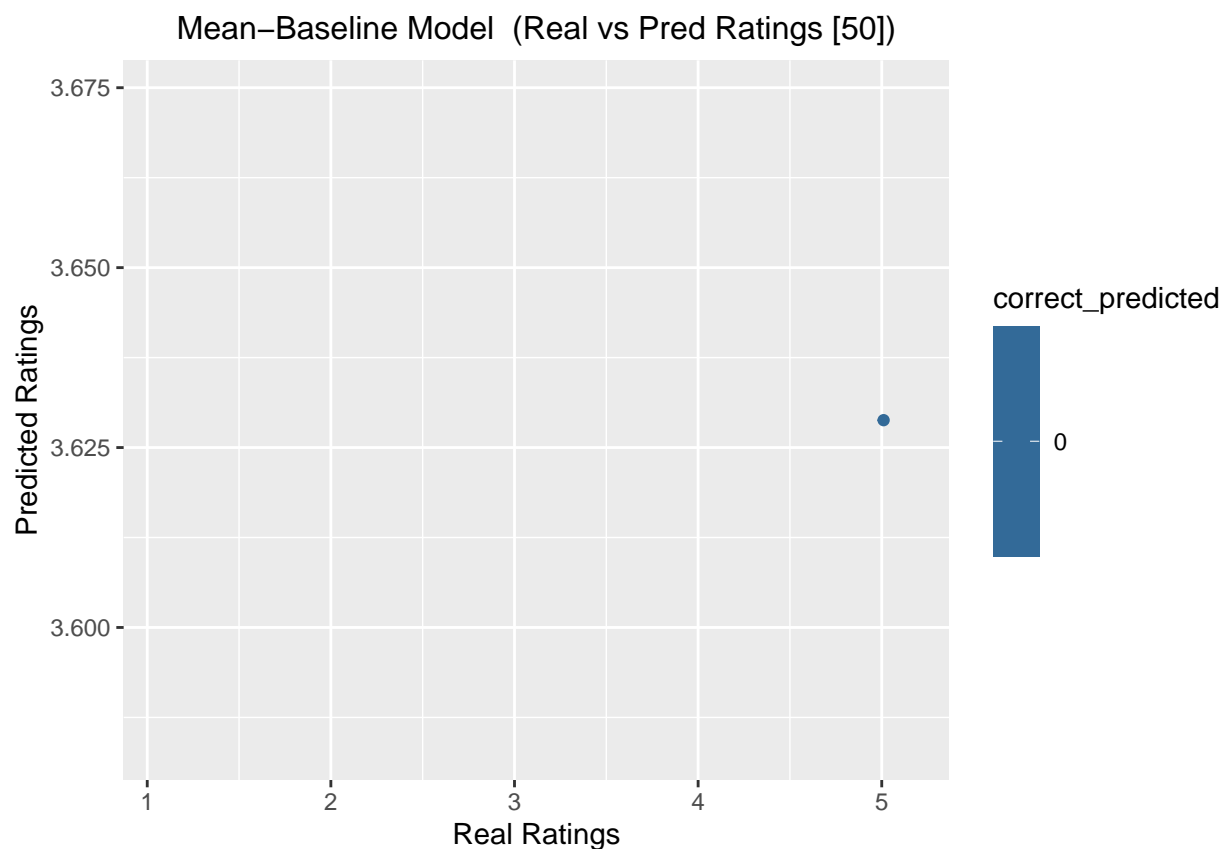
This model always predicts the mean of a dataset.

```
## [1] "The mean is: 3.52072752590941"
```

Naïve Mean-Baseline Model

The formula used is:

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



The RMSE for this model was 1.0582078, which requires improvement as this does not meet the baseline RMSE requirement of 0.8649.

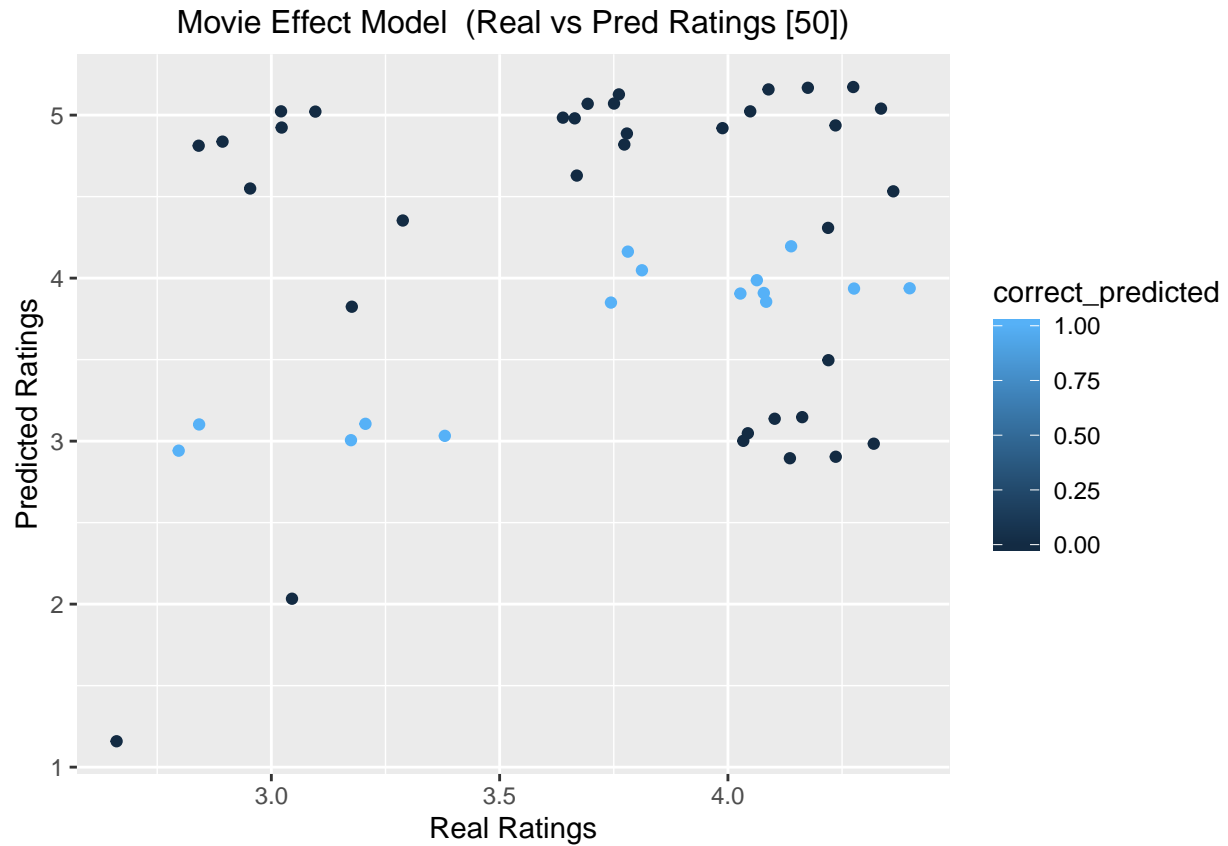
Movie-Effect Model

This model takes into account the fact that some movies are rated higher than others.

The formula used is:

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

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



The RMSE for this model was 0.9484903, which requires improvement as this does not meet the baseline RMSE requirement of 0.8649.

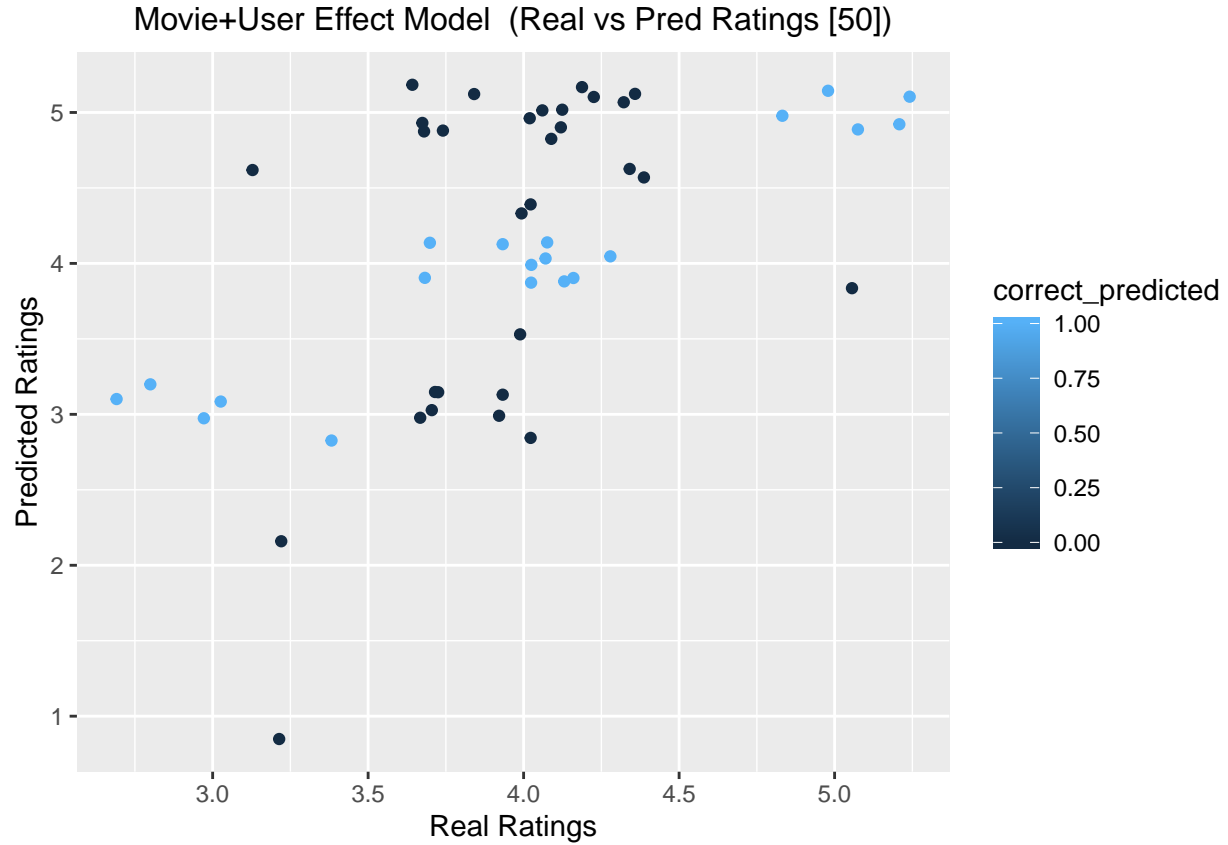
Movie and User Effect Model

This model takes into account the fact that some movies are rated higher than others and that users have different movie preferences and thus rate accordingly.

The formula used is:

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

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



The RMSE for this model was 0.8729667, which requires improvement as this is not meeting the baseline RMSE requirement of 0.8649.

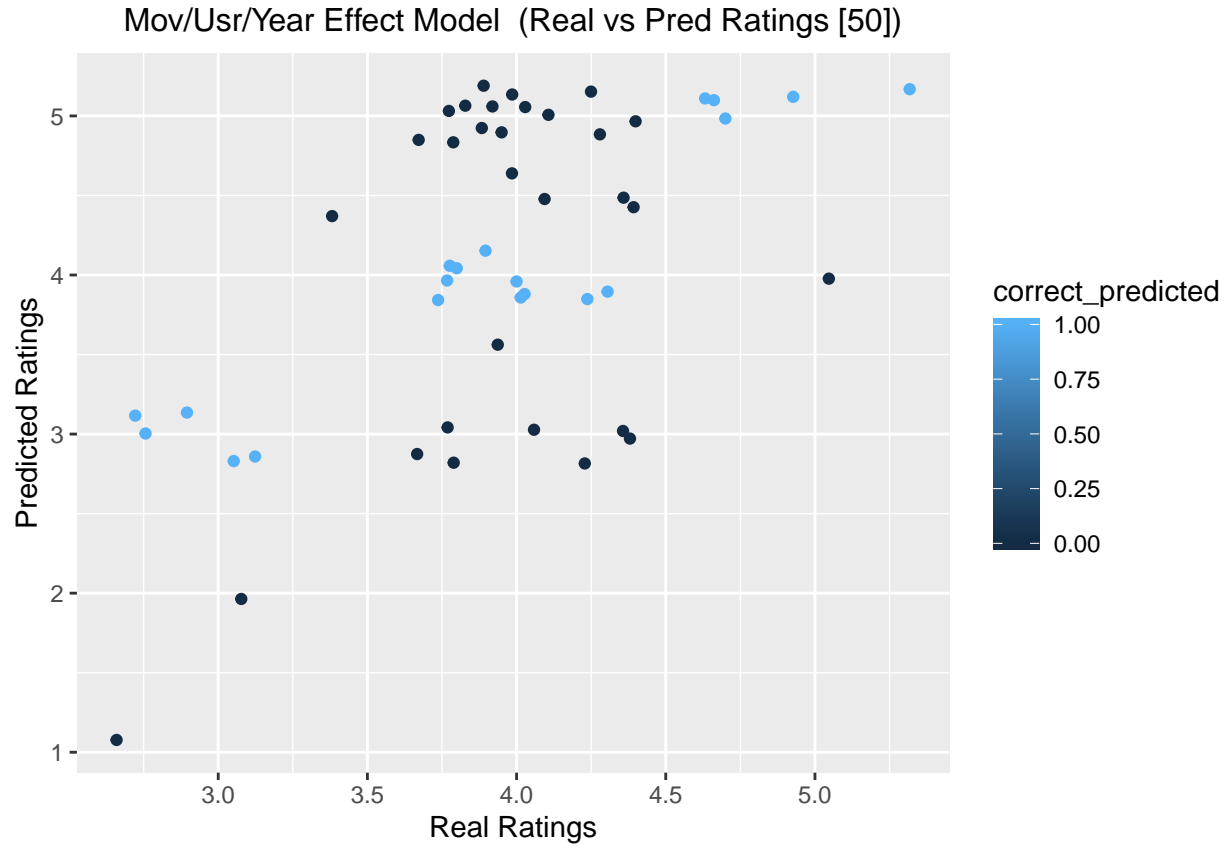
Movie and User and Year Effect Model

This model takes into account the fact that some movies are rated higher than others and that users have different movie preferences and thus rate accordingly. This model also accounts for the year the movie was rated.

The formula used is:

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

With $\hat{\mu}$ is the mean and $\epsilon_{u,i}$ is the independent errors sampled from the same distribution centered at 0. The b_i is a measure for the popularity of movie i , i.e. the bias of movie i . The b_u is a measure for the mildness of user u , i.e. the bias of user u . The b_r refers to the effect the year of rating has on the movie.



The RMSE for this model was 0.8729482, which requires improvement as this does not meet the baseline RMSE requirement of 0.8649.

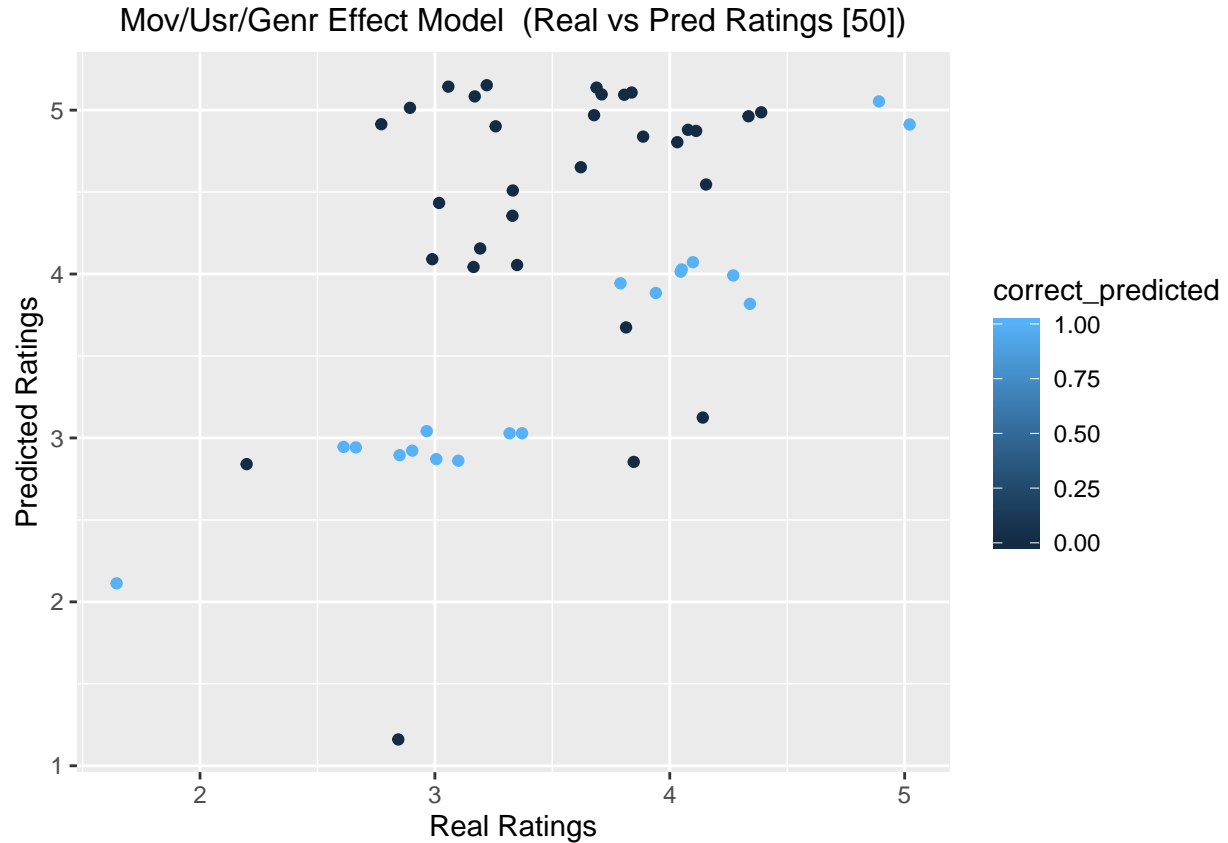
Movie and User and Genre Effect Model

This model takes into account the fact that some movies are rated higher than others and that users have different movie preferences and thus rate accordingly. This model also accounts for it's combined genres.

