Movielens - Building a Recommendation System

by Rafael Yan

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1 Introduction.

A recommendation system is a machine learning algorithm that predicts the rating or preference a user would give to a particular item. You might have used this kind of system in your daily life even without noticing it. Every time you use your favorite web browser it is most likely that some interesting ads are shown to you that conveniently meet your needs. Or maybe when listening to music on a streaming service you feel pleased with the songs that are played after your first pick. Well, that is thanks to recommendation systems that most of companies nowadays use in order to target their products for specific audiences. Google, Amazon, Netflix, Youtube, Spotify and Facebook are just a few examples of services that are guiding you through recommendation systems towards the most likely product you might purchase, watch, hear, follow or read.

The GroupLens reaserch lab generated the MovieLens dataset with over 20 million ratings over 27,000 movies by more than 138,000 users. The objective of this project is to show how to build a recommendation system which could predict the rating a user will give to a movie, based on this data. For this purpose we will use a 10 million version of the MovieLens dataset to make the computation a little easier.

A similar challenge was launched by Netflix in October 2006, in which they offer a million dollar award to the team who could improve their recommendation algorithm by 10%. They decided on a winner based on a metric called "Residual Mean Squared Error (RMSE)". To win the Netflix prize a participating team had to get an RMSE of approximately 0.857 (or smaller). On September 18, 2009, Netflix announced the team "BellKor's Pragmatic Chaos" as the winner of the challenge with a Test RMSE of 0.8567.

If we build an algorithm that predicts the rating for certain movies and consider that those predictions will have some errors which are the difference between the predicted rating and the true rating given by the users, then the smaller these differences, the better the algorithm has performed. The RMSE is just a way to measure these differences and this is the metric we will use to describe how well our recommendation algorithm performs.

As a beginner in the data science world, I have come across many interesting challenges like learning a programming language from scratch, diving into statistics and probability, dealing with great amounts of information and computationally heavy tasks and deciphering the information available regarding most of the concepts and techniques I have learn so far. Therefore, I have focused on explaining and illustrating many basic concepts in Layman's terms. Nonetheless, this paper also includes an important amount of information explaining technicalities and equations.

The reader will find throughout this paper the application of three main techniques: linear regression models (normalization of global effects), regularization, and matrix factorization.

2 Getting Started.

2.1 Machine Learning Basics.

Before going further, let's explain some basics of Machine Learning (ML):

1). ML means, as its name implies, teaching or training a machine to learn to do something. This can be achieved by building an algorithm. In this case, we want to train a machine to predict movie ratings.

2). There are different types of ML algorithms: supervised, semi-supervised, unsupervised and reinforcement. In this case, we use supervised algorithms, which means the machine is taught by example. In other words, we show to the machine a dataset (i.e. MovieLens) that includes inputs (i.e. users, movie titles, movie genres, dates of rating, etc.) and outputs (i.e. movie ratings), so the algorithm must find the way to determine new outputs given new inputs. This is one of the reasons why recommendation systems are a powerful tool, they improve the user experience by offering movies that best fit to their preferences or by showing a repertoire they might not discover otherwise due to the large movie inventory.

3). When using a supervised ML algorithm, it is implied that we have a dataset with the variables (inputs) and their results (outputs) which we will use to train our algorithm. But, how can we measure the accuracy of the algorithm if we are predicting movie ratings of movies or users that are not contained in our dataset but instead will be present in the future? How can we test our algorithm? Do we wait until the users rate new movies, we process this new information and then we measure how well our algorithm performs? Well, we certainly don't. Instead you split your dataset (the one you currently have), say 80%-20%. We can use the 80% of the data to train an algorithm and then test it in the 20% of the remaining data, simulating the movies that users will rate in the future. As we know the true ratings of the 20% contained in the test set, thus we can measure the accuracy of our predictions with a metric such the RMSE.

4). A train set in ML is used to perform all the calculations of the algorithm. On the other hand, a test set is only used to evaluate those calculations. Imagine that you are teaching a kid to multiply 1-digit number by 2, and you want to know how good is he at multiplications so you ask him to multiply a 1-digit number by 2. The kid will most likely answer correctly, but that doesn't mean he has understood the concept of multiplication, not even the concept of multiplying a number with more than 1-digit by 2. So testing his learnings that way would result in an over-optimistic assessment (this concept is called overfitting).

5). We can create many ML models for the same problem. Each one will result in different predictions and thus, will have different accuracy on its own. But we can "ensemble" different models so we can predict taking into account the results of each model. In an ensemble, the prediction is improved due to the evaluation of the ensemble as a whole. For example, if we want to predict which class of ticket a person buys (class "A", "B" or "C") and we train 10 ML algorithms and for a given user 6 models predict "A", 2 models predict "B" and 2 models predict "C", then we can evaluate that 60% of our models predict the same results, so it is most likely that this prediction would be the best one.

6). In ML there are parameters required in our model which are not features (variables) and they may change the result of the predictions. For example, if a model predicts based on how near is a user to a certain facility (i.e. gas stations), you should tell the model how to interpret the concept "near": it could be a distance (i.e. all gas stations within a given radius) or it could be a minimum of facilities (i.e. the 5 nearest gas stations). Both distance and minimum facilities would be parameters and different values of parameters will result in different estimates. This implies that depending on the value of the parameters the model would be more or less accurate. Therefore, a parameter can be tuned to optimize a model. A well known tuning technique is Cross Validation (CV).

2.2 Tools and Resources.

This project can be downloaded from this link. During the development of this project the following tools and resources were employed:

- Programming Language: R.
- Integrated Development Environment (IDE): RStudio.
- Operating System (OS): Microsoft Windows 10 Home Single Language.
- System Type: x64-based PC.
- Processor: Intel(R) Core(TM) i7-7700HQ CPU @ 2.80GHz, 2801 Mhz, 4 core processors, 8 thread processors.
- Installed Physical Memory (RAM): 8.00 GB.
- Total Physical Memory: 7.83 GB.
- Available Physical Memory: 1.46 to 2.4 GB.
- Code Hosting Service: GitHub.

2.3 Data Wrangling[1].

First of all, we download the MovieLens dataset from this link which has a zip file containing two files:

- movies.dat
- ratings.dat

Then we joined the two sets together and split the data into two sets:

- **validation**: contains only the 10% of the data and will be used as our *test set*.
- **edx**: contains the rest of the data and will be used as our *train set*.

If a userId or a movieId is just in the *test set*, then we will remove it and add it back to the *train set*. This will be helpful when building our model because we would expect to make predictions only of known users and known movies which are on our *train set*.

2.4 Data Exploration[2].

Both our train set (**edx**) and test set (**validation**) are composed by 6 columns or variables:

Table 1: First rows from edx set.

userId	movieId	rating	timestamp	title	genres
1	122	5	838985046	Boomerang (1992)	Comedy|Romance
1	185	5	838983525	Net, The (1995)	Action|Crime|Thriller
1	292	5	838983421	Outbreak (1995)	Action|Drama|Sci-Fi|Thriller
1	316	5	838983392	Stargate (1994)	Action|Adventure|Sci-Fi
1	329	5	838983392	Star Trek: Generations (1994)	Action|Adventure|Drama|Sci-Fi
1	355	5	838984474	Flintstones, The (1994)	Children|Comedy|Fantasy
1	356	5	838983653	Forrest Gump (1994)	Comedy|Drama|Romance|War
1	362	5	838984885	Jungle Book, The (1994)	Adventure|Children|Romance

The columns *title* and *genres* are variables of class character, the rest of the variables are numeric. Note that the column *title* contains the release year in parentheses, a movie can have several genres separated by a pipe operator "|". The column *timestamp* variable represents seconds since January 1, 1970 (so technically it is a date and we should treat it like so). So let us add two more columns to our dataset:

[1]This pdf section corresponds to section "Code Provided" of the R script.

[2]This pdf section corresponds to section "II. DATA EXPLORATION (DESCRIPTIVE STATISTICS)" and "III. RELATIONSHIP BETWEEN VARIABLES AND RATINGS" of the R script.

1. The premiere or release year of a movie (*year*): this represents an additional variable in our dataset and it is extracted from *title*.
2. The date a movie has been rated (*rating_date*): this is just a transformation of *timestamp*, hence is not an additional variable. If we just convert the *timestamp* from the actual format to a date format, we will end up with a huge list of unique dates, and thus there will be less ratings by each one of these dates. Instead we can transform the *timestamp* a way that many dates can be treated as one single group, and thus there will be more ratings by each one of these groups (this will be important for regularization). We will create a rating_date which is the first day of the week described in the *timestamp*.

Now the **edx** set looks like this:

Table 2: First rows from edx set with additional columns.

userId	movieId	rating	timestamp	title	genres	year	rating_date
1	122	5	838985046	Boomerang (1992)	Comedy|Romance	1992	1996-08-04
1	185	5	838983525	Net, The (1995)	Action|Crime|Thriller	1995	1996-08-04
1	292	5	838983421	Outbreak (1995)	Action|Drama|Sci-Fi|Thriller	1995	1996-08-04
1	316	5	838983392	Stargate (1994)	Action|Adventure|Sci-Fi	1994	1996-08-04
1	329	5	838983392	Star Trek: Generations (1994)	Action|Adventure|Drama|Sci-Fi	1994	1996-08-04
1	355	5	838984474	Flintstones, The (1994)	Children|Comedy|Fantasy	1994	1996-08-04
1	356	5	838983653	Forrest Gump (1994)	Comedy|Drama|Romance|War	1994	1996-08-04
1	362	5	838984885	Jungle Book, The (1994)	Adventure|Children|Romance	1994	1996-08-04

The *userId*, *movieId*, *timestamp*, *title*, *genres*, *year* and *rating_date* are our **independent variables**. On the other hand *rating* is our **dependent variable**. So, we will build a model which predicts *ratings* based on what we know about the users, the movies, the genres of the movies, the premiere year of a movie and the time a user has rated a movie.

Note that because *title* and *movieId* refers to the same item (the first one as a text and the last one as an ID) then we can consider just one of them. For simplicity we will choose *movieId* as the independent variable. The same thing happens with *timestamp* and *rating_date*. We will use *rating_date* as our independent variable because many *timestamp* dates can be grouped by the same *rating_date*.

Considering this, we have 5 variables we can use to train a model which predicts ratings but, are those variables meaningful to train a model? To answer this question we will first explore our data available in the **edx** set. Here are some descriptive statistics of our *train* set:

- **9,000,055** total observations, each one representing a rating of a movie given by a user.
- **10,677** unique movies (min ID = *1* and max ID = 6.5133×10^4).
- **69,878** unique users (min ID = *1* and max ID *71567*).
- **797** unique group of genres.
- The first rating was made on **1995**.
- The most recent rating was made on **2009**.
- The most frequent rating is 4 stars. Whole star ratings are more common than half star ratings:

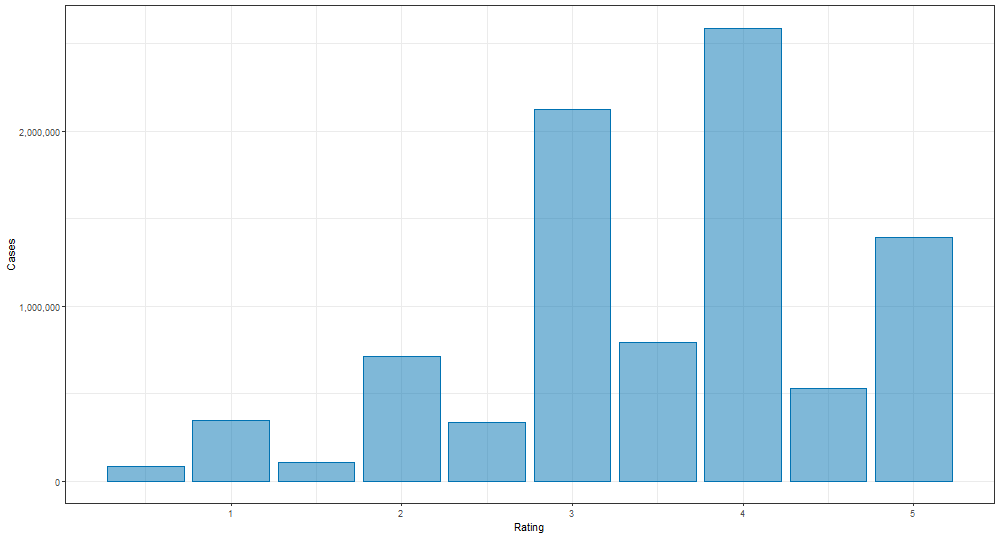


Figure 1: Frequence of ratings on edx set.

