ABSTRACT

SCHOLCOVER, FEDERICO. Using a Finite Mixture Model-Based Clustering Approach to Identify Move and Wait Strategies (Under the direction of Douglas J. Gillan).

Telerobotic platforms can be sent to places human cannot or should not go. They can explore space or search a collapsed building for survivors while keeping the human operator safe. However, distance between the human operator and the platform induces latency – a gap in time between when the operator sends a command, the platform executes the command, and when the operator receives feedback about the command’s execution. This latency negatively impacts task performance, and operators assume different strategies to compensate for increased latency. The strategy is known as the “Move and Wait” strategy, where operators make increasingly piecemeal movements as latency increases. The operators will move a little, wait to see the results, and then move again. Detection of strategy use has relied on coarse measures: visual inspection or trial-level outcomes, such as the proportion of time spent waiting. These measures do not allow for the detection of strategy use in-the-moment. We cannot say that a participant spent the first part of a trial using a strategy before transitioning to a different strategy. There is additional anecdotal evidence to suggest the existence of an intermediary strategy which current measures would be unable to detect. The work here addresses these issues by developing a novel method to define strategy use, by adapting the PRONET technique to continuous data. Continuous movement data was transformed into discrete clusters, using finite mixture models, and the transitions between these clusters were passed to a Pathfinder algorithm. Results demonstrate (1) this methods utility and (2) at supports the existence of the three aforementioned movement strategies.
Using a Finite Mixture Model-Based Clustering Approach to Identify Move and Wait Strategies

by
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DEDICATION

To the countless friends I have made throughout my life, in Florida and in North Carolina. I hope each of you know how important you are to me.
BIOGRAPHY

Federico “Freddy” Scholcover was born in Buenos Aires, Argentina and immigrated to the United States at the age of 4. Freddy grew up in Coral Springs, Florida where he developed a passion for wearing flipflops (as all Floridians should). Freddy earned a pair of B.S. degrees (with honors) from the University of Central Florida in 2014 before joining NC State’s Human Factors & Applied Cognition doctoral program. Freddy spent his time at NC State doing a little bit of everything: researching, teaching, working in industry, mentoring, networking. Now, he can include “graduating during a global pandemic” to that list. Freddy has accepted a position as a Postdoctoral Research Scholar with Arizona State University’s Center for Human, Artificial Intelligence, and Robot Teaming.
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INTRODUCTION

Imagine a collapsed building where survivors are likely trapped beneath the rubble. A rescue team needs to be able to get into the structure to locate and extract the victims of the collapse. However, the unstable structure poses a risk to the rescue team, as there is a risk for a secondary collapse. One hundred and thirty-five rescuers died while searching through rubble after the 1985 Mexico City Earthquake (Casper, Micire, & Murphy, 2000). How can we rescue survivors while minimizing the risk to the rescue crew (Casper & Murphy, 2003)? Telerobotic platforms (i.e. robots operated remotely by a human) allow humans to bring their presence and their expertise into a dangerous and/or distant environment. These platforms can explore space (Lester & Thronson, 2011), or the ocean (Eustice, Singh, Leonard, Walter, & Ballard, 2005), send a surgeon to a new location (Marescaux, Leroy, Rubino, Smith, Vix, Simone, & Mutter, 2002), and keep search and rescue teams safe (Murphy, Tadokoro, Nardi, Jacoff, Fiorini, Choset, & Erkmen, 2008).

Although such robots are useful, many issues emerge in the act of extending a human operator’s reach into a new location. Some of these issues are design-based, such as a limited field of view or failures to understand where the tool is oriented in space (for a review, see Chen, Haas, & Barnes, 2007). An unavoidable issue is based on the physical constraints of the task environment. When the operator and tool are far apart, there are delays between human input and tool/robot response, and between tool/robot response and audiovisual feedback. These communication delays, known as latency, cause a new set of performance issues (for a review, see Sheridan, 1993).

Latency always increases task difficulty: subjective workload increases (Lu, Zhang, Ersal, & Yang, 2019), tasks take longer (MacKenzie & Ware, 1993; Sheridan & Ferrell, 1963),
and more errors are made (Khasawneh, Rogers, Bertrand, Madathil, Gramopadhye 2019; Scholcover & Gillan, 2018; Scholcover & Gillan, under review). These issues possibly arise due to the difficulty of predicting the tool’s status after the latency period (McClelland & Campbell, 2010, 2013; Scholcover & Gillan, under review). These prediction difficulties likely increase cognitive workload, leading to the adoption of an alternative movement strategy (Scholcover & Gillan, under review).

The Move and Wait Strategy

To adapt to difficulties from latency, operators adopt a different control strategy that is akin to transitioning from a closed-loop to open-loop control scheme. When not experiencing any latency, participants will actively manipulate the tool -- a continuous movement strategy. However, at high latencies, they adopt a strategy to compensate, known as the Move and Wait strategy (Ferrell, 1965; Sheridan & Ferrell, 1963). In the Move and Wait strategy, participants move the robot in a piecemeal set of actions. They will move, wait to see the result, and then move again while taking any unexpected results into account (Hoffman, 1992). The use of this strategy is one of the oldest findings in the area of teleoperation with latency (Ferrell, 1965; Sheridan & Ferrell, 1963).

Despite how long the literature has been aware of the Move and Wait strategy, it has only been coarsely defined. It is broadly defined as a set of discrete movements, where further movement commands are paused until feedback is received (Hoffman, 1992; Hoffman & Karri, 2018). This broad definition is likely due to the difficulty of measuring strategy use, relying on relatively coarse measures lacking in specificity. The foundational paper on this topic, for example, relied on visual inspection to claim whether a participant engaged in the strategy,
which they confirmed by participant verbal reports and performance measures (Ferrell, 1965).

This has remained consistent in the literature, in that strategy differences are primarily described in an observational manner (Currie & Rochlis, 2004; Ferrell, 1965; Hoffman & Karri, 2018; Lane, Carignan, Sullivan, Akin, Hunt & Cohen, 2002). Evidence that a Move and Wait strategy was used, at best, relies on the proportion of time spent moving (Hill, 1976; Hoffman 1992; Scholcover & Gillan, 2018; Scholcover & Gillan, under review) or in visual inspection of control position graphs (see Figure 4 of Hoffman & Karri, 2018).

The exact pattern of behaviors that define the Move and Wait strategy have not been well defined nor has the transition point between continuous control and the more discrete control movements. Use of a Move and Wait strategy can be seen at the task level, detectable by changes in the proportion of time spent moving as a function of latency, the average move time per move, or by the total number of moves made (Hill, 1976). Currently, we can say that participants spend more time waiting in one trial versus another. However, these metrics are coarse and do not account for moment-to-moment strategy shifts -- We cannot detect strategy shifts that occur within a trial. We cannot say that a participant spent the first 10% of a trial using a continuous movement strategy before transitioning to a Move and Wait strategy, for example.

