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Analyzing large scale trajectory data to identify users with similar behavior

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ANALYZING LARGE SCALE TRAJECTORY DATA TO IDENTIFY USERS WITH SIMILAR BEHAVIOR

by

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ABSTRACT

In today’s society, social networks are a popular way to connect with friends and family and share what’s going on in your life. With the Internet connecting us all closer than ever before, it is increasingly common to use social networks to meet new friends online that share similar interests instead of only connecting with those you already know. For the problem of attempting to connect people with similar interests, this paper proposes the foundation for a Geo-social network that aims to extract the semantic meaning from users’ location history and use this information to find the similarity between users. Once the similarity scores are obtained, the results are examined to extract the groups of similar users for the Geo-social network. Computing similarity for a large number of users and then grouping based on the results is a computationally intensive task, but fortunately Apache Spark can be leveraged to execute the comparison and clustering of users in parallel across multiple computers, increasing the computation speed when compared to a centralized version and working quickly enough to suggest friends in real time for a given user.

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TABLE OF CONTENTS

Page

LIST OF ILLUSTRATIONS

Figure Page

NOMENCLATURE

Symbol	Description
t	Threshold for Maximum Time Between Two Locations
α	Threshold for Minimum Similarity Between Two Users
φ	Time Passed Between Two Trajectories

1. INTRODUCTION

1.1. BACKGROUND

Today, mobile devices with Internet are extremely common and almost all users of these devices utilize some form of location-based service at some point, such as using Google Maps to find nearby restaurants, getting directions from your current location or checking in on Facebook or any other social network. Along with these devices being so frequently used, more people are using GPS devices to record their location trajectories. All of this means that there is more data than ever to take advantage of and analyze. By looking at this large amount of trajectory data, it is possible to look at two different users GPS trajectory data in order to determine if two users would be compatible.

However, people in various locations will never come up as similar if their GPS data alone is considered. By looking at the locations in the real world it is possible to extract some semantic meaning of the places visited by the user. When the semantic meaning is obtained it is possible to identify users that have an overlap in interests, even if their actual geographic location does not overlap [1][2]. By giving a similarity score based on this semantic overlap, users can be clustered into groups that will identify similar social groups. These social groups can then be used to match similar users together for the Geo-Social network.

For this to be feasible, a similarity comparison between two trajectories that runs within a reasonable amount of time is needed. After retrieving the similarity score for all of the users in the dataset, a graph where users are connected if their similarity score is above a threshold can be created. By examining this graph, it is possible find groups of users that are connected to identify users who will most likely be compatible. By using

Spark, we can find the similarities between all users, which is a very computationally heavy task for a centralized approach. Afterwards, Spark is also used to identify the groups within the user dataset. To ensure that the groups contain users who are all very similar, the approach to be used will find maximal cliques in the graph. This means that all users in the group will be similar to every other user in the clique.

1.2. RELATED WORK

Two works [1] and [2], performed work that the similarity comparison used in this paper draws inspiration from, finding similar user based on location history. The objective of [1] is to estimate similarity between two users using the semantic meaning of the location data. [2] Looks to mine user similarity based on the GPS trajectories taken from the real world. The work from each of these papers lend themselves nicely to being used for creating a geo-social network and the approach in this paper is similar for the similarity comparison stage. One disadvantage to the method used in [2] that is addressed in this paper, is the problem of looping locations within the users' location history. The Bron & Kerbosch algorithm originally presented in [3], as well as improvements on the algorithm presented in [4] are used for finding all maximal cliques within the graph of users.

1.3. PROBLEM DEFINITION

The main goal of this work is to give a similarity score to the trajectory data of two different users and use the results to identify all cliques within the graph of users to set the stage for creation of a geo-social network. Before continuing, there are some terms that will be used frequently and are important to know in order to understand the approach.

A trajectory is a sequence of locations with information about the time spent at each location and the time it takes to travel between locations in the sequence. Below is an example of a trajectory.

$$Traj = p_1, p_2, p_3, \ldots p_n \colon where\ p_i = (location\ name, stay\ time, travel\ time) \tag{1}$$

Trajectories tell a lot about the users who submit them and are vital to the algorithm. Therefore, it is important to get a firm grasp on the idea of what a trajectory is and how it is visualized other works. Below, Figure 1.1 shows an example of some made up trajectories to be compared. By looking at these two trajectories and using our algorithm we can give a score that will give an idea of how similar the two trajectories are.

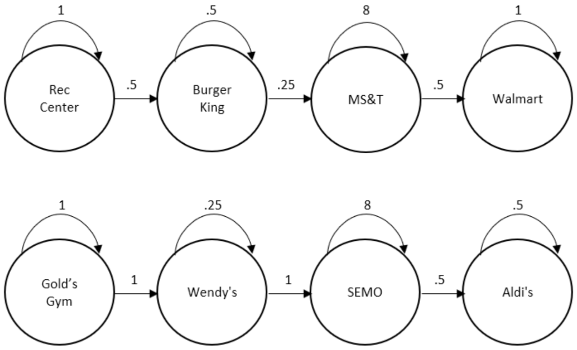


Figure 1.1. Two Different Trajectories

After finding the similarity score between all users, a graph will be constructed where the graphs vertices represent users, and an edge between nodes indicates a similarity over the chosen threshold, α. The approach that is used in this paper focuses on grouping the users by finding the cliques in the graph. A clique is a subset of vertices, all adjacent to each other, within a graph. Figure 1.2. below shows an example graph with 3 cliques.

