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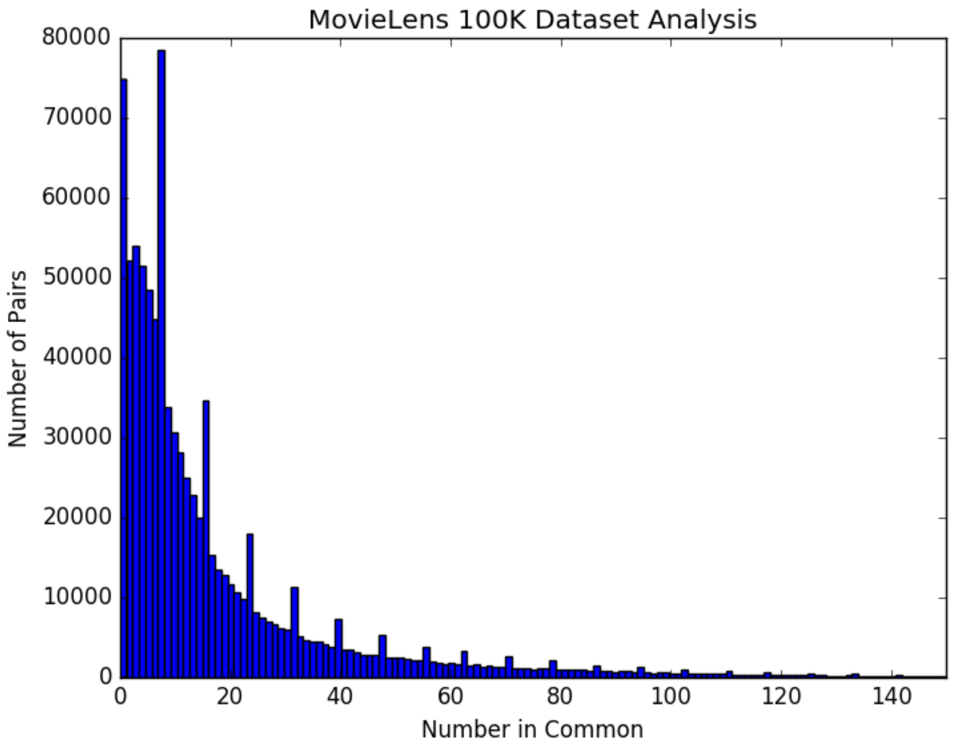
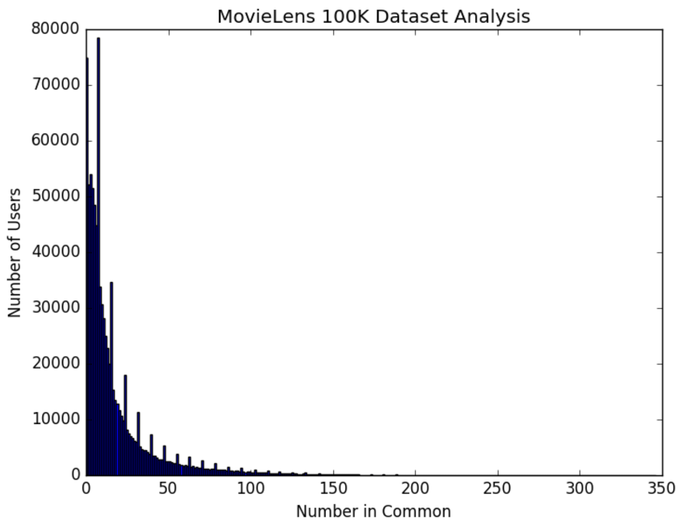
Assignment 4

## Problem 1

**A)** Mean number of common reviewed movies: **18.8079220449**
Median number of common reviewed movies: **10.0**





The above numbers and graphs were generated from code found in the file understanding_data.py. To run this file, enter in command line:

```
python understanding_data.py u.data
```