Now let us explore the behaviour of ratings (our dependent variable) based on our 5 independent variables separately. For this purpose we will group all our data by each element of each variable (i.e. each user in userId). Then we will summarize how many times we find this element in our dataset (*cases*) and which is the average rating considering all the cases we found (*avg_rating*). Here is an example:

Table 3: Summary by userId.

userId	**cases**	**avg_rating**
59269	6616	3.264586
67385	6360	3.197720
14463	4648	2.403615
68259	4036	3.576933
27468	4023	3.826871
19635	3771	3.498807
3817	3733	3.112510
63134	3371	3.268170
58357	3361	3.000744
27584	3142	3.001432

As shown on the table above user 59269 appears 6,616 times and his average rating is 3.2645859. The table shows only the first 10 *userId* ordered by *cases*.

Repeating this step for each variable we obtain the following scatter plots and histograms:

- Each pair of graphs defines a variable (i.e. movieId).
- Each dot in the scatter plot is a unique element (i.e. movie) of that variable.
- The dotted line in both graphs represents the mean rating by variable.
- On the top right of the histogram it is shown the average rating (*mean*) and the standard deviation (*sd*) of each variable.

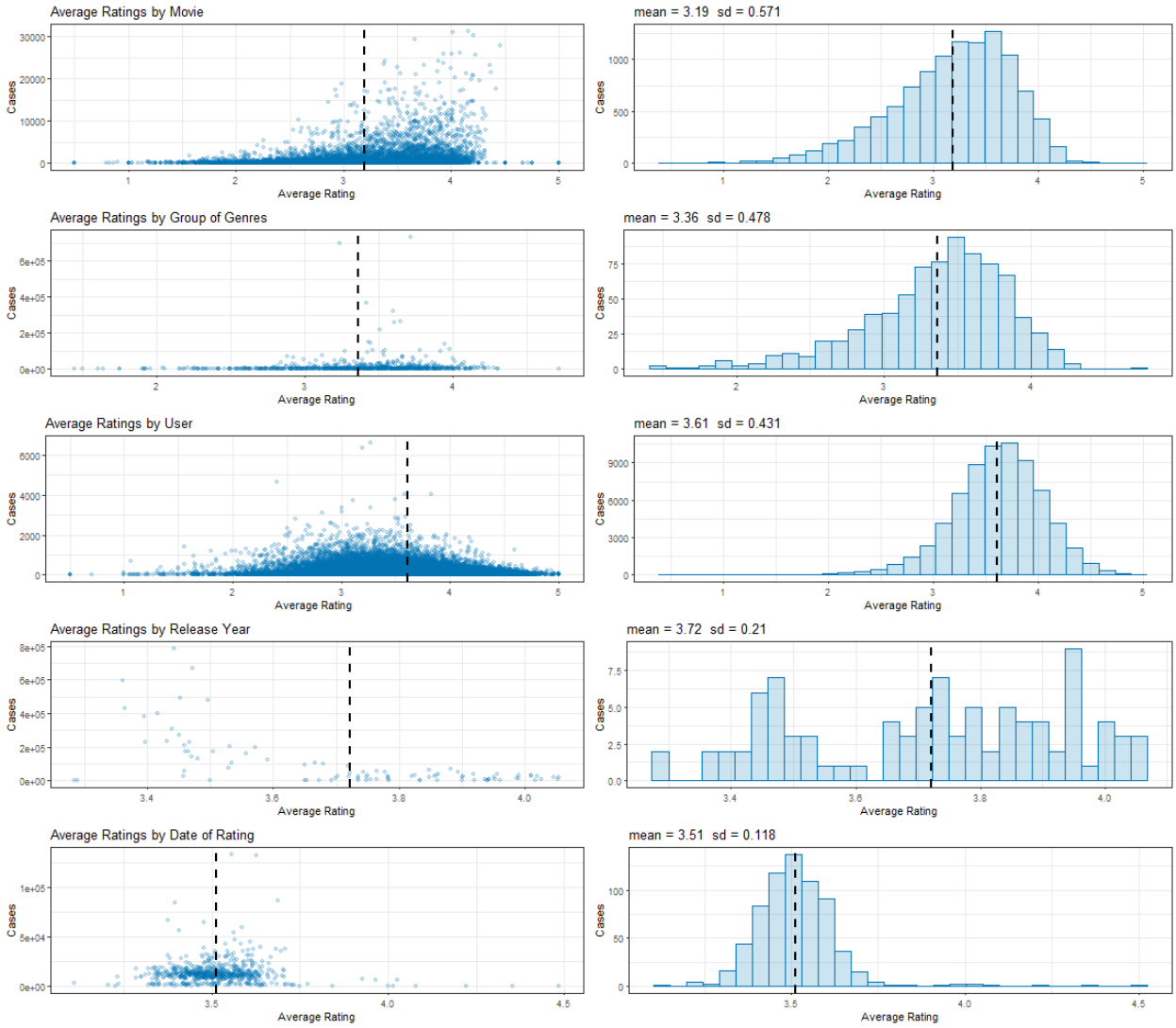


Figure 2: Average rating by variable.

From the figures above we can see that *movie*, *user* and *genre* histograms are more spread out than those of *year* and *date of rating*. Above each histogram is shown its corresponding standard deviation (sd). Larger standard deviation means greater variability. Variability in a feature is important to ML algorithms because it impacts the capacity of a model to use that feature: if a feature has little variance, then it has no ability to contribute to the model.

Hence, the first three variables (movie, genre and user) are more likely to help to make predictions than the last two variables (release year and date of rating). With this insight we can start to train our models.

3 Methods and Analysis.

3.1 Predictions and Evaluation of the Models[3].

Our goal in this project is to predict the rating any given user would assing to any given movie. Here is an example of some users and the movies they have rated in our **edx** set:

Table 4: Example of movie ratings by user.

userId	**Father of the Bride Part II (1995)**	**GoldenEye (1995)**	**Heat (1995)**	**Jumanji (1995)**	**Sabrina (1995)**	**Toy Story (1995)**
5					3	1
8	3		4	2.5		
10					3	
13				3		
14				3		3
18	1	4		3	2.5	3
19	3	4				

As we can see, no user has rated all movies. The challenge is to estimate a rating for all the missing values (we will use different algorithms with different approaches). If we do a good job then our estimates would be similar to the true ratings, we would evaluate the precision of our algorithm with the RMSE. Remember that we use the **validation** set as a sample of known true ratings where we can test our predictions. Suppose that we train a model with our **edx** set and the prediction we get from user "5" and movie "Heat" is 2.5 stars and we know that the true rating (from the **validation** set) is 3 stars. Then the error of our prediction would be:

$$error = true_{rating} - prediction = 3stars - 2.5stars = 0.5stars$$

If we repeat this calculation for all our predictions then we have to **sum** all our errors. We must consider that some values could be positive and some others could be negative, therefore we first **square** the errors so the positive values don't cancel out the negative values. Then we divide our result by the number of predictions we made in order to get the **mean** error. Note that since we previously squared our errors, then the unit of our result is $stars^2$ thus we **square root** it to turn it back to our original unit ($stars$). This value is known as the *Root Mean Square Error* or *RMSE*, and it can be written as:

$$RMSE = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(true_{rating_i} - prediction_i)^2}$$

Once we are able to predict all ratings for any given user and any given movie, then we can *recommend* movies to users just by showing them only those movies we predict they would like the most (movies with more stars). In this project we will just predict the ratings, we won't make the recommendation of the top "N" movies to the users.

3.2 Models Implemented.

The models we will train for our recommendation system follow one of the these approaches:

[3]This pdf section corresponds to section "IV RMSE FUNCTION" of the R script.

1. Linear regression. In this approach we will start from a baseline predictor (i.e. average rating of all movies) and then we will add the effect of a specific variable (i.e. movie effect, user effect, genre effect, etc.). Redarding this approach Yehuda Koren, one of the winner of the Netflix challenge, wrote in his article "The BellKor Solution to the Netflix Grand Prize" (Korean, 2009, p.9):

"Out of the numerous new algorithmic contributions, I would like to highlight one – those humble baseline predictors (or biases), which capture main effects in the data. While the literature mostly concentrates on the more sophisticated algorithmic aspects, we have learned that an accurate treatment of main effects is probably at least as significant as coming up with modeling breakthroughs".

To illustrate this model, let us take the following example:

- User effect: Isabella is an easygoing user so she tends to rate movies on average 0.4 stars higher than other users.
- Movie effect: Back to the Future is a classic movie and maybe is 0.6 stars higher than the average movie.
- Genre effect: Suppose that science fiction movies tend to be 0.8 lower than other film genres.

If the average of all movies is 3.5 stars (baseline predictor), then our prediction for Isabella rating Back to the Future would be:

3.5 stars (baseline) + 0.4 stars (user effect) + 0.6 stars (movie effect) - 0.8 (genre effect) = **3.7 stars**

2. Matrix factorization. This model detect patterns or latent factors between groups of movies or groups of users. Note that this interaction between groups of movies or users can't be accounted for with our first approach. To illustrate this model, consider the following example:

If Isabella likes Harry Potter Part-3 there's a good chance that she would enjoy the rest of the saga, moreover there is a chance that she would enjoy other films like Lord of the Rings, Star Wars, Indiana Jones, Pan's Labyrinth, Jurassic Park and Noah. Here are some assumptions why this may happen:

- The fan factor: Isabella is very into the Harry Potter world, she knows the story, the characters, the places, etc. so she would enjoy all the saga despite of the quality, the cast or the production of the film.
- The fantasy factor: Letting aside that she is a huge fan, in general she likes fantasy so she also will enjoy Lord of the Rings or Star Wars.
- The direction and production factor: Not only she likes fantasy but she likes very much Cuaron's films so maybe she will enjoy Pan's Labyrinth too.
- The music factor: Isabella loves John Williams' music, so maybe Jurassic Park has the right mix of fantasy and music she expects in a movie, and so has Star Wars.
- The cast factor: Besides, Isabella likes very much Emma Watson, so maybe Noah would be a nice choice for her.

Now if we consider that there are many patterns like the ones described above, theoretically, if we could realize of the presence of these patterns, we could decompose our prediction in these factors making our model more accurate.

One way we can obtain these patterns is with Principal Component Analysis (PCA) or Singular Value Decomposition (SVD) which allow us to find the correlations or the lack of correlation among the variables in a matrix, i.e. a user-movie ratings matrix where movies are columns, users are rows and the numbers inside the matrix are the ratings for each combination of column and row (user-movie). These methods will decompose our matrix in Principal Components that can be thought of as the patterns we are looking for.

This decomposition is called matrix factorization and the mathematical principles applied in these methods allow us to find the similarities among our movies and our users, no matter if the "latent factors" that give us these similarities are not interpretable. In other words, we don't have to be aware that a fan, music, fantasy, direction or cast factor exists, the method will just find those patterns.

PCA and SVD are in fact known as dimensionality reduction methods that we will use for matrix factorization purposes.

3.3 Linear Regression Models[4].

3.3.1 Baseline Predictor Model.

As we explained before, we will start from a baseline predictor which will be defined as the average of all the ratings in our **edx** set. This average would be our first prediction:

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

- $Y_{u,m}$ = the rating for user u and movie m.
- μ = the rating average of all movies in the **edx** set.
- $\epsilon_{u,m}$ = an independent error for user u and movie m sampled from the same distribution centered at 0.

If we want an estimate of μ, this is $\hat{\mu}$ where the hat symbol "^" means "estimate", then the Central Limit Theorem (CTL) tells us that we can just use μ, the rating average of all the observations in our dataset (3.5125). Thus, our prediction would be the following:

Table 5: Example of predictions of model 1.

user	movie	title	true rating	model 1
34	1	Toy Story (1995)	3.0	3.512465
157	1	Toy Story (1995)	5.0	3.512465
91	2	Jumanji (1995)	4.0	3.512465
481	2	Jumanji (1995)	3.0	3.512465
541	6	Heat (1995)	4.0	3.512465
530	6	Heat (1995)	4.0	3.512465
430	6874	Kill Bill: Vol. 1 (2003)	4.5	3.512465
481	6874	Kill Bill: Vol. 1 (2003)	5.0	3.512465
94	480	Jurassic Park (1993)	4.0	3.512465
268	480	Jurassic Park (1993)	5.0	3.512465

Note that the table above is just an extract of our entire prediction that we will be using for illustration purposes. To evaluate the performance of our first model we compare all the true ratings in our **validation** set with predictions in our **edx** set with our predictions in the **edx** set and obtain the RMSE of our algorithm:

Table 6: RMSE of model 1.