The formula used is:

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

With $\hat{\mu}$ is the mean and $\epsilon_{i,u}$ is the independent errors sampled from the same distribution centered at 0. The b_i is a measure for the popularity of movie i , i.e. the bias of movie i . The b_u is a measure for the mildness of user u , i.e. the bias of user u . The b_g refers to the genre effect.



The RMSE for this model was 0.8725783, which requires improvement as this does not meet the baseline RMSE requirement of 0.8649.

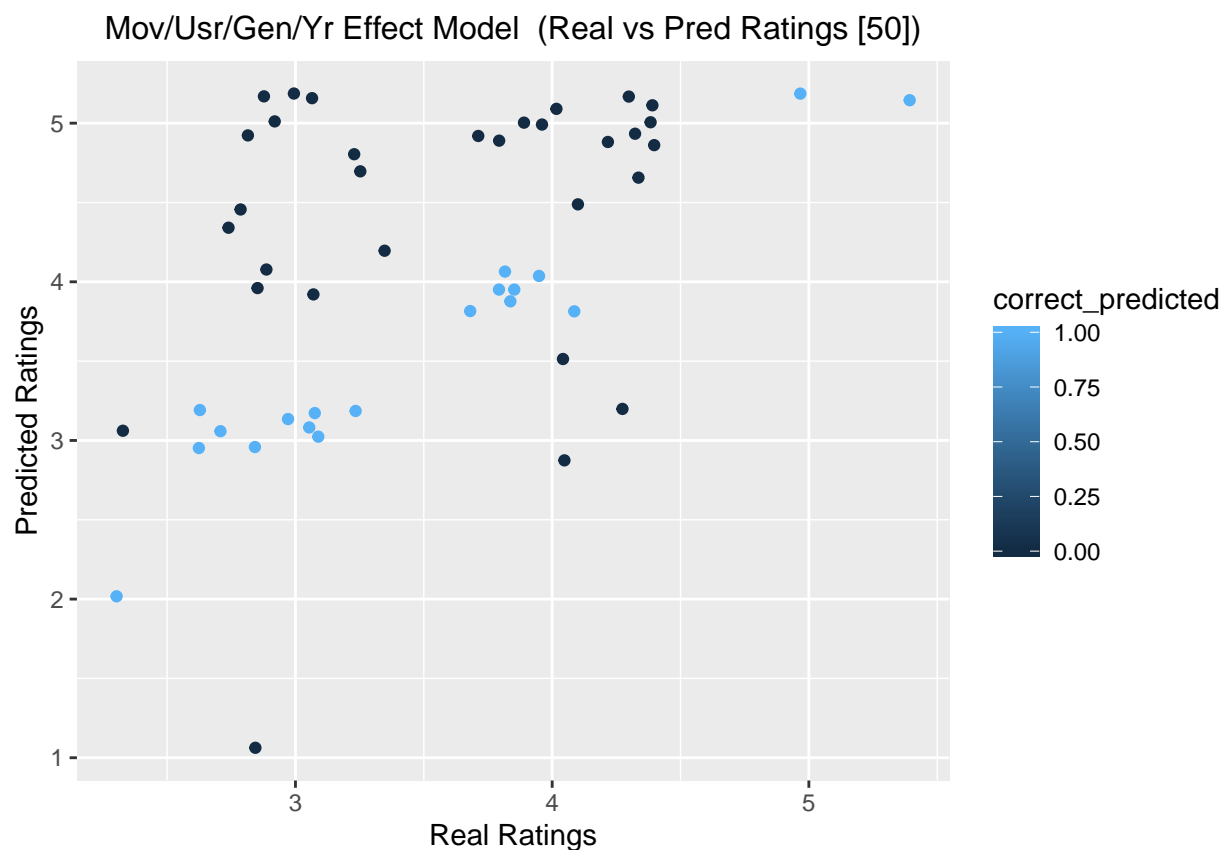
Movie and User and Year and Genre Effect Model

The model takes into account the fact that some movies are rated higher than others and that users have different movie preferences and thus rate accordingly. This model also accounts for the year the movie was rated and it's combined genres.

The formula used is:

$$Y_{u,i,r,g} = \hat{\mu} + b_i + b_u + b_r + b_g + \epsilon_{u,i,r,g}$$

With $\hat{\mu}$ is the mean and $\epsilon_{i,u}$ is the independent errors sampled from the same distribution centered at 0. The b_i is a measure for the popularity of movie i , i.e. the bias of movie i . The b_u is a measure for the mildness of user u , i.e. the bias of user u . The b_r refers to the effect the year of rating has on the movie. he b_g refers to the genre effect.



The RMSE for this model was 0.8725610, which requires improvement as this does not meet the baseline RMSE requirement of 0.8649.

Movie and User and Year and Genre Effect Models with 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_i , it necessary to use this basic equation:

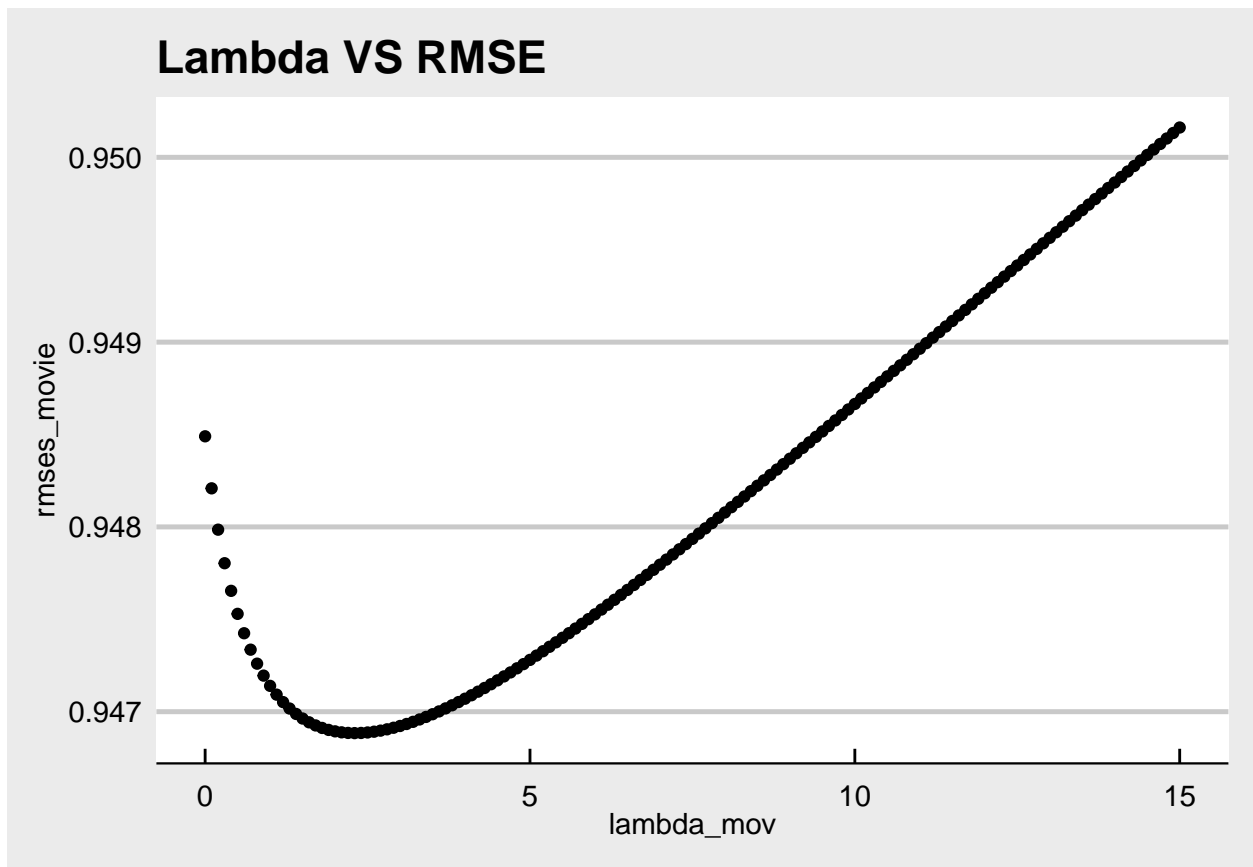
$$\frac{1}{N} \sum_{u,i} (y_{u,i} - \mu - b_i)^2 + \lambda \sum_i b_i^2$$

reduced to this equation:

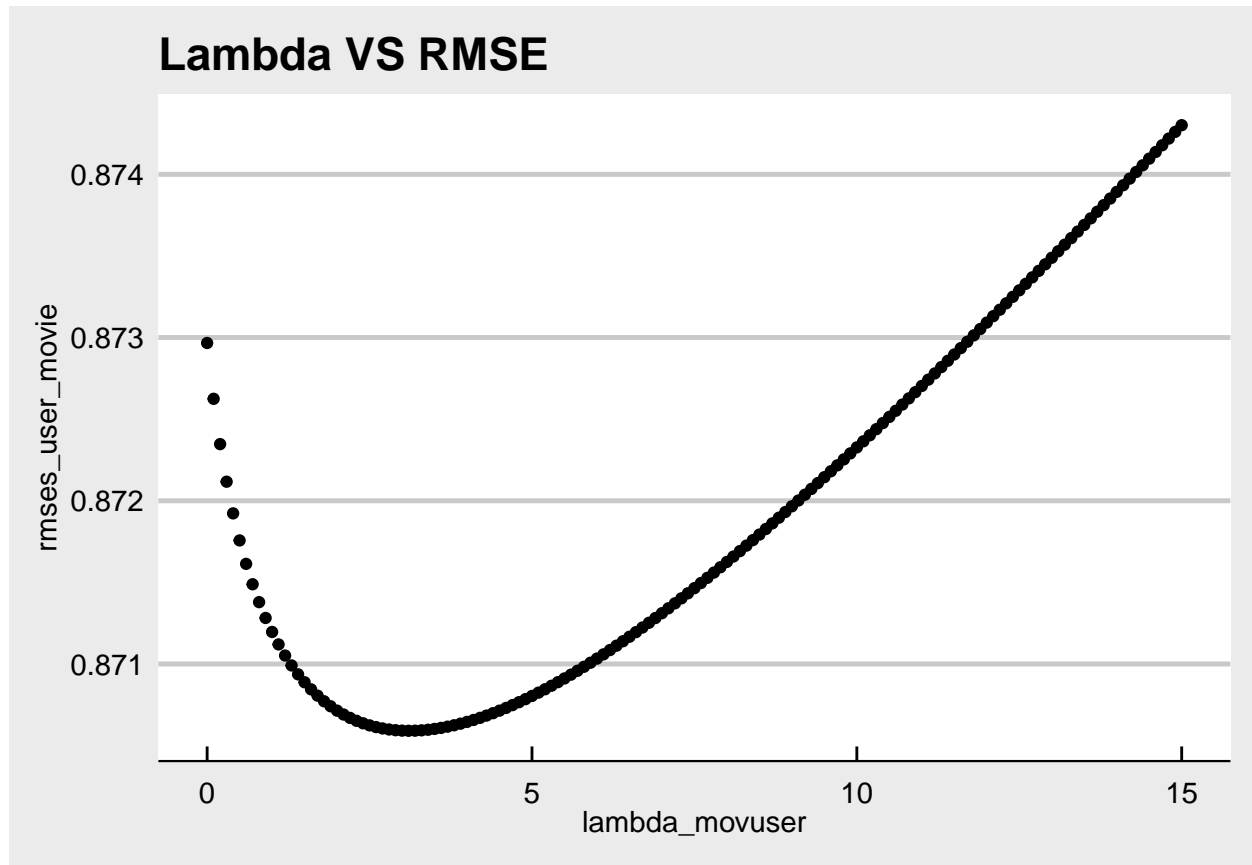
$$\hat{b}_i(\lambda) = \frac{1}{\lambda + n_i} \sum_{u=1}^{n_i} (Y_{u,i} - \hat{\mu})$$

Regularization was applied to the four models above, the results are shown below:

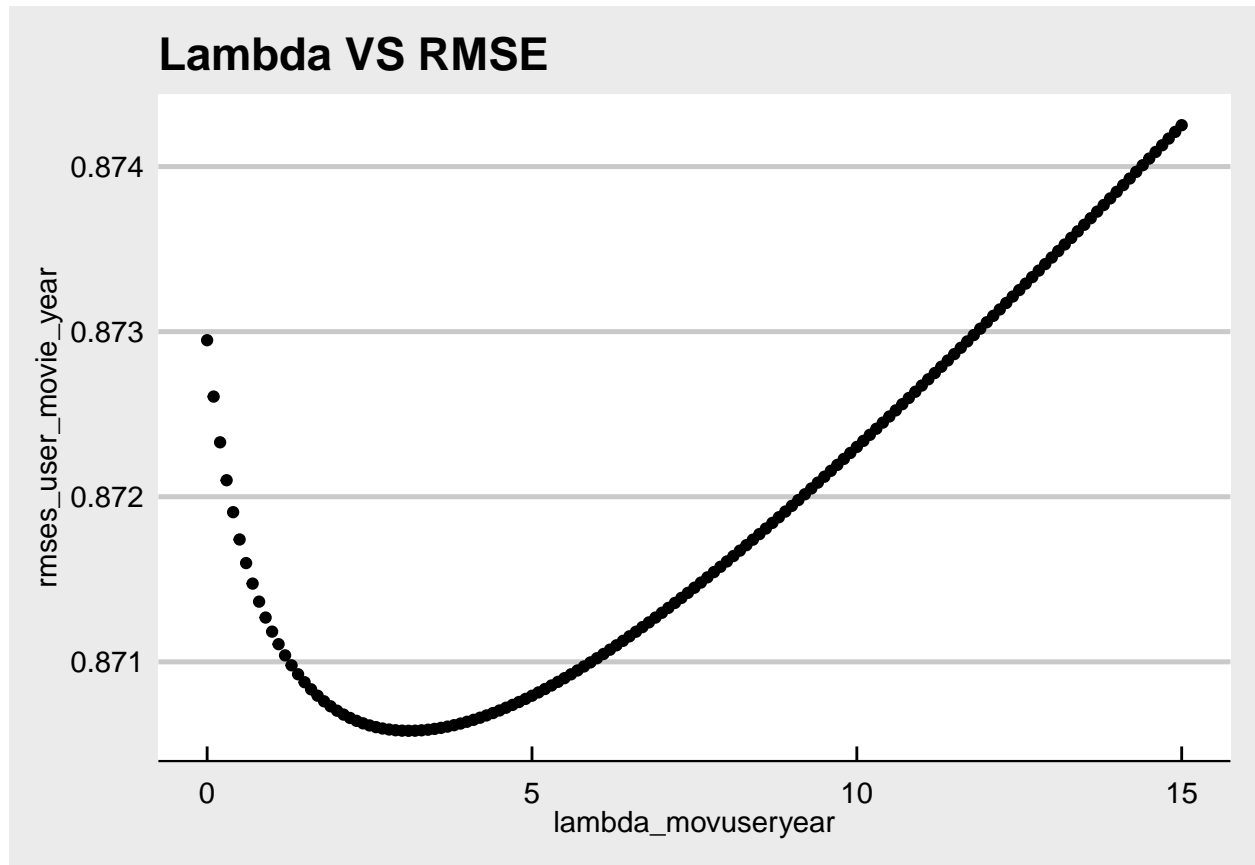
Movie Effects - Lambda Tuning Parameter



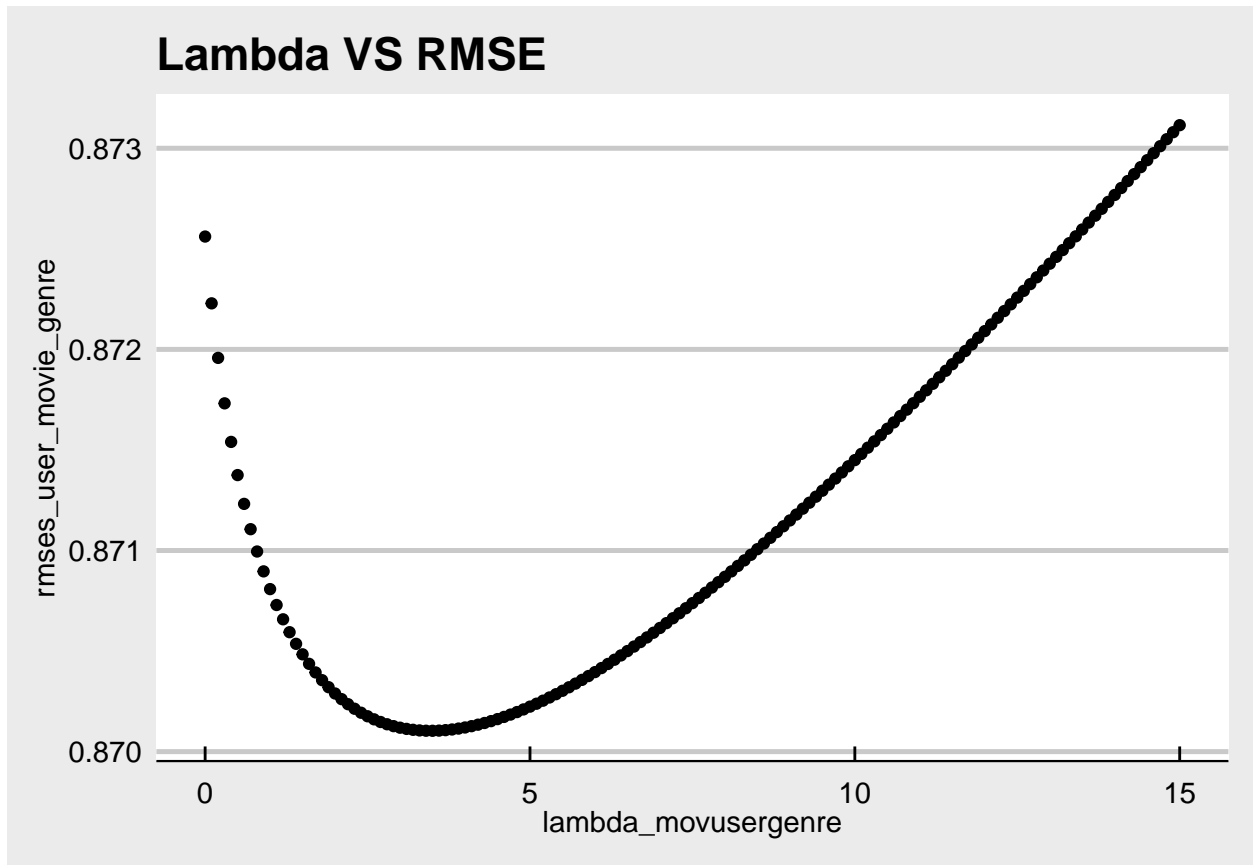
Movie + User Effects - Lambda Tuning Parameter