Along with this issue of not being able to differentiate between continuous and discrete strategy use in the moment, there have been reports of variations on the Move and Wait strategy dating back to the original Ferrel article (Ferrel, 1965; Hill, 1976; Hoffman & Karri, 2018; Rayman, Croome, Galbraith, McClure, Morady, Peterson, Smith, Subotic, Van Wmysberghe, Patel, & Primak, 2007; Scholcover & Gillan, under review). These variations are dependent on the task and context. Fitts Law-style target acquisition studies, for example, describe the transition from a continuous movement strategy, to a slower drag, to an eventual discrete Move
and Wait (Hoffman & Karri, 2018). Anecdotally, the authors have observed a third movement strategy during data collection (see Scholcover & Gillan, under review). This third strategy can best be described as a staccato movement (Rayman, et al. 2007), which anecdotally occurs at moderate latencies between where a continuous movement strategy and a Move and Wait strategy would be expected (Scholcover & Gillan, under review). The Staccato movement strategy is characterized by rapid inputs, with very little pause time in between. This may be equivalent to Hoffman et al.’s (2018) slow drag movement. The possible existence of a third movement strategy suggests that some nuance is lost when movement strategy is bifurcated as either continuous or discrete (i.e. Move and Wait).

**PRONET Application of the Pathfinder Network Algorithm**

Movement strategies can be thought of as a sequence of discrete actions. A continuous movement strategy is a series of relatively long moves, with very little pauses time in between. A Move and Wait strategy is a series of shorter movements with moderate pauses in between. A Staccato strategy is a series of very short movements with very little pause time in between. A movement strategy is both its constituent components (short moves, long moves, short waits) and their sequence (e.g. short move $\rightarrow$ moderate wait). One approach to uncovering these sequences is the PRONET technique, as it is designed to describe patterns of behavior (Cooke, Neville, & Rowe, 1996).

The PRONET technique begins with a matrix of transition frequencies or conditional probabilities. It counts the number of times a discrete event is followed by another discrete event (e.g. a long move followed by a short wait). It generates a two-way matrix where the rows and columns represent all possible events. The frequency of transitioning from each individual event
(represented by the row) to an event (represented by the column) is then counted (Cooke & Gillan, 1999).

The transition matrix is then passed on to the Pathfinder Network Algorithm—a method of describing the relationships between objects, using graph theory to represent the relationships as a network (Schvaneveldt, Dearholt, & Durso, 1988; Schvaneveldt, Durso, & Dearholt, 1989), wherein the objects might be concepts (see Goldsmith, Johnson, & Acton 1991 for an example) or actions (Cooke et al., 1996). The objects are represented as nodes in the network and their relationship is represented as links between the nodes. Highly related nodes are directly connected to each other, while unrelated nodes are indirectly connected through one or more nodes. The Pathfinder algorithm looks for the minimum number of links to describe that relationship, using a specified distance parameter to describe these dissimilarities and maximum number of links between any two nodes. If given a transition matrix, the resulting Pathfinder network is a description of the types of movement strategies a person might engage in. The distance parameter, the Minkowski r-metric, defines how the distance between nodes is calculated. The q parameter constrains the maximum number of links between any two nodes. A pathfinder network with \( r = \infty \) and \( q = n - 1 \), where n is the number of nodes, is known as the minimal Pathfinder network, as it will have the fewest number of links (Schvaneveldt, et al., 1989). This is considered the “default” setting.

It is generally recommended to use a transition matrix of conditional probabilities when applying the PRONET technique. Conditional probabilities better represent low frequency events by accounting for absolute frequency differences of the initial event (Cooke & Gillan, 1999). The Pathfinder network resulting from a conditional probability matrix best describes where someone will transition to, given an initial starting spot (e.g. if a person begins at event A, which event is
most likely to occur next?). However, the conditional probability matrix may also overstate the role of a low frequency event. For example, there may be an initial action that occurred only twice that transitioned to a different action once. The Pathfinder analysis, using a conditional probability matrix, would assign that relationship a higher link weight than an initial action that occurred 1000 times and transitioned to a different action 300 times. Conversely, a raw frequency transition matrix would better highlight the absolute differences in the initial state – better describing which initial states are most likely to occur and where will they transition to. If the goal of the analysis is to know the overall pattern of behaviors, such as a movement strategy, then a raw frequency matrix would be better. If the goal of the analysis is to know the likelihood of some behavior, given an initial behavior, then a conditional probability matrix is better.

While the PRONET technique is useful for describing the patterns of behaviors between discrete events, movement strategies only have two events, moves and waits, and these events always occur in the same order… a move is followed by a wait, which is followed by a move. The key differentiator between movement strategies is the length of time of each move and each wait. To be able to apply the PRONET technique to uncover strategy differences, we need a way of representing these continuous actions as discrete events.

**Clustering as a Means of Data Recovery**

A data-driven approach to representing these continuous moves and waits as discrete events is through clustering. Clustering techniques attempt to find natural groups within a dataset, grouping together like-observations. In this case, grouping together movement events that are alike. Movements (and waits) originating from the same strategy are likely to be more similar to each other than they are to movements originating from other strategies and would
therefore belong to the same cluster. By clustering the individual movements, we are likely to discover discrete movement types. A type of movement associated with the Staccato strategy, a type of movement associated with the Move and Wait strategy, etc. The act of finding clusters in the data can be thought of as recovering unobserved data (Oberski, 2016), in this case, the unobserved discrete movement types.

A clustering solution can be thought of as a categorical variable (movement type), where the number of clusters is equivalent to the number of levels in the categorical variable (G-many type). The assignment for each observation to a cluster is their level (movement type A). The labels for each level (e.g., staccato move) -- sometimes compared to reading tea leaves (Bauer, 2005) -- are defined by a subject matter expert after observations have been clustered.

A good cluster solution is defined by both cohesion (i.e., the relatedness of the points in a cluster), and isolation (i.e., the degree of separation between clusters). Different clustering techniques will tend to emphasize either cohesion or isolation (Cormack, 1971). Modern clustering approaches attempt to model the data as being generated from a finite mixture of statistical distributions which represent a finite number of latent clusters. A cluster is synonymous with the underlying statistical distribution used to model it.