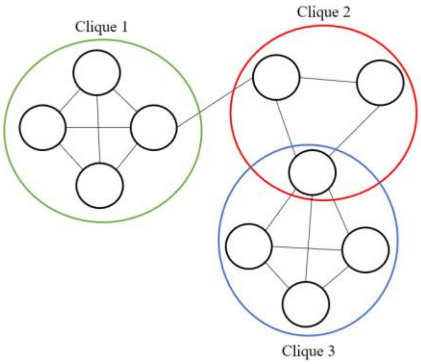


Figure 1.2. Example Three Clique Graph

2. SEMANTIC TRAVEL MATCHING

2.1. MAXIMUM TRAVEL MATCHING

The approach used in [1] involves finding and measuring the length of the maximal travel matches found when comparing two user's trajectories. A regular travel match between two sub-sequences is found when a given constant maximum time difference between stay times, t, and two sub-sequences of trajectories $T_1(a_1, a_2, \dots a_n)$ and $T_2(b_1, b_2, \dots b_n)$ meet the following conditions

1. $\forall\ i\ \epsilon\ [1, k]: a_i = b_i$

2. $\forall\ i\ \epsilon\ [2, k]: The\ travel\ time\ between\ two\ locations\ a_i\ and\ a_{i+1}\ and$ $b_i\ and\ b_{i+1}\ is\ less\ than\ the\ maximum\ time\ difference\ constant\ t.$

Furthermore, a travel match is maximal if it has no more locations that match within the time constraint to be added on to the start, somewhere in the middle, or the end of the travel match.

Finding the maximum travel match between two sequences tells a lot about how similar they are. If two people have a long match in things that they do throughout the day and how long they do these things, it is very likely that they share similar interests or at the very least a similar lifestyle. One important thing to note is that using the maximum travel match to compute the similarity score causes the score to have no upper bound, even if two trajectories are matching exactly, they could always be matching with one more location added.

2.2. SEMANTIC TRAVEL MATCHING

As discussed previously, the goal is of the algorithm is to be able to compare location trajectories that do not share any geographic overlap. Simply checking if the names of the locations match may not suffice for finding an actual match. For example, if two people are both college students at different schools that spend 10 hours and school then return immediately home every day, simply comparing the value of Missouri S&T to Mizzou or their GPS values would not indicate a match, although for all intents and purposes, these two locations are semantically similar, and certainly indicate a level of similarity just below an exact match. To address this problem, a tree to represent a semantic location hierarchy will be constructed that can be referenced when comparing two different trajectories. The lower level you go on the tree, the closer the semantic meaning of the locations and as you climb the tree the descriptions become more general.

For example, Taco Bell and McDonalds would both be at the same level of the tree under a node named Fast Food Restaurants which might be under an even more general category labeled Food. Creating a tree that had all possible values we would need would take an extremely long time and would be a whole research project on its own, so for now a simple semantic hierarchy tree that demonstrates the effectiveness of this approach will be used for the current implementation of the algorithm.

In the future a much more in-depth tree will be a requirement. One project has already worked on creating a web that links together the English language together based on the semantic similarity of words called WordNet [5]. The use of WordNet will eventually replace the sample semantic hierarchy tree in the future when looking to scale outward and accept even more types of location input data, but for the remainder of this paper, the simple tree shown in Figure 2.1. below will be used.

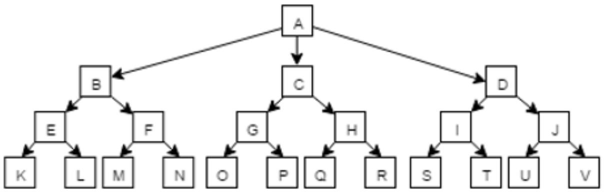


Figure 2.1. Sample Location Hierarchy Tree

For the sample tree above, the top node A is null. B, C, and D represent Food, Recreation, and Education categories. The next row (in order) represents Fast Food, Groceries, Fitness, Baseball, College and K-12. The lowest row (in order) represents McDonalds, Burger King, Walmart, Aldis, Gold’s Gym, Rec Center, Yoga Planet, Busch Stadium, Batting Cage, Missouri S&T, Southeast Missouri University, Rolla High School and Mark Twain Elementary.