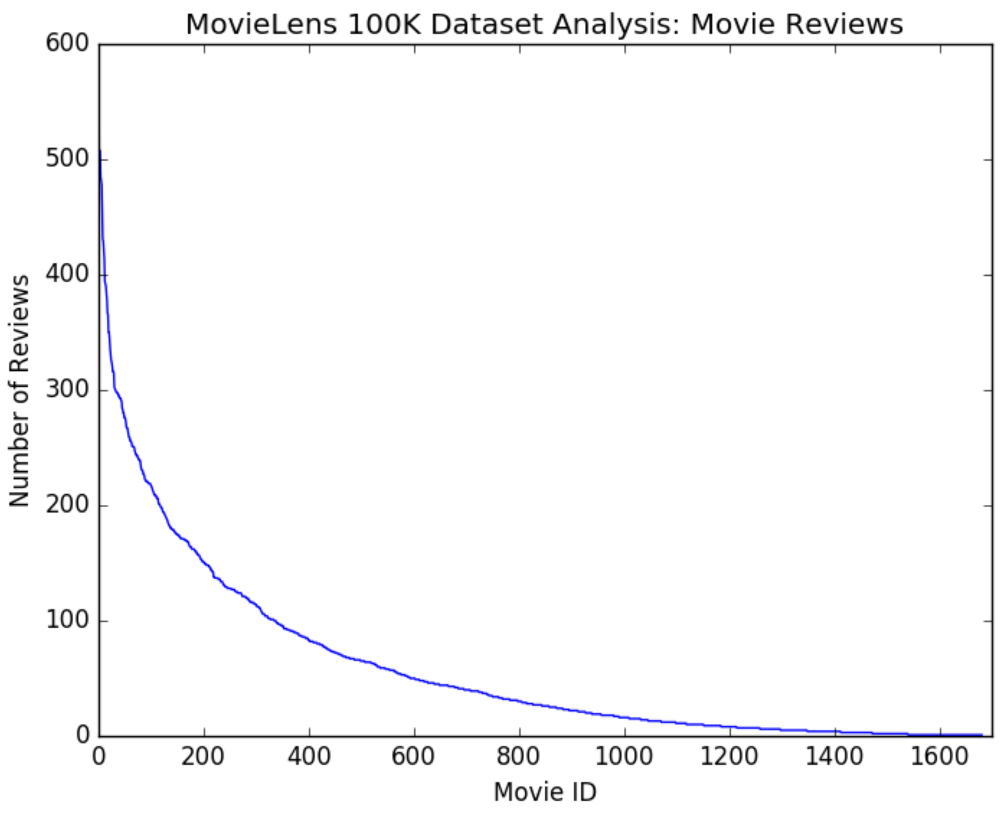
I created two histograms. The first histogram constrains the x-axis such that it focuses on the concentrated lower end of the distribution. I did this because I think it creates a more telling visual of the data, and is easier to read. The second histogram has an x-axis that goes up to 350, such that this graph covers the entire distribution. Because the right end of the distribution consists of outliers, where one given pair had a high number of common reviews, it is hard to see this data representation on the large-scale graph. That being said, it does more accurately represent the entire data representation, so I thought it was important to include it.

When designing both histograms, I set it such that the number of bins is the same as the number of individual common quantities. Meaning, each bar represents a distinct number of common movie reviews between a pair of users, and the height of the bar represents how many pairs of users had that same common quantity. I did this such that no quantities were aggregated, and that the histogram would accurately represent the distribution.

**B)** 141 movies have the minimum number of reviews (1 review). 1 movie has the maximum number of reviews (583). I think this distribution follows the general notion of Zipf's law. There are 1,682 movies, thus the film with the maximum number of reviews is ranked 1,682nd in the frequency table. According to the law, there should be 1,682 times more movies ranked first in the frequency table. In this case, there are 141 films with the minimum number of reviews, and only one film with the maximum number of reviews. Thus, this data distribution follows the skewed trend where higher ranked terms (more reviews) have fewer occurrences (fewer movies), but does not follow the law to the exact numerical definition. This trend can be very clearly seen in the graph below.

**Movie 50** had the maximum number of reviews with: **583 reviews**
The following movies had the minimum number of reviews with: **1 review**
['1653', '1655', '1621', '1627', '1626', '1625', '1624', '1579', '1343', '1507', '1505', '1618', '1619', '1616', '1614', '1613', '1363', '1543', '1548', '1601', '1603', '1604', '1606', '1156', '1557', '1525', '1526', '814', '1492', '1493', '1494', '1498', '1122', '1235', '1236', '1482', '1486', '1130', '1572', '1571', '1570', '1577', '1576', '1575', '1574', '830', '1582', '1583', '1580', '1581', '1586', '1373', '1584', '1457', '1458', '1587', '1595', '1596', '1593', '1599', '1447', '1452', '1453', '857', '852', '1476', '1309', '1559', '1681', '1680', '1682', '1461', '1460', '1310', '1533', '1536', '1678', '1679', '1674', '1675', '1676', '1677', '1670', '1671', '1673', '677', '1414', '1320', '1325', '1329', '1520', '711', '1669', '1668', '1667', '1666', '1665', '1663', '1661', '1660', '599', '1546', '1339', '1352', '1659', '1650', '1651', '1657', '1654', '1633', '1349', '1348', '1340', '1341', '1645', '1647', '1641', '1640', '1649', '1648', '1515', '1510', '1563', '1564', '1566', '1567', '1630', '1632', '1634', '1635', '1636', '1637',

```
'1638', '1366', '1568', '1569', '1561', '1562', '1565', '1201', '1364']
```



The above numbers and graphs were generated from code found in the file understanding_data.py. To run this file, enter in command line:
python understanding_data.py u.data

**Problem Two**

**A)** I think approach A is a more suitable solution to the issue posed by missing reviews. Users are only allowed to rate a movie from 1-5. Meaning, if the rating is set to be 0, it clearly represents a missing rating. In turn, if a user has rated a movie and another user has not, Manhattan Distance will always appropriately count this difference when measuring the distance between two users. With approach B, a missing rating will be substituted with the mean. There is a chance that this average rating is the same number as the rating of the user who actually rated the film. In turn, Manhattan Distance would mistakenly consider this as a similarity between two users, when in reality that does not accurately represent how they viewed the film. Approach B does not correctly distinguish unrated films from the pool of data, and in turn could consider erroneous similarities. Moreover, it is important to note when users have both chosen not to rate a given film, as it is telling of their profile. Approach A will correctly account for when users have both not rated a given movie, for they will both be 0.
For example, imagine the following two users rating 5 movies.

```
1) 1    1       3       1
2) 1            1
```

In this scenario, we are going to compare user 1 and user 2. With Approach A, user1 and user2's missing reviews would be substituted with 0s and would appear like below.

| | | | | |
|---|---|---|---|---|
| 1) 1 | 1 | 3 | 1 | 0 |
| 2) 1 | 0 | 1 | 0 | 0 |

In turn, the Manhattan Distance would be 1+2+1 = 3. This correctly captures the similarity that they did not review the fifth film. It also captures two key differences where user1 reviewed the film and user2 did not.