These finite mixture models are a type of soft-clustering approach. Observations are given a likelihood of belonging to a cluster. This contrasts with hard clustering techniques where an observation wholly belongs to cluster A or cluster B. The advantage of assuming a mixture of distributions is that these likelihoods come directly from the distributions. An observation can have a 70% likelihood of belonging to A, 20% to B, and 10% to C. However, hard clustering can be seen as a special case of soft clustering, where an observation is assigned to the cluster with the highest likelihood.
The task in clustering is to find (1) the best fit between the mixture of distributions and the data and (2) the correct number of underlying distributions. That is, clustering is about finding how many clusters there are and their location in space. In the context of movement types, the types of movements are equitable to the number of clusters (i.e. five clusters implies five types of discrete movements), with these movements defined by the parameters of the underlying distribution, which includes a mean and variance. Once we have these discrete movement types, we can apply the PRONET technique to extract the pattern of movements that define a strategy.

**Gaussian Mixture Models**

The most common type of mixture modeling approach is the Gaussian Mixture Model (GMM; Melnykov & Maitra, 2010). A GMM models a cluster solution as a mixture of G-many multivariate Gaussian distributions. A multivariate Gaussian distribution is an extension of the classic Gaussian distribution (commonly referred to as the Normal distribution), into two or more dimensions. The task of a GMM is twofold: (1) find the best fit between G-many mixtures and the data and (2) find the value of G. GMMs use the approach to finding the best fit and the value of G.

First, the location of each of the G mixtures is initialized with a random guess somewhere within the data set. Then an iterative approach, known as the Expectation-Maximization (EM) Algorithm (Dempster, Laid, & Rubin, 1977), is used to move and distort each distribution until a measure of fit between the distribution and the data, known as the likelihood estimate, is maximized. Occasionally, the EM algorithm will fail to converge on a maximum likelihood estimate due to singularities or degeneracies in the data. An alternative procedure has been
proposed, which uses a maximum a posteriori (MAP) estimator instead. More information on the EM algorithm and the types of model parameterizations can be found in Appendix 3.

Once the EM algorithm converges, the Bayesian information criterion (BIC; Schwarz, 1978) is used as a measure of model fit and is calculated from the maximized log-likelihood function with a penalty term for the model complexity (Fraley, Raftery, Murphy, Scrucca, 2012). BIC has consistently shown superior performance (Steele & Raftery, 2009) to other criterion measures of model fit exist, such as the Akaike Information Criterion (AIC; Akaike, 1973, 1974), adjusted BIC (Sclove, 1987), Deviance Information Criterion (DIC; Spiegelhalter, Best, Carlin, & Van Der Linde, 2002), or the Integrated Complete Likelihood (ICL; Biernacki, Celeux, & Govaert, 2000). Unfortunately, based on the initialization of the EM Algorithm, the model can converge to a locally maximized likelihood estimate rather than a globally-maximized solution (Baudry & Celeux, 2015; Figueiredo & Jain, 2002), leading to a suboptimal model fit. There are multiple approaches to initializing the EM algorithm to combat this. One approach is to run the algorithm multiple times with different random initializations. However, this is computationally intensive. Another approach leans on a different style of clustering, known as agglomerative clustering, to find a good initialization (Figueiredo & Jain, 2002). Agglomerative clustering is a bottom up approach which iteratively combines observations into clusters until they all belong to a single cluster. The R package mclust (Scrucca, et al., 2016) provides multiple initialization options, using model-based hierarchical agglomerative clustering as the default approach (Scrucca et. al., 2016). Model-based agglomerative clustering is commonly used as a cluster initializer as it tends to converge towards a good result and is computationally efficient, only having to be run once for multiple numbers of mixture components (Scrucca & Raftery, 2015).
BIC generally finds the solution that best approximates the data, rather than the actual number of clusters, as it generally improves with more mixture components (Baudry, Raftery, Celeux, Lo, & Gottardo, 2010; Biernacki, et al., 2000; Scrucca, et al., 2016). That is, it overestimates the number of mixture components relative to the number of clusters. Given that any non-Gaussian distribution can be modeled as a mixture of multiple Gaussians, any data set which originates from a non-Gaussian distribution will be best approximated by more mixture components than actual clusters (Baudry, et al., 2010). This can be extremely misleading for any inferences made from the number of mixtures.

A solution exists to account for data originating from non-Gaussian distributions, by conceptually delineating between a mixture component and a cluster. A cluster is now defined as a combination of related mixture components, where these related mixture components approximate a single statistical distribution (Baudry, et al., 2010). The data from a single cluster are generated from a single statistical distribution (Gaussian or non-Gaussian), which is approximated by multiple multivariate Gaussian mixtures.

Baudry et al. (2010) developed an approach that uses this approximation as a way to derive the correct number of clusters while maintaining the optimized model fit, by using a combination of BIC and the Integrated Complete Likelihood (ICL) criterion (Biernacki, et al., 2000). The ICL criterion is equivalent to BIC with an additional entropy parameter that measures how well the mixtures are separated. If two mixtures are not well separated, then they are likely to be approximating a single distribution. The less separation between mixtures, the larger the entropy parameter and the worse the ICL (Biernacki, et al., 2000).

Baudry et al. (2010) suggest first generating a mixture model that best fits the data using BIC. That is, finding the number of mixtures that best fit the data, likely a number of mixtures
greater than the actual number of underlying clusters. Then, the mixtures are iteratively merged using the entropy criterion into a single cluster. Once entropy is minimized, the process stops. This leads to a set of clusters that are fewer than the number of mixture components, but still fit the data very well. In graphing the number of clusters on the x-axis and the entropy on the y-axis, there is likely to be an elbow. That is, a point where entropy starts to increase rapidly as a function of the clusters. Baudry et al. (2010) suggest using the location of the elbow as the stop point for the merge.

Current Study

To find movement strategies, one can take the GMM approach outlined above to movement events and apply the PRONET technique to the results. Once the continuous movement events are transformed into discrete clusters, a transition matrix between the clusters can be generated (e.g. Cluster 1 was followed by Cluster 2 100 times) and provided to the Pathfinder algorithm. The resulting Pathfinder network would then serve as a representation of the types of movement strategies that participants might use. Applying this approach to movement data from a latency study is likely to be a strong step in defining the possible movement strategies that might occur.