The semantic travel matching is performed at each level of the tree (aside from the level 0 null node). The score obtained at the end of the comparison of each level is adjusted based on how far down the tree the current level is. For example, during the comparison at the lowest level, Missouri S&T and SEMO would not indicate a match, but at the next highest level, their locations would both be simplified to College and would be a location match. The score adjustment for each level is shown in the equation below.

$$\text{Adjusted Score} = \text{Score} * 2^{level-1} \tag{2}$$

To measure the similarity of two trajectories, there is a max allowable difference in time t and a time passed for each trajectory, φ, which is initially 0. Then starting at the initial location for each user, a check is done to see if the locations at the current are the same. If they are, add to the matching score and move to the next location, adding stay and travel time to each trajectories time passed. If the locations do not match, there are two possible paths. The first is to compare the current location of the first trajectory with the next location of the second trajectory, incrementing the second trajectory's time passed. The second is if the next location for the second user cannot be reached without surpassing max difference in time. The check will move T_2 to the last matching location and increment T_1 to the next location, increasing T_1's time. Once this process is over, the algorithm moves up a level of the semantic hierarchy tree and repeats, this time adding less points for each match than the lower level.

2.3. SEMANTIC TRAVEL MATCHING EXAMPLE

To demonstrate, a comparison between T_1 and T_2 , which are shown above as the top and bottom trajectories respectively in Figure 1.1. above. The comparison will be run with an initial matching score = 8 at level = 1, and max time difference of 2. First, the algorithm compares Rec Center and Golds Gym and it is a match, and the score is increased. The T_1 time is equal to 1.5 and T_2 to 2. Compare Burger King and McDonald's, which are not equal at the current level, so move T_1 to next T_2 location with time of 3.25. Next, comparison between Burger King and SEMO not a match, so we move to next T_2 location, surpassing the given t. So now, T_1 goes to MS&T with time 2.25 and T_2 goes back to McDonalds with time 2. They are not a match so T_2 goes to SEMO with time 3.25. SEMO and MS&T do not match so move T_2 to Aldi's with time 11.25. The max time difference has been reached and now the algorithm moves back to SEMO and move, T_1 to Walmart with time 10.75. Max time difference has been reached so move T_2 to Aldi's with time 11.25. Finally, compare to Walmart and it is not a match so finish for this level, with score 8. Now the matching score is adjusted for the current level, which keeps it at 8. If continued, the process would then be repeated moving up one level one the semantic hierarchy tree. After each level is calculated the score for each level is then combined as the final similarity score between the two users.

It can be seen how this approach would be computationally intensive and impractical for a large amount of data with a centralized approach. That is where Spark comes in. Multiple comparisons can be computed in parallel using a Spark DataFrame with our trajectory comparison algorithm as a user defined function that is executed between each pair of users at a given level in our dataset at the same time. In this way, it is possible to not only spread out the comparison of users, but also each individual hierarchy level between the nodes in the Spark cluster.

2.4. ISSUE OF LOOPING LOCATIONS

Throughout the day, it may be very common for users to visit the same location multiple times. For example, the user leaves his home to go to school, then returns home for lunch and heads back to school again until finally heading home for the day. The similarity comparison algorithms given in [1] and [2] does not deal with this issue and seeing as this would likely be a frequent scenario when analyzing the entire day of users, the similarity comparison in this paper has been modified to be able to handle looping locations. When constructing the adjacency matrix used to find the maximal length path, each repeat location will have its own node in the graph instead of looping caused from returning back up the tree. Figure 2.2. shows and example of a looping trajectory.

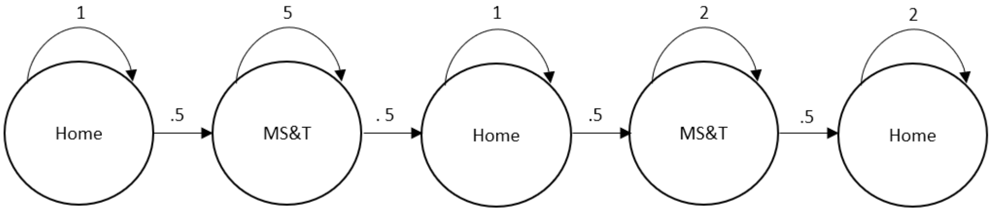


Figure 2.2. Looping Location Trajectory

3. MAXIMAL CLIQUE FINDING

3.1. BRON-KERBOSCH ALGORITHM

After computing the similarity between all users, the graph of users will be constructed to leverage graph theory to find the cliques within the users. Each node in the graph will indicate a user in the dataset, and an edge between two nodes will indicate a similarity score over a certain threshold, α. Within this graph, the goal is to find all the groups of users that are fully connected to each other, which indicates that their locations throughout the day are semantically similar.

After first testing a naïve approach for clique finding, the Bron-Kerbosch algorithm has proven to be the best method to use when finding all cliques within the user similarity graph. This approach was chosen because, although it may have a higher complexity than other clique finding algorithms, it is one of the best for finding all maximal cliques in practice [4]. Another benefit of using the Bron-Kerbosch algorithm, or any clique finding as our method for grouping similar users together, is that this type of “clustering” does not require any cluster validation because it is already guaranteed that every user in the clique is above the similarity threshold with all other users in the group.