ID	Method	RMSE
1	average	1.061202

3.3.2 Average + Movie Effect Model.

Now we will add the movie effect to our baseline predictor. This represents how many stars on average is a movie above or under the rating average of all the dataset. Our model now would be described as follows:

[4]This pdf section corresponds to section "V. NORMALIZATION EFFECTS MODELS" of the R script.

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

- $Y_{u,m}$ = the rating we predict for user u and movie m.
- μ = the rating average of all movies in the **edx** set.
- b_m = bias due to the movie effect.
- $\epsilon_{u,m}$ = an independent error for user u and movie m sampled from the same distribution centered at 0.

In this case the Least Squares Estimate of b_m which minimizes our RMSE is the average of $Y_{u,m} - \hat{\mu}$ for each movie m:

$$\hat{b_m} = \frac{1}{n_m}\sum^{n_m}(Y_{u,m} - \hat{\mu})$$

where:

- $\hat{b_m}$ = estimate of the bias or effect for movie m.
- n_m = number of ratings of movie m.
- $\hat{\mu}$ = estimate of the average of all ratings (model 1).

So, first we will calculate the mean rating of each movie and then we will substract $\hat{\mu}$ which we can estimate using the following piece of code:

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

b_m <- edx %>%
  group_by(movieId,title) %>%
  summarize(mean_rating = mean(rating), mu = mu ,b_m = mean(rating - mu))

prediction <- mu + validation %>%
  left_join(b_m, by='movieId') %>%
  .$b_m %>%
  as.data.frame()
```

movieId	title	mean_rating	mu	b_m
1	Toy Story (1995)	3.927638	3.512465	0.4151725
2	Jumanji (1995)	3.205399	3.512465	-0.3070658
3	Grumpier Old Men (1995)	3.146984	3.512465	-0.3654817
4	Waiting to Exhale (1995)	2.864299	3.512465	-0.6481659
5	Father of the Bride Part II (1995)	3.068672	3.512465	-0.4437933
6	Heat (1995)	3.815284	3.512465	0.3028191
7	Sabrina (1995)	3.358589	3.512465	-0.1538759
8	Tom and Huck (1995)	3.134592	3.512465	-0.3778732
9	Sudden Death (1995)	2.997805	3.512465	-0.5146601
10	GoldenEye (1995)	3.425825	3.512465	-0.0866405

From what we can see Toy Story (1995) tend to be rated 0.4151725 stars above the average rating and Jumanji (1995) tend to be rated -0.3070658 stars below the average rating.

Now we are ready to predict based on the average rating and the movie effect, here are some examples:

Table 7: Example of predictions of model 1 and model 2.

user	movie	title	true rating	model 1	model 2
34	1	Toy Story (1995)	3.0	3.512465	3.927638
157	1	Toy Story (1995)	5.0	3.512465	3.927638
91	2	Jumanji (1995)	4.0	3.512465	3.205399
481	2	Jumanji (1995)	3.0	3.512465	3.205399
541	6	Heat (1995)	4.0	3.512465	3.815284
530	6	Heat (1995)	4.0	3.512465	3.815284
430	6874	Kill Bill: Vol. 1 (2003)	4.5	3.512465	3.902361
481	6874	Kill Bill: Vol. 1 (2003)	5.0	3.512465	3.902361
94	480	Jurassic Park (1993)	4.0	3.512465	3.663522
268	480	Jurassic Park (1993)	5.0	3.512465	3.663522

Note that the RMSE of this model is lower than the one of our first algorithm:

Table 8: RMSE of first two models.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087

3.3.3 Average + Genre, User, Premiere Year or Date of Rating Effect Models.

In the next models we will apply the same approach as in our previous model. This time we will consider the rating average of all observations plus the bias due to the effects of genre, user, premiere year and date of rating. We will analyze each effect separately using the following models:

$$Y_{u,m} = \mu + b_g + \epsilon_{u,m}$$
$$Y_{u,m} = \mu + b_u + \epsilon_{u,m}$$
$$Y_{u,m} = \mu + b_y + \epsilon_{u,m}$$
$$Y_{u,m} = \mu + b_d + \epsilon_{u,m}$$

- $Y_{u,m}$ = the rating for user u and movie m.
- μ = the rating average of all movies in the **edx** set.
- b_g = bias due to the genre effect.
- b_u = bias due to the user effect.
- b_y = bias due to the year effect.
- b_d = bias due to the date of rating effect.
- $\epsilon_{u,m}$ = an independent error for user u and movie m sampled from the same distribution centered at 0.

The Least Squares Estimate of b_g, b_u, b_y and b_d which minimizes our RMSE is the average of $Y_{u,m}$ - $\hat{\mu}$. In this case, the average of $Y_{u,m}$ is calculated in each equation by a different effect: genre, user, year and date. Therefore, the bias of each variable is determined by the following piece of code:

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

b_g <- edx %>%
  group_by(genres) %>%
  summarize(b_g = mean(rating - mu))

b_u <- edx %>%
  group_by(userId) %>%
  summarize(b_u = mean(rating - mu))

b_y <- edx %>%
  group_by(year) %>%
  summarize(b_y = mean(rating - mu))

b_d <- edx %>%
  group_by(rating_date) %>%
  summarize(b_d = mean(rating - mu))

# prediction for genre effect:
prediction <- mu + validation %>%
  left_join(b_g, by='genres') %>%
  .$b_g %>%
  as.data.frame()

# prediction for user effect:
prediction <- mu + validation %>%
  left_join(b_u, by='userId') %>%
  .$b_u %>%
  as.data.frame()

# prediction for year effect:
prediction <- mu + validation %>%
  left_join(b_y, by='year') %>%
  .$b_y %>%
  as.data.frame()

# prediction for date of rating effect:
prediction <- mu + validation %>%
  left_join(b_d, by='rating_date') %>%
  .$b_d %>%
  as.data.frame()
```

The RMSE of these models are:

Table 9: RMSE of models 1 to 6.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018

Here are some examples of the predictions applying each model:

Table 10: Example of predictions of model 1 to model 6.

user	movie	title	true rating	model 1	model 2	model 3	model 4	model 5	model 6
34	1	Toy Story (1995)	3.0	3.512465	3.927638	3.786856	2.734835	3.442880	3.556944
157	1	Toy Story (1995)	5.0	3.512465	3.927638	3.786856	4.160000	3.442880	3.626599
91	2	Jumanji (1995)	4.0	3.512465	3.205399	3.390070	3.724719	3.442880	3.587538
481	2	Jumanji (1995)	3.0	3.512465	3.205399	3.390070	4.118971	3.442880	3.611736
541	6	Heat (1995)	4.0	3.512465	3.815284	3.461289	3.441861	3.442880	3.583683
530	6	Heat (1995)	4.0	3.512465	3.815284	3.461289	3.642857	3.442880	3.927142
430	6874	Kill Bill: Vol. 1 (2003)	4.5	3.512465	3.902361	3.461289	3.815790	3.459295	3.611736
481	6874	Kill Bill: Vol. 1 (2003)	5.0	3.512465	3.902361	3.461289	4.118971	3.459295	3.412347
94	480	Jurassic Park (1993)	4.0	3.512465	3.663522	3.541762	3.317757	3.496722	3.483927
268	480	Jurassic Park (1993)	5.0	3.512465	3.663522	3.541762	3.611111	3.496722	3.538801

When analyzing the effects separately the ones which seem to perform better are *movie*, *user* and *genre*, while *year* and *date of rating* have little improvement respect the average alone. We expected this based on the scatter plots and the histograms we built in the previous chapter.

3.3.4 Average + Movie + User Effect Model.

As you may noticed using global effects separately didn't improve our predictions very much. The best RMSE until now is 0.9439087 this means our error is almost of 1 star.

Let us try to capture the movie and user effect (our two best models) in the same algorithm:

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

The Least Squares Estimate of b_m and b_u which minimizes our RMSE are:

- Movie bias[5]:

$$\hat{b_m} = \frac{1}{n_m} \sum^{n_m} (Y_{u,m} - \hat{\mu})$$

[5]This is the same equation as the one we used in model 2.

- User bias:

$$\hat{b_u} = \frac{1}{n_u}\sum^{n_u}(Y_{u,m} - \hat{\mu} - \hat{b_m})$$

where:

- $\hat{b_u}$ = estimate of the bias or effect for user u.
- n_u = number of ratings of user u.
- $\hat{\mu}$ = estimate of the average of all ratings (model 1).
- $\hat{b_m}$ = estimate of the bias or effect for movie m which we calculate with the first equation.

Both equations can be calculated with the next piece of code:

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

b_m <- edx %>%
  group_by(movieId) %>%
  summarize(b_m = mean(rating - mu))

b_u <- edx %>%
  left_join(b_m,by="movieId") %>%
  group_by(userId) %>%
  summarize(b_u = mean(rating - mu - b_m))

prediction <- validation %>%
  left_join(b_m, by='movieId') %>%
  left_join(b_u, by='userId') %>%
  mutate(pred = mu + b_m + b_u) %>%
  .$pred %>%
  as.data.frame()
```

The RMSE for this model is shown in the following table. The other results are shown for comparison purposes:

Table 11: RMSE of models 1 to 7.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488

We can see that our model had a significant improvement. Here are some results of models 2 (movie effect alone), 4 (user effect alone) and 7 (movie and user effect together):

Table 12: Example of predictions of model 2, 4 and 7.

user	movie	title	true rating	model 2	model 4	model 7
34	1	Toy Story (1995)	3.0	3.927638	2.734835	3.433689
157	1	Toy Story (1995)	5.0	3.927638	4.160000	4.863637
91	2	Jumanji (1995)	4.0	3.205399	3.724719	3.202967
481	2	Jumanji (1995)	3.0	3.205399	4.118971	3.816242
541	6	Heat (1995)	4.0	3.815284	3.441861	3.867987
530	6	Heat (1995)	4.0	3.815284	3.642857	4.225466
430	6874	Kill Bill: Vol. 1 (2003)	4.5	3.902361	3.815790	4.189686
481	6874	Kill Bill: Vol. 1 (2003)	5.0	3.902361	4.118971	4.513204
94	480	Jurassic Park (1993)	4.0	3.663522	3.317757	3.672228
268	480	Jurassic Park (1993)	5.0	3.663522	3.611111	3.927797

When mixing both effects now we see that our lowest prediction is less than 0 and our higher prediction is greater than 5 which in fact are out of the real rating parameters:

```
## [1] -0.4545803  6.0873129
```

So we can fix this with the next piece of code:

```
prediction <- validation %>%
  left_join(b_m, by='movieId') %>%
  left_join(b_u, by='userId') %>%
  mutate(pred = ifelse(mu + b_m + b_u < 0,0,ifelse(mu + b_m + b_u >5,5,mu + b_m + b_u))) %>%
  .$pred %>%
  as.data.frame()
```

We will refer to this prediction as *model 8* and it is just the prediction of *model 7* with the out of range (OOR) correction. The RMSE now is:

Table 13: RMSE of models 1 to 8.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488
8	average + movie + user effect (OOR correction)	0.8651772

3.3.5 Average + All Effects Model.

The next model will consider all of the effects together. This time we will correct from the beginning all the predictions that are out of range. The equation of our model is:

$$Y_{u,m} = \mu + b_m + b_u + b_g + b_y + b_d + \epsilon_{u,m}$$

The Least Squares Estimate of the biases which minimizes our RMSE are:

- Movie bias[6]:
$$\hat{b_m} = \frac{1}{n_m}\sum^{n_m}(Y_{u,m} - \hat{\mu})$$
- User bias[7]:
$$\hat{b_u} = \frac{1}{n_u}\sum^{n_u}(Y_{u,m} - \hat{\mu} - \hat{b_m})$$
- Genre bias:
$$\hat{b_g} = \frac{1}{n_g}\sum^{n_g}(Y_{u,m} - \hat{\mu} - \hat{b_m} - \hat{b_u})$$
- Year bias:
$$\hat{b_y} = \frac{1}{n_y}\sum^{n_y}(Y_{u,m} - \hat{\mu} - \hat{b_m} - \hat{b_u} - \hat{b_g})$$
- Date of rating bias:
$$\hat{b_d} = \frac{1}{n_d}\sum^{n_d}(Y_{u,m} - \hat{\mu} - \hat{b_m} - \hat{b_u} - \hat{b_g} - \hat{b_y})$$

where:

- $\hat{b_{...}}$ = estimate of the bias or effect for user u, genre g, year y and date d.
- $n_{...}$ = number of ratings of user u, genre g, year y and date d.
- $\hat{\mu}$ = estimate of the average of all ratings (model 1).

These equations can be calculated with the next piece of code:

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

b_m <- edx %>%
  group_by(movieId) %>%
  summarize(b_m = mean(rating - mu))

b_u <- edx %>%
  left_join(b_m,by="movieId") %>%
  group_by(userId) %>%
  summarize(b_u = mean(rating - mu - b_m))

b_g <- edx %>%
  left_join(b_m,by="movieId") %>%
```