With Approach B, user1 and user2's missing reviews would be substituted with the mean rating, and would appear like below.

| | | | | |
|---|---|---|---|---|
| 1) 1 | 1 | 3 | 1 | 1.5 |
| 2) 1 | 1 | 1 | 1 | 1 |

In turn, the Manhattan Distance would be 2+.5 = 2.5. Because user2's substituted mean rating matched user1's rating in both cases, the algorithm interpreted these comparisons as two similarities and did not account for them in the distance. This method does not clearly distinguish unrated films, and the means of substitution can be mistaken as a matched rating. Moreover, both users were missing the 5th review, and had different substituted means. Though it truly was a similarity that they did not review a given film, this was counted as a difference within the distance.

In conclusion, Approach A ensures that unrated films have a unique numeric value; as a result, there cannot be false matches between user ratings when one user's substitution matches the other's true rating, and false mismatches when two users have different substituted means. As a result, this is a more accurate approach to calculating Manhattan Distance.

**B)** I think Pearson Correlation would be better for item-based collaborative filtering. Euclidean distance is helpful when you want to know the actual numeric distance between two given objects. However, in this scenario we simply want to know how similar two movies are to one another. As a result, Pearson Correlation would provide a better indicator, as it holistically analyzes trends, and produces a similarity measure. Moreover, Pearson Correlation is a great distance measures when comparing high dimensional vectors. Because each vector consists of 943 elements, Pearson Correlation would provide more telling info.

For example, imagine the following two vectors:

| | | | | | |
|---|---|---|---|---|---|
| 1) [1 | 1 | 3 | 1 | 3 | 4] |
| 2) [1 | 2 | 1 | 1 | 1 | 1] |

The Pearson's Coefficient of the above vectors is -.43
Euclidean Distance = $\sqrt{18}$

This coefficient represents the overarching relationship between the two vectors. As multidimensional vectors, this coefficient is far more telling and helpful in identifying similarity trends than a raw distance as found through the Euclidean method.

**Problem 3**
Fully implemented in user_cf.py and item_cf.py files. They can be run using the below format:

```
python user_cf.py <datafile> <userID> <movieID> <distance> <k> <i>
python item_cf.py <datafile> <userID> <movieID> <distance> <k> <i>
```

**Problem 4**
**A)** I chose to use MSE (mean squared error) to assess the accuracy of a given variant. MSE takes the difference between the actual rating and predicted rating, squares it, and then averages these values across the entire sample. For example, if you have a sample of 50 draws, you would take the first draw, find the squared difference between the actual and predicted, and then do the same for the following 49 samples. Once these squared differences are all summed, one can divide them by 50 and find the MSE across the entire sample. In a more formulaic form, for n draws in a given sample:

$$\text{MSE}_{\text{sample}} = \frac{1}{n}\sum(actual - predicted)^2$$

Given the following tests, I will take the 50 individual MSEs, and find the average MSE.
I thought it was important to not just capture how often a variant is incorrect, but to find the extent to which a variant is incorrect. Because ratings can be a range of numbers, not a binary system, one variant may be incorrect more often, but on average makes closer predictions. For example, variant1 could get a prediction right 50% of the time, but the other 50% it is on average off by 5 points. On the other hand, variant2 could only be right 40% of the time, but the other 60% it is only off on average by 1 point. MSE would be able to recognize that variant2, on average, returns closer results, even if it is not completely correct as often as variant1.

**B)** Null Hypothesis: There is no significant difference between the two variants' error measures. Unfortunately, I ran all of the tests in their entirety and did not store the error arrays for each variant. In turn, when I looked to analyze the statistical significance between the error measures, I did not have all of the necessary data. You can see from the graphs in each section that I did indeed run the tests in the entirety the first time however. I went to office hours and discussed with Ethan my options given time constraints. As a result, we determined that rerunning each variant with a smaller sample size, storing the results, and using these arrays to find pvalues was the best way to design my statistical test. This is an inherently limited approach, but looking at each of the graphs below, there aren't any major outliers in the dataset, so it provides a relatively accurate sampled representation of the larger distribution. In each section below, you will find a graph representing the full dataset for the variant, the average MSE, the subset of the MSEs I used for statistical analysis, and the resulting pvalues.