The Bron-Kerbosch algorithm is a simple backtracking procedure that works recursively to solve sub problems using three sets of nodes. The three sets are called *R*, *X*, and *P*. *R* contains the nodes that are required to be included in the partial clique. *X* contains the nodes that are going to be excluded from the clique. *P* contains the nodes that have not yet been considered. The algorithm finds maximal cliques that include all the vertices in *R*, some of the vertices in *P* and none of the vertices in *X*. In each recursive call to the algorithm, *P* and *X* are disjoint sets where the union contains the vertices that form a clique when they are added to *R*. When *P* and *X* are both empty, there are no more nodes that can be added to *R* and *R* is output as a maximal clique [3].

In the first call of the algorithm, *R* and *X* are set to the empty set and *P* is the set of all vertices in the graph. Each recursive call considers the vertices in *P* in turn. For each vertex *v* chosen from *P*, a recursive call is made in which *v* is added to *R* and all neighbors of *v* are considered, in order, to find the clique one vertex at a time. Then *v* is moved from *P* to *X* to stop it from being considered in future cliques and then moves to the next vertex within *P*.

If the graph running the Bron-Kerbosch algorithm has a large amount of non-maximal cliques, the algorithm will degrade to be fairly inefficient due to making a recursive call for each clique even if it is not maximal. Since this may happen quite often in a graph that models social networks, it makes sense to modify the approach to adjust for this issue. The modified approach works by adding a pivot vertex chosen from the union of P and X. Since any maximal clique must have either the pivot vertex or a node which is not adjacent to the pivot, the number of vertices that need to be searched will be lowered in most common cases [4].

Further specializing the Bron-Kerbosch for finding social groups, an additional check that R is greater than two before reporting it as a clique is made. This will ensure that only groups are being reported as opposed to every edge in the graph, which would be far too many to be useful. Since the goal of each call of the Bron-Kerbosch algorithm is to find all cliques a given user is a part of, another modification is made to initialize *P* as all of the neighbors of the user that is being considered. This is due to the fact that any clique a user is in has to be composed entirely of its neighbors.

Algorithm 1: Modified Bron-Kerbosch Pivot

```
BKPiv(R, P, X):
    If P and X = {} and Length(R) > 2:
        Return R as a maximal clique
    Select a pivot vertex $u \in P \cup X$
    For vertex v in $P \setminus$ Neighbors(u):
        BKPiv( $R \cup \{v\}$, $P \cap$ Neighbors(v), $X \cap$ Neighbors(v))
        $P = P \setminus \{v\}$
        $X = X \cup \{v\}$
```

3.2. BRON-KERBOSCH EXAMPLE

Since the Bron-Kerbosch algorithm is key for constructing the geo-social network, an example of running through the procedure will be given for the example graph given in Figure 3.1. below. In this example, cliques of size two are returned to clearly show how the algorithm runs normally, but as mentioned previously, the program implementation will not return these “edge” cliques.

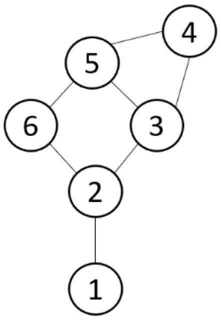


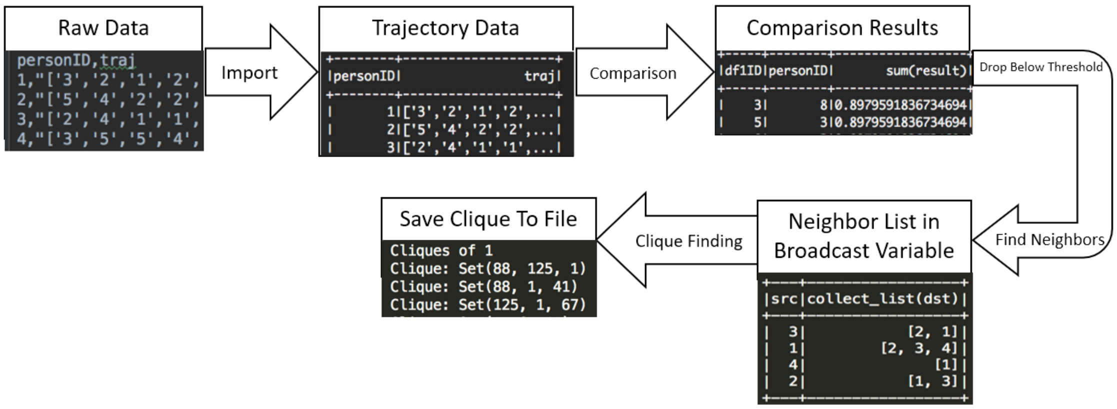
Figure 3.1. Example Graph for Bron-Kerbosch Algorithm