Movie + User + Year Effects - Lamba Tuning Parameter



Movie + User + Year + Genre Effects - Lamba Tuning Parameter



From the regularization results, the model that took into account both movie+user+genre+year effects yielded to lowest RMSE results of 0.8701036 with a lambda value of 3.5 when using the training and test datasets. This model will be tested on the validation set for final results.

Testing optimized model on validation set

When testing the optimized model on the validation set, the RMSE is 0.8644548 which exceeds the baseline RMSE requirement of 0.8649.

```
min_lambda_val_set <- 3.5

# Calculate Predicted Ratings from Min Lambda
mu <- mean(edx$rating)
# Calculate the average by user
b_i <- edx %>% group_by(movieId) %>% summarize(b_i = sum(rating -
  mu)/(n() + min_lambda_val_set))

# Calculate the average by user
b_u <- edx %>% left_join(b_i, by = "movieId") %>% group_by(userId) %>%
  summarize(b_u = sum(rating - b_i - mu)/(n() + min_lambda_val_set))

b_u_r <- edx %>% left_join(b_i, by = "movieId") %>% left_join(b_u,
  by = "userId") %>% group_by(yearOfRate) %>% summarize(b_u_r = sum(rating -
  b_i - mu_hat - b_u)/(n() + min_lambda_val_set))

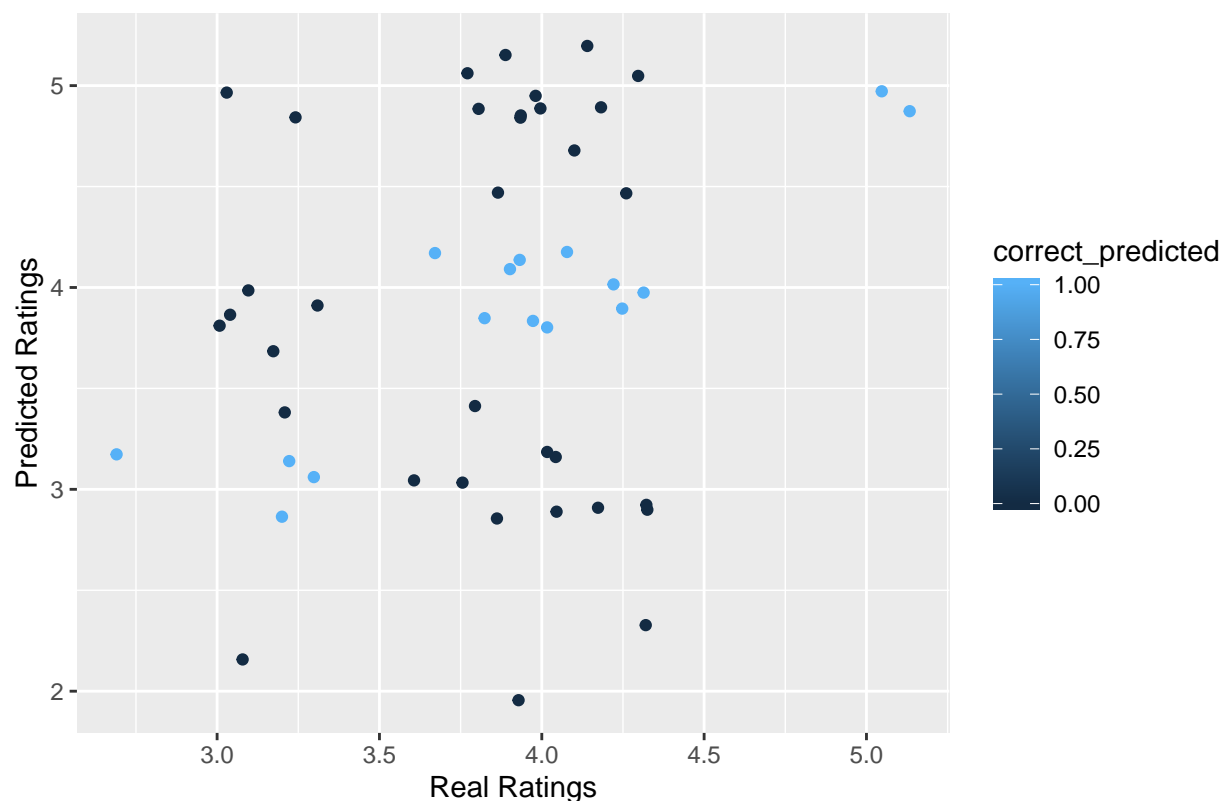
b_u_g <- edx %>% left_join(b_i, by = "movieId") %>% left_join(b_u,
  by = "userId") %>% left_join(b_u_r, by = "yearOfRate") %>%
  group_by(genres) %>% summarize(b_u_g = sum(rating - b_i -
  mu_hat - b_u - b_u_r)/(n() + min_lambda_val_set))

# Compute the predicted ratings on test_set dataset
predicted_ratings <- validation %>% left_join(b_i, by = "movieId") %>%
  left_join(b_u, by = "userId") %>% left_join(b_u_r, by = "yearOfRate") %>%
  left_join(b_u_g, by = "genres") %>% mutate(pred = mu_hat +
  b_i + b_u + b_u_r + b_u_g) %>% .$pred

rmse_val_res <- RMSE(predicted_ratings, validation$rating)

# Plot Predictions
Pred_Plot(round(predicted_ratings), validation$rating, "Regularized Model 1")
```

Regularized Model 1 (Real vs Pred Ratings [50])



```
rmse_results <- rmse_results %>% add_row(Dataset = "edx/validation",
  Model = "Regularized Movie+User+Year+Genre Effect Model",
  RMSE = rmse_val_res, Accuracy = mean(round(predicted_ratings/0.5) *
    0.5 == validation$rating), Lambda = as.character(min_lambda_val_set))
rmse_results %>% kable() %>% kable_styling(bootstrap_options = c("striped"),
  position = "center", font_size = 10, full_width = FALSE) %>%
  footnote(general = "RMSE's for Model 1", footnote_as_chunk = T)
```

Dataset	Model	RMSE	Accuracy	Lambda
Train/Test	Naive Mean-Baseline Model	1.0582078	0.0544756	NA
Train/Test	Movie Effect Model	0.9484903	0.2241301	NA
Train/Test	Move+User Effect Model	0.8729667	0.2435335	NA
Train/Test	Mov/Usr/Year Effect Model	0.8729482	0.2436686	NA
Train/Test	Mov/Usr/Genr Effect Model	0.8725783	0.2439640	NA
Train/Test	Movie+User+Year+Genre Effect Model	0.8725610	0.2441842	NA
Train/Test	Regularized Movie Effect Model	0.9468840	0.2230638	2.3
Train/Test	Regularized Movie+User Effect Model	0.8705907	0.2428126	3.1
Train/Test	Regularized Movie+User+Year Effect Model	0.8705824	0.2430829	3.1
Train/Test	Regularized Movie+User+Year+Genre Effect Model	0.8701036	0.2433432	3.5
edx/validation	Regularized Movie+User+Year+Genre Effect Model	0.8644548	0.2484252	3.5

Note: RMSE's for Model 1

5.4.2 Model 2 - Matrix Factorization with Parallel Stochastic Gradient Descent Model

Matrix factorization was empirically shown to be a better model than traditional nearest-neighbor based approaches in the Netflix Prize competition and KDD Cup 2011. The goal is to approximate the incomplete matrix A by WH^T , where W and H are rank- k matrices. Matrix factorization offers superior speed and accuracy when compared to model 1 in this report.

This algorithm uses a recosystem library, which is an R wrapper of the LIBMF library developed by Yu-Chin Juan, Wei-Sheng Chin, Yong Zhuang, Bo-Wen Yuan, Meng-Yuan Yang, and Chih-Jen Lin (<http://www.csie.ntu.edu.tw/~cjlin/libmf/>), an open source library for recommender system using parallel matrix factorization. (Chin, Yuan, et al. 2015)

```
# Create algorithm datasets
edx_fact <- edx %>% select(movieId, userId, rating)
validation_fact <- validation %>% select(movieId, userId, rating)
# Convert to Matrix
edx_fact <- as.matrix(edx_fact)
validation_fact <- as.matrix(validation_fact)

# write to disk
write.table(edx_fact, file = "trainingset.txt", sep = " ", row.names = FALSE,
            col.names = FALSE)
write.table(validation_fact, file = "validationset.txt", sep = " ",
            row.names = FALSE, col.names = FALSE)

# Initialize train and test sets
set.seed(1, sample.kind = "Rounding")
training_dataset <- data_file("trainingset.txt")
validation_dataset <- data_file("validationset.txt")

# Create Reco Object
r = Reco()

# Create Tuning Parameters
opts = r$tune(training_dataset, opts = list(dim = c(10, 20, 30),
      lrate = c(0.1, 0.2), costp_l1 = 0, costq_l1 = 0, nthread = 1,
      niter = 10))

# Train Model
r$train(training_dataset, opts = c(opts$min, nthread = 1, niter = 20))
```

## iter	tr_rmse	obj
## 0	0.9736	1.2042e+007
## 1	0.8721	9.8790e+006
## 2	0.8378	9.1536e+006
## 3	0.8168	8.7473e+006
## 4	0.8012	8.4729e+006
## 5	0.7892	8.2723e+006
## 6	0.7795	8.1204e+006
## 7	0.7713	7.9959e+006
## 8	0.7646	7.9044e+006
## 9	0.7588	7.8245e+006
## 10	0.7537	7.7575e+006
## 11	0.7492	7.7015e+006

```
## 12      0.7452 7.6522e+006
## 13      0.7415 7.6098e+006
## 14      0.7382 7.5712e+006
## 15      0.7351 7.5374e+006
## 16      0.7322 7.5068e+006
## 17      0.7296 7.4768e+006
## 18      0.7271 7.4528e+006
## 19      0.7249 7.4299e+006
```

```
# write predictions to a tempfile on HDisk
```

```
stored_prediction = tempfile()
```

```
# Run Prediction
```

```
r$predict(validation_dataset, out_file(stored_prediction))
```

```
## prediction output generated at C:\Users\EstelleR\AppData\Local\Temp\RtmpWMvM5C\file46d837fe290b
```

```
real_ratings <- read.table("validationset.txt", header = FALSE,
  sep = " ")$V3
pred_ratings <- scan(stored_prediction)
```

```
# Determine RMSE
```

```
rmse_of_model_mf <- RMSE(pred_ratings, real_ratings)
rmse_results <- rmse_results %>% add_row(Dataset = "edx/validation",
  Model = "Matrix Factorization with Parallel Stochastic Gradient Descent",
  RMSE = rmse_of_model_mf, Accuracy = mean(round(pred_ratings/0.5) *
    0.5 == validation$rating), Lambda = "NA")
```

```
rmse_results %>% filter(RMSE <= 0.8) %>% kable() %>% kable_styling(bootstrap_options = c("striped"),
  position = "center", font_size = 10, full_width = FALSE) %>%
  footnote(general = "RMSE for Model 2", footnote_as_chunk = T)
```

Dataset	Model	RMSE	Accuracy	Lambda
edx/validation	Matrix Factorization with Parallel Stochastic Gradient Descent	0.7829341	0.2753943	NA

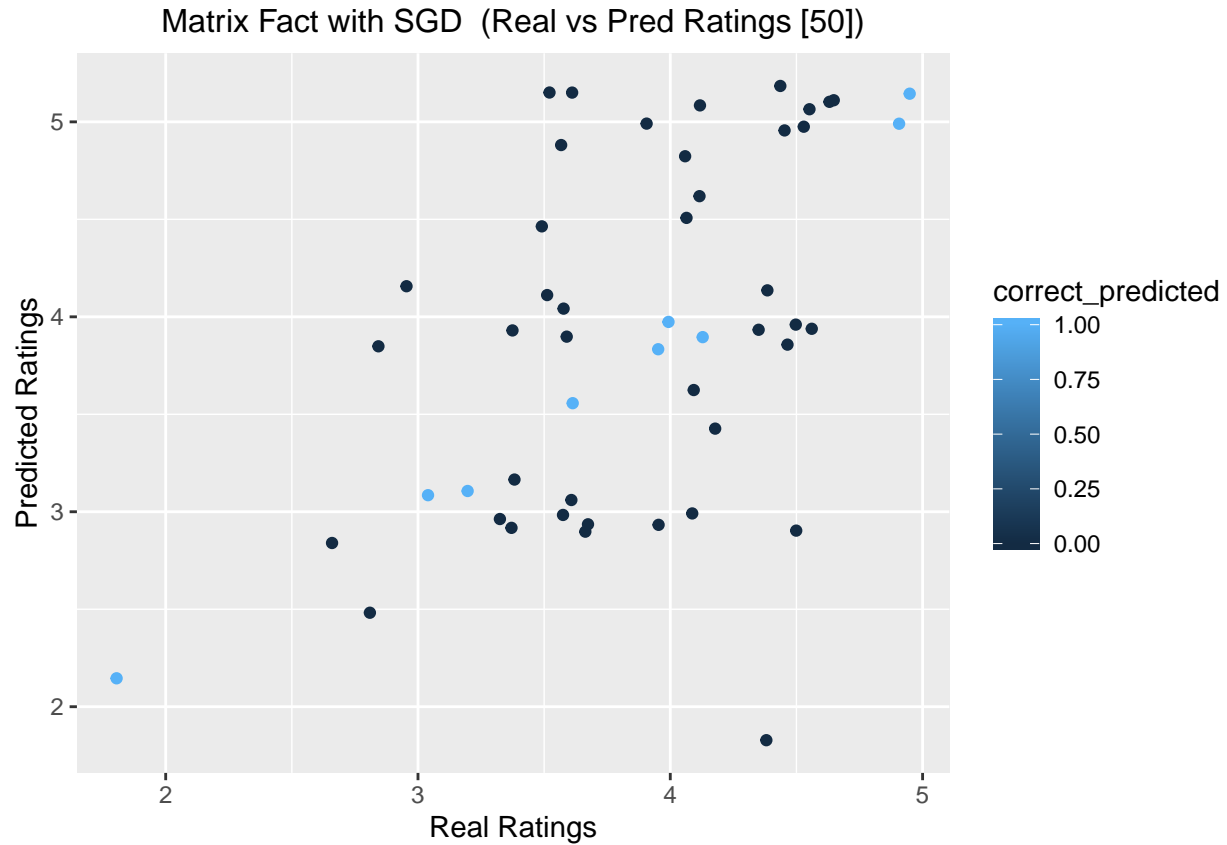
Note: RMSE for Model 2

```
# Compare Predictions
```

```
pred_ratings_rounded <- pred_ratings
pred_ratings_rounded <- round(pred_ratings_rounded/0.5) * 0.5
```

```
# Plot Predictions
```

```
Pred_Plot(pred_ratings_rounded, real_ratings, "Matrix Fact with SGD")
```



When testing the SGD Model on the validation set, the RMSE is 0.7829341 which exceeds the baseline RMSE requirement of 0.8649.