[6] This is the same equation as the one we used in model 2.
[7] This is the same equation as the one we used in model 7.

```
  left_join(b_u,by="userId") %>%
  group_by(genres) %>%
  summarize(b_g = mean(rating - mu - b_m - b_u))

b_d <- edx %>%
  left_join(b_m,by="movieId") %>%
  left_join(b_u,by="userId") %>%
  left_join(b_g,by="genres") %>%
  group_by(rating_date) %>%
  summarize(b_d = mean(rating - mu - b_m - b_u - b_g))

b_y <- edx %>%
  left_join(b_m,by="movieId") %>%
  left_join(b_u,by="userId") %>%
  left_join(b_g,by="genres") %>%
  left_join(b_d,by="rating_date") %>%
  group_by(year) %>%
  summarize(b_y = mean(rating - mu - b_m - b_u - b_g - b_d))

prediction <- validation %>%
  left_join(b_m, by='movieId') %>%
  left_join(b_u, by='userId') %>%
  left_join(b_g, by='genres') %>%
  left_join(b_d,by="rating_date") %>%
  left_join(b_y,by="year") %>%
  mutate(pred = ifelse(mu + b_m + b_u + b_g + b_d + b_y < 0,
                       0,
                       ifelse(mu + b_m + b_u + b_g + b_d + b_y >5,
                              5,
                              mu + b_m + b_u + b_g + b_d + b_y))) %>%
  .$pred %>%
  as.data.frame()
```

The RMSE for this model is shown in the following table. The other results are shown for comparison purposes:

Table 14: RMSE of models 1 to 9.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488
8	average + movie + user effect (OOR correction)	0.8651772
9	average + all effects	0.8644178

Here are some results of models 8 and 9:

Table 15: Example of predictions of models 8 and 9.

user	movie	title	true rating	model 8	model 9
34	1	Toy Story (1995)	3.0	3.433689	3.366152
157	1	Toy Story (1995)	5.0	4.863637	4.803003
91	2	Jumanji (1995)	4.0	3.202967	3.164558
481	2	Jumanji (1995)	3.0	3.816242	3.732063
541	6	Heat (1995)	4.0	3.867987	3.808501
530	6	Heat (1995)	4.0	4.225466	4.216872
430	6874	Kill Bill: Vol. 1 (2003)	4.5	4.189686	4.165081
481	6874	Kill Bill: Vol. 1 (2003)	5.0	4.513204	4.500259
94	480	Jurassic Park (1993)	4.0	3.672228	3.639648
268	480	Jurassic Park (1993)	5.0	3.927797	3.894359

3.4 Regularization Models[8].

One problem with our predictions in the last model, which seems to be the best in terms of the RMSE, is that the estimates of the biases b_m, b_u, b_g, b_y and b_d are prone to be larger (positive or negative) when there is just a **few samples** when estimated. Let us count the movies which were rated 20 or fewer times:

```
movies_20_less <- nrow(edx %>%
                         group_by(movieId) %>%
                         summarize(cases = n()) %>%
                         ungroup() %>%
                         filter(cases<=20))
movies_20_less
```

```
## [1] 1933
```

These movies represent 18.1043364% of all the movies in the **edx** set and will cause b_m to be larger and hence increase our RMSE.

Here are the number of users that rated 20 or fewer movies:

```
users_20_less <- nrow(edx %>%
                        group_by(userId) %>%
                        summarize(cases = n()) %>%
                        ungroup() %>%
                        filter(cases<=20))
users_20_less
```

```
## [1] 4966
```

These users represent 7.1066716% of all the users in the **edx** set and will cause b_u to be larger and hence increase our RMSE.

To better illustrate this idea let us take our Least Squares Estimate which minimizes our RMSE in *model 2* (the average of $Y_{u,m} - \hat{\mu}$ for each movie m):

[8]This pdf section corresponds to section "V.X Model 10 Regularization" of the R script

$$\hat{b_m} = \frac{1}{n_m}\sum^{n_m}(Y_{u,m} - \hat{\mu})$$

Suppose that movie m_x has 1,000 ratings (n_m) and m_y has only 10 ratings, then the average of $Y_{u,m} - \hat{\mu}$ will be very precise for movie m_x since it is calculated with 1,000 observations. On the other hand, our estimate for movie m_y will be calculated with only 10 observations, which will lead us to a very inaccurate prediction.

Regularization is a technique we can use to penalize large estimates that are produced when using small samples. Therefore, we will minimize the following equation with the penalty term λ:

$$\frac{1}{N}\sum_{u,m}(y_{u,m} - \mu - b_m - b_u - b_g - b_y - b_d)^2 + \lambda(\sum_m b_m^2 + \sum_u b_u^2 + \sum_g b_g^2 + \sum_y b_y^2 + \sum_d b_d^2)$$

The optimal values for the estimates with regularization are:

- Movie effect:

$$\hat{b_m}(\lambda) = \frac{1}{(\lambda + n_m)}\sum^{n_m}(Y_{u,m} - \hat{\mu})$$

- User effect:

$$\hat{b_u}(\lambda) = \frac{1}{(\lambda + n_u)}\sum^{n_u}(Y_{u,m} - \hat{\mu} - \hat{b_m}(\lambda))$$

- Genre effect:

$$\hat{b_g}(\lambda) = \frac{1}{(\lambda + n_g)}\sum^{n_g}(Y_{u,m} - \hat{\mu} - \hat{b_m}(\lambda) - \hat{b_u}(\lambda))$$

- Year effect:

$$\hat{b_y}(\lambda) = \frac{1}{(\lambda + n_y)}\sum^{n_y}(Y_{u,m} - \hat{\mu} - \hat{b_m}(\lambda) - \hat{b_u}(\lambda) - \hat{b_g}(\lambda))$$

- Date of rating effect:

$$\hat{b_d}(\lambda) = \frac{1}{(\lambda + n_d)}\sum^{n_d}(Y_{u,m} - \hat{\mu} - \hat{b_m}(\lambda) - \hat{b_u}(\lambda) - \hat{b_g}(\lambda) - \hat{b_y}(\lambda))$$

where:

- λ = penalty term.
- $n_{...}$ = the number of ratings for movie m, user u, genre g, year y and date of rating d.
- $\hat{b_{...}}$ = the bias due to movie, user, genre, year and date of rating effect.

Hence, the equation of our model is:

$$Y_{u,m} = \mu + b_m(\lambda) + b_u(\lambda) + b_g(\lambda) + b_y(\lambda) + b_d(\lambda) + \epsilon_{u,m}$$

Let us consider that λ equals 1, if n is very large, then λ won't change our estimate very much since the term $\lambda + n$ (1 + n) in the denominator will be larger and thus, similar to n (the result is not affected by the regularization penalty). But if n is small, then our estimate will be shrunken towards zero since $\lambda + n$ (1 + n) in the denominator will be smaller (the result is affected by the regularization penalty).

Note that lambda (λ) is a **parameter** that can be **tuned**, thus we can seek the best value of λ which minimizes the RMSE. This means that we need to evaluate different values of λ to see which one leads us to the best prediction. But **we can't use our test set** (*validation set*) to seek for the best λ so we will use **cross-validation** (CV) to accomplish our goal using 10 folds (k-folds) of our **edx** set as follows:

- We build 10 samples of our **edx** set with the 90% of the observations where we train the model and tune for λ
- We build 10 samples with the remaining 10% of the observations to estimate the RMSE in this set and find the best λ.
- Note that we use part of the train set to find the λ, we're not using the **validation** set.

The code we can use for tuning for λ is:

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

# We create 10 folds to perform CV
k_folds_index <- createFolds(edx$movieId,k=10,list=TRUE,returnTrain = TRUE)

mu <- mean(edx$rating)

# Range adjusted from 3.5 to 5.5 after analysis, but it can be any range.
lambdas <- seq(3.5,5.5,.15)

# Partitioning train set in two:
# train_fold = 90% of the k_th fold, and,
# validation_fold = 10% of the remaining data.

# Here is an example of the 1st fold
k <- 1

# This is the train set used for cross validation where k indicates the number of the fold.
train_fold <- edx[k_folds_index[[k]],]

# This is the validation set used for the cross validation
validation_fold <- edx[-k_folds_index[[k]],]

# Now we can tune for lambda with the following function.
# We are going to use the first fold (k = 1).
# So let's test our function (this could take several minutes):

rmses <- sapply(lambdas,function(lambda){
  b_m <- train_fold %>%
    group_by(movieId) %>%
    summarize(b_m = sum(rating - mu)/(n()+lambda))

  b_u <- train_fold %>%
    left_join(b_m, by="movieId") %>%
    group_by(userId) %>%
    summarize(b_u = sum(rating - mu - b_m)/(n()+lambda))

  b_g <- train_fold %>%
    left_join(b_m,by="movieId") %>%
    left_join(b_u,by="userId") %>%
    group_by(genres) %>%
    summarize(b_g = sum(rating - mu - b_m - b_u)/(n()+lambda))

  b_d <- train_fold %>%
    left_join(b_m,by="movieId") %>%
    left_join(b_u,by="userId") %>%
```

```
    left_join(b_g,by="genres") %>%
    group_by(rating_date) %>%
    summarize(b_d = sum(rating - mu - b_m - b_u - b_g)/n()+lambda)

  b_y <- train_fold %>%
    left_join(b_m,by="movieId") %>%
    left_join(b_u,by="userId") %>%
    left_join(b_g,by="genres") %>%
    left_join(b_d,by="rating_date") %>%
    group_by(year) %>%
    summarize(b_y = sum(rating - mu - b_m - b_u - b_g - b_d)/(n()+lambda))

  prediction <- validation_fold %>%
    left_join(b_m, by='movieId') %>%
    left_join(b_u, by='userId') %>%
    left_join(b_g, by='genres') %>%
    left_join(b_d, by="rating_date") %>%
    left_join(b_y, by="year") %>%
    mutate(pred = ifelse(mu + b_m + b_u + b_g + b_d + b_y < 0,
                         0,
                         ifelse(mu + b_m + b_u + b_g + b_d + b_y >5,
                                5,
                                mu + b_m + b_u + b_g + b_d + b_y)))