The initial call will have the sets as *R* = {}, *X* = {}, *P* = {1, 2, 3, 4, 5, 6}. The pivot u is chosen as 5 from *P* U *X*. Now there are 3 nodes that will be iterated over in *P* \ N(u): 5, 2, 1. The first iteration of the loop *v* = 5. The recursive call is made with *R* = {5}, *P* = {3, 4, 6}, *X* = {}. Now, either 3 or 4 will be chosen as the pivot and two second recursive calls for 6 and which of 3 or 4 that was not chosen as the pivot. In the end, these calls will return the cliques of {3, 4, 5} and {4, 5} as well as adding 5 to *X* to no longer be considered and removing it from *P*. In the second iteration of the original call *v* = 2 will make a recursive call where *R* = {2}, *P* = {1, 3, 6}, and *X* = {}. In the end, this call will eventually make three second recursive calls that will return {2, 6}, {2, 3}, and {1, 2} as cliques. As before, node 2 is then added to *X* and removed from *P* to be no longer considered. The last iteration will have *v* = 1. It will make the first recursive call, where *R* = {1}, *P* = {}, and *X* = {4}. Since *P* is empty and *X* is not, it will not return any cliques and the Bron-Kerbosch algorithm completes.

3.3. PROGRAM SPECIFIC IMPLEMENTATION DETAILS

The storage of graph information is put together with the idea of using the Bron-Kerbosch algorithm. The neighbors for each node are collected and stored in Spark broadcast variable so these neighbor lists can be accessed at any time from any node in the cluster. The users that are actually a part of the user graph after dropping all connections below the similarity threshold are saved in another Spark broadcast variable so that only valid nodes are considered. As briefly mentioned before, the neighbors of the user being currently analyzed for cliques is found from the broadcast variable and sent as *P* when the clique finding function is called. This ensures that no irrelevant cliques are considered. The Bron-Kerbosch algorithm is called using a Spark user defined function on each node in the user graph so cliques for each user can be found. Each clique a node is a member of is written to a file, so the groups a user is a part of can be easily accessed later for creating the Geo-Social network.

Below in Figure 3.2. is a complete overview of the process the program goes through from trajectory input data to outputting the cliques.



```
personID,traj
1,"['3','2','1','2',
2,"['5','4','2','2',
3,"['2','4','1','1',
4,"['3','5','5','4',
```

```
+--------+--------------------+
|personID|                traj|
+--------+--------------------+
|       1|['3','2','1','2',...|
|       2|['5','4','2','2',...|
|       3|['2','4','1','1',...|
```

```
+-----+--------+------------------+
|df1ID|personID|       sum(result)|
+-----+--------+------------------+
|    3|       8|0.8979591836734694|
|    5|       3|0.8979591836734694|
```

```
+---+-----------------+
|src|collect_list(dst)|
+---+-----------------+
|  3|           [2, 1]|
|  1|        [2, 3, 4]|
|  4|              [1]|
|  2|           [1, 3]|
+---+-----------------+
```

```
Cliques of 1
Clique: Set(88, 125, 1)
Clique: Set(88, 1, 41)
Clique: Set(125, 1, 67)
```

Figure 3.2. Complete Process Overview

4. EXPERIMENT AND RESULTS

4.1. EXPERIMENTAL DESIGN

To test the approach, the two crucial phases of the similarity grouping are tested separately. This is due to the fact that when testing for a large number of users, performing some transformations on the data in Spark on a single computer was very time consuming, and not representative of the actual time it would take to compute the similarity between all users and to use the similarity results to find all maximal cliques within the graph. To help avoid some of this issue, the testing was divided into two portions. The first testing the similarity comparison and the second testing the clique finding approach. Goals for future testing involve utilizing Spark on a cluster so that the large transformations can be performed. Comparing the execution of each algorithm on a large amount of data with a centralized version is an important result to show that a Spark approach is preferred, however, it is not realistic that a Geo-Social network would constantly receive 100,000 users at the exact same time that all need to be computed.

Another set of tests that are much more applicable for implementing a Geo-Social network is testing the time it takes to compute the similarity for a single new user and to find cliques of the new user. These tests are much more realistic and show that a Geo-Social Network is feasible to be run in real time after all of the heavy similarity calculations have been done offline.

4.2. GRAPH GENERATION

As real-life input graphs for the clique finding will likely resemble a social network, testing on a uniform randomly generated graph is not the best approach. A uniform random graph gives a large overestimation of the stress that would be put on the clique finding algorithm when compared to real user data due to the substantial number of connections between users all over the graph. A uniform random graph does not model users and their communities very well and gives the clique finding algorithm little to work with in finding meaningful groups. Generating a different type of graph in order to test the algorithm properly would be a better approach. A simple graph to model social networks and clearly test the effectiveness of the clique finding algorithm is the Relaxed Caveman graph [6]. This graph is essentially a ring of cliques linked to form a connected graph. Additional connections between cliques are also added to mimic a real network as well as test the algorithm with a slightly more complicated graph. We can adjust some parameters when generating the relaxed caveman graph, such as the connection probability between cliques, the density of these connections and the minimum and maximum of the sub-components.

4.3. TESTING RESULTS

Despite not utilizing the full power of Spark by using only a single computer, the results of the experiments were still very promising for the Spark implementation. The biggest issue are the expensive DataFrame transformations, and when those are removed from the equation, the ability of Spark to utilize multiple threads showed over the centralized approach. However, this is a very real issue for the future and it will need to be tested on multiple nodes to see if the data transformations are sped up simply by scaling out, or if more efficient transformations need to be found. The results for single user addition into the network were also favorable and show that running this approach in real time for construction of a Geo-Social network is possible.