To better define movement strategies, we will use a four-step exploratory hybrid PRONET-clustering approach: (1) First, we will explore combinations of variables that might be useful as components in finding movement strategies: move time, wait time, and “context” variables, such as a participant’s sensitivity to time and reported workload. There is some evidence to suggest that these context variables affect when the transition in movement strategy occurs (Scholcover & Gillan, 2018; Scholcover & Gillan, under review). (2) At the second stage,
cluster solutions deemed sufficient at the previous stage will be tested to ensure they vary as a function of latency, supporting that the cluster solution is clustering around movement types and not some third variable. (3) Cluster solutions deemed sufficient at the previous stage will then have the PRONET technique applied to their cluster transitions. The resulting pathfinder networks are expected to illustrate movement strategies. We expect to find, at least, a continuous movement strategy that is most prominent at low latencies and a Move and Wait strategy that is most prominent at high latencies. We may be able to detect the existence of Staccato movement strategy at this stage. We expect this strategy to be most prominent at latencies between where continuous and Move and Wait strategies are most prominent. (4) For the strategies to have practical significance, their use should lead to different performance outcomes. Controlling for latency and route clearance, utilization of these movement strategies should be predictive of trial-level performance outcomes, such as trial completion time, total distance traveled per trial, and the total number of errors committed per trial. Data for the clustering procedure will be sourced from a pre-existing dataset, used in Scholcover and Gillan (under review). To generate the data, participants navigated a course multiple times, across multiple levels of latency, as well as different horizontal route clearances. Movement and positional data were recorded at approximately 60 frames per second.

**METHOD**

The following is a short summary of how the data were collected; see Scholcover and Gillan (under review) for a full description. Ninety participants from the North Carolina State undergraduate psychology participant pool completed two sets of tasks, a magnitude estimation task (Stevens, 1956) and a route navigation task.
**Magnitude Estimation Task**

In the magnitude estimation task, participants reported the duration of white squares, ranging in duration from 0.067 seconds to 2 seconds. Participants estimated the duration of a white square relative to another white square (the standard). They were informed that the standard was on the screen for 100 units of duration and to report subsequent stimuli as a ratio of the standard. Participants completed 10 training trials and 90 experimental trials. Durations were randomly presented in a blocked fashion (30 possible durations, 3 times total). Participants responded using the number keys on the keyboard. They were reminded of the standard length after every 10th trial.

To derive a single measure of temporal sensitivity, a regression line was fit for each participant’s data to derive the exponent of Steven’s Power Law (Stevens, 1957). The logarithm of the actual duration was used to predict the logarithm of their reported duration. The regression estimate ($B_1$) is equivalent to $\alpha$ in Steven’s Power Law, which is a measure of the degree of sensitivity to changes.

**Route Navigation Task**

The route navigation had participants navigate a computerized route multiple times, with varying amounts of latency and horizontal clearance per trial. The participants were represented on the course by a cube, which was 1.2 meters in length, width and height. They moved the cube using the W/A/S/D keys on a standard QWERTY keyboard to move forward/left/back/right respectively and the Q/E keys to rotate counter-/clockwise.

Per trial latency ranged from 0 to 1 second of latency, in 0.125 second steps. The horizontal clearance of the route varied per trial, from 4 meters to 10 meters in 0.75-meter steps.
There were a total of nine possible latencies and nine possible clearances, for a total of 81 possible combinations. Participants completed three training trials, all at 7 meters of clearance. Each training trial increased in latency, from 0 seconds, to .5 seconds, and finally 1 second. Afterwards, they completed nine trials. Participants experienced each level of latency and each level of clearance once, but not all combinations. Trials were randomized prior to the study such that there would be an equal number of completed trials per cell (10) at the completion of the study. One participant was mis-assigned, so the number of completed trials per cell varies from 9 to 11 for a total of 810 completed trials. After each trial, participants completed the NASA-TLX, which is a measure of workload (Hart & Staveland, 1988). The route (see Figure 1) was constructed similarly to the route in Scholcover and Gillan (2018), mirrored about the vertical axis. Participants received a negative feedback tone if they came in contact with the walls. Behavioral data were recorded on a frame-by-frame basis at approximately 60 frames per second, with the program designed to smooth variations in the frame rate. The participant’s inputs, the cube’s positional data and heading were recorded once for each frame along with a timestamp.

The frame-by-frame data was aggregated into “events,” such that they were coded as either continuous inputs (move) or not-inputs (wait). Changes in input, while continuously inputting (e.g. holding W, then holding W and E, then holding just E), were considered a continuous input. Data were collated into a series of events, where each event consisted of the length of time that a participant moved, the latency, the horizontal clearance, NASA-TLX workload score, the time of the post-move wait, the starting position, and the ending position. There were a total of 94,260 candidate events. There were 792 events that did not have a post-move wait event and were not included in the data set. These events consisted of the final
movement in most trials, as participants would move continuously into the finish marker (and therefore had no wait time afterwards). For 26 trials, participants made a single continuous movement across the map. These incomplete cases were omitted from analysis.

In addition to the variables used in clustering, three additional trial-level variables will be used as outcome variables in the fourth stage of the analysis to test the predictive utility of the clusters: trial completion time, number of errors (discrete number of times contacting the course boundary), and the total distance traveled.

Figure 1. Route Layout. B and E mark the beginning and end, respectively.
RESULTS

Model Generation

Four variables were evaluated for their contribution to movement strategies: At least one of two movement variables (move time and post-move wait time; see Table 1) crossed with two context variables (temporal sensitivity and workload; see Table 2). These variable sets were modeled as Gaussian Mixtures, using the mclust 5 (Fraley & Raftery, 1999, 2003, 2006; Fraley et al., 2012; Scrucca et al., 2016) R package (R Core Team, 2018). Figure 2 shows the entire model building and evaluation process.

Table 1. Movement Variable Sets to be Used in Clustering.

<table>
<thead>
<tr>
<th>Clustering Variables</th>
<th>Move</th>
<th>Wait</th>
<th>Move &amp; Wait</th>
</tr>
</thead>
<tbody>
<tr>
<td>Move Time*</td>
<td>✓</td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>Wait Time*</td>
<td></td>
<td>✓</td>
<td>✓</td>
</tr>
</tbody>
</table>

Note: Random noise was added to the move time and wait time for each observation, between -1/120th and +1/120th sec., to discourage the clustering procedure from clustering around the framerate of 60 frames per second.

Table 2. Trial-Level Variable Sets to be Used in Clustering.

<table>
<thead>
<tr>
<th>Clustering Variables</th>
<th>None</th>
<th>TLX</th>
<th>Temporal Sensitivity</th>
<th>Both</th>
</tr>
</thead>
<tbody>
<tr>
<td>NASA-TLX</td>
<td>✓</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Temporal Sensitivity</td>
<td></td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
</tbody>
</table>

Each Gaussian Mixture consisted of anywhere between 1 and 26 mixture components, using the V hyperparameters for the univariate variable sets and the VVV hyperparameters for the multivariate variable sets. GMMs were fit using MAP estimation. For each of the twelve variable sets, the modeling procedure was repeated 50 times (600 total runs) using a different stratified random sample of the data. The samples were stratified on trials, such that movements from five trials of each of the latency and clearance combinations were included in the training
set. Each run randomly sampled 405 trials. They were sampled without replacement within a run. The remaining trials were held out from the clustering procedure, to be used in the test set if that specific run was selected.