In order to calculate the pvalue I leveraged the Scipy's t-test for two independent samples. I called the following in command line where list1 and list2 are set as the outputted arrays for the corresponding variants.

```
        scipy.stats.ttest_ind(list1, list2)
```

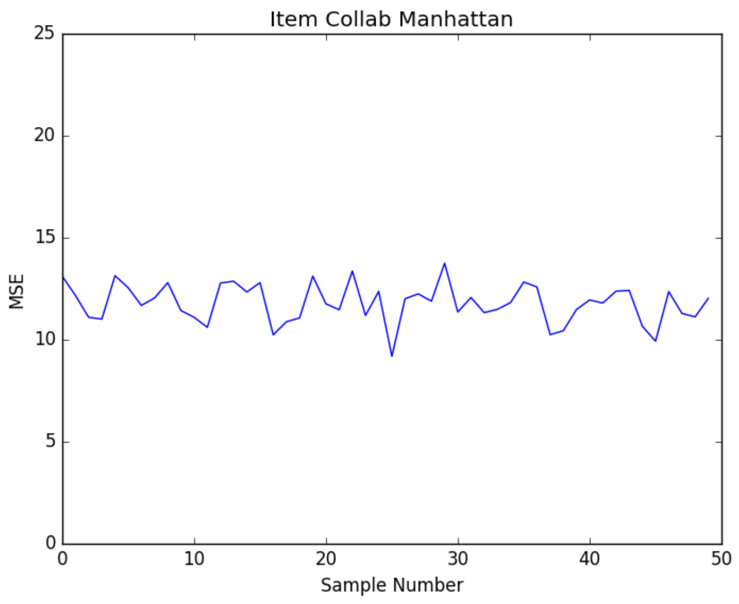
I will be using a 95% confidence interval, meaning if the pvalue is less than .05 (5%), then the difference in error is statistically significant

**C)** The following parameters were kept constant across the two comparisons:

datafile = u.data (samples are serialized), k = 5, iFlag = 1

iFlag was set to 1 for both variants so that the eligible dataset members were kept constant, and the entire testing set could be used within each variant. I thought allowing all data members to be used within the variant, including those with missing reviews, would provide more accurate, raw results of each approach. Filtering the data skews it such that it always has neighbors with reviews, and doesn't necessarily represent a variant's effectiveness with the entire, unfiltered dataset. I also chose to do k=5 neighbors because I hoped to provide a sufficient sampling of "similar" data points, while maintaining computational speed. I did not want to overfit my data and choose too low of a k, but I also did not want to extend the runtime or underfit the dataset. Instead of plotting one final graph comparing the average MSE per variant, I thought it would be more telling to have one graph per variant to determine whether the variants act similarly or not. It's imperative to know if any outliers, etc. impacted the given variant's MSE. As a result, these graphs are a visual depiction that can be used to gauge variant similarity.

**Item-Based where Distance =1 (Manhattan):**

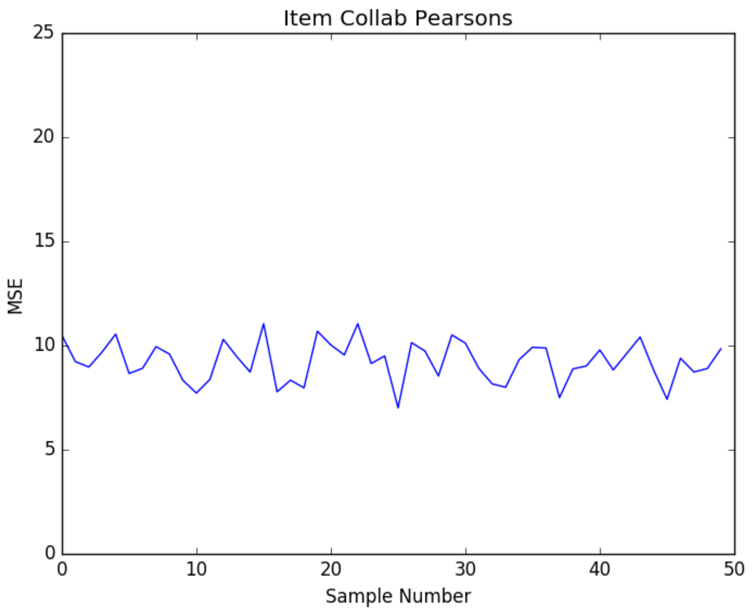


This experiment was conducted by running: python item_experiment.py u.data 1 5 1

The average MSE across the 50 samples was **11.794**. In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data:
[13.11, 12.17, 11.1, 11.01, 13.14]

**Item-Based where Distance = 0 (Pearson):**



This experiment was conducted by running: python item_experiment.py u.data 0 5 1

The average MSE across the 50 samples was **9.2296**. In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data:
[10.49, 9.23, 8.97, 9.7, 10.55]

P-Value = 0.0033823287820232417

Pearson correlation performed better than Manhattan distance because 9.2296 < 11.794. This result is statistically significant because the pvalue < .05, showing the error distributions are relatively different. In turn, we reject the null hypothesis.

Meaning, Pearson correlation produced more accurate predictions than Manhattan distance with a lower average MSE. This correlates to my intuitions in 2b, as I expected Pearson's correlation to be a more effective means in determining the similarity between two high-dimensional vectors that Euclidean distance. Euclidean distance echoes the inherent concern of Manhattan distance, as they both focus on the raw value distance between each element, and sum it across elements. Pearson's correlation further manipulates these calculations to provide a more overarching analysis on the similarity between two vectors, ranging from -1 to 1. Because this data is extremely high dimensional, I assumed the aggregated approach of Manhattan distance would have compromised performance compared to Pearson correlation.