4.3.1. Similarity Comparison Results. Similarity testing for the full set of users is an extremely computationally heavy task. In a true Geo-Social network this part of the process would take place offline on a large cluster to handle the amount of data and calculations that need to be done in order to find the similarity between all users at each level of the hierarchy tree. Although the goal was to test for the same increments of users as the clique testing, it was only feasible to test up to 50,000 users due to the very long run time. The results obtained are in Figure 4.1. Although this would take place offline and the time would not be as much of an issue, it would still be good to look for improving the efficiency of the similarity comparison itself which at this point is somewhat outdated. Using multiple nodes would yield a very large increase in speed due to the fact the DataFrame that has to be used to contain all of the rows for each pair of users at each level in the tree becomes massive very quickly as the number of users grow. It is impossible to store this huge table in main memory on a single computer and leads to a slowdown of the algorithm.

4.3.2. Clique Finding Results. The clique finding process had less issues than the similarity comparison, and the times were quite fast. For very low number of users the centralized approach is slightly faster than the Spark version, but as the number of users increase it can be quickly seen the benefits of parallelizing and using multiple threads. The overhead for setting up the Spark program seems to take most of the time for the test cases examined while finding the cliques for all users is quite fast due to the modified Bron-Kerbosch.

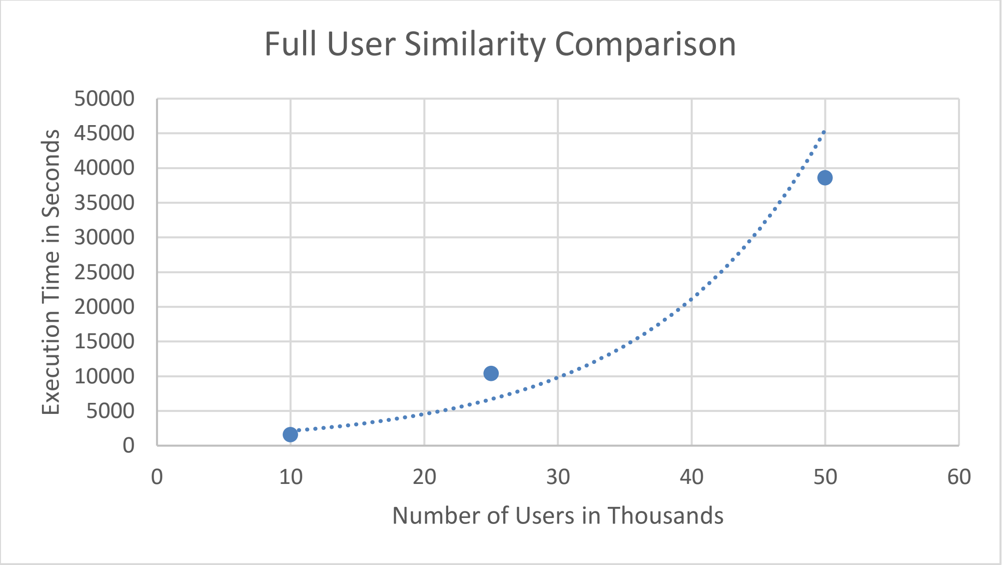


Figure 4.1. Full Similarity Comparison

Results for Clique Finding are in Figure 4.2. It is also important to note again that the power of multiple nodes is not being used and finding the cliques for each user is a task that can be distributed across a cluster because finding the cliques of a given user is not dependent on anything besides the list of neighbors, which is stored in a broadcast variable that can be accessed from any node. In the future, when the neighbor list is large, and a cluster is being used, it would be better to only send the neighbor lists of the users being analyzed to the correct node.