6 Results

From the two models tested, the Matrix factorization with stochastic gradient descent model performed better when comparing it to model 1 (which follows the Netflix approach of 2011) in terms of RMSE.

Final RMSE Results

Dataset	Model	RMSE	Accuracy	Lambda
edx/validation	Regularized Movie+User+Year+Genre Effect Model	0.8644548	0.2484252	3.5
edx/validation	Matrix Factorization with Parallel Stochastic Gradient Descent	0.7829341	0.2753943	NA

Note: Final Results

7 Conclusion

From hours of testing different models and configurations, it was clear from research that matrix factorization model offers superior performance when applied to recommender systems (as seen in the RMSE results). When implemented on the supplied validation dataset, an RMSE of 0.7829341 was obtained.

By incorporating various features into model 1, a small improvement was seen on the RMSE.

Recommendations

-Split larger datasets into smaller training and tests sets for testing algorithms to avoid wasting time. - Spending time analyzing data before developing models/algorithms will help to achieve the goal faster.

Future Work

-Use the recommenderlab package to explore this project further. Baseline simulations was ran but it resulted in an RMSE of exceeding 0.9. -Use single-value decomposition and matrix facotorization to expand on model 1. -Consider time effects on model 1. -Modify tuning parameters for model 2 to optimize RMSE.

8 References

- <https://github.com/AlessandroCorradini/Harvard-Data-Science-Professional/tree/master/09%20-%20PH125.9x%20-%20Capstone>
- <https://rpubs.com/jeknov/movieRec>
- <https://github.com/gideonvos/MovieLens/blob/master/MovieLensProject.R>
- <https://redroy44.github.io/2017/02/03/movielens/>
- https://github.com/mmurray2073/harvardx_datascience/blob/master/Capstone_MovieLens_MichaelMurray.R
- <https://cran.r-project.org/web/packages/recosystem/vignettes/introduction.html>
- <https://www.analyticsvidhya.com/blog/2016/12/practical-guide-to-implement-machine-learning-with-caret-package-in-r-with-practice-problem/>
- http://rstudio-pubs-static.s3.amazonaws.com/493393_e53177fe25844f788d0bebafa8e7035f.html
- Chin, Wei-Sheng, Bo-Wen Yuan, Meng-Yuan Yang, Yong Zhuang, Yu-Chin Juan, and Chih-Jen Lin. 2015. “LIBMF: A Library for Parallel Matrix Factorization in Shared-Memory Systems.” https://www.csie.ntu.edu.tw/~cjlin/papers/libmf/libmf_open_source.pdf.
- Chin, Wei-Sheng, Yong Zhuang, Yu-Chin Juan, and Chih-Jen Lin. 2015a. “A Fast Parallel Stochastic Gradient Method for Matrix Factorization in Shared Memory Systems.” ACM TIST.
- http://www.csie.ntu.edu.tw/~cjlin/papers/libmf/libmf_journal.pdf. 2015b. “A Learning-Rate Schedule for Stochastic Gradient Methods to Matrix Factorization.” PAKDD.
- http://www.csie.ntu.edu.tw/~cjlin/papers/libmf/mf_adaptive_pakdd.pdf.
- <https://researcher.watson.ibm.com/researcher/files/us-phaas/rj10482Updated.pdf>
- <https://bookdown.org/yihui/rmarkdown/>

9 Environmental Variables

```
# Print OS
print("Operating System:")

## [1] "Operating System:"

version

##
## platform      _
## arch          x86_64-w64-mingw32
## os            mingw32
## system        x86_64, mingw32
## status
## major         3
## minor         6.2
## year          2019
## month         12
## day           12
## svn rev       77560
## language      R
## version.string R version 3.6.2 (2019-12-12)
## nickname      Dark and Stormy Night

# Print Installed Packages
print("All installed packages")

## [1] "All installed packages"

installed.packages()

##           Package           LibPath
## annotate      "annotate"      "C:/Users/EstelleR/Documents/R/win-library/3.6"
## AnnotationDbi "AnnotationDbi"    "C:/Users/EstelleR/Documents/R/win-library/3.6"
## arules        "arules"        "C:/Users/EstelleR/Documents/R/win-library/3.6"
## askpass       "askpass"       "C:/Users/EstelleR/Documents/R/win-library/3.6"
## assertthat    "assertthat"    "C:/Users/EstelleR/Documents/R/win-library/3.6"
## backports     "backports"     "C:/Users/EstelleR/Documents/R/win-library/3.6"
## base64enc     "base64enc"     "C:/Users/EstelleR/Documents/R/win-library/3.6"
## BH            "BH"            "C:/Users/EstelleR/Documents/R/win-library/3.6"
## Biobase       "Biobase"       "C:/Users/EstelleR/Documents/R/win-library/3.6"
## BiocGenerics  "BiocGenerics"  "C:/Users/EstelleR/Documents/R/win-library/3.6"
## BiocManager   "BiocManager"   "C:/Users/EstelleR/Documents/R/win-library/3.6"
## BiocVersion   "BiocVersion"   "C:/Users/EstelleR/Documents/R/win-library/3.6"
## bit           "bit"           "C:/Users/EstelleR/Documents/R/win-library/3.6"
## bit64         "bit64"         "C:/Users/EstelleR/Documents/R/win-library/3.6"
## bitops        "bitops"        "C:/Users/EstelleR/Documents/R/win-library/3.6"
## blob          "blob"          "C:/Users/EstelleR/Documents/R/win-library/3.6"
## boot          "boot"          "C:/Users/EstelleR/Documents/R/win-library/3.6"
## brew          "brew"          "C:/Users/EstelleR/Documents/R/win-library/3.6"
## broom         "broom"         "C:/Users/EstelleR/Documents/R/win-library/3.6"
```

## callr	"callr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## caret	"caret"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## cellranger	"cellranger"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## cli	"cli"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## clipr	"clipr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## clisymbols	"clisymbols"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## colorspace	"colorspace"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## commonmark	"commonmark"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## covr	"covr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## crayon	"crayon"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## crosstalk	"crosstalk"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## curl	"curl"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## data.table	"data.table"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## DBI	"DBI"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## dbplyr	"dbplyr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## desc	"desc"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## devtools	"devtools"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## digest	"digest"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## dplyr	"dplyr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## dslabs	"dslabs"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## DT	"DT"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## e1071	"e1071"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ellipsis	"ellipsis"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## evaluate	"evaluate"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## fansi	"fansi"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## farver	"farver"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## fastAdaboost	"fastAdaboost"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## fastmap	"fastmap"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## forcats	"forcats"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## foreach	"foreach"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## foreign	"foreign"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## formatR	"formatR"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## fs	"fs"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## gam	"gam"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## genefilter	"genefilter"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## generics	"generics"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ggplot2	"ggplot2"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ggrepel	"ggrepel"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ggthemes	"ggthemes"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## gh	"gh"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## git2r	"git2r"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## glue	"glue"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## gower	"gower"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## gridExtra	"gridExtra"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## gtable	"gtable"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## gutenbergr	"gutenbergr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## haven	"haven"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## hexbin	"hexbin"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## highr	"highr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## HistData	"HistData"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## hms	"hms"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## htmltools	"htmltools"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## htmlwidgets	"htmlwidgets"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## httpuv	"httpuv"	"C:/Users/EstelleR/Documents/R/win-library/3.6"

## httr	"httr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## hunspell	"hunspell"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ini	"ini"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ipred	"ipred"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## IRanges	"IRanges"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## irlba	"irlba"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ISOcodes	"ISOcodes"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## iterators	"iterators"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## janeaustenr	"janeaustenr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## jsonlite	"jsonlite"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## kableExtra	"kableExtra"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## kernlab	"kernlab"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## KernSmooth	"KernSmooth"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## knitr	"knitr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## labeling	"labeling"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## Lahman	"Lahman"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## later	"later"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## lava	"lava"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## lazyeval	"lazyeval"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## lifecycle	"lifecycle"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## lubridate	"lubridate"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## magrittr	"magrittr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## markdown	"markdown"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## MASS	"MASS"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## MatrixModels	"MatrixModels"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## matrixStats	"matrixStats"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## memoise	"memoise"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## Metrics	"Metrics"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## mgcv	"mgcv"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## mime	"mime"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ModelMetrics	"ModelMetrics"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## modelr	"modelr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## munsell	"munsell"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## naivebayes	"naivebayes"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## nlme	"nlme"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## numDeriv	"numDeriv"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## openssl	"openssl"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## pdftools	"pdftools"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## pillar	"pillar"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
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## pkgload	"pkgload"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## plogr	"plogr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## plotly	"plotly"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## plyr	"plyr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## praise	"praise"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## prettyunits	"prettyunits"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## processx	"processx"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## prodlim	"prodlim"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## progress	"progress"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## promises	"promises"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## proxy	"proxy"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## pryr	"pryr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ps	"ps"	"C:/Users/EstelleR/Documents/R/win-library/3.6"

## purrr	"purrr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## qpdf	"qpdf"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## quantreg	"quantreg"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## R6	"R6"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## randomForest	"randomForest"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
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## rcmdcheck	"rcmdcheck"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## RColorBrewer	"RColorBrewer"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## Rcpp	"Rcpp"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## RcppProgress	"RcppProgress"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## RCurl	"RCurl"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## readr	"readr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## readxl	"readxl"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## recipes	"recipes"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## recommenderlab	"recommenderlab"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## ecosysystem	"ecosysystem"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## registry	"registry"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rematch	"rematch"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## remotes	"remotes"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## reprex	"reprex"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## reshape2	"reshape2"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rex	"rex"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rlang	"rlang"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rmarkdown	"rmarkdown"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## roxygen2	"roxygen2"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rprojroot	"rprojroot"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## RSQLite	"RSQLite"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rstudioapi	"rstudioapi"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rversions	"rversions"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## rvest	"rvest"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## S4Vectors	"S4Vectors"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## scales	"scales"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## selectr	"selectr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## sessioninfo	"sessioninfo"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## shiny	"shiny"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## slam	"slam"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## SnowballC	"SnowballC"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## sourcetools	"sourcetools"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## SparseM	"SparseM"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## SQUAREM	"SQUAREM"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## stopwords	"stopwords"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## stringi	"stringi"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## stringr	"stringr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## survival	"survival"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## sys	"sys"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## testthat	"testthat"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## textdata	"textdata"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tibble	"tibble"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tidyr	"tidyr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tidyselect	"tidyselect"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tidytext	"tidytext"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tidyverse	"tidyverse"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## timeDate	"timeDate"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tinytex	"tinytex"	"C:/Users/EstelleR/Documents/R/win-library/3.6"

## titanic	"titanic"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## tokenizers	"tokenizers"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## triebeard	"triebeard"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## urltools	"urltools"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## usethis	"usethis"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## utf8	"utf8"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## vctr	"vctr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## viridisLite	"viridisLite"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## webshot	"webshot"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## whisker	"whisker"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## withr	"withr"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## xfun	"xfun"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## XML	"XML"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## xml2	"xml2"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## xopen	"xopen"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## xtable	"xtable"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## yaml	"yaml"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## zeallot	"zeallot"	"C:/Users/EstelleR/Documents/R/win-library/3.6"
## base	"base"	"C:/Program Files/R/R-3.6.2/library"
## boot	"boot"	"C:/Program Files/R/R-3.6.2/library"
## class	"class"	"C:/Program Files/R/R-3.6.2/library"
## cluster	"cluster"	"C:/Program Files/R/R-3.6.2/library"
## codetools	"codetools"	"C:/Program Files/R/R-3.6.2/library"
## compiler	"compiler"	"C:/Program Files/R/R-3.6.2/library"
## datasets	"datasets"	"C:/Program Files/R/R-3.6.2/library"
## foreign	"foreign"	"C:/Program Files/R/R-3.6.2/library"
## graphics	"graphics"	"C:/Program Files/R/R-3.6.2/library"
## grDevices	"grDevices"	"C:/Program Files/R/R-3.6.2/library"
## grid	"grid"	"C:/Program Files/R/R-3.6.2/library"
## KernSmooth	"KernSmooth"	"C:/Program Files/R/R-3.6.2/library"
## lattice	"lattice"	"C:/Program Files/R/R-3.6.2/library"
## MASS	"MASS"	"C:/Program Files/R/R-3.6.2/library"
## Matrix	"Matrix"	"C:/Program Files/R/R-3.6.2/library"
## methods	"methods"	"C:/Program Files/R/R-3.6.2/library"
## mgcv	"mgcv"	"C:/Program Files/R/R-3.6.2/library"
## nlme	"nlme"	"C:/Program Files/R/R-3.6.2/library"
## nnet	"nnet"	"C:/Program Files/R/R-3.6.2/library"
## parallel	"parallel"	"C:/Program Files/R/R-3.6.2/library"
## rpart	"rpart"	"C:/Program Files/R/R-3.6.2/library"
## spatial	"spatial"	"C:/Program Files/R/R-3.6.2/library"
## splines	"splines"	"C:/Program Files/R/R-3.6.2/library"
## stats	"stats"	"C:/Program Files/R/R-3.6.2/library"
## stats4	"stats4"	"C:/Program Files/R/R-3.6.2/library"
## survival	"survival"	"C:/Program Files/R/R-3.6.2/library"
## tcltk	"tcltk"	"C:/Program Files/R/R-3.6.2/library"
## tools	"tools"	"C:/Program Files/R/R-3.6.2/library"
## translations	"translations"	"C:/Program Files/R/R-3.6.2/library"
## utils	"utils"	"C:/Program Files/R/R-3.6.2/library"
##	Version	Priority
## annotate	"1.64.0"	NA
## AnnotationDbi	"1.48.0"	NA
## arules	"1.6-4"	NA
## askpass	"1.1"	NA
## assertthat	"0.2.1"	NA

## backports	"1.1.5"	NA
## base64enc	"0.1-3"	NA
## BH	"1.72.0-2"	NA
## Biobase	"2.46.0"	NA
## BiocGenerics	"0.32.0"	NA
## BiocManager	"1.30.10"	NA
## BiocVersion	"3.10.1"	NA
## bit	"1.1-14"	NA
## bit64	"0.9-7"	NA
## bitops	"1.0-6"	NA
## blob	"1.2.0"	NA
## boot	"1.3-24"	"recommended"
## brew	"1.0-6"	NA
## broom	"0.5.3"	NA
## callr	"3.4.0"	NA
## caret	"6.0-84"	NA
## cellranger	"1.1.0"	NA
## cli	"2.0.0"	NA
## clipr	"0.7.0"	NA
## clisymbols	"1.2.0"	NA
## colorspace	"1.4-1"	NA
## commonmark	"1.7"	NA
## covr	"3.4.0"	NA
## crayon	"1.3.4"	NA
## crosstalk	"1.0.0"	NA
## curl	"4.3"	NA
## data.table	"1.12.8"	NA
## DBI	"1.1.0"	NA
## dbplyr	"1.4.2"	NA
## desc	"1.2.0"	NA
## devtools	"2.2.1"	NA
## digest	"0.6.23"	NA
## dplyr	"0.8.3"	NA
## dslabs	"0.7.3"	NA
## DT	"0.11"	NA
## e1071	"1.7-3"	NA
## ellipsis	"0.3.0"	NA
## evaluate	"0.14"	NA
## fansi	"0.4.0"	NA
## farver	"2.0.1"	NA
## fastAdaboost	"1.0.0"	NA
## fastmap	"1.0.1"	NA
## forcats	"0.4.0"	NA
## foreach	"1.4.7"	NA
## foreign	"0.8-74"	"recommended"
## formatR	"1.7"	NA
## fs	"1.3.1"	NA
## gam	"1.16.1"	NA
## genefilter	"1.68.0"	NA
## generics	"0.0.2"	NA
## ggplot2	"3.2.1"	NA
## ggrepel	"0.8.1"	NA
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## gh	"1.0.1"	NA

## git2r	"0.26.1"	NA
## glue	"1.3.1"	NA
## gower	"0.2.1"	NA
## gridExtra	"2.3"	NA
## gtable	"0.3.0"	NA
## gutenbergr	"0.1.5"	NA
## haven	"2.2.0"	NA
## hexbin	"1.28.0"	NA
## highr	"0.8"	NA
## HistData	"0.8-4"	NA
## hms	"0.5.2"	NA
## htmltools	"0.4.0"	NA
## htmlwidgets	"1.5.1"	NA
## httpuv	"1.5.2"	NA
## httr	"1.4.1"	NA
## hunspell	"3.0"	NA
## ini	"0.3.1"	NA
## ipred	"0.9-9"	NA
## IRanges	"2.20.1"	NA
## irlba	"2.3.3"	NA
## ISOcodes	"2019.12.22"	NA
## iterators	"1.0.12"	NA
## janeaustenr	"0.1.5"	NA
## jsonlite	"1.6"	NA
## kableExtra	"1.1.0"	NA
## kernlab	"0.9-29"	NA
## KernSmooth	"2.23-16"	"recommended"
## knitr	"1.26"	NA
## labeling	"0.3"	NA
## Lahman	"7.0-1"	NA
## later	"1.0.0"	NA
## lava	"1.6.6"	NA
## lazyeval	"0.2.2"	NA
## lifecycle	"0.1.0"	NA
## lubridate	"1.7.4"	NA
## magrittr	"1.5"	NA
## markdown	"1.1"	NA
## MASS	"7.3-51.5"	"recommended"
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## Metrics	"0.1.4"	NA
## mgcv	"1.8-31"	"recommended"
## mime	"0.8"	NA
## ModelMetrics	"1.2.2"	NA
## modelr	"0.1.5"	NA
## munsell	"0.5.0"	NA
## naivebayes	"0.9.6"	NA
## nlme	"3.1-143"	"recommended"
## numDeriv	"2016.8-1.1"	NA
## openssl	"1.4.1"	NA
## pdftools	"2.3"	NA
## pillar	"1.4.3"	NA
## pkgbuild	"1.0.6"	NA