The default mclust initialization procedure was altered to increase the representation of less frequent but longer events. The initialization for mclust uses hierarchical agglomerative clustering, which samples a maximum of 2000 events from the training set. Although this number can be increased, anything much larger exceeds computational limits. Given that each training data set had approximately 45,000 events, less frequent but longer events (i.e. long moves) were much less likely to be used in the model initialization, increasing the likelihood that the specific model converged to a local maximum. To account for this, the initialization used a weighted sampling procedure, where the likelihood of selecting an event was weighted based on the percentage of the completion time spent moving for that observation. That is, an event that was 50% of the trials completion time in duration was ten times as likely to be sampled relative to an event that was 5% of the trial’s completion time. By repeating this procedure 50 times per variable set, we were able to average out the effects of any one random subsample.

**Model Selection**

As can be seen in Figure 3, including the NASA-TLX as a modeling variable leads to decreases in model fit, as measured by BIC, relative to all other models. Similarly, including both moves and waits decreased model fit relative to all other models. As such, both sets of models will be omitted from further discussion. Comprehensive analysis of all variable sets, including those dropped from further discussion, can be found in Appendix 1 through 12 (see Table 3).
After fitting the mixture components, the mixture components were collapsed into clusters following the procedure in Baudry et al. (2010). The number of clusters was selected using a two-piece piecewise linear regression function on the entropy-by-components graph. The breakpoint in the piecewise regression was selected as the final number of clusters, derived from combining iteratively the mixture components. Figure 4 shows the entropy plot for the final run selected from each variable set, as well as the breakpoint for the piecewise linear regression functions.
Table 4. Summary of all 600 runs.

<table>
<thead>
<tr>
<th>Variables</th>
<th># of Mixture Components</th>
<th># of Clusters</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Percentile</td>
<td>25th</td>
<td>50th</td>
</tr>
<tr>
<td>M</td>
<td>10</td>
<td>12</td>
<td>14</td>
</tr>
<tr>
<td>M, TLX</td>
<td>22</td>
<td>23.5</td>
<td>26</td>
</tr>
<tr>
<td>M, TLX, TS</td>
<td>25.25</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>M, TS</td>
<td>24</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>M, W</td>
<td>25</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>M, W, TLX</td>
<td>25</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>M, W, TLX, TS</td>
<td>25.25</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>M, W, TS</td>
<td>25</td>
<td>26</td>
<td>26</td>
</tr>
<tr>
<td>W</td>
<td>9</td>
<td>9.5</td>
<td>10</td>
</tr>
<tr>
<td>W, TLX</td>
<td>24</td>
<td>25.5</td>
<td>26</td>
</tr>
<tr>
<td>W, TLX, TS</td>
<td>25</td>
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<td>26</td>
</tr>
<tr>
<td>W, TS</td>
<td>24.25</td>
<td>26</td>
<td>26</td>
</tr>
</tbody>
</table>

Note: M - Move, TLX - NASA TLX, TS - Temporal Sensitivity, and W – Wait

Figure 3. Summary of Model Fits. Note that the inner band is 50% of the data and the outer band is 100%.
As can be seen in Figure 3 and
Table 4, whereas temporal sensitivity improved model fit, the vast majority of models including temporal sensitivity contained more than 12 clusters. The univariate models of Move-Only and Wait-Only had comparatively fewer clusters, with a median of six and three clusters, respectively. In line with the stated goal of finding the most parsimonious solution, models with temporal sensitivity will be dropped from further discussion (see appendices for analysis related to models using temporal sensitivity). Along similar lines as above, simultaneously including both moves and waits in the model decreased parsimony (as well as failed the step 2 check in varying with latency). The univariate models (Move-Only and Wait-Only) were retained for further discussion.

![Figure 4](image-url)  
**Figure 4.** Entropy-by-Components Graph for the Final Candidate Models. The vertical line is the breakpoint for the piecewise regression.
To select a representative run from each variable set, we used an unconventional approach. Classically, the “best” model is the model with the highest BIC\(^1\) (Steele & Raftery, 2009). However, BIC-based model comparisons rely on both models being applied to samples of the same size, as the penalty to the log-likelihood scales with the sample size. The repeated stratified subsampling procedure occurred at the trial level, resulting in models having different observation counts, and therefore different log-likelihood penalties. Instead, we selected the model that is the most similar to all other models, as measured by the Adjusted Rand Index (ARI). The Adjusted Rand Index measures the degree of similarity between two cluster solutions. It does this by looking at the degree to which pairs of values are in the same cluster in both clustering solutions, correcting for chance pairings. It ranges from approximately 0 to 1 (Hubert & Arabie, 1985; Rand, 1971).

For each variable set, each of the 50 runs was applied to each specific run’s training subsample (leading to a 50 by 50 matrix), and an ARI for each pairing was derived. The run with the highest median ARI across all training samples was selected to represent the overall variable set.

---

\(^1\) Classically, a lower BIC is better. However, the mclust package removes the negative component from BIC calculations, flipping the relationship.
Table 5 shows the final model selected for each candidate variable set, along with the number of clusters, the number of mixture components, the BIC for the training set, and the median ARI. Descriptives for both the mixture components and clusters can be found in the related appendices (see Table 3). The selected run for the Move-Only Cluster solution can be seen in Table 6 and Figure 5. The selected run for the Wait-Only cluster solution can be seen in Table 7 and Figure 6.
### Table 5. Summary of final candidate models.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Appendix</th>
<th># of Clusters</th>
<th># of Mixtures</th>
<th>BIC</th>
<th># of Obs.</th>
<th>Median ARI</th>
</tr>
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<tbody>
<tr>
<td>M</td>
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<td>10</td>
<td>-33180</td>
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<tr>
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</tr>
<tr>
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<td>46516</td>
<td>0.89</td>
</tr>
<tr>
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</tr>
<tr>
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<tr>
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<td>39068.54</td>
<td>52210</td>
<td>0.63</td>
</tr>
</tbody>
</table>

Note: M - Move, TLX - NASA TLX, TS - Temporal Sensitivity, and W – Wait

### Table 6. Cluster Summary for Move-Only Solution.

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.12 (0.04)</td>
<td></td>
<td></td>
<td></td>
<td>0.47</td>
<td>0.04</td>
</tr>
<tr>
<td>2</td>
<td>0.28 (0.04)</td>
<td></td>
<td></td>
<td></td>
<td>0.09</td>
<td>0.02</td>
</tr>
<tr>
<td>3</td>
<td>0.46 (0.07)</td>
<td></td>
<td></td>
<td></td>
<td>0.09</td>
<td>0.03</td>
</tr>
<tr>
<td>4</td>
<td>1.05 (0.34)</td>
<td></td>
<td></td>
<td></td>
<td>0.28</td>
<td>0.20</td>
</tr>
<tr>
<td>5</td>
<td>3.10 (0.80)</td>
<td></td>
<td></td>
<td></td>
<td>0.05</td>
<td>0.11</td>
</tr>
<tr>
<td>6</td>
<td>9.62 (6.60)</td>
<td></td>
<td></td>
<td></td>
<td>0.02</td>
<td>0.11</td>
</tr>
</tbody>
</table>
Figure 5. Observations with Assigned Clusters (Combined) for Move-Only Solution.
Table 7. Cluster Summary for Wait-Only Solution.