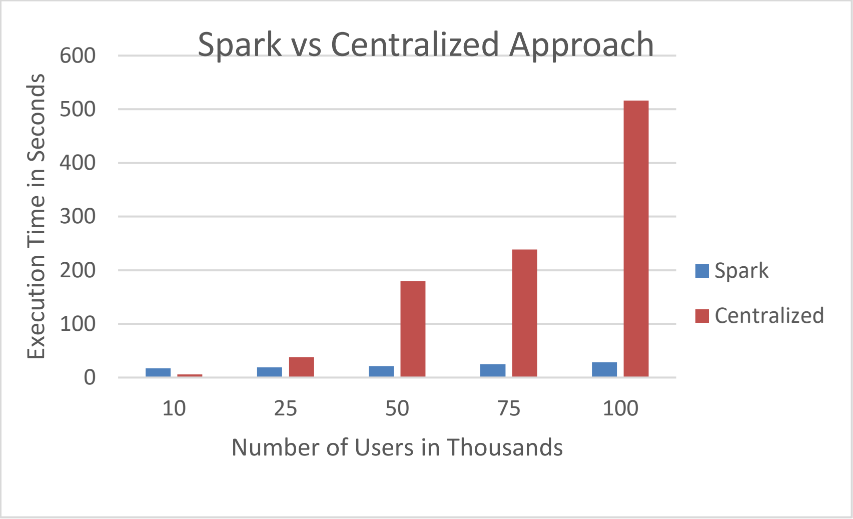


Figure 4.2. Comparing Spark with Centralized for Clique Finding

4.3.3. Single User Addition. The time it takes to add a single user into the network is very import to ensure it is realistic to run the Geo-Social network in real time. Adding a single user for clique finding takes almost no time given that the neighbors have already been found. Increasing the number of users does not increase the time to find a particular user’s cliques due to the fact that the goal is still simply to find the cliques they are in. Increasing the number of users will only increase the search space (neighbors of the given user) by a negligible amount in the context of the Bron-Kerbosch algorithm. Results are below in Figure 4.3.

Adding a single user for similarity takes a bit longer but still a reasonable amount of time for a real time application. Increasing the number of users obviously has a much higher effect here, due to the fact a comparison must be made with every other user. The results can be seen in Figure 4.4. In the future, when using more nodes with Spark, these single comparisons can be spread out between the cluster decreasing the computation time.

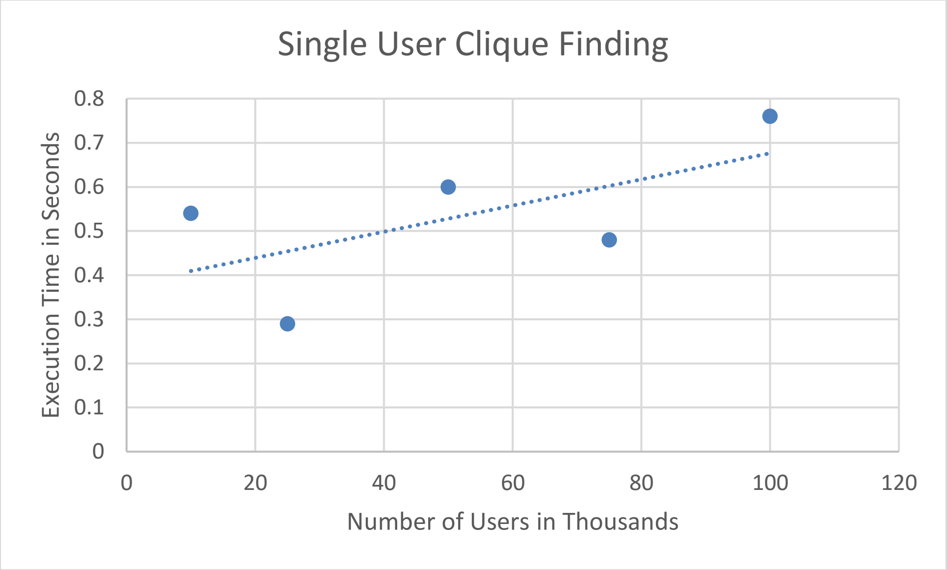


Figure 4.3. Single User Clique Finding Results

To get real time results with a very large number of users, it would be an option to allow users to control how long they would like to search for similar users depending on if they would rather have faster matches or more quality matches.

For these results, keep in mind that the overhead of setting up the Spark program takes about 15 seconds, so the clique finding itself takes less than a second and the similarity comparison takes about 30 seconds for 100,000 users. The results show the time to actually perform the task after the Spark program has been set up. When combining the two approaches, it is clear that the similarity comparison is where to focus further efforts to decrease the runtime of the algorithm. Looking at possible ways to further parallelize the similarity comparison could also be an option for improvement. The results are shown in the chart in Figure 4.5.