  # Since we splitted the data 90%-10% it is possible that some observations result in NA
  # when left-joining. So we identify those observations and substract them from both sets
  # and calculate RMSE only with the remaining observations:

  index_preserve <- which(!is.na(prediction$pred))
  p <- prediction$pred[index_preserve]
  v <- validation_fold$rating[index_preserve]

  return(RMSE(p,v))
})
```

The result of our tuning process is:

Table 16: Tuning results for Lambda using Cross-Validation.

lambdas	rmses1	rmses2	rmses3	rmses4	rmses5	rmses6	rmses7	rmses8	rmses9	rmses10
3.50	0.8636884	0.8649804	0.8635590	0.8650831	0.8637605	0.8640203	0.8642252	0.8645307	0.8643483	0.8643300
3.65	0.8636830	0.8649750	0.8635528	0.8650776	0.8637559	0.8640145	0.8642196	0.8645257	0.8643404	0.8643223
3.80	0.8636784	0.8649703	0.8635475	0.8650730	0.8637521	0.8640096	0.8642148	0.8645215	0.8643333	0.8643154
3.95	0.8636747	0.8649665	0.8635431	0.8650693	0.8637491	0.8640054	0.8642108	0.8645181	0.8643271	0.8643093
4.10	0.8636717	0.8649633	0.8635393	0.8650663	0.8637469	0.8640020	0.8642076	0.8645155	0.8643216	0.8643041
4.25	0.8636694	0.8649610	0.8635364	0.8650640	0.8637454	0.8639995	0.8642052	0.8645137	0.8643170	0.8642995
4.40	0.8636679	0.8649594	0.8635342	0.8650625	0.8637446	0.8639976	0.8642035	0.8645125	0.8643131	0.8642958
4.55	0.8636671	0.8649584	0.8635327	0.8650618	0.8637445	0.8639965	0.8642025	0.8645121	0.8643100	0.8642928
4.70	0.8636670	0.8649582	0.8635320	0.8650617	0.8637451	0.8639961	0.8642022	0.8645123	0.8643075	0.8642905
4.85	0.8636675	0.8649586	0.8635319	0.8650623	0.8637464	0.8639964	0.8642026	0.8645133	0.8643058	0.8642889
5.00	0.8636688	0.8649597	0.8635325	0.8650636	0.8637483	0.8639974	0.8642037	0.8645148	0.8643048	0.8642880
5.15	0.8636706	0.8649614	0.8635338	0.8650656	0.8637508	0.8639991	0.8642054	0.8645170	0.8643044	0.8642878
5.30	0.8636730	0.8649638	0.8635356	0.8650682	0.8637540	0.8640014	0.8642077	0.8645198	0.8643047	0.8642882
5.45	0.8636760	0.8649667	0.8635381	0.8650714	0.8637578	0.8640043	0.8642107	0.8645233	0.8643057	0.8642892

The following plot shows the results for each fold in our previous table. The red dotted lines indicates the intercept of the λ which minimizes the RMSE:

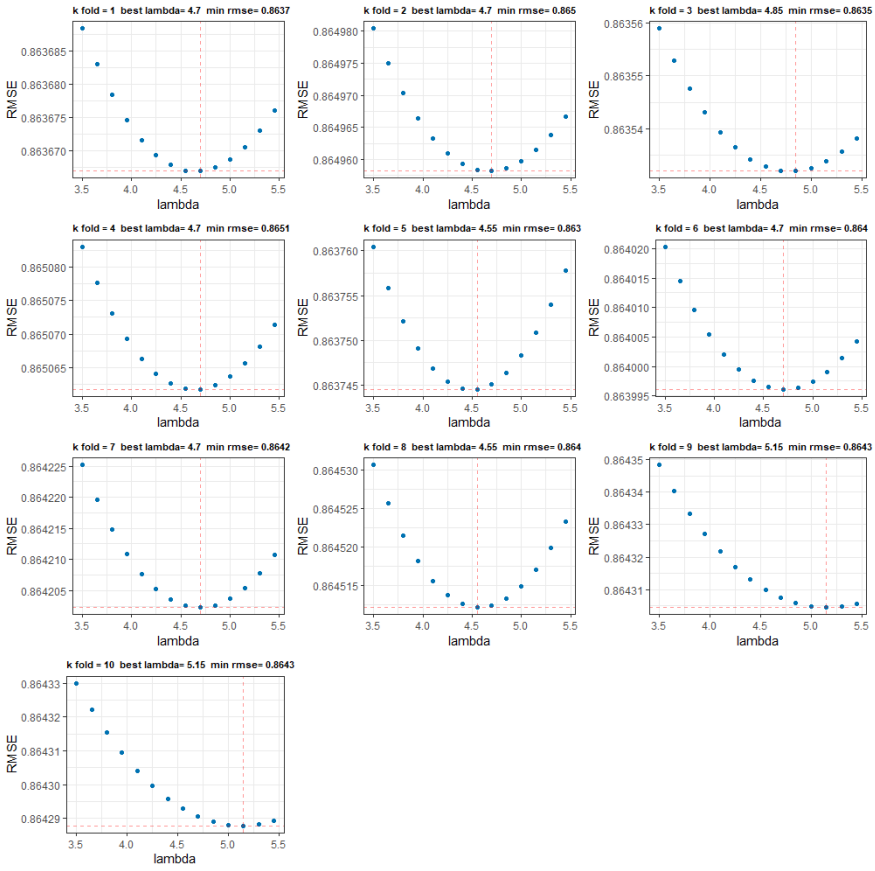


Figure 3: Best Lambda using Cross Validation with 10 folds

With these results we calculate the mean RMSE of the 10 k-folds for each value of λ:

Table 17: Mean RMSE for each value of Lambda.

lambdas	mean_rmse
3.50	0.8642526
3.65	0.8642467
3.80	0.8642416
3.95	0.8642373
4.10	0.8642338
4.25	0.8642311
4.40	0.8642291
4.55	0.8642278
4.70	0.8642273
4.85	0.8642274
5.00	0.8642282
5.15	0.8642296
5.30	0.8642316
5.45	0.8642343

The value of λ with the lowest mean RMSE is the best lambda (our tuned penalty parameter). In this case our best λ equals to 4.7 (mean RMSE = 0.8642273).

Now we can train our model with our penalty term $\lambda = 4.7$ with the following piece of code:

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

# We define best lambda as:

best_lambda <- 4.7

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

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

b_g <- edx %>%
  left_join(b_m,by="movieId") %>%
  left_join(b_u,by="userId") %>%
  group_by(genres) %>%
  summarize(b_g = sum(rating - mu - b_m - b_u)/(n()+best_lambda))

b_d <- edx %>%
  left_join(b_m,by="movieId") %>%
  left_join(b_u,by="userId") %>%
  left_join(b_g,by="genres") %>%
  group_by(rating_date) %>%
  summarize(b_d = sum(rating - mu - b_m - b_u - b_g)/n()+best_lambda)

b_y <- edx %>%
  left_join(b_m,by="movieId") %>%
  left_join(b_u,by="userId") %>%
  left_join(b_g,by="genres") %>%
  left_join(b_d,by="rating_date") %>%
  group_by(year) %>%
  summarize(b_y = sum(rating - mu - b_m - b_u - b_g - b_d)/(n()+best_lambda))

prediction <- validation %>%
  left_join(b_m, by='movieId') %>%
  left_join(b_u, by='userId') %>%
  left_join(b_g, by='genres') %>%
  left_join(b_d, by="rating_date") %>%
  left_join(b_y, by="year") %>%
  mutate(pred = ifelse(mu + b_m + b_u + b_g + b_d + b_y < 0,
                       0,
                       ifelse(mu + b_m + b_u + b_g + b_d + b_y >5,
                              5,
                              mu + b_m + b_u + b_g + b_d + b_y))) %>%
  .$pred %>%
  as.data.frame()
```

The RMSE for this model 10 is shown in the following table:

Table 18: RMSE of models 1 to 10.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488
8	average + movie + user effect (OOR correction)	0.8651772
9	average + all effects	0.8644178
10	average + all effects with regularization	0.8639582

Here are some results of models 9 and 10:

Table 19: Example of predictions of models 9 and 10.

user	movie	title	true rating	model 9	model 10
34	1	Toy Story (1995)	3.0	3.366152	3.374955
157	1	Toy Story (1995)	5.0	4.803003	4.737930
91	2	Jumanji (1995)	4.0	3.164558	3.168552
481	2	Jumanji (1995)	3.0	3.732063	3.723915
541	6	Heat (1995)	4.0	3.808501	3.812605
530	6	Heat (1995)	4.0	4.216872	4.249858
430	6874	Kill Bill: Vol. 1 (2003)	4.5	4.165081	4.111632
481	6874	Kill Bill: Vol. 1 (2003)	5.0	4.500259	4.490765
94	480	Jurassic Park (1993)	4.0	3.639648	3.647496
268	480	Jurassic Park (1993)	5.0	3.894359	3.882399

One final adjustment we will try is to test regularization only for the strongest effects (*movie*, *user* and *genre*)[9]. Hence, the equation of our model is:

$$Y_{u,m} = \mu + b_m(\lambda) + b_u(\lambda) + b_g(\lambda) + b_y + b_d + \epsilon_{u,m}$$

And as we can see in the following table, using a penalty term just on some effects produces a similar RMSE:

[9]The code can be found on section "V.XI Model 11 Average + Regularization Best Effects" of the R script

Table 20: RMSE of models 1 to 11.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488
8	average + movie + user effect (OOR correction)	0.8651772
9	average + all effects	0.8644178
10	average + all effects with regularization	0.8639582
11	average + best effects regularization	0.8639540

3.5 Matrix Factorization Models.

So far, the algorithms implemented have considered just global and isolated factors (i.e. movie effect, user effect, etc.), those are the bias in ratings considering a specific effect. But there are in fact other latent factors that can explain most of the variation in the ratings we observed.

Our models, as explained by Rafael Irizarry in his book Introduction to Data Science: *"[. . .] leaves out an important source of variation related to the fact that groups of movies have similar rating patterns and groups of users have similar patterns"* (Irizarry, 2020, p.626).

As we explained on **chapter 3.2** we will use matrix factorization to detect these patterns between groups of movies and groups of users using Principal Component Analysis (PCA) and Singular Value Decomposition (SVD)[10].

3.5.1 PCA and SVD examples.

PCA and SVD have two benefits, among others:

- Reducing the dimensions of a data set making it smaller and easier to explore, manipulate and visualize and,
- Capturing the "latent factors" or "patterns" between groups of variables and groups of observations.

First we will illustrate the importance of PCA and SVD with a simple example and, in the next section, we will explain the concepts behind this techniques. So, let us get started with the following matrix:

[10]Here are two links that clearly explain the basics of dimension reduction: 1). Josh Starmer's "StatQuest: PCA main ideas in only 5 minutes!!!"; 2). Luis Serrano's "Principal Component Analysis (PCA)"; and 3). Abhigyan's "Importance of Dimensionality Reduction!!"

Table 21: Example of Matrix 15 x 10.

	var1	var2	var3	var4	var5	var6	var7	var8	var9	var10
obs1	0.2196078	0.2078431	0.2196078	0.2313725	0.2549020	0.2784314	0.2980392	0.3058824	0.3098039	0.3098039
obs2	0.2941176	0.2862745	0.2431373	0.2549020	0.2784314	0.2980392	0.3098039	0.3176471	0.3176471	0.3137255
obs3	0.3568627	0.3450980	0.3647059	0.3607843	0.3568627	0.3529412	0.3490196	0.3490196	0.3529412	0.3568627
obs4	0.4196078	0.4156863	0.3882353	0.3843137	0.3803922	0.3764706	0.3764706	0.3764706	0.3764706	0.3764706
obs5	0.4352941	0.4392157	0.4196078	0.4196078	0.4196078	0.4196078	0.4196078	0.4156863	0.4117647	0.4078431
obs6	0.4156863	0.4313725	0.4431373	0.4470588	0.4549020	0.4549020	0.4549020	0.4470588	0.4392157	0.4352941
obs7	0.4039216	0.4274510	0.4470588	0.4549020	0.4666667	0.4745098	0.4745098	0.4627451	0.4470588	0.4392157
obs8	0.3607843	0.3843137	0.4313725	0.4431373	0.4588235	0.4705882	0.4705882	0.4549020	0.4352941	0.4235294
obs9	0.3411765	0.3647059	0.4078431	0.4196078	0.4431373	0.4549020	0.4549020	0.4352941	0.4117647	0.3960784
obs10	0.3803922	0.4039216	0.3882353	0.4039216	0.4274510	0.4431373	0.4392157	0.4196078	0.3960784	0.3764706
obs11	0.3960784	0.3803922	0.4235294	0.4196078	0.3607843	0.4000000	0.3882353	0.4117647	0.3333333	0.3098039
obs12	0.4156863	0.3960784	0.3960784	0.4274510	0.4352941	0.4235294	0.4000000	0.4235294	0.4823529	0.5529412
obs13	0.4352941	0.4117647	0.4039216	0.3764706	0.4000000	0.3725490	0.3960784	0.3607843	0.3686275	0.3372549
obs14	0.4352941	0.4078431	0.4392157	0.3372549	0.3294118	0.2980392	0.3725490	0.3529412	0.3647059	0.2745098
obs15	0.4196078	0.3921569	0.3568627	0.3058824	0.3450980	0.3647059	0.3843137	0.4000000	0.4313725	0.3803922

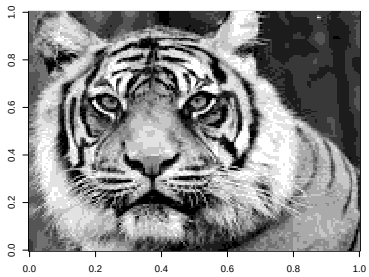
This is in fact an extract of a bigger matrix:

```
dim(example_matrix_dim_reduction)
```

```
## [1] 168 138
```

As we can see this matrix has 168 observations and 138 variables or features where each feature represents a dimension, hence we are dealing with a high dimensional matrix. The higher the number of features, the harder it is to analyze, make computations, visualize and train the data. What's more, it turns out that many of the features are irrelevant to the data because they account little variability. So we can decompose our original matrix into different matrices of fewer dimensions while keeping most of the relevant information.