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.02 (0.01)</td>
<td>0.03</td>
<td>0.00</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.59 (0.49)</td>
<td>0.97</td>
<td>0.40</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>4.98 (2.75)</td>
<td>0.00</td>
<td>0.00</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 6. Observations with Assigned Clusters (Combined) for Wait-Only Solution.

Evaluating Cluster Solutions

At this stage of analysis, the chosen model parameters were used to analyze the test data. To support that cluster solutions were coalescing around movement strategies, a $\chi^2$-like test was used, measuring the relationship between latency and mean cluster frequency. This approach uses a Monte Carlo simulation to create a null distribution from the marginal values, randomly generating a series of contingency tables and their associated $\chi^2$ values. The $\chi^2$ for the observed contingency table is then compared to this simulated distribution. Probability values, in this case,
describe how much more extreme the observed contingency table is relative to the null distribution generated from 10,000,000.

Table 8. Mean Freq. of Cluster for Move-Only Cluster Solution

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Latency</th>
<th>Marginal Means</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0</td>
<td>125</td>
</tr>
<tr>
<td>1</td>
<td>50.33</td>
<td>16.79</td>
</tr>
<tr>
<td>2</td>
<td>9.43</td>
<td>6.42</td>
</tr>
<tr>
<td>3</td>
<td>7.65</td>
<td>8.05</td>
</tr>
<tr>
<td>4</td>
<td>14.2</td>
<td>17.76</td>
</tr>
<tr>
<td>5</td>
<td>3.58</td>
<td>3.87</td>
</tr>
<tr>
<td>6</td>
<td>2.05</td>
<td>1.71</td>
</tr>
<tr>
<td>Marginal Means</td>
<td>14.54</td>
<td>9.10</td>
</tr>
</tbody>
</table>

\( \chi^2 = 60.11, p = .02 \)

Table 9. Mean Freq. of Cluster for Wait-Only Cluster Solution

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Latency</th>
<th>Marginal Means</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0</td>
<td>125</td>
</tr>
<tr>
<td>1</td>
<td>4.92</td>
<td>4.50</td>
</tr>
<tr>
<td>2</td>
<td>56.40</td>
<td>45.18</td>
</tr>
<tr>
<td>3</td>
<td>0.02</td>
<td>0.00</td>
</tr>
<tr>
<td>Marginal Means</td>
<td>20.45</td>
<td>16.56</td>
</tr>
</tbody>
</table>

\( \chi^2 = 22.48, p = .007 \)

The cluster assignments for both the Move-Only (\( \chi^2 = 60.11, p = .02 \); Table 8) and Wait-Only cluster solutions (\( \chi^2 = 22.48, p = .007 \); Table 9) were not independent of latency, supporting that those cluster solutions were capturing an element of movement strategy. However, as can be seen in Table 7 and Table 9, Cluster 2 of the Wait-Only cluster solution contained the vast majority of observations (97%) and trial time (40% compared to <1% for both 1 and 3). This lessens the practical significance of that cluster solution, and the Wait-Only solution will be dropped from further discussion. Analysis related to the Wait-Only solution, such as the Pathfinder analysis or mixed effects models, can be found in Appendix 1.9.
Understanding Movement Patterns with the PRONET Technique

Following the PRONET technique, transition matrices between clusters for the remaining cluster solution (Move-Only) were passed to a Pathfinder analysis (Schvaneveldt, Durso, & Dearholt, 1989), using the R comato (Muehlin, 2018) and igraph (Csardi & Nepusz, 2006) packages. Transition matrices used raw frequencies, as we are interested in the overall strategy differences, rather than parsing out the effects of the initial condition. Pathfinder network parameters were set to minimize the overall structure (fewest links), which occurs when \( q = n - 1 \) and \( r = \infty \).

Figure 7 shows a Pathfinder network of the transitions between clusters for the Move-Only cluster solution. The network structure of these clusters is indicative of a continuous move strategy found at low latencies, characterized by the Cluster 6 \( (M = 9.62 \text{ sec}, SD = 6.60) \) to Cluster 4 \( (M = 1.05 \text{ sec}, SD = 0.34) \) cycle \( (6 \rightarrow 4 \text{ cycle}) \). The network structure is also indicative of the classic Move and Wait strategy, characterized by the Cluster 5 \( (M = 3.10 \text{ sec}, SD = 0.80) \) to Cluster 4 \( (M = 1.05 \text{ sec}, SD = 0.34) \) cycle \( (5 \rightarrow 4 \text{ cycle}) \) and the Cluster 4 to Cluster 4 cycle \( (4 \rightarrow 4 \text{ cycle}) \). These cycles are indicative of the classic Move and Wait strategy given the relatively moderate movement times of Clusters 5 and 4 and their rapid increase in frequency as a function of latency (see Table 8).

There are also a set of cycles \( (2 / 3 \rightarrow 1 \rightarrow 4; 1 \rightarrow 1; 1 \rightarrow 4) \) typified by much shorter and more frequent movements (Cluster 1, \( M = 0.12 \text{ sec}, SD = 0.04 \); Cluster 2, \( M = 0.28 \text{ sec}, SD = 0.04 \); Cluster 3, \( M = 0.46 \text{ sec}, SD = 0.07 \)). These cycles support the existence of a Staccato strategy (or strategies), where participants are rapidly pressing a single button. This may be the equivalent of the slower cursor drag seen in Hoffman et al. (2018). This equivalency is supported by its change in frequency with latency -- from 50.33 occurrences at 0 seconds of latency to
133.41 at .875 sec -- followed by a drop-off down to 82.07 at 1 second. That is, cycles typified by Cluster 1 are likely to be intermediary strategies existing between continuous and discrete movements, such as the Staccato strategy. The $2 \rightarrow 1$ and $3 \rightarrow 1$ links may actually represent an acceleration button press, given that they exit directly to Cluster 1 and that both have very low counts (both at 9% of all observations) and extremely low proportion of total time (2% and 3% respectively). Given their ancillary role in the overall Staccato strategy represented by the $4 \rightarrow 2$ / $3 \rightarrow 1 \rightarrow 1$ and $1 \rightarrow 1$ cycles, discussion about these will be subsumed into the overall discussion on the Staccato strategy.