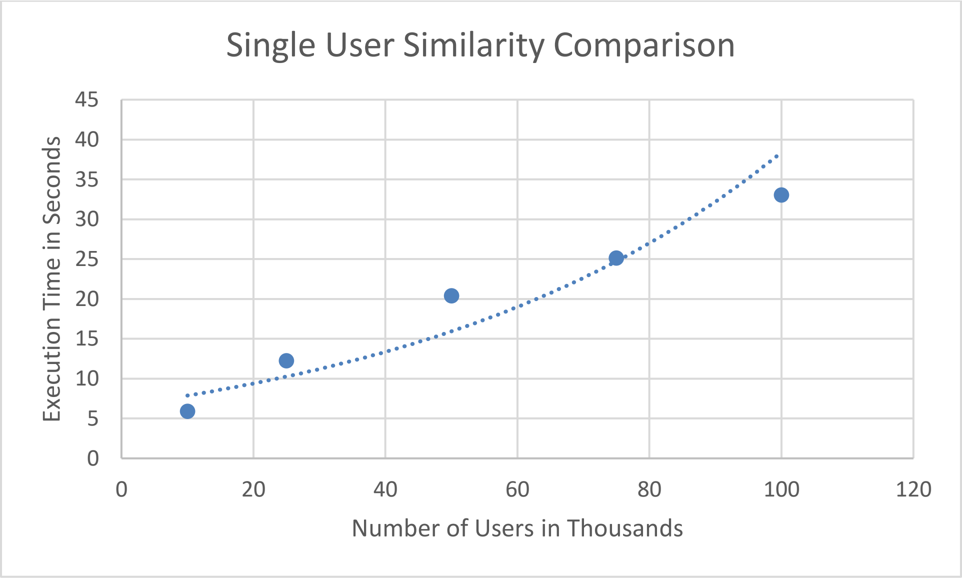


Figure 4.4. Single User Similarity Results

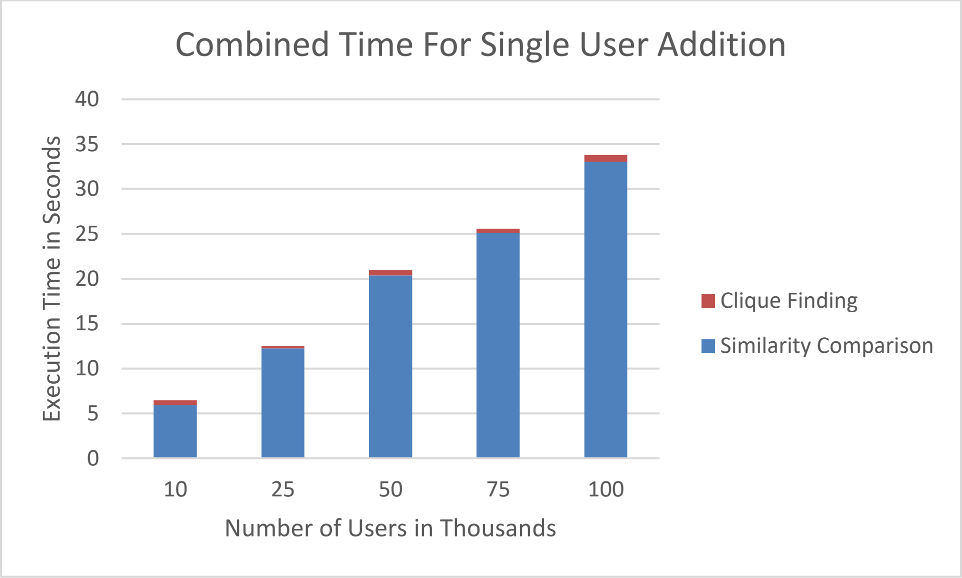


Figure 4.5. Full Process Single User Addition

5. CONCLUSIONS

5.1. FUTURE WORK

Through this project, a great deal has been learned about how to use the Spark framework to perform our desired computation on a large dataset. Currently, the largest limiting factor for computation time is manipulation of the Spark DataFrames to get the data in a format to be entered to the algorithms and intermediate processing of the results rather than slow execution of the algorithms themselves. If this manipulation can be reduced, great improvements in speed would result. These manipulations may be running slowly because large datasets are being operated on using a single computer with a limited main memory. When the main memory is full, the process slows down considerable as a large amount of swapping is needed to work with all of the data.

As mentioned previously, implementing the program in a cloud environment is the next major goal that will make a dramatic difference in the number of users that can be analyzed. Since the approach is designed to utilize this framework, the results would be greatly improved when the true benefits of Spark are used.

Additionally, there is another version of the Bron-Kerbosch algorithm that looks at the ordering of the recursive calls to minimize the number of calls that are made. The order of the recursive calls is found by looking at the degeneracy ordering of the subgraph that is being considered. The degeneracy ordering approach can also be combined with pivoting to get a further optimized approach for finding cliques in graphs that have the structure of a social network. In the future, switching to using this combined approach will undoubtedly increase the speed of clique finding.

When the program is running more smoothly over multiple nodes, generating slightly more complicated graphs to test the clique finding algorithm is also a good step forward. Stochastic block model graphs are frequently used for creating graphs containing communities, without being as rigid as the relaxed caveman where every “community” is a standalone clique [7]. Another benefit of testing on this type of graph, is it will allow for multiple cliques in the same community to be grouped together, if desired, to obtain different levels of similarity for groups.

Another approach that could be considered is instead of using the fairly rigid clique finding would be using a K-Distance Cliques approach. This algorithm detailed in [8] allows cliques to be composed of all users which are reachable with *k* jumps instead of just 1 jump required by a standard clique. This could allow for granularization of cliques by being able to identify general communities with higher values of *k* and more specific groups with lower values of *k*.

5.2. FINAL THOUGHTS

This paper successfully implements a parallel version of the similarity comparison algorithm in Spark as well as develops a modified version of the Bron-Kerbosch clique finding algorithm. Once the combined Spark program is implemented in a cloud environment, the scale which can be handled will increase greatly. The clique finding algorithm is working correctly for observed test cases and outputs all cliques that each user is a part of. Although there are some issues with the speed of parts of the process, the single user addition is fast enough, even on a single node, to run at real time for the creation of a Geo-Social network. With this information it will be possible to construct a geo-social network to connect users with similar interests together, even if their locations are far apart.

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VITA

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