We can visualize our previous model as an image. In fact, both rows and columns in the matrix represent pixels and the values inside the matrix which are numbers between 0 and 1 represent different scales of color. So the image that is stored in our matrix looks like this:



With PCA and SVD we can decompose our matrix into elements of fewer dimensions which represent patterns between our observations and patterns between our variables, like this:

```
pca <- prcomp(img, center = TRUE, scale = FALSE)

# Principal Components
n <- 13
# First Matrix
dim(pca$x[,1:n])
```

```
## [1] 168  13
```

```
# A Vector
length(pca$sdev[1:n])
```

```
## [1] 13
```

```
# Second Matrix
dim(t(pca$rotation[,1:n]))
```

```
## [1]  13 138
```

Note the dimensions of our 3 elements:

- The first matrix $(168 * 13)$ captures the patterns between our 168 observations.
- The second matrix $(13 * 138)$ captures the patterns between our 138 variables.
- Lastly, the vector contains the 13 most important components of our data (those which account for most of the variability)

We can obtain the same results with SVD:

```
svd <- svd(scale(img,scale=FALSE,center=TRUE))

# Principal Components
n <- 13
# First Matrix
dim(svd$u[,1:n])
```

```
## [1] 168  13
```

```
# A Vector
length(svd$d[1:n])
```

```
## [1] 13
```

```
# Second Matrix
dim(t(svd$v[,1:n]))
```

```
## [1]  13 138
```

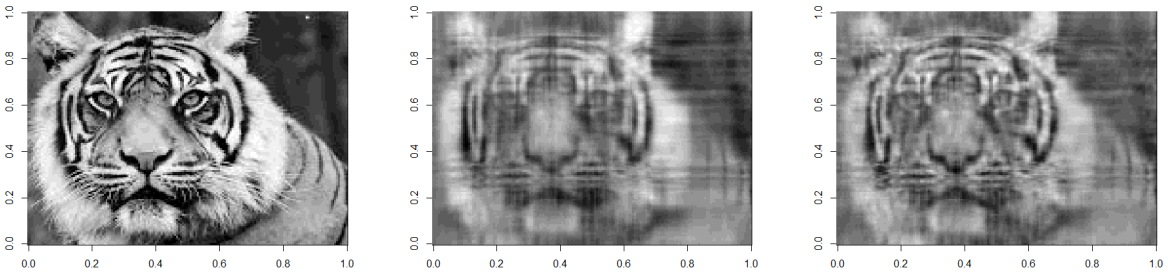
The three elements of SVD are similar to those we obtained with PCA. Now we can visualize an image for the original matrix, the transformed matrix using PCA and the transformed matrix using SVD:

- Original Matrix.
- Low Rank Approximation Matrix using PCA (13 PCs).
- Low Rank Approximation Matrix using SVD (13 PCs).

```r
# Low Rank Approximation Matrix using PCA with 13 principal components:
approx_img_pca <-  sweep(pca$x[,1:n,drop=FALSE],2,pca$sdev[1:n],"*") %*%
  t(pca$rotation[,1:n,drop=FALSE])

# Low Rank Approximation Matrix using SVD with 13 principal components:
approx_img_svd <- t(t(svd$u[,1:n,drop=FALSE]) * svd$d[1:n]) %*%
  t(svd$v[,1:n,drop=FALSE])

# Here are the 3 images to compare results:
image(img, col = pal(20))
image(approx_img_pca, col = pal(20))
image(approx_img_svd, col = pal(20))
```



Notice how similar are the last 2 pictures (transformed matrices) to our original matrix (first picture). These transformed matrices are using only 13 components to find patterns. his means that only with 13 components we accounted most of the variability of our original matrix. That is why these 3 pictures looks alike.

3.5.2 PCA and SVD basics.

Some main ideas about PCA and SVD are:

- Both are *orthogonal linear transformations* that turn the original data into a new coordinate system, where the origin is the center of the data.
- Centering the data around the origin means we calculate the average of each variable and then subtract it from the data, therefore each variable (column) will have a mean of zero.
- To perform the linear transformation we calculate the covariance matrix V, then we calculate its corresponding eigenvalues λ_i (magnitude) and eigenvectors v_i (direction), such that $V * v_i = \lambda_i * v_i$.
- The number of eigenvectors and eigenvalues i are either the number of variables or the number of observations, whichever is smaller.
- Because of the covariance matrix is **square and symmetric**, the eigenvalues λ_i are real numbers; because of the covariance matrix is **positive semi-definite**, the eigenvalues λ_i are non negative, and because of the covariance matrix is **symettric** the eigenvectors v_i are perpendicular (orthogonal), even in high dimensional data.
- Each eigenvector v_i can be intepreted as an axis called *Principal Component (PC)* where we can project our data (like the "photograph" of our data taken from that spot). So, if we think of multi-dimensional data, there are several axes or PCs and we can think of our transformation as an ellipsoid that fit our data in those axes:

  - The direction of the axis is determined by the eigenvector and,
  - Its form along each axis (long or short ellipsoid) is determined by the eigenvalues (magnitude).

- The larger the eigenvalue λ_i of a PC, the more variability it takes into account, thus, it better defines the original data. Therefore, we order PCs by size of eigenvalues in decreasing order.

PCA transforms a $n * m$ matrix $\mathbf{M}$ (with $m \leq n$) into a new matrix $\mathbf{M_t}$ which can be decomposed into:

- Matrix $\mathbf{x}$ of $n * m$ dimensions, and
- Matrix **rotation** of $m * m$ dimensions.

$$M \approx M_t = x * rotation^T$$

where,

- x = the coordinates of the observations into the axes of the orthogonal linear transformation.
- *rotation* = matrix of eigenvectors.

SVD transforms a $n * m$ matrix $\mathbf{M}$ (with $m \leq n$) into a new matrix $\mathbf{M_t}$ which can be decomposed into:

$$M \approx M_t = U * d * V^T$$

where,

- U = matrix of eigenvalues compressed to the unit vector.
- d = diagonal matrix with standard deviations of each component, sorted decreasingly.
- V = matrix of eigenvectors.

3.5.3 PCA and SVD in R.

The following code shows the way to obtain the same results either with PCA or SVD in R[11]:

```
# Matrix example
m <- matrix(sample(1:10, 16, replace=T),4,4)

# Perform transformation
pca <- prcomp(m,center=TRUE,scale=FALSE)
svd <- svd(scale(m,scale=FALSE,center=TRUE))

# Matrix of coordinates
pca$x
t(t(svd$u) * svd$d)

# Matrix of eigenvectors
pca$rotation
svd$v

# Variance
pca$sdev^2
svd$d^2/(nrow(m) - 1)
```

[11] The full code can be found in the R script "02_pca_svd_explained"

```r
# Low Rank Approximation Matrix
approx_matrix_pca <- sweep(pca$x[,1:n,drop=FALSE],2,pca$sdev[1:n],"*") %*%
  t(pca$rotation[,1:n,drop=FALSE])
approx_matrix_svd <-(svd$u[,1:n,drop=FALSE] * svd$d[1:n]) %*%
  t(svd$v[,1:n,drop=FALSE])
```

3.5.4 Matrix Completion[12].

The example of dimension reduction we showed in the previous chapter it is possible only when there is no missing values on our matrix. And as we can recall, our actual matrix is pretty sparse:

Table 22: Example of movie ratings by user.

userId	Father of the Bride Part II (1995)	GoldenEye (1995)	Heat (1995)	Jumanji (1995)	Sabrina (1995)	Toy Story (1995)
5					3	1
8	3		4	2.5		
10					3	
13				3		
14				3		3
18	1	4		3	2.5	3
19	3	4				

This makes sense, since normally the repertoire is huge but our capacity to see or rate all movies is limited. Think for instance of Amazon's inventory and compare it to the products that you have bought, looked at or searched for up until now. These would be just a few items from the whole inventory. So, let us calculate the sparsity of our ratings matrix.

Since there are movies and users with just a few number of ratings, we will create a matrix only with the most rated movies and the most assiduous users. In this case we will consider only those which have at least 100 cases:

```r
# Movies with at least 100 ratings
best_movies <- edx %>%
  group_by(movieId) %>%
  summarize(cases = n()) %>%
  filter(cases >= 100) %>%
  .$movieId

# Users with at least 100 ratings
best_users <- edx %>%
  group_by(userId) %>%
  summarize(cases = n()) %>%
  filter(cases >= 100) %>%
  .$userId

# Dataset with our best selection (at least 100 ratings)
edx_best_observations <- edx %>%
  filter(movieId %in% best_movies, userId %in% best_users)
```

[12]This pdf section corresponds to section "VI. MATRIX FACTORIZATION" of the R script.

As we can see, our matrix kept a huge amount of observations:

```
nrow(edx_best_observations)
```

```
## [1] 6780215
```

Now we transform our dataset and create a user-movie matrix with all the ratings available:

```
edx_sparse_matrix <- sparseMatrix(
  as.integer(factor(edx_best_observations$userId)),
  as.integer(factor(edx_best_observations$movieId)),
  x=edx_best_observations$rating)

# The dimension of our matrix is:
dim(edx_sparse_matrix)
```

```
## [1] 24115  5711
```

Our matrix has 24115 users and 5711 movies. The sparsity of this matrix can be calculated with the following piece of code:

```
# The sparsity of our matrix (the proportion of missing values) is defined as:
sparsity <- 1 - ( length(edx_sparse_matrix@x) / edx_sparse_matrix@Dim[1] / edx_sparse_matrix@Dim[2])
sparsity
```

```
## [1] 0.9507684
```

Note that 95.08% of all the ratings is missing. In order to perform PCA or SVD we need to **complete** our matrix. So, we will try 2 different techniques of matrix completion:

1). Replace missing values with zeros: As explained by Rafael Irizarry in his book Introduction to Data Science: *"In general, the choice of how to fill in missing data, or if one should do it at all, should be made with care"* (Irizarry, 2020, p. 642) . If we have the true ratings in our user-movie matrix and we substract the prediction we obtained with our last linear model, then we obtain the *rating residuals* for each known user-movie combination in our matrix. Then we will replace the missing ratings by zeros. Note that because the residuals are centered at zero, imputing zeros to the missing values **will not affect our matrix**. Finally, we will apply PCA to the residuals matrix to detect the patterns between groups of movies and groups of users and then we will sum this residuals to our last linear model. By doing this we train a model that considers the regularized global effects (of the linear models) and the "latent patterns" (obtained with matrix factorization).

2). Replace missing values using Expectation-Maximization (EM): As explained by Jason Brownlee (2019) in his article "A Gentle Introduction to Expectation-Maximization (EM Algorithm)"[13] *"The EM algorithm is an iterative approach that cycles between two modes. The first mode attempts to estimate the missing or latent variables, called the estimation-step or E-step. The second mode attempts to optimize the parameters of the model to best explain the data, called the maximization-step or M-step."*. We will use the **eimpute** function in R which iterates using EM and then approximates the completed matrix via truncated SVD.

Other techniques that can be used for matrix completion are: Convex Relaxation, Stochastic Gradient Descent (SGD) and Alternating Least Squares Minimization (ALS).

[13] https://machinelearningmastery.com/expectation-maximization-em-algorithm/

3.5.5 Regularized Global Effects + PCA Model[14].

In this model we will use our last regularized global effects equation:

$$Y_{u,m} = \mu + b_m(\lambda) + b_u(\lambda) + b_g(\lambda) + b_y + b_d + \epsilon_{u,m}$$

And then add "n" factors ("latent patterns") obtained with PCA:

$$\sum_{pc=1}^{n} (x_{u,pc} * rotation_{m,pc})$$

where,

- n = number of principal components to consider. This is a parameter, hence it can be tuned.
- $x_{u,pc}$ = the coordinate of user u into the principal component pc.
- $rotation_{m,pc}$ = the eigenvector of movie m and the principal component pc.

Therefore, the equation of this models is:

$$Y_{u,m} = \mu + b_m(\lambda) + b_u(\lambda) + b_g(\lambda) + b_y + b_d + \sum_{pc=1}^{n} (x_{u,pc} * rotation_{m,pc}) + \epsilon_{u,m}$$

To begin with our calculations we obtain the residuals substracting the true ratings minus the prediction of our regularized linear model, we create a matrix of the residuals for each user (row) and movie (column). The missing values as explained before will be replaced by zeros.