## pkgconfig	"2.0.3"	NA
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## plotly	"4.9.1"	NA
## plyr	"1.8.5"	NA
## praise	"1.0.0"	NA
## prettyunits	"1.0.2"	NA
## processx	"3.4.1"	NA
## prodlim	"2019.11.13"	NA
## progress	"1.2.2"	NA
## promises	"1.1.0"	NA
## proxy	"0.4-23"	NA
## pryr	"0.1.4"	NA
## ps	"1.3.0"	NA
## purrr	"0.3.3"	NA
## qpdf	"1.1"	NA
## quantreg	"5.54"	NA
## R6	"2.4.1"	NA
## randomForest	"4.6-14"	NA
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## rcmdcheck	"1.3.3"	NA
## RColorBrewer	"1.1-2"	NA
## Rcpp	"1.0.3"	NA
## RcppProgress	"0.4.1"	NA
## RCurl	"1.95-4.12"	NA
## readr	"1.3.1"	NA
## readxl	"1.3.1"	NA
## recipes	"0.1.8"	NA
## recommenderlab	"0.2-5"	NA
## recosystem	"0.4.2"	NA
## registry	"0.5-1"	NA
## rematch	"1.0.1"	NA
## remotes	"2.1.0"	NA
## reprex	"0.3.0"	NA
## reshape2	"1.4.3"	NA
## rex	"1.1.2"	NA
## rlang	"0.4.2"	NA
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## roxygen2	"7.0.2"	NA
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## RSQLite	"2.1.5"	NA
## rstudioapi	"0.10"	NA
## rversions	"2.0.1"	NA
## rvest	"0.3.5"	NA
## S4Vectors	"0.24.1"	NA
## scales	"1.1.0"	NA
## selectr	"0.4-2"	NA
## sessioninfo	"1.1.1"	NA
## shiny	"1.4.0"	NA
## slam	"0.1-47"	NA
## SnowballC	"0.6.0"	NA
## sourcetools	"0.1.7"	NA
## SparseM	"1.78"	NA
## SQUAREM	"2017.10-1"	NA

## stopwords	"1.0"	NA
## stringi	"1.4.3"	NA
## stringr	"1.4.0"	NA
## survival	"3.1-8"	"recommended"
## sys	"3.3"	NA
## testthat	"2.3.1"	NA
## textdata	"0.3.0"	NA
## tibble	"2.1.3"	NA
## tidyr	"1.0.0"	NA
## tidyselect	"0.2.5"	NA
## tidytext	"0.2.2"	NA
## tidyverse	"1.3.0"	NA
## timeDate	"3043.102"	NA
## tinytex	"0.18"	NA
## titanic	"0.1.0"	NA
## tokenizers	"0.2.1"	NA
## triebeard	"0.3.0"	NA
## urltools	"1.7.3"	NA
## usethis	"1.5.1"	NA
## utf8	"1.1.4"	NA
## vctrs	"0.2.1"	NA
## viridisLite	"0.3.0"	NA
## webshot	"0.5.2"	NA
## whisker	"0.4"	NA
## withr	"2.1.2"	NA
## xfun	"0.11"	NA
## XML	"3.98-1.20"	NA
## xml2	"1.2.2"	NA
## xopen	"1.0.0"	NA
## xtable	"1.8-4"	NA
## yaml	"2.2.0"	NA
## zeallot	"0.1.0"	NA
## base	"3.6.2"	"base"
## boot	"1.3-23"	"recommended"
## class	"7.3-15"	"recommended"
## cluster	"2.1.0"	"recommended"
## codetools	"0.2-16"	"recommended"
## compiler	"3.6.2"	"base"
## datasets	"3.6.2"	"base"
## foreign	"0.8-72"	"recommended"
## graphics	"3.6.2"	"base"
## grDevices	"3.6.2"	"base"
## grid	"3.6.2"	"base"
## KernSmooth	"2.23-16"	"recommended"
## lattice	"0.20-38"	"recommended"
## MASS	"7.3-51.4"	"recommended"
## Matrix	"1.2-18"	"recommended"
## methods	"3.6.2"	"base"
## mgcv	"1.8-31"	"recommended"
## nlme	"3.1-142"	"recommended"
## nnet	"7.3-12"	"recommended"
## parallel	"3.6.2"	"base"
## rpart	"4.1-15"	"recommended"
## spatial	"7.3-11"	"recommended"

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## splines      "3.6.2"      "base"
## stats        "3.6.2"      "base"
## stats4       "3.6.2"      "base"
## survival     "3.1-8"      "recommended"
## tcltk        "3.6.2"      "base"
## tools        "3.6.2"      "base"
## translations "3.6.2"      NA
## utils        "3.6.2"      "base"
##
## Depends
## annotate     "R (>= 2.10), AnnotationDbi (>= 1.27.5), XML"
## AnnotationDbi "R (>= 2.7.0), methods, utils, stats4, BiocGenerics (>= 2.29.2), Biobase (>= 1.17.0)"
## arules       "R (>= 3.4.0), Matrix (>= 1.2-0)"
## askpass      NA
## assertthat   NA
## backports    "R (>= 3.0.0)"
## 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 (>= 3.6.0)"
## bit          "R (>= 2.9.2)"
## bit64        "R (>= 3.0.1), bit (>= 1.1-12), utils, methods, stats"
## bitops       NA
## blob         NA
## boot         "R (>= 3.0.0), graphics, stats"
## brew         NA
## broom        "R (>= 3.1)"
## callr        NA
## caret        "R (>= 3.2.0), lattice (>= 0.20), ggplot2"
## cellranger   "R (>= 3.0.0)"
## cli          "R (>= 2.10)"
## clipr        NA
## clisymbols   NA
## colorspace   "R (>= 3.0.0), methods"
## commonmark   NA
## covr         "R (>= 3.1.0), methods"
## crayon       NA
## crosstalk    NA
## curl         "R (>= 3.0.0)"
## data.table   "R (>= 3.1.0)"
## DBI          "methods, R (>= 3.0.0)"
## dbplyr       "R (>= 3.1)"
## desc         "R (>= 3.1.0)"
## devtools     "R (>= 3.0.2), usethis (>= 1.5.0)"
## digest       "R (>= 3.1.0)"
## 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 (>= 3.1)"
## foreach           "R (>= 2.5.0)"
## foreign           "R (>= 3.0.0)"
## formatR           "R (>= 3.0.2)"
## fs                "R (>= 3.1)"
## gam               "stats, splines, foreach"
## genefilter        NA
## generics          "R (>= 3.1)"
## ggplot2           "R (>= 3.2)"
## ggrepel           "R (>= 3.0.0), ggplot2 (>= 2.2.0)"
## ggthemes          "R (>= 3.3.0)"
## gh                NA
## git2r             "R (>= 3.1)"
## glue              "R (>= 3.1)"
## gower             NA
## gridExtra         NA
## gtable            "R (>= 3.0)"
## gutenbergr        "R (>= 2.10)"
## haven             "R (>= 3.2)"
## hexbin            "R (>= 2.0.1), methods"
## highr             "R (>= 3.2.3)"
## HistData          NA
## hms               NA
## htmltools         "R (>= 2.14.1)"
## htmlwidgets       NA
## httpuv            "R (>= 2.15.1)"
## httr              "R (>= 3.2)"
## hunspell          "R (>= 3.0.2)"
## ini               NA
## ipred             "R (>= 2.10)"
## IRanges           "R (>= 3.1.0), methods, utils, stats, BiocGenerics (>= 0.25.3), \nS4Vectors (>= 0.23.2)"
## irlba             "Matrix"
## ISOcodes          "R (>= 3.5.0)"
## iterators         "R (>= 2.5.0), utils"
## janeaustenr       "R (>= 3.1.2)"
## jsonlite          "methods"
## kableExtra        "R (>= 3.1.0)"
## kernlab           "R (>= 2.10)"
## KernSmooth        "R (>= 2.5.0), stats"
## knitr             "R (>= 3.2.3)"
## labeling          NA
## Lahman            "R (>= 2.10)"
## later             NA
## lava              "R (>= 3.0)"
## lazyeval          "R (>= 3.1.0)"
## lifecycle         "R (>= 3.2)"
## lubridate         "methods, R (>= 3.0.0)"
## magrittr          NA
## markdown          "R (>= 2.11.1)"
## MASS              "R (>= 3.1.0), grDevices, graphics, stats, utils"
## MatrixModels      "R (>= 3.0.1)"
## matrixStats       "R (>= 2.12.0)"

```



```

## memoise          NA
## Metrics          NA
## mgcv             "R (>= 2.14.0), nlme (>= 3.1-64)"
## mime            NA
## ModelMetrics     "R (>= 3.2.2)"
## modelr           "R (>= 3.2)"
## munsell          NA
## naivebayes       NA
## nlme             "R (>= 3.4.0)"
## numDeriv         "R (>= 2.11.1)"
## openssl          NA
## pdftools         NA
## pillar           NA
## pkgbuild         "R (>= 3.1)"
## pkgconfig        NA
## pkgload          NA
## plogr            NA
## plotly           "R (>= 3.2.0), ggplot2 (>= 3.0.0)"
## plyr             "R (>= 3.1.0)"
## praise           NA
## prettyunits      NA
## processx         NA
## prodlim          "R (>= 2.9.0)"
## progress         NA
## promises         NA
## proxy            "R (>= 3.4.0)"
## pryr             "R (>= 3.1.0)"
## ps               "R (>= 3.1)"
## purrr            "R (>= 3.2)"
## qpdf             NA
## quantreg         "R (>= 2.6), stats, SparseM"
## R6               "R (>= 3.0)"
## randomForest     "R (>= 3.2.2), stats"
## rappdirs         "R (>= 2.14), methods"
## rcmdcheck        NA
## RColorBrewer     "R (>= 2.0.0)"
## Rcpp             "R (>= 3.0.0)"
## RcppProgress     NA
## RCurl            "R (>= 3.0.0), methods, bitops"
## readr            "R (>= 3.1)"
## readxl           NA
## recipes          "R (>= 3.1), dplyr"
## recommenderlab   "R (>= 2.10.0), Matrix, arules, proxy, registry"
## recosystem       "R (>= 3.3.0), methods"
## registry         "R (>= 2.6.0)"
## rematch          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)"
## rprojroot        "R (>= 3.0.0)"

```

```

## 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"
## slam             "R (>= 3.4.0)"
## SnowballC        NA
## sourcetools       "R (>= 3.0.2)"
## SparseM          "R (>= 2.15), methods"
## SQUAREM          "R (>= 3.0)"
## stopwords        "R (>= 2.10)"
## stringi          "R (>= 2.14)"
## stringr          "R (>= 3.1)"
## survival         "R (>= 3.4.0)"
## sys              NA
## testthat         "R (>= 3.1)"
## textdata         NA
## tibble           "R (>= 3.1.0)"
## tidyr            "R (>= 3.1)"
## tidyselect       "R (>= 3.1)"
## 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)"
## triebeard        NA
## urltools         "R (>= 2.10)"
## usethis          "R (>= 3.2)"
## utf8             "R (>= 2.10)"
## vctrs            "R (>= 3.2)"
## viridisLite      "R (>= 2.10)"
## webshot          "R (>= 3.0)"
## whisker          NA
## withr            "R (>= 3.0.2)"
## xfun             NA
## XML              "R (>= 2.13.0), methods, utils"
## xml2             "R (>= 3.1.0)"
## xopen            "R (>= 3.1)"
## xtable           "R (>= 2.10.0)"
## yaml             NA
## zeallot          NA
## base             NA
## boot             "R (>= 3.0.0), graphics, stats"
## class            "R (>= 3.0.0), stats, utils"
## cluster          "R (>= 3.3.0)"
## codetools        "R (>= 2.1)"
## compiler         NA
## datasets         NA
## foreign          "R (>= 3.0.0)"

```

```

## graphics      NA
## grDevices     NA
## grid          NA
## KernSmooth    "R (>= 2.5.0), stats"
## lattice       "R (>= 3.0.0)"
## MASS          "R (>= 3.1.0), grDevices, graphics, stats, utils"
## Matrix        "R (>= 3.2.0)"
## methods       NA
## mgcv          "R (>= 2.14.0), nlme (>= 3.1-64)"
## nlme          "R (>= 3.4.0)"
## nnet          "R (>= 2.14.0), stats, utils"
## parallel      NA
## rpart         "R (>= 2.15.0), graphics, stats, grDevices"
## spatial       "R (>= 3.0.0), graphics, stats, utils"
## splines       NA
## stats         NA
## stats4        NA
## survival      "R (>= 3.4.0)"
## tcltk         NA
## tools         NA
## translations  NA
## utils         NA
##              Imports
## annotate      "Biobase, DBI, xtable, graphics, utils, stats, methods,\nBiocGenerics (>= 0.13.8), RC"
## AnnotationDbi "DBI, RSQLite, S4Vectors (>= 0.9.25)"
## arules        "stats, methods, graphics, utils"
## askpass       "sys (>= 2.1)"
## assertthat    "tools"
## backports     "utils"
## base64enc     NA
## BH            NA
## Biobase       "methods"
## BiocGenerics  "methods, utils, graphics, stats, parallel"
## BiocManager   "utils"
## BiocVersion   NA
## bit           NA
## bit64         NA
## bitops        NA
## blob          "methods, prettyunits, rlang, vctrs (>= 0.2.0)"
## boot         NA
## brew          NA
## broom         "backports, dplyr, generics (>= 0.0.2), methods, nlme, purrr,\nreshape2, stringr, tibble"
## callr         "processx (>= 3.4.0), R6, utils"
## caret         "foreach, methods, plyr, ModelMetrics (>= 1.1.0), nlme,\nreshape2, stats, stats4, utils"
## cellranger    "rematch, tibble"
## cli           "assertthat, crayon (>= 1.3.4), glue, methods, utils, fansi"
## clipr         "utils"
## clisymbols    NA
## colorspace    "graphics, grDevices, stats"
## commonmark    NA
## covr          "digest, stats, utils, jsonlite, rex, httr, crayon, withr (>= 1.0.2), yaml"
## crayon        "grDevices, methods, utils"
## crosstalk     "htmltools (>= 0.3.5), jsonlite, lazyeval, R6, shiny (>= 0.11),\nggplot2"
## curl          NA

```

```

## data.table      "methods"
## DBI              NA
## dbplyr          "assertthat (>= 0.2.0), DBI (>= 1.0.0), dplyr (>= 0.8.0), glue\n(>= 1.2.0), methods, p
## desc            "assertthat, utils, R6, crayon, rprojroot"
## devtools        "callr, cli, covr (>= 3.2.0), crayon, desc, digest, DT,\nellipsis (>= 0.3.0), glue, g
## digest          "utils"
## dplyr           "assertthat (>= 0.2.0), glue (>= 1.3.0), magrittr (>= 1.5),\nmmethods, pkgconfig, R6, l
## dslabs          "ggplot2"
## DT              "htmltools (>= 0.3.6), htmlwidgets (>= 1.3), jsonlite (>=\n0.9.16), magrittr, crossta
## 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"
## formatR        NA
## fs              "methods, Rcpp"
## gam             NA
## genefilter      "BiocGenerics (>= 0.31.2), AnnotationDbi, annotate, Biobase,\ngraphics, methods, stat
## generics        "methods"
## ggplot2         "digest, grDevices, grid, gtable (>= 0.1.1), lazyeval, MASS,\nmgc, reshape2, rlang (>
## ggrepel         "grid, Rcpp, scales (>= 0.3.0)"
## ggthemes        "ggplot2 (>= 3.0.0), graphics, grid, methods, purrr, scales,\nstringr, tibble"
## gh              "ini, jsonlite, httr"
## git2r           "graphics, utils"
## glue            "methods"
## gower           NA
## gridExtra       "gtable, grid, grDevices, graphics, utils"
## gtable          "grid"
## gutenbergr      "dplyr, readr, purrr, urltools, stringr, lazyeval"
## haven           "forcats (>= 0.2.0), hms, Rcpp (>= 0.11.4), readr (>= 0.1.0),\nrlang (>= 0.4.0), tibble
## hexbin          "lattice, grid, graphics, grDevices, stats, utils"
## highr           NA
## HistData        NA
## hms             "methods, pkgconfig, rlang, vctrs (>= 0.2.0)"
## htmltools       "utils, digest, Rcpp, 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"
## ini             NA
## ipred           "rpart (>= 3.1-8), MASS, survival, nnet, class, prodlim"
## IRanges         "stats4"
## irlba           "stats, methods"
## ISOcodes        NA
## iterators       NA
## janeaustenr     NA
## jsonlite        NA
## kableExtra      "knitr (>= 1.16), magrittr, stringr (>= 1.0), xml2 (>= 1.1.1),\nrvest, rmarkdown (>=
## kernlab         "methods, stats, grDevices, graphics"

```