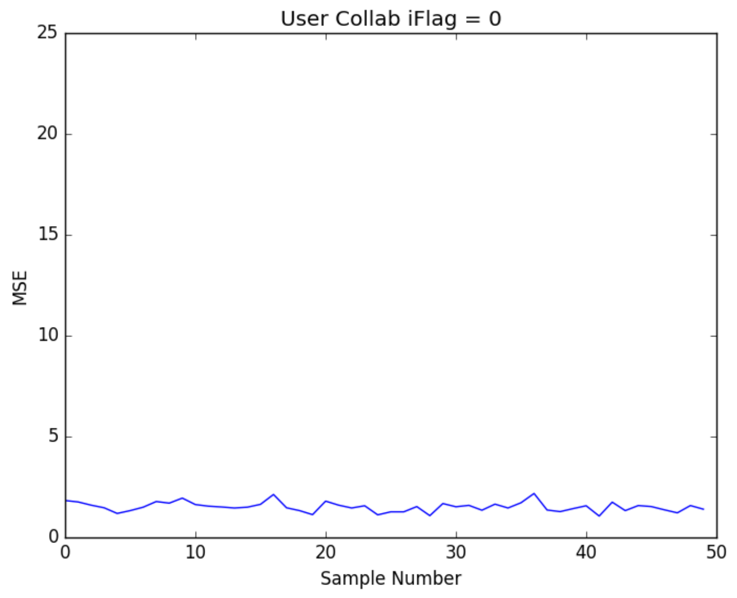
**D)** The following parameters were kept constant across the two comparisons:

datafile = u.data (samples are serialized), distance = 0 (Pearson's), k = 5

Pearson's distance was used for both variants so that the distance measure was kept constant, and vectors were compared in the same way. If the distance was Pearson for one, and Manhattan for the other, results may be skewed depending on which measure is better suited for the dataset. Computing two vector's Pearson's relationship is faster than finding Manhattan distance. Because each test required 50*100 = 5,000 iterations, I chose to expedite it in this way. Also, since it's highly dimensional data, I assume these will return better results, as done in part C. I also chose to do k=5 neighbors because I hoped to provide a sufficient sampling of "similar" data points, while maintaining computational speed. I did not want to overfit my data and choose too low of a k, but I also did not want to extend the runtime or underfit the dataset.

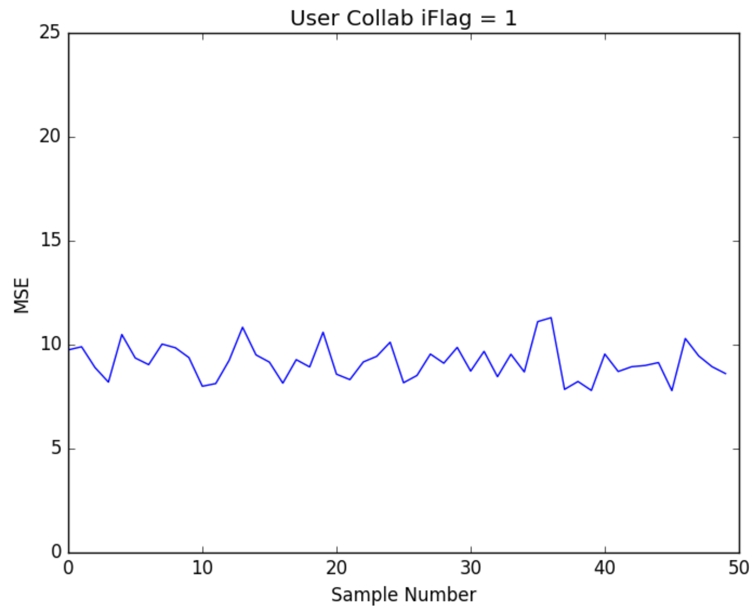
Instead of plotting one final graph comparing the average MSE per variant, I thought it would be more telling to have one graph per variant to determine whether the variants act similarly or not. It's imperative to know if any outliers, etc. impacted the given variant's MSE. As a result, these graphs are a visual depiction that can be used to gauge variant similarity.

**User-Based where iFlag = 0:**



The experiment was conducted by running: python experiment.py u.data 0 5 0
The average MSE across the 50 samples was **1.5154**. In the figure to the left, each individual sample's MSE is plotted against the iteration number.
Statistical Analysis Data:
[1.83, 1.76, 1.6, 1.47, 1.19]

**User-Based where iFlag = 1:**



The experiment was conducted by running: python experiment.py u.data 0 5 1

The average MSE across the 50 samples was **9.1886.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.
Statistical Analysis Data:
[9.75, 9.9, 8.9, 8.2, 10.49]

P-Value = 6.5196659023822529e-08

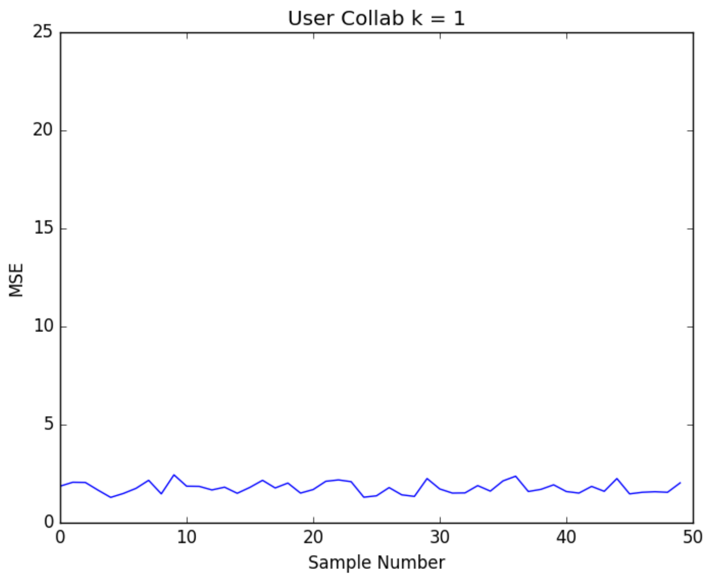
iFlag = 0 performed better than iFlag =1 because 1.5154 < 9.1886. This result is statistically significant because the pvalue is far less than .05, showing the error distributions are incredibly different. Given my model, I can say with 95% confidence that Pearson correlation performs better than Manhattan distance for item-based collaboration filtering. In turn, we reject the null hypothesis.