Figure 7. Pathfinder Network of Cluster Transitions for Move-Only Solution.
The changes from Figure 7 to Figure 8 (.5 sec) and Figure 8 (1 sec) further support the role of Cluster 1 as an indicator of a Staccato strategy and Cluster 5 as an indicator of a Move and Wait strategy, respectively. This is highlighted by the change of the 4 → 5 link at 0.5 sec of latency (see Figure 8, middle panel) to 1 → 5 at 1 sec of latency (see Figure 8, right panel). Given that the Staccato strategy is likely an intermediary between the continuous movement strategy typified by the 6 → 4 link and the Move and Wait strategy typified by the 5 → 4 link, it’s logical that the Staccato strategy and Move and Wait strategy become more connected at higher latencies through the 1 → 5 link.

Cluster 4 acts as a central node (Gillan, Breedin & Cooke, 1992) between these longer movements and the much shorter movements, suggesting a central role across all movement strategies. Given its moderate duration, high frequency across latencies, and close relationship to the continuous movement (Cluster 6), shorter Move-and-Wait movement (Cluster 5) and rapid-fire Staccato move (Cluster 1), Cluster 4 may be indicative of a strategy invariant, existing across all movement strategies. It may also indicate an artifact of the route design in the experiment, as
the central region of the map requires zigzag movements whose length approximately match the duration of Cluster 4. Figure 8 supports this view of Cluster 4 as an invariant, either due to a strategy invariant or route artifact. Figure 8A shows that Cluster 6 (long move) cycles with Cluster 4, linking the longer continuous movement with the shorter, 1-second movements. Cluster 4, in this role, may be indicative of course adjustments while Cluster 6 is a likely indicator of a continuous movement strategy.

![Change in Network Similarity by Latency](image)

**Figure 9.** Change in Frequency-Based Pathfinder Network Similarity.

Figure 9 compares the Pathfinder networks constructed from the transition matrix, subset at each latency, with the subsequent latency. The network similarity score is a measure of the number of links in common between two networks, ranging from 0 for no shared links to 1 when the network links are the same. Figure 9 has three regions of stability or change. The first region
occurs during the transition from 0 sec of latency until approximately .250 sec of latency. Here, the networks are extremely dissimilar relative to the rest of the range. This dissimilarity indicates a drastic behavioral shift, likely from a continuous movement strategy to a more discrete strategy (i.e., the staccato strategy). Next, there is a region of relative stability from approximately .250 sec to .750 sec. The final region occurs beginning at the .750 sec to .875 sec transition. This is where there is a dip in the similarity graph, suggesting another large behavioral change, although not as drastic as the initial change. This is where the change mentioned earlier, the 4 → 5 link changing to 1 → 5 link, occurs (see Figure 8). This change suggests a behavior shift that is less drastic, but still occurs nonetheless, shifting from a primarily Staccato strategy to a Move and Wait strategy.

**Predicting Task Outcomes**

The remaining cluster solution (Move-Only) was analyzed using linear mixed-effects models, using the lme4 (Bates, Maechler, Bolker, & Walker, 2015) and lmerTest R packages (Kuznetsova, Brockhoff, & Christensen, 2017). The goal for this analysis is primarily to demonstrate that reliance on different strategies leads to different performance outcomes, further validating the hybrid GMM-PRONET approach. Additionally, this analysis serves to support further the strategy labels given in the previous section. That is, the coefficients for a cluster related to the continuous movement strategy should show outcomes, such as increased errors, that match the given strategy.

One mixed-effects model was run per dependent variable: completion time, number of errors, and total distance traveled. Independent variables for each model were all centered, and included both trial latency and trial clearance. Additionally, centered terms were included for the
proportion of total time in each of the assigned clusters. There was an additional random-intercept term ($\mu_{0j}$) to account for within-participant effects.

Note that, even without centering, the proportion of time spent in each cluster does not always sum to one for two reasons. Time spent moving and time spent waiting were mutually exclusive, and therefore both were only included in four of twelve variable sets. Additionally, most trials had a small period that was ineligible for clustering, as some moves were not always followed by waits. These actions were omitted from all models. This avoids issues related to designs where the independent variables are a proportion, rather than absolute quantities. This is akin to deciding how much sugar to put in a glass of sweet tea: the correct amount depends on how much tea is in the glass. In these cases, the independent variables are inherently related. As the proportion of one goes up (tea), the proportion of the other inherently goes down (sugar). For trials that were included with some eligible time, the ineligible time ranged from 0% of the observations in a trial to 99.13% of the observations in a trial ($Md = 5.34\%$).

As seen in Table 10, the Move-Only cluster solution predicts completion time ($Marg. R^2 = 0.67$), the total number of errors ($Marg. R^2 = 0.38$), and total distance traveled ($Marg. R^2 = 0.49$). Clusters 2 and 3 failed to predict any outcome variables (with one exception). As can be seen in Table 6, Clusters 2 and 3 contributed 18% of all moves but only 5% of the total task time in the training set. Their effects likely disappeared as they play a role solely in the larger 1→4 Staccato cycle and the model already accounts for the effects of clusters 1 and 4. In a sense, Cluster 1 is the primary driver in the 1→4 cycle, with Clusters 2 & 3 playing a minor supporting role.
**Table 10. Linear Mixed-Effects Models for Move-Only Cluster Solution**

<table>
<thead>
<tr>
<th>Fixed Effects</th>
<th>Completion Time (min.)</th>
<th># of Errors</th>
<th>Total Distance Traveled</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>B (SE)</td>
<td>B (SE)</td>
<td>B (SE)</td>
</tr>
<tr>
<td>Intercept</td>
<td>3.35 (0.10) ***</td>
<td>11.58 (1.29) ***</td>
<td>701.55 (6.44) ***</td>
</tr>
<tr>
<td>Latency (sec.)</td>
<td>2.89 (0.12) ***</td>
<td>20.24 (1.58) ***</td>
<td>153.29 (7.42) ***</td>
</tr>
<tr>
<td>Clearance (meters)</td>
<td>-0.29 (0.02) ***</td>
<td>-3.34 (0.25) ***</td>
<td>-10.30 (1.17) ***</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 1</td>
<td>2.19 (0.62) ***</td>
<td>-4.35 (7.84)</td>
<td>92.73 (37.35) *</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 2</td>
<td>0.85 (0.77)</td>
<td>2.11 (9.88)</td>
<td>70.75 (46.67)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 3</td>
<td>0.41 (0.69)</td>
<td>0.72 (8.82)</td>
<td>82.77 (41.59) *</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 4</td>
<td>-1.29 (0.35) ***</td>
<td>-2.12 (4.47)</td>
<td>94.96 (21.31) ***</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 5</td>
<td>-1.95 (0.37) ***</td>
<td>17.97 (4.76) ***</td>
<td>114.12 (22.56) ***</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 6</td>
<td>-1.27 (0.22) ***</td>
<td>12.96 (2.84) ***</td>
<td>70.83 (13.50) ***</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Rand. Effects</th>
<th>Var. (SD)</th>
<th>Var. (SD)</th>
<th>Var. (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subject</td>
<td>0.34 (0.58) **</td>
<td>45.65 (6.76) ***</td>
<td>1429.84 (37.81) ***</td>
</tr>
<tr>
<td>Residual</td>
<td>0.45 (0.67)</td>
<td>73.48 (8.57)</td>
<td>1603.09 (40.04)</td>
</tr>
</tbody>
</table>