Our resulting matrix looks like this:

Table 23: Extract of Residuals from UserId - MovieId Matrix.

1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
-2.964295	0.0000000	0	0	0.0000000	0.0000000	-0.4136615	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
0.000000	-0.8608151	0	0	-0.2328866	0.0379914	0.0000000	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	0.0000000	0	0	0
0.000000	0.0000000	0	0	0.0000000	0.0000000	-0.3875601	0	0	0

Now we perform PCA using the matrix of residuals with the following piece of code:

```
pca_edx_residuals <- prcomp(edx_model_11_dense)
```

This process can take several minutes (at least 1 hour), so we can check the results in the following object:

[14]This pdf section corresponds to section "VI.III Model 12 Average + Regularization Best Effects + PCA" of the R script

```
pca_edx_residuals <- readRDS("rda/pca_edx_residuals.rda")
```

saveRDS(dim_pca_x,"rda/dim_pca_x.rda") saveRDS(dim_pca_rotation,"rda/dim_pca_rotation.rda")

The PCA results consist of:

- A matrix **x** with the coordinates of users projected into each PC and dimensions 24115 x 5711.
- A matrix **rotation** of eigenvectors and dimensions 5711 x 5711.
- A vector **sdev** with the standard deviations of each PC.

The variance explained by each Principal Component is shown in the following graph:

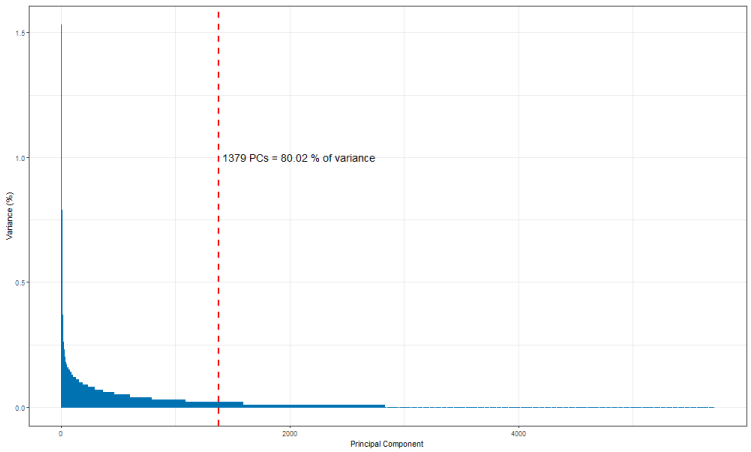


Figure 4: Variance accounted for each PC (Scree plot).

In our graph above we can see that 1379 components explain approximately 80% of the variance of our data. This means that the rest of the components account only the remaining 20%, thus we can leave them out and still train a model which fits the original data very accurately (as we previously illustrated with the tiger's image).

Now we will explore the first 2 PCs of the variables (movies). We will show how movies are projected on the first Principal Component (PC1) and the second Principal Component (PC2):

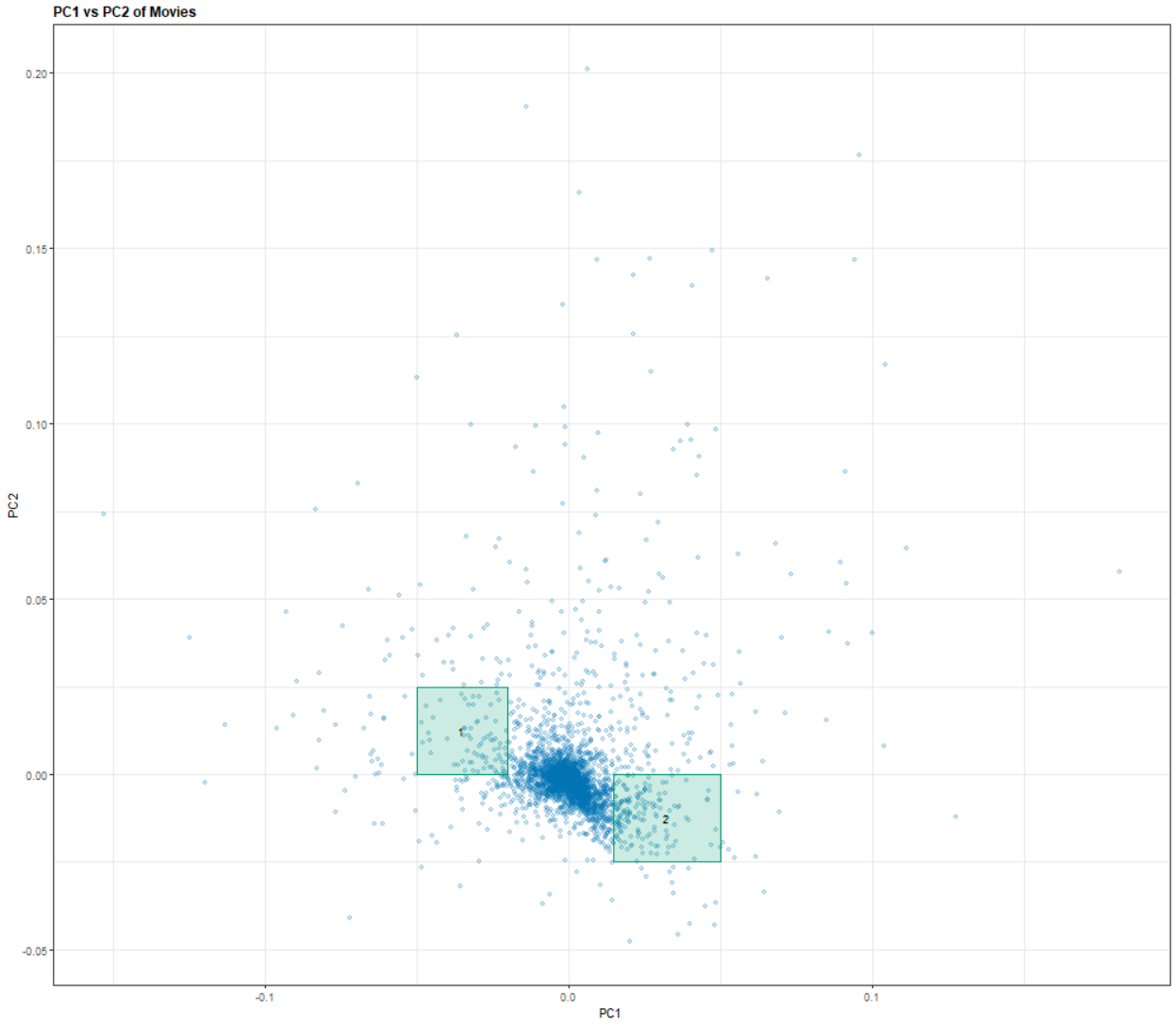


Figure 5: Movies projected on PC1 and PC2.

For illustration purposes, we will focus just on the movies in the first 2 cuadrants. The picture of the first cuadrant is:

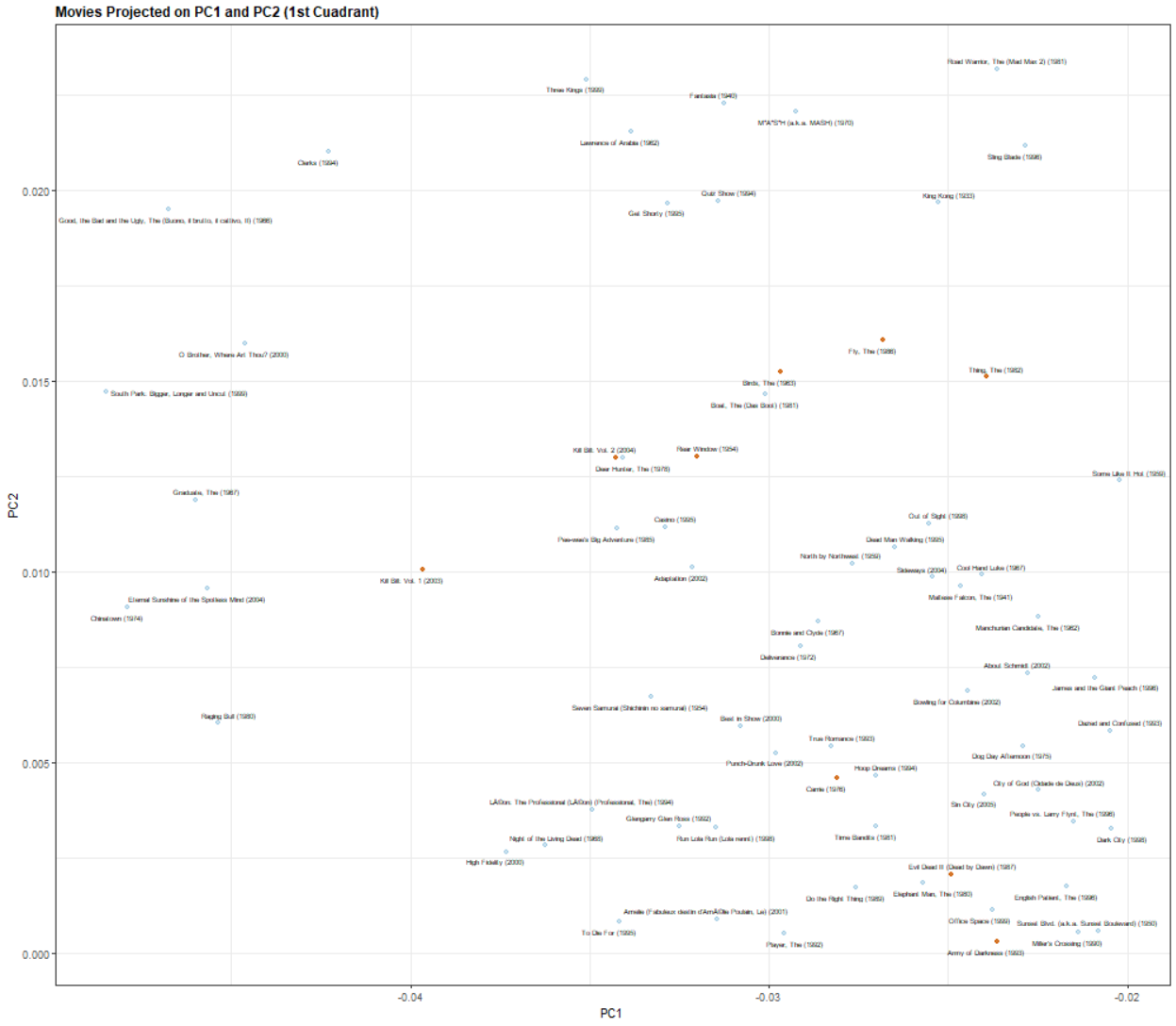


Figure 6: Movies projected on PC1 and PC2 (First Cuadrant).

We can observe that, from the point of view of PC1 and PC2, there are similarities among some gruesome movies like Kill Bill 1 and Kill Bill 2, Evil Dead II and Army of Darkness (Evil Dead III), and some horror movies like Hitchcock's Rear Window and The Birds and some others like The Fly, The Thing and Carrie.