When the iFlag is 0, meaning missing reviews cannot be included in the k closest neighbors, the algorithm produces more accurate predictions and lower average MSE. This is what I expected because there are so many missing reviews that often times the predicted value defaults to 0. By ensuring only similar reviewed movies are within the k closest neighbors, this algorithm ensures that the predicted value is a non-missing rating, and in turn produces more accurate predictions with a lower error rate.

**D)** Based on the above tests, the best settings are: distance = 0 (Pearson's), iFlag = 0.
These conditions were held constant for the below User-Based Collab Filtering tests.

Instead of plotting one final graph comparing the average MSE per variant, I thought it would be more telling to have one graph per variant to determine whether the variants act similarly or not. It's imperative to know if any outliers, etc. impacted the given variant's MSE. As a result, these graphs are a visual depiction that can be used to gauge variant similarity.

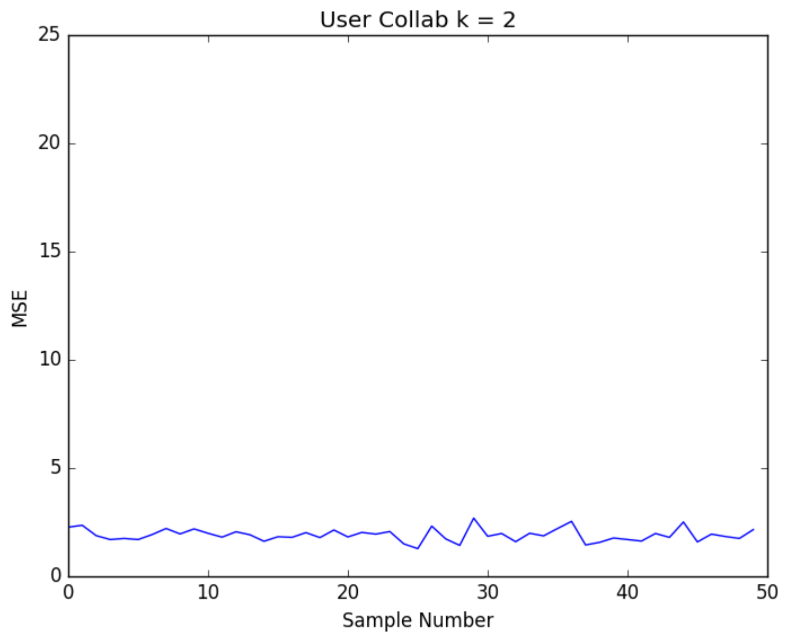
**User-Based K=1**



The average MSE across the 50 samples was: **1.7734.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data:
[1.86, 2.06, 2.05, 1.66, 1.29]

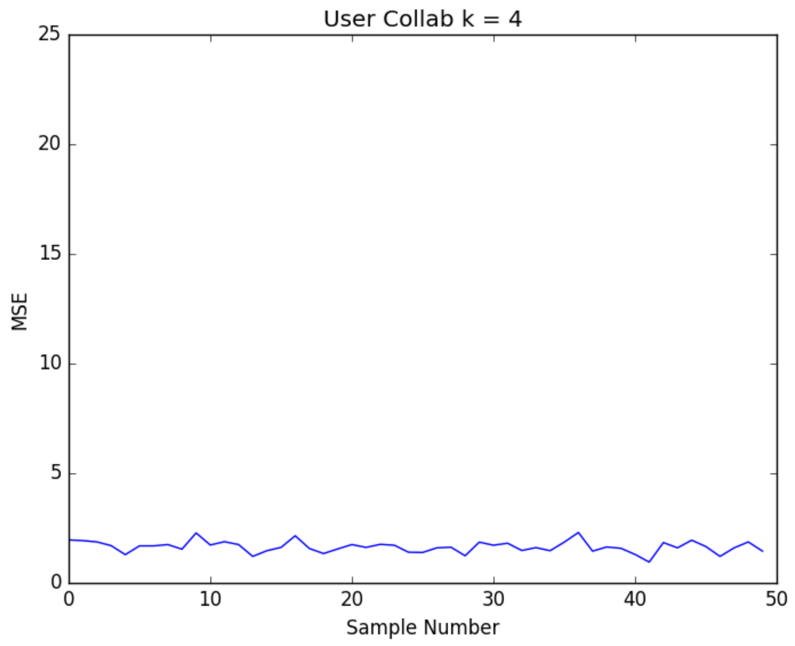
## User-Based K=2



The average MSE across the 50 samples was: **1.9098.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data: [2.27, 2.36, 1.88, 1.7, 1.75]