```

## KernSmooth      NA
## knitr            "evaluate (>= 0.10), highr, markdown, stringr (>= 0.6), yaml\n(>= 2.1.19), methods, x
## labeling         NA
## Lahman           "dplyr"
## later            "Rcpp (>= 0.12.9), rlang"
## lava             "grDevices, graphics, methods, numDeriv, stats, survival,\nSQUAREM, utils"
## lazyeval         NA
## lifecycle        "glue, rlang (>= 0.4.0)"
## lubridate        "stringr, Rcpp (>= 0.12.13),"
## magrittr         NA
## markdown         "utils, xfun, mime (>= 0.3)"
## MASS             "methods"
## MatrixModels     "stats, methods, Matrix (>= 1.1-5)"
## matrixStats      NA
## memoise          "digest (>= 0.6.3)"
## Metrics          NA
## mgcv             "methods, stats, graphics, Matrix, splines, utils"
## mime             "tools"
## ModelMetrics     "Rcpp, data.table"
## modelr           "broom, dplyr, magrittr, purrr (>= 0.2.2), rlang (>= 0.2.0),\ntibble, tidyr (>= 0.8.0)
## munsell          "colorspace, methods"
## naivebayes       NA
## nlme             "graphics, stats, utils, lattice"
## numDeriv         NA
## openssl          "askpass"
## pdftools         "Rcpp (>= 0.12.12), qpdf"
## pillar           "cli, crayon (>= 1.3.4), fansi, rlang (>= 0.3.0), utf8 (>= \n1.1.0), vctrs (>= 0.2.0)"
## pkgbuild         "callr (>= 3.2.0), cli, crayon, desc, prettyunits, R6,\nrprojroot, withr (>= 2.1.2)"
## pkgconfig        "utils"
## pkgload          "desc, methods, pkgbuild, rlang, rprojroot, rstudioapi, utils,\nwithr"
## plogr            NA
## plotly           "tools, scales, httr, jsonlite (>= 1.6), magrittr, digest,\nviridisLite, base64enc, h
## plyr             "Rcpp (>= 0.11.0)"
## praise           NA
## prettyunits      "magrittr, assertthat, methods"
## 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"
## proxy            "stats, utils"
## pryr             "stringr, codetools, methods, Rcpp (>= 0.11.0)"
## ps               "utils"
## purrr            "magrittr (>= 1.5), rlang (>= 0.3.1)"
## qpdf             "Rcpp, askpass, curl"
## quantreg         "methods, graphics, Matrix, MatrixModels"
## R6               NA
## randomForest     NA
## rappdirs         NA
## rcmdcheck        "callr (>= 3.1.1.9000), cli (>= 1.1.0), crayon, desc (>= \n1.2.0), digest, pkgbuild, p
## RColorBrewer     NA
## Rcpp             "methods, utils"
## RcppProgress     NA
## RCurl            NA
## 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, lubridate, magrittr, Matrix,\npurrr (>= 0.2.3), rlang
## recommenderlab  "methods, utils, stats, irlba, recosystem"
## recosystem      "Rcpp (>= 0.11.0)"
## registry        "utils"
## rematch         NA
## 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             "magrittr, 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, methods, pkgload\n(>= 1.0.2), purrr (>= 0
## rprojroot       "backports"
## RSQLite         "bit64, blob (>= 1.2.0), DBI (>= 1.1.0), memoise, methods,\nnpkgconfig, Rcpp (>= 0.12.
## rstudioapi      NA
## rversions       "curl, utils, xml2 (>= 1.0.0)"
## rvest           "httr (>= 0.5), magrittr, selectr"
## S4Vectors       NA
## scales          "farver (>= 2.0.0), labeling, munsell (>= 0.5), R6,\nRColorBrewer, viridisLite, lifecyc
## 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, d
## slam            "stats"
## SnowballC       NA
## sourcetools     NA
## SparseM         "graphics, stats, utils"
## SQUAREM         NA
## stopwords       "ISOcodes"
## stringi         "tools, utils, stats"
## stringr         "glue (>= 1.2.0), magrittr, stringi (>= 1.1.7)"
## survival        "graphics, Matrix, methods, splines, stats, utils"
## sys            NA
## testthat        "cli, crayon (>= 1.3.4), digest, ellipsis, evaluate, magrittr,\nmethods, pkgload, pra
## textdata        "fs, readr, tibble, rappdirs"
## tibble          "cli, crayon (>= 1.3.4), fansi (>= 0.4.0), methods, pillar (>=\n1.3.1), pkgconfig, rl
## tidyr           "dplyr (>= 0.8.2), ellipsis (>= 0.1.0), glue, magrittr, purrr,\nRcpp, rlang, stringi,
## tidyselect      "glue (>= 1.3.0), purrr, rlang (>= 0.2.2), Rcpp (>= 0.12.0)"
## tidytext        "rlang, dplyr, stringr, hunspell, generics, Matrix, tokenizers,\n\nnjaneaustrn, purrr (
## 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)"
## triebeard       "Rcpp"
## urltools        "Rcpp, methods, triebeard"
## usethis         "clipr (>= 0.3.0), clisymbols, crayon, curl (>= 2.7), desc, fs\n(>= 1.3.0), gh, git2r
## utf8           NA
## vctrs           "backports, ellipsis (>= 0.2.0), digest, glue, rlang (>=\n0.4.0), zeallot"
## viridisLite     NA
## webshot         "magrittr, jsonlite, callr"
## whisker         NA
## withr           "stats, graphics, grDevices"
## xfun            "stats, tools"

```

## XML	NA
## xml2	"Rcpp, methods"
## xopen	"processx"
## xtable	"stats, utils"
## yaml	NA
## zeallot	NA
## base	NA
## boot	NA
## class	"MASS"
## cluster	"graphics, grDevices, stats, utils"
## codetools	NA
## compiler	NA
## datasets	NA
## foreign	"methods, utils, stats"
## graphics	"grDevices"
## grDevices	NA
## grid	"grDevices, utils"
## KernSmooth	NA
## lattice	"grid, grDevices, graphics, stats, utils"
## MASS	"methods"
## Matrix	"methods, graphics, grid, stats, utils, lattice"
## methods	"utils, stats"
## mgcv	"methods, stats, graphics, Matrix, splines, utils"
## nlme	"graphics, stats, utils, lattice"
## nnet	NA
## parallel	"tools, compiler"
## rpart	NA
## spatial	NA
## splines	"graphics, stats"
## stats	"utils, grDevices, graphics"
## stats4	"graphics, methods, stats"
## survival	"graphics, Matrix, methods, splines, stats, utils"
## tcltk	"utils"
## tools	NA
## translations	NA
## utils	NA
##	LinkingTo
## annotate	NA
## AnnotationDbi	NA
## arules	NA
## askpass	NA
## assertthat	NA
## backports	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
## cellranger         NA
## cli                NA
## clipr              NA
## clisymbols         NA
## colorspace         NA
## commonmark         NA
## covr               NA
## crayon             NA
## crosstalk          NA
## curl               NA
## data.table         NA
## DBI                NA
## dbplyr             NA
## desc               NA
## devtools           NA
## digest             NA
## dplyr              "BH, plogr (>= 0.2.0), Rcpp (>= 1.0.1)"
## 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
## formatR            NA
## fs                 "Rcpp"
## gam                NA
## genefilter         NA
## generics           NA
## ggplot2            NA
## ggrepel            "Rcpp"
## ggthemes           NA
## gh                 NA
## git2r              NA
## glue               NA
## gower              NA
## gridExtra          NA
## gtable             NA
## gutenbergr         NA
## haven              "Rcpp"
## hexbin             NA
## highr              NA
## HistData           NA
## hms                NA
## htmltools          "Rcpp"

```



```

## htmlwidgets      NA
## httpuv           "Rcpp, BH, later"
## httr             NA
## hunspell         "Rcpp (>= 0.12.12)"
## ini              NA
## ipred            NA
## IRanges          "S4Vectors"
## irlba            "Matrix"
## ISOcodes         NA
## iterators        NA
## janeaustenr      NA
## jsonlite         NA
## kableExtra       NA
## kernlab          NA
## KernSmooth       NA
## knitr            NA
## labeling         NA
## Lahman           NA
## later            "Rcpp, BH"
## lava             NA
## lazyeval         NA
## lifecycle        NA
## lubridate        "Rcpp,"
## magrittr         NA
## markdown         NA
## MASS             NA
## MatrixModels     NA
## matrixStats      NA
## memoise          NA
## Metrics          NA
## mgcv             NA
## mime             NA
## ModelMetrics     "Rcpp"
## modelr           NA
## munsell          NA
## naivebayes       NA
## nlme             NA
## numDeriv         NA
## openssl          NA
## pdftools         "Rcpp"
## pillar           NA
## pkgbuild         NA
## pkgconfig        NA
## pkgload          NA
## plogr            NA
## plotly           NA
## plyr             "Rcpp"
## praise           NA
## prettyunits      NA
## processx         NA
## prodlim          "Rcpp"
## progress         NA
## promises         "later, Rcpp"
## proxy            NA

```

```

## pryr          "Rcpp"
## ps            NA
## purrr         NA
## qpdf          "Rcpp"
## quantreg      NA
## R6            NA
## randomForest  NA
## rappdirs      NA
## rcmdcheck     NA
## RColorBrewer  NA
## Rcpp          NA
## RcppProgress  NA
## RCurl         NA
## readr         "Rcpp, BH"
## readxl        "progress, Rcpp"
## recipes       NA
## recommenderlab NA
## recosystem    "Rcpp, RcppProgress"
## registry      NA
## rematch       NA
## remotes       NA
## reprex        NA
## reshape2      "Rcpp"
## rex           NA
## rlang          NA
## rmarkdown     NA
## roxygen2       "Rcpp"
## rprojroot     NA
## RSQLite        "BH, plogr (>= 0.2.0), Rcpp"
## rstudioapi     NA
## rversions      NA
## rvest          NA
## S4Vectors      NA
## scales         NA
## selectr        NA
## sessioninfo    NA
## shiny          NA
## slam           NA
## SnowballC      NA
## sourcetools    NA
## SparseM        NA
## SQUAREM        NA
## stopwords      NA
## stringi        NA
## stringr        NA
## survival       NA
## sys            NA
## testthat       NA
## textdata       NA
## tibble         NA
## tidyr          "Rcpp"
## tidyselect     "Rcpp (>= 0.12.0),"
## tidytext       NA
## tidyverse      NA

```

```

## timeDate      NA
## tinytex       NA
## titanic       NA
## tokenizers    "Rcpp"
## triebeard     "Rcpp"
## urltools      "Rcpp"
## usethis       NA
## utf8          NA
## vctrs         NA
## viridisLite   NA
## webshot       NA
## whisker       NA
## withr         NA
## xfun          NA
## XML           NA
## xml2          "Rcpp (>= 0.12.12)"
## xopen         NA
## xtable        NA
## yaml          NA
## zeallot       NA
## base          NA
## boot          NA
## class         NA
## cluster       NA
## codetools     NA
## compiler      NA
## datasets      NA
## foreign       NA
## graphics      NA
## grDevices     NA
## grid          NA
## KernSmooth    NA
## lattice       NA
## MASS          NA
## Matrix        NA
## methods       NA
## mgcv          NA
## nlme          NA
## nnet          NA
## parallel      NA
## rpart         NA
## spatial       NA
## splines       NA
## stats         NA
## stats4        NA
## survival      NA
## tcltk         NA
## tools         NA
## translations  NA
## utils         NA
##              Suggests
## 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.UC"
## arules        "pmml, XML, arulesViz, testthat"

```

```

## askpass          "testthat"
## assertthat       "testthat, covr"
## backports        NA
## base64enc        NA
## BH               NA
## Biobase           "tools, tkWidgets, ALL, RUnit, golubEsets"
## BiocGenerics      "Biobase, S4Vectors, IRanges, GenomicRanges, DelayedArray,\nBiostrings, Rsamtools, Ann"
## BiocManager       "BiocStyle, BiocVersion, remotes, testthat, withr, curl, knitr"
## BiocVersion       NA
## bit              NA
## 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, brms,\nbtergm, car, caret, c"
## callr            "cliapp, covr, crayon, fansi, knitr, pingr, ps, rmarkdown,\nrprojroot, spelling, test"
## caret            "BradleyTerry2, e1071, earth (>= 2.2-3), fastICA, gam (>=\n1.15), ipred, kernlab, kni"
## cellranger       "covr, testthat (>= 1.0.0), knitr, rmarkdown"
## cli              "callr, covr, htmlwidgets, knitr, mockery, rmarkdown,\nrstudioapi, prettycode, testth"
## clipr            "covr, knitr, rmarkdown, rstudioapi (>= 0.5), testthat (>=\n2.0.0)"
## clisymbols       "testthat"
## colorspace       "datasets, utils, KernSmooth, MASS, kernlab, mvtnorm, vcd,\nntcltk, shiny, shinyjs, gg"
## commonmark       "curl, testthat, xml2"
## covr             "R6, knitr, rmarkdown, htmltools, DT (>= 0.2), testthat,\nrlang, rstudioapi (>= 0.2),"
## crayon           "mockery, rstudioapi, testthat, withr"
## crosstalk        NA
## curl             "spelling, testthat (>= 1.0.0), knitr, jsonlite, rmarkdown,\nmagrittr, httpuv (>= 1.4"
## data.table       "bit64, curl, R.utils, knitr, xts, nanotime, zoo, yaml"
## DBI              "blob, covr, hms, knitr, magrittr, rmarkdown, rprojroot,\nRSQLite (>= 1.1-2), testtha"
## dbplyr           "bit64, covr, knitr, Lahman, nycflights13, RMariaDB (>=\n1.0.2), rmarkdown, RMySQL (>"
## desc             "covr, testthat, whoami, withr"
## devtools         "BiocManager, bitops, curl (>= 0.9), evaluate, foghorn (>=\n1.1.0), gmailr (> 0.7.0),"
## digest           "tinytest, knitr, rmarkdown"
## dplyr            "bit64, callr, covr, crayon (>= 1.3.4), DBI, dbplyr, dtplyr,\nggplot2, hms, knitr, Lah"
## dslabs           NA
## DT               "knitr (>= 1.8), rmarkdown, shiny (>= 1.2.0)"
## 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"
## foreign          NA
## formatR          "codetools, shiny, testit, rmarkdown, knitr"
## fs               "testthat, covr, pillar (>= 1.0.0), crayon, rmarkdown, knitr,\nwithr, spelling"
## gam              "akima"
## genefilter       "class, hgu95av2.db, tkWidgets, ALL, ROC, DESeq, pasilla,\nRColorBrewer, BiocStyle, kn"
## generics         "covr, pkgload, testthat, tibble"
## ggplot2          "covr, dplyr, ggplot2movies, hexbin, Hmisc, knitr, lattice,\nmapproj, maps, maptools,"
## ggrepel          "knitr, rmarkdown, testthat, gridExtra, devtools, prettydoc"

```

```

## ggthemes      "dplyr, covr, extrafont, glue, knitr, lattice, lintr, maps,\nmapproj, pander, rlang,
## gh            "covr, pingr, testthat"
## git2r         "getPass"
## glue          "testthat, covr, magrittr, crayon, knitr, rmarkdown, DBI,\nRSQLite, R.utils, forcats,
## gower         "tinytest (>= 0.9.3),"
## 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"
## hexbin        "marray, affy, Biobase, limma"
## highr         "knitr, testit"
## HistData      "gtools, KernSmooth, maps, ggplot2, scales, proto, grid,\nreshape, plyr, lattice, jpeg
## hms           "crayon, lubridate, pillar (>= 1.1.0), testthat"
## htmltools     "markdown, testthat, withr"
## htmlwidgets  "knitr (>= 1.8)"
## 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"
## ini          "testthat"
## ipred         "mvtnorm, mlbench, TH.data"
## IRanges       "XVector, GenomicRanges, Rsamtools, GenomicAlignments,\nGenomicFeatures, BSgenome.Cel
## irlba         NA
## ISOcodes      NA
## iterators     "RUnit, foreach"
## janeaustenr   "dplyr, testthat"
## jsonlite      "httr, curl, plyr, testthat, knitr, rmarkdown, R.rsp, sp"
## kableExtra    "testthat, magick, formattable, dplyr"
## kernlab       NA
## KernSmooth    "MASS"
## knitr         "formatR, testit, digest, rgl (>= 0.95.1201), codetools,\nrmarkdown, htmlwidgets (>=
## labeling      NA
## Lahman        "lattice, ggplot2, googleVis, data.table, vcd, reshape2,\ntidyr, zipcode, knitr, rmar
## later         "knitr, rmarkdown, testthat"
## lava         "KernSmooth, Matrix, Rgraphviz, data.table, ellipse, fields,\nforeach, geepack, gof (
## lazyeval      "knitr, rmarkdown (>= 0.2.65), testthat, covr"
## lifecycle     "covr, crayon, knitr, rmarkdown, testthat (>= 2.1.0)"
## lubridate     "testthat, knitr, covr"
## magrittr      "testthat, knitr"
## markdown      "knitr, RCurl"
## MASS          "lattice, nlme, nnet, survival"
## MatrixModels  NA
## matrixStats   "base64enc, ggplot2, knitr, microbenchmark, R.devices, R.rsp"
## memoise       "testthat, aws.s3, httr, covr"
## Metrics       "testthat"
## mgcv          "parallel, survival, MASS"
## mime          NA
## ModelMetrics  "testthat"
## modelr        "compiler, covr, ggplot2, testthat"
## munsell       "ggplot2, testthat"
## naivebayes    "knitr"
## nlme          "Hmisc, MASS"
## numDeriv      NA
## openssl       "testthat, digest, knitr, rmarkdown, jsonlite, jose, sodium"
## pdftools      "jpeg, png, webp, tesseract, testthat"