The picture of the second cuadrant is:

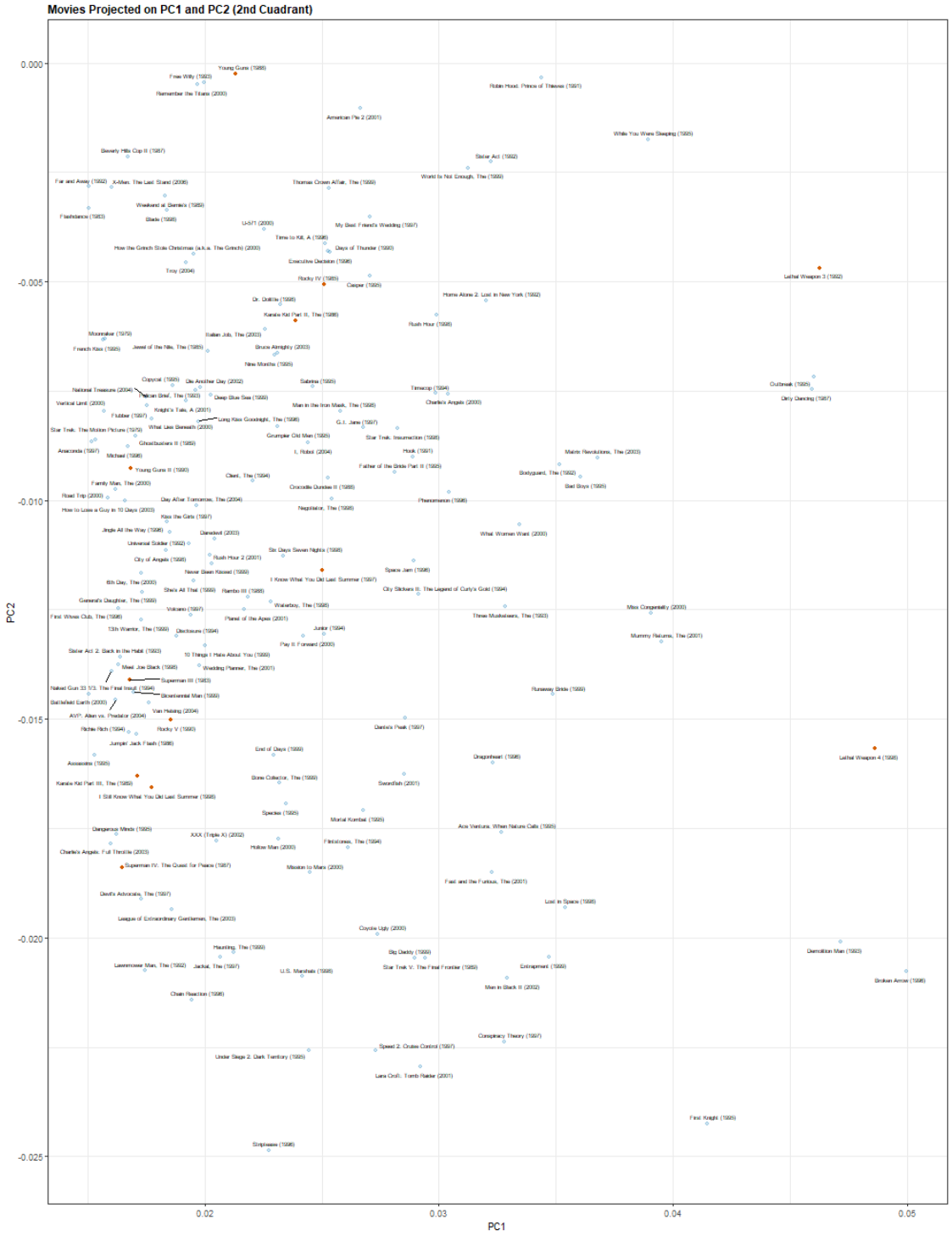


Figure 7: Movies projected on PC1 and PC2 (Second Cuadrant).

Here we observe many sequels like Karate Kid Part II and Part III, Lethal Weapon 3 and Lethal Weapon 4, I Know What You Did Last Summer and I Still Know What You Did Last Summer, Rocky IV and Rocky V, Superman III and Superman IV, and Young Guns and Young Guns II.

Note that despite we are showing only two PCs since higher-dimensions (specially more than three) are more difficult to visualize, we can detect some patterns in our data. We can use as many PCs as we need to make our prediction more accurate.

Now we are ready to make predictions using these results. Remember that we only used the best observations (number of ratings >= 100) in PCA. Therefore, for all the remaining movies and users for which we don't have a PCA we will predict only with the Regularized Global Effects equation. Note that the number of PCs to consider in this model is a *parameter*, thus it can be tuned. However, i did not use any tuning technique since the calculations were very expensive. For this model i defined 40 PCs which gives us the following rmse:[15]:

Table 24: RMSE of models 1 to 12.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488
8	average + movie + user effect (OOR correction)	0.8651772
9	average + all effects	0.8644178
10	average + all effects with regularization	0.8639582
11	average + best effects regularization	0.8639540
12	average + best effects regularization + pca	0.8338059

We can observe that this last model has an improvement of 3.49% over our previous model. Here are some results of models 11 and 12:

Table 25: Example of predictions of models 11 and 12.

user	movie	title	true rating	model 11	model 12
34	1	Toy Story (1995)	3.0	3.375434	3.694323
157	1	Toy Story (1995)	5.0	4.734081	4.734081
91	2	Jumanji (1995)	4.0	3.168754	3.145050
481	2	Jumanji (1995)	3.0	3.723372	3.672923
541	6	Heat (1995)	4.0	3.812804	3.881913
530	6	Heat (1995)	4.0	4.251571	4.251571
430	6874	Kill Bill: Vol. 1 (2003)	4.5	4.108840	4.108840
481	6874	Kill Bill: Vol. 1 (2003)	5.0	4.490061	4.604305
94	480	Jurassic Park (1993)	4.0	3.647870	3.859515
268	480	Jurassic Park (1993)	5.0	3.881632	3.881632

3.5.6 Expectation Maximization + Truncated SVD Model[16].

Now we will perform EM and truncated SVD using the **eimpute** function of the *eimpute* package. This function *"Efficiently impute missing values for a large scale matrix"* as explained in the RDocumentation.

We can perform EM + truncated SVD with the next piece of code:

[15]The code to obtain the rmse is in section "VI.III.IV Final Prediction" of the R script.
[16]This pdf section corresponds to section "VI.IV Model 13 EM + Truncated SVD" of the R script

```r
# Install package
if(!require(eimpute)) install.packages("eimpute", repos = "http://cran.us.r-project.org")
library(eimpute)

# We define rank= 40 for approximating the low-rank matrix:

rank <- 40
impute_matrix <- eimpute(edx_best_observation_dense, rank) # this might take 10-15 minutes
edx_em_svd_matrix <- impute_matrix[["x.imp"]]

# We assign the user and the movie ids to the name of the rows and columns, respectively:

colnames(edx_em_svd_matrix) <- colnames(edx_best_observation_dense)
rownames(edx_em_svd_matrix) <- rownames(edx_best_observation_dense)
```

Here is an extract of our low-rank approximation matrix:

Table 26: Extraction of user-movie matrix using EM adn truncated SVD.

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
8	3.775122	2.500000	2.967880	3.045211	3.000000	4.000000	2.705373	3.413097	2.901393	3.626875
10	3.174974	3.323997	2.944546	3.389261	3.128438	3.045664	3.000000	3.386666	3.465124	3.232114
13	3.775423	3.000000	3.024289	2.826213	3.062942	3.676802	3.046081	3.232827	3.491365	3.636127
18	3.000000	3.000000	2.599571	2.777535	1.000000	3.852150	2.500000	2.986784	3.503943	4.000000
19	4.073113	3.086415	3.448288	3.047579	3.000000	3.013860	3.778713	3.271568	2.772632	4.000000
30	5.000000	4.408288	4.000000	3.897089	3.987945	4.437596	4.986236	3.806352	3.362880	4.393979
34	3.846005	3.000000	4.000000	2.503261	3.000000	3.557167	2.977195	3.000000	3.000000	2.588530
35	3.000000	2.903018	2.946770	3.576333	3.068020	4.363749	2.914173	3.514600	3.280207	2.796093
36	4.000000	3.000000	3.000000	3.445679	3.236180	5.000000	3.150968	3.024788	2.780520	3.000000
38	3.486158	3.394425	4.068886	3.751635	3.799400	3.649723	4.149239	3.937765	3.832716	4.000000

Now we are ready to make predictions using these results. Remember that we only used the best observations (number of ratings >= 100) to estimate our low-rank approximation matrix with EM and truncated SVD. Therefore, for all the remaining movies and users that we don't have in our matrix we will predict only with the Regularized Global Effects equation. Note that the **rank** in eimpute is a *parameter*, thus it can be tuned. However, we will use the same rank as PCs of our previous model (rank = 40). This gives us the following rmse[17]:

[17]The code to obtain the rmse is in section "VI.IV.III Final Prediction" of the R script.

Table 27: RMSE of models 1 to 13.

ID	Method	RMSE
1	average	1.0612018
2	average + movie effect	0.9439087
3	average + genre effect	1.0184056
4	average + user effect	0.9783360
5	average + year effect	1.0500259
6	average + rating date effect	1.0575018
7	average + movie + user effect	0.8653488
8	average + movie + user effect (OOR correction)	0.8651772
9	average + all effects	0.8644178
10	average + all effects with regularization	0.8639582
11	average + best effects regularization	0.8639540
12	average + best effects regularization + pca	0.8338059
13	regularization + em + truncated svd	0.8210000

We can observe that this last model has an improvement of 1.54% over the regularization + pca model. Here are some results of models 12 and 13:

Table 28: Example of predictions of models 12 and 13.

user	movie	title	true rating	model 12	model 13
34	1	Toy Story (1995)	3.0	3.694323	3.846005
157	1	Toy Story (1995)	5.0	4.734081	4.734081
91	2	Jumanji (1995)	4.0	3.145050	3.046957
481	2	Jumanji (1995)	3.0	3.672923	3.319152
541	6	Heat (1995)	4.0	3.881913	3.777974
530	6	Heat (1995)	4.0	4.251571	4.251571
430	6874	Kill Bill: Vol. 1 (2003)	4.5	4.108840	4.108840
481	6874	Kill Bill: Vol. 1 (2003)	5.0	4.604305	5.000000
94	480	Jurassic Park (1993)	4.0	3.859515	4.760803
268	480	Jurassic Park (1993)	5.0	3.881632	3.881632

3.6 Ensemble

Finally, we will ensemble our two best algorithms, model 12 and model 13, to see if we can improve our prediction a little bit. Our final prediction will be estimated as the average of model 12 and model 13 predictions using this piece of code:

```
prediction_results <- prediction_results %>%
  mutate(ensemble = (avg_best_effects_regularization_pca + regularization_em_svd) / 2)
```

4 Results and Conclusions.

To sum up, we have trained a total of 14 models:

Table 29: RMSE of trained models.

ID	Method	RMSE	Description
1	average	1.0612018	rating average of all the observations in the dataset
2	average + movie effect	0.9439087	rating average of all observations plus bias due to movie effect
3	average + genre effect	1.0184056	rating average of all observations plus bias due to genre effect
4	average + user effect	0.9783360	rating average of all observations plus bias due to user effect
5	average + year effect	1.0500259	rating average of all observations plus bias due to year effect
6	average + rating date effect	1.0575018	rating average of all observations plus bias due to rating date effect
7	average + movie + user effect	0.8653488	rating average of all observations plus bias due to movie and user effect
8	average + movie + user effect (OOR correction)	0.8651772	rating average of all observations plus bias due to movie and user effect with out of range correction
9	average + all effects	0.8644178	rating average of all observations plus bias due to movie, user, genre, year and date of rating effect
10	average + all effects with regularization	0.8639582	rating average of all observations plus bias due to all effect with regularization
11	average + best effects regularization	0.8639540	rating average of all observations plus bias due to all effect with regularization on movie, user and genre effects
12	average + best effects regularization + pca	0.8338059	regularization model plus PCA
13	regularization + em + truncated svd	0.8210000	regularization model plus Expectation-Matimization and truncated SVD
14	ensemble	0.8110796	ensemble of regularization + pca and regularization + em + truncated svd

Note that our ensemble (model 14) has an improvement of 1.21% over the second best model (model 13). And an improvement of 23.57% over our first model.

- *Model 1* uses a baseline predictor: the **average of all ratings**. Thus, every prediction is the same no matter the movie or the user. This represents a naive approach.
- *Models 2 to 6* predicts based on **global effects separately**. These effects or biases are: movie, user, genre, premiere year and date of rating. These models demonstrate to have little improvement over our first model, and this makes sense since we are not taking into account the interaction among all these effects together.
- *Model 7 to 9* predicts based on a **combination of global effects**. This resulted in much more accurate models since we take into account the interaction among all the global effects.
- *Model 10 and 11* uses **regularization** in global effects to penalyze biases that were estimated with small sample sizes. But still, these models leave out an important variation: the similarities between groups of movies and groups of users. Here we used Cross-Validation (CV) to find the best penalty term of λ.
- *Model 12 and 13* uses different techniques of **matrix factorization** that helped us to find "latent patterns" between different groups of movies and users, which in the end led us to an important improvement in our prediction. To accomplish this we used Principal Component Analysis (PCA) and Expectation-Maximization (EM) with truncated Singular Value Decomposition (SVD). This last method was way faster and has a better result. Despite we did not tune the parameters *number of PCs* or *rank* we could have used Cross-Validation to find the best values of both parameters.
- *Model 14* **ensembles** the predictions from models 12 and 13 by estimating the average of both models. This final algorithm proved to be the best model in terms of RMSE:

Table 30: Best model based on RMSE.

	ID	Method	RMSE
14	14	ensemble	0.8110796