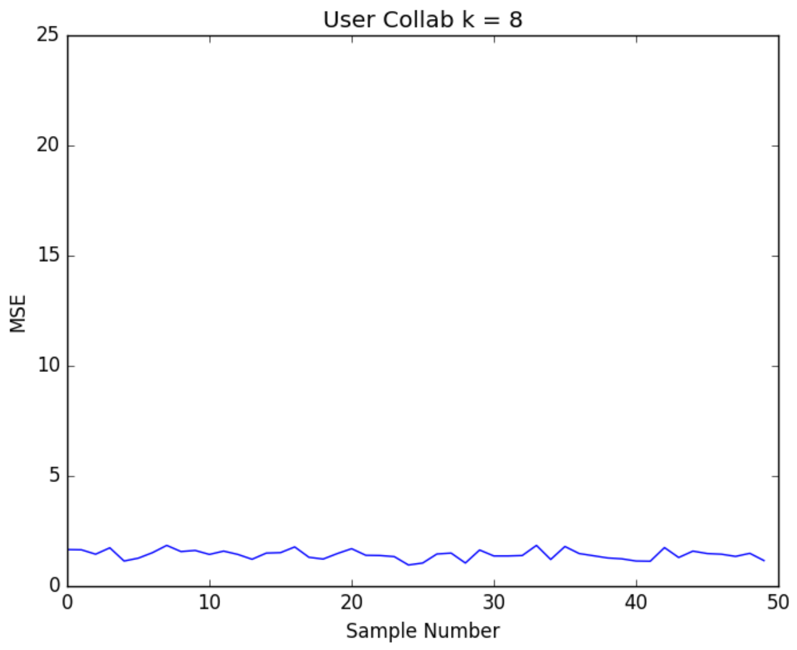
## User-Based K=4



The average MSE across the 50 samples was: **1.6458.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data: [1.96, 1.93, 1.87, 1.7, 1.29]

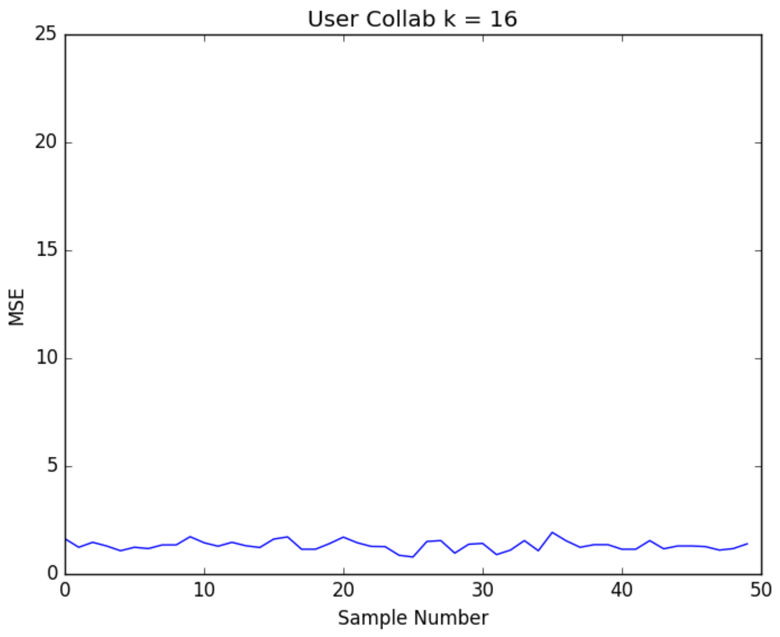
## User-Based K=8



The average MSE across the 50 samples was: **1.4336.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data: [1.66, 1.65, 1.45, 1.74, 1.14]

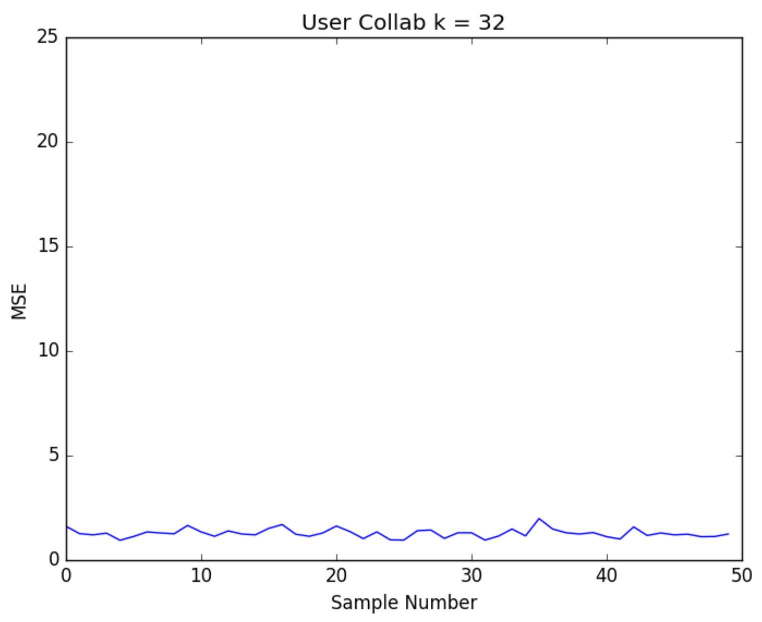
## User-Based K=16



The average MSE across the 50 samples was: **1.3246.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data: [1.64, 1.24, 1.47, 1.3, 1.08]

## User-Based K=32



K=32: the average MSE across the 50 samples was: **1.2876.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data:
[1.62, 1.27, 1.21, 1.29, 0.95]

K = 32 has the lowest error rate of 1.2876.
Below are the pvalues when comparing the error distributions of the adjacent k values.