```

```

## pillar "knitr, lubridate, testthat (>= 2.0.0), withr"
## pkgbuild "Rcpp, testthat, covr"
## pkgconfig "covr, testthat, disposables (>= 1.0.3)"
## pkgload "bitops, covr, Rcpp, testthat"
## plogr "Rcpp"
## plotly "MASS, maps, ggthemes, GGally, testthat, knitr, devtools,\nshiny (>= 1.1.0), shinytes
## plyr "abind, covr, doParallel, foreach, iterators, itertools,\ntcltk, testthat"
## praise "testthat"
## prettyunits "testthat"
## processx "callr (>= 3.2.0), codetools, covr, crayon, curl, debugme,\nparallel, testthat, withr
## prodlim NA
## progress "Rcpp, testthat, withr"
## promises "testthat, future, knitr, rmarkdown"
## proxy "cba"
## pryr "testthat (>= 0.8.0)"
## ps "callr, covr, curl, pingr, processx (>= 3.1.0), R6, rlang,\ntestthat, tibble"
## purrr "covr, crayon, dplyr (>= 0.7.8), knitr, rmarkdown, testthat,\ntibble, tidyselect"
## qpdf "testthat"
## quantreg "tripack, akima, MASS, survival, rgl, logspline, nor1mix,\nFormula, zoo, R.rsp"
## R6 "knitr, microbenchmark, pryr, testthat, ggplot2, scales"
## randomForest "RColorBrewer, MASS"
## rappdirs "testthat, roxygen2"
## rcmdcheck "covr, knitr, mockery, rmarkdown, testthat"
## RColorBrewer NA
## Rcpp "RUnit, inline, rbenchmark, knitr, rmarkdown, pinp, pkgKitten\n(>= 0.1.2)"
## RcppProgress "RcppArmadillo, devtools, roxygen2, testthat"
## RCurl "Rcompression, 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,\nkernlab, knitr, modelda
## recommenderlab "ROCR, testthat"
## recosystem "knitr, prettydoc"
## registry NA
## rematch "covr, testthat"
## remotes "brew, callr, codetools, curl, covr, git2r (>= 0.23.0), knitr,\nmockery, pkgbuild (>=
## rerex "covr, devtools, fortunes, knitr, miniUI, rprojroot,\nrstudioapi, shiny, styler (>= 1
## reshape2 "covr, lattice, testthat (>= 0.8.0)"
## rex "testthat, knitr, rmarkdown, dplyr, ggplot2, Hmisc, stringr,\nrvest, roxygen2, covr"
## rlang "cli, covr, crayon, magrittr, methods, pillar, rmarkdown,\ntestthat (>= 2.3.0)"
## rmarkdown "shiny (>= 0.11), tufte, testthat, digest, dygraphs, tibble,\nfs, pkgdown, callr (>= 1
## roxygen2 "covr, devtools, knitr, rmarkdown, testthat (>= 2.1.0),\nR.methodsS3, R.oo"
## rprojroot "testthat, mockr, knitr, withr, rmarkdown"
## RSQLite "DBItest (>= 1.7.0), knitr, rmarkdown, testthat"
## rstudioapi "testthat, knitr, rmarkdown"
## rversions "mockery, testthat"
## rvest "covr, knitr, png, rmarkdown, spelling, stringi (>= 0.3.1),\ntestthat"
## S4Vectors "IRanges, GenomicRanges, SummarizedExperiment, Matrix,\nDelayedArray, ShortRead, graph
## scales "bit64, covr, dichromat, hms, testthat (>= 2.1.0), ggplot2"
## selectr "testthat, XML, xml2"
## sessioninfo "callr, covr, mockery, testthat"
## shiny "datasets, Cairo (>= 1.5-5), testthat (>= 2.1.1), knitr (>= 1.6), markdown, rmarkdown
## slam NA
## SnowballC NA
## sourcetools "testthat"

```

```

## SparseM      NA
## SQUAREM      "setRNG"
## stopwords    "covr, lintr, quanteda, spelling, testthat"
## stringi      NA
## stringr      "covr, htmltools, htmlwidgets, knitr, rmarkdown, testthat"
## survival     NA
## sys          "unix (>= 1.4), spelling, testthat"
## testthat     "covr, curl (>= 0.9.5), devtools, knitr, rmarkdown, usethis,\nvctrs (>= 0.1.0), xml2"
## textdata     "knitr, rmarkdown, testthat (>= 2.1.0)"
## tibble       "bench, covr, dplyr, htmltools, import, knitr, mockr,\nnycflights13, rmarkdown, testthat"
## tidyr        "covr, jsonlite, knitr, repurrrsive (>= 1.0.0), rmarkdown,\nreadr, testthat (>= 2.1.0)"
## tidyselect   "covr, dplyr, testthat"
## 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"
## triebeard    "knitr, rmarkdown, testthat"
## urltools     "testthat, knitr"
## usethis      "covr, knitr, magick, pkgdown (>= 1.1.0), rmarkdown, roxygen2,\nspelling (>= 1.2), sty"
## utf8         "knitr, rmarkdown, testthat"
## vctrs        "bit64, covr, crayon, generics, knitr, pillar (>= 1.4.1),\nnpkgdown, rmarkdown, testthat"
## viridisLite  "hexbin (>= 1.27.0), ggplot2 (>= 1.0.1), testthat, covr"
## webshot      "httpuv, knitr, rmarkdown, shiny"
## whisker      "markdown"
## withr        "testthat, covr, lattice, DBI, RSQLite, methods, knitr,\nrmarkdown"
## xfun         "testit, parallel, rstudioapi, tinytex, mime, markdown, knitr,\nhtmltools, base64enc, "
## 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"
## zeallot      "testthat, knitr, rmarkdown, purrr, magrittr"
## base         "methods"
## boot         "MASS, survival"
## class        NA
## cluster      "MASS, Matrix"
## codetools    NA
## compiler     NA
## datasets     NA
## foreign      NA
## graphics     NA
## grDevices    "KernSmooth"
## grid         "lattice"
## KernSmooth   "MASS"
## lattice      "KernSmooth, MASS, latticeExtra"
## MASS         "lattice, nlme, nnet, survival"
## Matrix       "expm, MASS"
## methods      "codetools"
## mgcv         "parallel, survival, MASS"
## nlme         "Hmisc, MASS"
## nnet         "MASS"
## parallel     "methods"

```

```

## rpart                "survival"
## spatial              "MASS"
## splines              "Matrix, methods"
## stats                "MASS, Matrix, SuppDists, methods, stats4"
## stats4              NA
## survival            NA
## tcltk               NA
## tools               "codetools, methods, xml2, curl, commonmark"
## translations        NA
## utils               "methods, xml2, commonmark"
##                     Enhances
## annotate            NA
## AnnotationDbi       NA
## arules              NA
## askpass             NA
## assertthat          NA
## backports           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
## cellranger          NA
## cli                 NA
## clipr               NA
## clisymbols          NA
## colorspace          NA
## commonmark          NA
## covr                NA
## crayon              NA
## crosstalk           NA
## curl                NA
## data.table          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              "compiler, doMC, RUnit, doParallel"
## foreign              NA
## formatR              NA
## fs                   NA
## gam                  NA
## genefilter           NA
## generics             NA
## ggplot2              "sp"
## ggrepel              NA
## ggthemes             NA
## gh                   NA
## git2r                NA
## glue                 NA
## gower                NA
## gridExtra            NA
## gtable               NA
## gutenbergr           NA
## haven                NA
## hexbin               NA
## highr                NA
## HistData             NA
## hms                  NA
## htmltools            "knitr"
## htmlwidgets          "shiny (>= 1.1)"
## httpuv               NA
## httr                 NA
## hunspell             NA
## ini                  NA
## ipred                NA
## IRanges              NA
## irlba                 NA
## ISOcodes             NA
## iterators            NA
## janeaustenr          NA
## jsonlite             NA
## kableExtra           NA
## kernlab              NA
## KernSmooth           NA
## knitr                 NA
## labeling             NA
## Lahman               NA
## later                NA
## lava                 NA
## lazyeval             NA
## lifecycle            NA
## lubridate            "chron, fts, timeSeries, timeDate, tis, tseries, xts, zoo"
## magrittr             NA
## markdown             NA
## MASS                 NA

```

```

## MatrixModels      NA
## matrixStats       NA
## memoise           NA
## Metrics           NA
## mgcv              NA
## mime              NA
## ModelMetrics      NA
## modelr            NA
## munsell           NA
## naivebayes        NA
## nlme              NA
## numDeriv          NA
## openssl           NA
## pdftools          NA
## pillar            NA
## pkgbuild          NA
## pkgconfig         NA
## pkgload           NA
## plogr             NA
## plotly            NA
## plyr              NA
## praise            NA
## prettyunits       NA
## processx          NA
## prodlim           NA
## progress          NA
## promises          NA
## proxy             NA
## pryr              NA
## ps                NA
## purrr             NA
## qpdf              NA
## quantreg          NA
## R6                NA
## randomForest      NA
## rappdirs          NA
## rcmdcheck          NA
## RColorBrewer      NA
## Rcpp              NA
## RcppProgress      NA
## RCurl             NA
## readr             NA
## readxl            NA
## recipes           NA
## recommenderlab    NA
## recosystem        NA
## registry          NA
## rematch           NA
## remotes           NA
## reprex            NA
## reshape2          NA
## rex               NA
## rlang             NA
## rmarkdown         NA

```

## roxygen2	NA
## rprojroot	NA
## RSQLite	NA
## rstudioapi	NA
## rversions	NA
## rvest	NA
## S4Vectors	NA
## scales	NA
## selectr	NA
## sessioninfo	NA
## shiny	NA
## slam	"Matrix, SparseM, spam"
## SnowballC	NA
## sourcetools	NA
## SparseM	NA
## SQUAREM	NA
## stopwords	NA
## stringi	NA
## stringr	NA
## survival	NA
## sys	NA
## testthat	NA
## textdata	NA
## tibble	NA
## tidyr	NA
## tidyselect	NA
## tidytext	NA
## tidyverse	NA
## timeDate	NA
## tinytex	NA
## titanic	NA
## tokenizers	NA
## triebeard	NA
## urltools	NA
## usethis	NA
## utf8	NA
## vctrs	NA
## viridisLite	NA
## webshot	NA
## whisker	NA
## withr	NA
## xfun	NA
## XML	NA
## xml2	NA
## xopen	NA
## xtable	NA
## yaml	NA
## zeallot	NA
## base	NA
## boot	NA
## class	NA
## cluster	NA
## codetools	NA
## compiler	NA

## datasets	NA	
## foreign	NA	
## graphics	NA	
## grDevices	NA	
## grid	NA	
## KernSmooth	NA	
## lattice	"chron"	
## MASS	NA	
## Matrix	"MatrixModels, graph, SparseM, sfsmisc"	
## methods	NA	
## mgcv	NA	
## nlme	NA	
## nnet	NA	
## parallel	"snow, nws, Rmpi"	
## rpart	NA	
## spatial	NA	
## splines	NA	
## stats	NA	
## stats4	NA	
## survival	NA	
## tcltk	NA	
## tools	NA	
## translations	NA	
## utils	NA	
##	License	License_is_FOSS
## annotate	"Artistic-2.0"	NA
## AnnotationDbi	"Artistic-2.0"	NA
## arules	"GPL-3"	NA
## askpass	"MIT + file LICENSE"	NA
## assertthat	"GPL-3"	NA
## backports	"GPL-2 GPL-3"	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"	NA
## bit64	"GPL-2"	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
## cellranger	"MIT + file LICENSE"	NA
## cli	"MIT + file LICENSE"	NA
## clipr	"GPL-3"	NA
## clisymbols	"MIT + file LICENSE"	NA
## colorspace	"BSD_3_clause + file LICENSE"	NA
## commonmark	"BSD_2_clause + file LICENSE"	NA
## covr	"GPL-3"	NA
## crayon	"MIT + file LICENSE"	NA

## crosstalk	"MIT + file LICENSE"	NA
## curl	"MIT + file LICENSE"	NA
## data.table	"MPL-2.0 file LICENSE"	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
## formatR	"GPL"	NA
## fs	"GPL-3"	NA
## gam	"GPL-2"	NA
## genefilter	"Artistic-2.0"	NA
## generics	"GPL-2"	NA
## ggplot2	"GPL-2 file LICENSE"	NA
## ggrepel	"GPL-3 file LICENSE"	NA
## ggthemes	"GPL-2"	NA
## gh	"MIT + file LICENSE"	NA
## git2r	"GPL-2"	NA
## glue	"MIT + file LICENSE"	NA
## gower	"GPL-3"	NA
## gridExtra	"GPL (>= 2)"	NA
## gtable	"GPL-2"	NA
## gutenbergr	"GPL-2"	NA
## haven	"MIT + file LICENSE"	NA
## hexbin	"GPL-2"	NA
## highr	"GPL"	NA
## HistData	"GPL"	NA
## hms	"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
## ini	"GPL-3"	NA
## ipred	"GPL (>= 2)"	NA
## IRanges	"Artistic-2.0"	NA
## irlba	"GPL-3"	NA
## ISOcodes	"GPL-2"	NA
## iterators	"Apache License (== 2.0)"	NA
## janeaustenr	"MIT + file LICENSE"	NA
## jsonlite	"MIT + file LICENSE"	NA

## kableExtra	"MIT + file LICENSE"	NA
## kernlab	"GPL-2"	NA
## KernSmooth	"Unlimited"	NA
## knitr	"GPL"	NA
## labeling	"MIT + file LICENSE Unlimited"	NA
## Lahman	"GPL"	NA
## later	"GPL (>= 2)"	NA
## lava	"GPL-3"	NA
## lazyeval	"GPL-3"	NA
## lifecycle	"GPL-3"	NA
## lubridate	"GPL (>= 2)"	NA
## magrittr	"MIT + file LICENSE"	NA
## markdown	"GPL-2"	NA
## MASS	"GPL-2 GPL-3"	NA
## MatrixModels	"GPL (>= 2)"	NA
## matrixStats	"Artistic-2.0"	NA
## memoise	"MIT + file LICENSE"	NA
## Metrics	"BSD_3_clause + file LICENSE"	NA
## mgcv	"GPL (>= 2)"	NA
## mime	"GPL"	NA
## ModelMetrics	"GPL (>= 2)"	NA
## modelr	"GPL-3"	NA
## munsell	"MIT + file LICENSE"	NA
## naivebayes	"GPL-2"	NA
## nlme	"GPL (>= 2) file LICENCE"	NA
## numDeriv	"GPL-2"	NA
## openssl	"MIT + file LICENSE"	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
## plotly	"MIT + file LICENSE"	NA
## plyr	"MIT + file LICENSE"	NA
## praise	"MIT + file LICENSE"	NA
## prettyunits	"MIT + file LICENSE"	NA
## processx	"MIT + file LICENSE"	NA
## prodlim	"GPL (>= 2)"	NA
## progress	"MIT + file LICENSE"	NA
## promises	"MIT + file LICENSE"	NA
## proxy	"GPL-2"	NA
## pryr	"GPL-2"	NA
## ps	"BSD_3_clause + file LICENSE"	NA
## purrr	"GPL-3 file LICENSE"	NA
## qpdf	"Apache License 2.0"	NA
## quantreg	"GPL (>= 2)"	NA
## R6	"MIT + file LICENSE"	NA
## randomForest	"GPL (>= 2)"	NA
## rappdirs	"MIT + file LICENSE"	NA
## rcmdcheck	"MIT + file LICENSE"	NA
## RColorBrewer	"Apache License 2.0"	NA
## Rcpp	"GPL (>= 2)"	NA
## RcppProgress	"GPL (>= 3)"	NA

## RCurl	"BSD"	NA
## readr	"GPL (>= 2) file LICENSE"	NA
## readxl	"GPL-3"	NA
## recipes	"GPL-2"	NA
## recommenderlab	"GPL-2"	NA
## recosystem	"BSD_3_clause + file LICENSE"	NA
## registry	"GPL-2"	NA
## rematch	"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
## rprojroot	"GPL-3"	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 LICENSE"	NA
## sessioninfo	"GPL-2"	NA
## shiny	"GPL-3 file LICENSE"	NA
## slam	"GPL-2"	NA
## SnowballC	"BSD_3_clause + file LICENSE"	NA
## sourcetools	"MIT + file LICENSE"	NA
## SparseM	"GPL (>= 2)"	NA
## SQUAREM	"GPL (>= 2)"	NA
## stopwords	"MIT + file LICENSE"	NA
## stringi	"file LICENSE"	"yes"
## stringr	"GPL-2 file LICENSE"	NA
## survival	"LGPL (>= 2)"	NA
## sys	"MIT + file LICENSE"	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
## triebeard	"MIT + file LICENSE"	NA
## urltools	"MIT + file LICENSE"	NA
## usethis	"GPL-3"	NA
## utf8	"Apache License (== 2.0) file LICENSE"	NA
## vctrs	"GPL-3"	NA
## viridisLite	"MIT + file LICENSE"	NA
## webshot	"GPL-2"	NA
## whisker	"GPL-3"	NA