P-Value (k=32, k=16): 0.60283718813952569
P-Value (k=32, k=8): 0.12577503005628449
P-Value (k=32, k=4): 0.018422208517155279
P-Value (k=32, k=2): 0.003049667929751951
P-Value (k=32, k=1): 0.020439977478433111

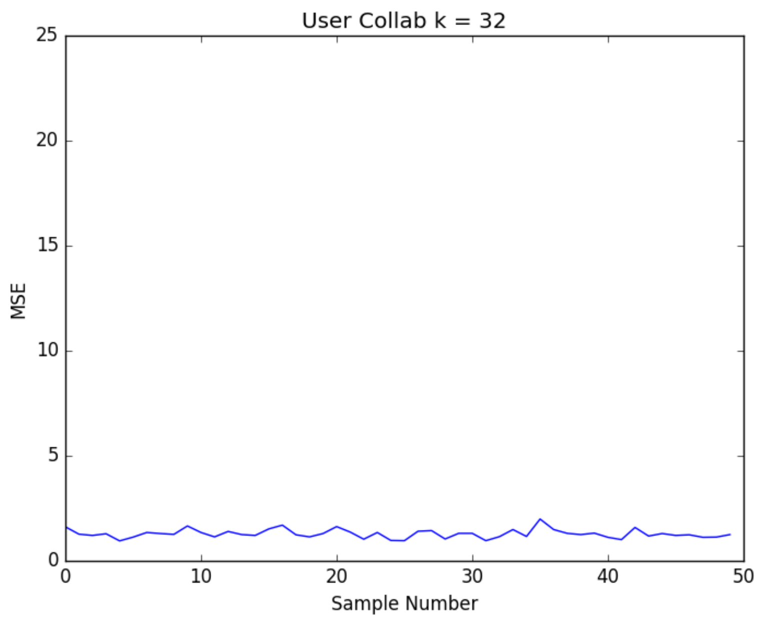
While k=32 produces the lowest average MSE, its error distribution is not significantly different than that of k=16 and k=8 because the corresponding pvalues are greater than .05. In turn, we fail to reject the null hypothesis, and cannot assert that k=32 performs significantly better than k=16 or k=8. That being said, the pvalues are lower than .05 for k=4, k=2, and k=1, meaning its error distribution is significantly different than theirs. In turn, under our model, we can reject the null hypothesis regarding these k values, and assert that k=32 performs significantly better than k=4, k=2, and k=1.

**F)** Based on the above tests, the "best" settings are: distance = 0 (Pearson's), iFlag = 0, k =32. These conditions were applied to the following two tests.

Instead of plotting one final graph comparing the average MSE per variant, I thought it would be more telling to have one graph per variant to determine whether the variants act similarly or not.

It's imperative to know if any outliers, etc. impacted the given variant's MSE. As a result, these graphs are a visual depiction that can be used to gauge variant similarity.

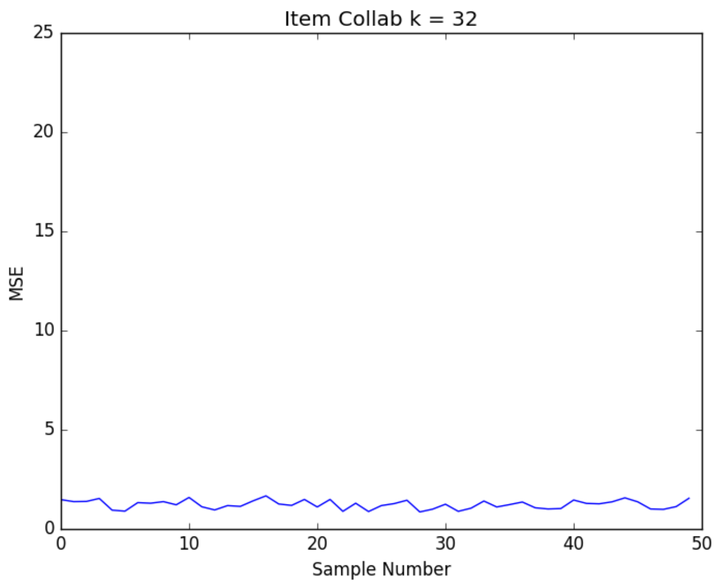
## User-Based With Best Settings



The average MSE across the 50 samples was: **1.2876.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data:
[1.62, 1.27, 1.21, 1.29, 0.95]

## Item-Based With Best Settings



The average MSE across the 50 samples was: **1.235.** In the figure to the left, each individual sample's MSE is plotted against the iteration number.

Statistical Analysis Data:
[1.48, 1.38, 1.39, 1.54, 0.95]

P-Value = 0.60606922146646069

Under “optimal” conditions, item-based performed better than user-based because 1.235< 1.2876. However, this result is not statistically significant under my model because the pvalue > .05, showing the error distributions are not significantly different. In turn, we fail to reject the null hypothesis, and cannot say with confidence that item-based performs better than user-based.