## withr	"GPL (>= 2)"	NA
## xfun	"MIT + file LICENSE"	NA
## XML	"BSD_2_clause + file LICENSE"	NA
## xml2	"GPL (>= 2)"	NA
## xopen	"MIT + file LICENSE"	NA
## xtable	"GPL (>= 2)"	NA
## yaml	"BSD_3_clause + file LICENSE"	NA
## zeallot	"MIT + file LICENSE"	NA
## base	"Part of R 3.6.2"	NA
## boot	"Unlimited"	NA
## class	"GPL-2 GPL-3"	NA
## cluster	"GPL (>= 2)"	NA
## codetools	"GPL"	NA
## compiler	"Part of R 3.6.2"	NA
## datasets	"Part of R 3.6.2"	NA
## foreign	"GPL (>= 2)"	NA
## graphics	"Part of R 3.6.2"	NA
## grDevices	"Part of R 3.6.2"	NA
## grid	"Part of R 3.6.2"	NA
## KernSmooth	"Unlimited"	NA
## lattice	"GPL (>= 2)"	NA
## MASS	"GPL-2 GPL-3"	NA
## Matrix	"GPL (>= 2) file LICENCE"	NA
## methods	"Part of R 3.6.2"	NA
## mgcv	"GPL (>= 2)"	NA
## nlme	"GPL (>= 2) file LICENCE"	NA
## nnet	"GPL-2 GPL-3"	NA
## parallel	"Part of R 3.6.2"	NA
## rpart	"GPL-2 GPL-3"	NA
## spatial	"GPL-2 GPL-3"	NA
## splines	"Part of R 3.6.2"	NA
## stats	"Part of R 3.6.2"	NA
## stats4	"Part of R 3.6.2"	NA
## survival	"LGPL (>= 2)"	NA
## tcltk	"Part of R 3.6.2"	NA
## tools	"Part of R 3.6.2"	NA
## translations	"Part of R 3.6.2"	NA
## utils	"Part of R 3.6.2"	NA
##	License_restricts_use	OS_type MD5sum NeedsCompilation Built
## annotate	NA	NA NA "no" "3.6.1"
## AnnotationDbi	NA	NA NA "no" "3.6.1"
## arules	NA	NA NA "yes" "3.6.2"
## askpass	NA	NA NA "yes" "3.6.1"
## assertthat	NA	NA NA "no" "3.6.1"
## backports	NA	NA NA "yes" "3.6.1"
## base64enc	NA	NA NA "yes" "3.6.0"
## BH	NA	NA NA "no" "3.6.1"
## Biobase	NA	NA NA "yes" "3.6.1"
## BiocGenerics	NA	NA NA "no" "3.6.1"
## BiocManager	NA	NA NA "no" "3.6.1"
## BiocVersion	NA	NA NA "no" "3.6.0"
## bit	NA	NA NA "yes" "3.6.0"
## bit64	NA	NA NA "yes" "3.6.0"
## bitops	NA	NA NA "yes" "3.6.0"

## blob	NA	NA	NA	"no"	"3.6.1"
## boot	NA	NA	NA	"no"	"3.6.2"
## brew	NA	NA	NA	NA	"3.6.0"
## broom	NA	NA	NA	"no"	"3.6.1"
## callr	NA	NA	NA	"no"	"3.6.1"
## caret	NA	NA	NA	"yes"	"3.6.1"
## cellranger	NA	NA	NA	"no"	"3.6.1"
## cli	NA	NA	NA	"no"	"3.6.1"
## clipr	NA	NA	NA	"no"	"3.6.1"
## clisymbols	NA	NA	NA	"no"	"3.6.2"
## colorspace	NA	NA	NA	"yes"	"3.6.1"
## commonmark	NA	NA	NA	"yes"	"3.6.2"
## covr	NA	NA	NA	"yes"	"3.6.2"
## crayon	NA	NA	NA	"no"	"3.6.1"
## crosstalk	NA	NA	NA	"no"	"3.6.2"
## curl	NA	NA	NA	"yes"	"3.6.1"
## data.table	NA	NA	NA	"yes"	"3.6.1"
## DBI	NA	NA	NA	"no"	"3.6.1"
## dbplyr	NA	NA	NA	"no"	"3.6.1"
## desc	NA	NA	NA	"no"	"3.6.2"
## devtools	NA	NA	NA	"no"	"3.6.2"
## digest	NA	NA	NA	"yes"	"3.6.1"
## dplyr	NA	NA	NA	"yes"	"3.6.1"
## dslabs	NA	NA	NA	"no"	"3.6.1"
## DT	NA	NA	NA	"no"	"3.6.2"
## e1071	NA	NA	NA	"yes"	"3.6.1"
## ellipsis	NA	NA	NA	"yes"	"3.6.1"
## evaluate	NA	NA	NA	"no"	"3.6.1"
## fansi	NA	NA	NA	"yes"	"3.6.1"
## farver	NA	NA	NA	"yes"	"3.6.1"
## fastAdaboost	NA	NA	NA	"yes"	"3.6.2"
## fastmap	NA	NA	NA	"yes"	"3.6.2"
## forcats	NA	NA	NA	"no"	"3.6.1"
## foreach	NA	NA	NA	"no"	"3.6.1"
## foreign	NA	NA	NA	"yes"	"3.6.2"
## formatR	NA	NA	NA	"no"	"3.6.2"
## fs	NA	NA	NA	"yes"	"3.6.1"
## gam	NA	NA	NA	"yes"	"3.6.2"
## genefilter	NA	NA	NA	"yes"	"3.6.1"
## generics	NA	NA	NA	"no"	"3.6.1"
## ggplot2	NA	NA	NA	"no"	"3.6.1"
## ggrepel	NA	NA	NA	"yes"	"3.6.2"
## ggthemes	NA	NA	NA	"no"	"3.6.2"
## gh	NA	NA	NA	"no"	"3.6.2"
## git2r	NA	NA	NA	"yes"	"3.6.2"
## glue	NA	NA	NA	"yes"	"3.6.1"
## gower	NA	NA	NA	"yes"	"3.6.1"
## gridExtra	NA	NA	NA	"no"	"3.6.2"
## gtable	NA	NA	NA	"no"	"3.6.1"
## gutenbergr	NA	NA	NA	"no"	"3.6.1"
## haven	NA	NA	NA	"yes"	"3.6.1"
## hexbin	NA	NA	NA	"yes"	"3.6.2"
## highr	NA	NA	NA	"no"	"3.6.1"
## HistData	NA	NA	NA	"no"	"3.6.1"

## hms	NA	NA	NA	"no"	"3.6.1"
## htmltools	NA	NA	NA	"yes"	"3.6.1"
## htmlwidgets	NA	NA	NA	"no"	"3.6.1"
## httpuv	NA	NA	NA	"yes"	"3.6.2"
## httr	NA	NA	NA	"no"	"3.6.1"
## hunspell	NA	NA	NA	"yes"	"3.6.1"
## ini	NA	NA	NA	"no"	"3.6.2"
## ipred	NA	NA	NA	"yes"	"3.6.1"
## IRanges	NA	NA	NA	"yes"	"3.6.1"
## irlba	NA	NA	NA	"yes"	"3.6.2"
## ISOcodes	NA	NA	NA	"no"	"3.6.2"
## iterators	NA	NA	NA	"no"	"3.6.1"
## janeaustenr	NA	NA	NA	"no"	"3.6.1"
## jsonlite	NA	NA	NA	"yes"	"3.6.1"
## kableExtra	NA	NA	NA	"no"	"3.6.2"
## kernlab	NA	NA	NA	"yes"	"3.6.1"
## KernSmooth	NA	NA	NA	"yes"	"3.6.2"
## knitr	NA	NA	NA	"no"	"3.6.1"
## labeling	NA	NA	NA	"no"	"3.6.0"
## Lahman	NA	NA	NA	"no"	"3.6.1"
## later	NA	NA	NA	"yes"	"3.6.2"
## lava	NA	NA	NA	"no"	"3.6.1"
## lazyeval	NA	NA	NA	"yes"	"3.6.1"
## lifecycle	NA	NA	NA	"no"	"3.6.1"
## lubridate	NA	NA	NA	"yes"	"3.6.1"
## magrittr	NA	NA	NA	"no"	"3.6.1"
## markdown	NA	NA	NA	"yes"	"3.6.1"
## MASS	NA	NA	NA	"yes"	"3.6.2"
## MatrixModels	NA	NA	NA	"no"	"3.6.1"
## matrixStats	NA	NA	NA	"yes"	"3.6.2"
## memoise	NA	NA	NA	"no"	"3.6.1"
## Metrics	NA	NA	NA	"no"	"3.6.2"
## mgcv	NA	NA	NA	"yes"	"3.6.2"
## mime	NA	NA	NA	"yes"	"3.6.2"
## ModelMetrics	NA	NA	NA	"yes"	"3.6.1"
## modelr	NA	NA	NA	"no"	"3.6.1"
## munsell	NA	NA	NA	"no"	"3.6.1"
## naivebayes	NA	NA	NA	"no"	"3.6.2"
## nlme	NA	NA	NA	"yes"	"3.6.2"
## numDeriv	NA	NA	NA	"no"	"3.6.0"
## openssl	NA	NA	NA	"yes"	"3.6.1"
## pdftools	NA	NA	NA	"yes"	"3.6.1"
## pillar	NA	NA	NA	"no"	"3.6.2"
## pkgbuild	NA	NA	NA	"no"	"3.6.2"
## pkgconfig	NA	NA	NA	"no"	"3.6.1"
## pkgload	NA	NA	NA	"yes"	"3.6.2"
## plogr	NA	NA	NA	"no"	"3.6.1"
## plotly	NA	NA	NA	"no"	"3.6.2"
## plyr	NA	NA	NA	"yes"	"3.6.1"
## praise	NA	NA	NA	"no"	"3.6.2"
## prettyunits	NA	NA	NA	"no"	"3.6.1"
## processx	NA	NA	NA	"yes"	"3.6.1"
## prodlim	NA	NA	NA	"yes"	"3.6.1"
## progress	NA	NA	NA	"no"	"3.6.1"

## promises	NA	NA	NA	"yes"	"3.6.2"
## proxy	NA	NA	NA	"yes"	"3.6.2"
## pryr	NA	NA	NA	"yes"	"3.6.2"
## ps	NA	NA	NA	"yes"	"3.6.1"
## purrr	NA	NA	NA	"yes"	"3.6.1"
## qpdf	NA	NA	NA	"yes"	"3.6.1"
## quantreg	NA	NA	NA	"yes"	"3.6.1"
## R6	NA	NA	NA	"no"	"3.6.1"
## randomForest	NA	NA	NA	"yes"	"3.6.1"
## rappdirs	NA	NA	NA	"yes"	"3.6.1"
## rcmdcheck	NA	NA	NA	"no"	"3.6.2"
## RColorBrewer	NA	NA	NA	"no"	"3.6.0"
## Rcpp	NA	NA	NA	"yes"	"3.6.1"
## RcppProgress	NA	NA	NA	"no"	"3.6.2"
## RCurl	NA	NA	NA	"yes"	"3.6.0"
## readr	NA	NA	NA	"yes"	"3.6.1"
## readxl	NA	NA	NA	"yes"	"3.6.1"
## recipes	NA	NA	NA	"no"	"3.6.1"
## recommenderlab	NA	NA	NA	"no"	"3.6.2"
## recosystem	NA	NA	NA	"yes"	"3.6.2"
## registry	NA	NA	NA	"no"	"3.6.0"
## rematch	NA	NA	NA	"no"	"3.6.1"
## remotes	NA	NA	NA	"no"	"3.6.2"
## reprex	NA	NA	NA	"no"	"3.6.1"
## reshape2	NA	NA	NA	"yes"	"3.6.1"
## rex	NA	NA	NA	"no"	"3.6.2"
## rlang	NA	NA	NA	"yes"	"3.6.1"
## rmarkdown	NA	NA	NA	"no"	"3.6.1"
## roxygen2	NA	NA	NA	"yes"	"3.6.2"
## rprojroot	NA	NA	NA	"no"	"3.6.2"
## RSQLite	NA	NA	NA	"yes"	"3.6.2"
## rstudioapi	NA	NA	NA	"no"	"3.6.1"
## rversions	NA	NA	NA	"no"	"3.6.2"
## rvest	NA	NA	NA	"no"	"3.6.1"
## S4Vectors	NA	NA	NA	"yes"	"3.6.1"
## scales	NA	NA	NA	"no"	"3.6.1"
## selectr	NA	NA	NA	"no"	"3.6.1"
## sessioninfo	NA	NA	NA	"no"	"3.6.2"
## shiny	NA	NA	NA	"no"	"3.6.2"
## slam	NA	NA	NA	"yes"	"3.6.2"
## SnowballC	NA	NA	NA	"yes"	"3.6.0"
## sourcetools	NA	NA	NA	"yes"	"3.6.2"
## SparseM	NA	NA	NA	"yes"	"3.6.2"
## SQUAREM	NA	NA	NA	"no"	"3.6.0"
## stopwords	NA	NA	NA	"no"	"3.6.1"
## stringi	NA	NA	NA	"yes"	"3.6.0"
## stringr	NA	NA	NA	"no"	"3.6.1"
## survival	NA	NA	NA	"yes"	"3.6.2"
## sys	NA	NA	NA	"yes"	"3.6.1"
## testthat	NA	NA	NA	"yes"	"3.6.2"
## textdata	NA	NA	NA	"no"	"3.6.1"
## tibble	NA	NA	NA	"yes"	"3.6.1"
## tidyr	NA	NA	NA	"yes"	"3.6.1"
## tidyselect	NA	NA	NA	"yes"	"3.6.1"

## tidytext	NA	NA	NA	"no"	"3.6.1"
## tidyverse	NA	NA	NA	"no"	"3.6.1"
## timeDate	NA	NA	NA	"no"	"3.6.0"
## tinytex	NA	NA	NA	"no"	"3.6.1"
## titanic	NA	NA	NA	"no"	"3.6.1"
## tokenizers	NA	NA	NA	"yes"	"3.6.1"
## triebeard	NA	NA	NA	"yes"	"3.6.1"
## urltools	NA	NA	NA	"yes"	"3.6.1"
## usethis	NA	NA	NA	"no"	"3.6.2"
## utf8	NA	NA	NA	"yes"	"3.6.1"
## vctrs	NA	NA	NA	"yes"	"3.6.2"
## viridisLite	NA	NA	NA	"no"	"3.6.1"
## webshot	NA	NA	NA	"no"	"3.6.2"
## whisker	NA	NA	NA	"no"	"3.6.1"
## withr	NA	NA	NA	"no"	"3.6.1"
## xfun	NA	NA	NA	"no"	"3.6.1"
## XML	NA	NA	NA	"yes"	"3.6.0"
## xml2	NA	NA	NA	"yes"	"3.6.1"
## xopen	NA	NA	NA	"no"	"3.6.2"
## xtable	NA	NA	NA	"no"	"3.6.1"
## yaml	NA	NA	NA	"yes"	"3.6.0"
## zeallot	NA	NA	NA	"no"	"3.6.1"
## base	NA	NA	NA	NA	"3.6.2"
## boot	NA	NA	NA	"no"	"3.6.2"
## class	NA	NA	NA	"yes"	"3.6.2"
## cluster	NA	NA	NA	"yes"	"3.6.2"
## codetools	NA	NA	NA	"no"	"3.6.2"
## compiler	NA	NA	NA	NA	"3.6.2"
## datasets	NA	NA	NA	NA	"3.6.2"
## foreign	NA	NA	NA	"yes"	"3.6.2"
## graphics	NA	NA	NA	"yes"	"3.6.2"
## grDevices	NA	NA	NA	"yes"	"3.6.2"
## grid	NA	NA	NA	"yes"	"3.6.2"
## KernSmooth	NA	NA	NA	"yes"	"3.6.2"
## lattice	NA	NA	NA	"yes"	"3.6.2"
## MASS	NA	NA	NA	"yes"	"3.6.2"
## Matrix	NA	NA	NA	"yes"	"3.6.2"
## methods	NA	NA	NA	"yes"	"3.6.2"
## mgcv	NA	NA	NA	"yes"	"3.6.2"
## nlme	NA	NA	NA	"yes"	"3.6.2"
## nnet	NA	NA	NA	"yes"	"3.6.2"
## parallel	NA	NA	NA	"yes"	"3.6.2"
## rpart	NA	NA	NA	"yes"	"3.6.2"
## spatial	NA	NA	NA	"yes"	"3.6.2"
## splines	NA	NA	NA	"yes"	"3.6.2"
## stats	NA	NA	NA	"yes"	"3.6.2"
## stats4	NA	NA	NA	NA	"3.6.2"
## survival	NA	NA	NA	"yes"	"3.6.2"
## tcltk	NA	NA	NA	"yes"	"3.6.2"
## tools	NA	NA	NA	"yes"	"3.6.2"
## translations	NA	NA	NA	NA	"3.6.2"
## utils	NA	NA	NA	"yes"	"3.6.2"