| Marg. R²      | 0.67       | 0.38       | 0.49       |
| Cond. R²      | 0.81       | 0.61       | 0.73       |
| ICC<sub>null</sub> | 0.13       | 0.23       | 0.20       |
| # of Trials   | 379        | 379        | 379        |
| # of Participants | 90         | 90         | 90         |

*p < .05, **p < .01, ***p < .001, +p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.

Cluster 1 is the only statistically significant cluster where the proportion of time spent moving in it increases completion time. Cluster 1 is indicative of a movement pattern that is counter-productive to finishing a trial quickly. This may imply that the 1→4 Staccato cycle is inherently inefficient from a time perspective, a half measure that is worse than either alternative.
It may also be indicative of a Speed-Error tradeoff that leans towards slower movement and fewer errors. The pattern of error results support this, although the Cluster 1 coefficient is nonsignificant ($p = .58$). When looking at the total distance traveled results, the role of Cluster 1 as an indicator of a staccato movement is further supported. The coefficient for Cluster 1 ($B = 92.73, SE = 37.35, t(347.48)= 2.48, p = .01$) is directly between those for Cluster 5 ($B = 114.11, SE = 22.56, t(333.38)= 5.06, p < .001$) and 6 ($B = 70.83, SE = 13.50, t(338.59)= 5.25, p <.001$), although a Z-test of the coefficients (using eq. 4 in Paternoster, Brame, Mazerolle, & Piquero, 1998) failed to find a significant difference from each other (all $p > .37$).

Increased use of Clusters 5 (indicative of a Move-and-Wait strategy) and 6 (indicative of a continuous strategy) both decreased completion time. While odd that the coefficient for Cluster 5 ($B = -1.95, SE = 0.37, t(330.19)= -5.22, p < .001$) was larger in magnitude than Cluster 6 ($B = -1.27, SE = 0.22, t(337.19)= -5.67, p < .001$), a Z-test of the coefficients again failed to find a significant difference ($Z = -0.29, p = .39$). This difference (while not significant) may also be due to the effects of latency being averaged out, and that a continuous movement strategy may quickly become inefficient at even low latencies relative to a move and wait strategy.

**Final Model Selection**

Rather than selecting between multiple sufficient models based on their relative merits, the Move-Only model is the only model to pass the criteria laid out at the beginning. It had a high model fit relative to other solutions, met the parsimony criteria, and varied as a function of latency. Although the Wait-Only model met those criteria as well, the vast majority of observations and trial time were in one of the three clusters. From that perspective, it had poorer utility relative to the Move-Only solution. Additionally, as can be seen in Figure 78 of Appendix
1.9, the PRONET analysis was not informative for the Wait-Only solution, either. It is therefore providential that the Move-Only solution did relatively well in predicting performance, with moderately high $R^2$ values.

**DISCUSSION**

This study presents a novel method to detect changes in control strategy across levels of latency. Prior work relied primarily on verbal reports, measures at the trial level, or on the visual inspection of displacement graphs (Currie & Rochlis, 2004; Ferrell, 1965; Hill, 1976; Hoffman, 1992; Hoffman & Karri, 2018; Lane, Carignan, Sullivan, Akin, Hunt & Cohen, 2002; Scholcover & Gillan, 2018; Scholcover & Gillan, under review). However, those measures could not account for specific moment-to-moment strategy shifts; they are unable to point at a specific moment in time and claim that a specific control strategy was being used. The method demonstrated here is a strong initial step in accomplishing just that. By combining the available movements into clusters and applying the PRONET technique -- using a modified Gaussian Mixture Modeling approach, generating a transition matrix from the clusters, and then passing the transition matrix to a Pathfinder analysis -- we were able to identify three distinct movement cycles. These cycles are indicative of three hypothesized behavioral patterns in a task with latency. These behavioral patterns, the kernel of control strategy, can be identified in situ. We can point to a moment in time and say, “This participant is currently engaged in a Move and Wait strategy.” This approach supersedes the need for a subject matter expert to observe the occurrence of these strategies.

In accomplishing the aforementioned goal, we were able to identify the minimum amount of information needed to define a control strategy: *just* move time. Other measures decreased model fit (temporal sensitivity; including move time and wait time simultaneously), parsimony
(workload), or had poor explanatory power (wait time). This is fortuitous for a few reasons. Defining movement strategies using movement time has strong face validity. Collecting move time is also a trace method, asking nothing additional of the participant as they complete the primary task. This contrasts with measures of workload or temporal sensitivity, which requires the participant to complete a measure outside of the primary task.

The failure of the context variables in this process (i.e., workload, temporal sensitivity) can likely be attributed to the structure of the data, as the hierarchical structure was not well represented in the analysis method. That is, temporal sensitivity was collected once per person and workload was collected once per trial, whereas move time was collected over 100 times per trial. This led to an overrepresentation of the context variables relative to move times and wait times in the clustering procedure. Although we found that move time alone is sufficient, future studies may be interested in understanding structural changes in movement strategy as a function of these context variables.

This work furthered the discussion on intermediate control strategies that may exist between continuous movement and the move-and-wait strategy. The three movement loops align fairly well with the classic continuous control strategy (6→4), the move-and-wait strategy (5→4, 4→4), and the postulated third, intermediate, Staccato strategy (1→4). These three strategies are connected to each other by a central movement (Cluster 4), which may be a key transition component of all movements.

There is a general pattern throughout the literature in that performance decreases with increased latency. However, the exact latency(s) where these performance drops are detectable varies with the task. Some studies find no effect of latency below 1.5 seconds of latency (Lane et al., 2002) but others find an effect of latency as low as .075 seconds of latency (Mackenzie et al.,
1993). These differences are entirely due to the design of the task and the tool. The more complex the task and the tool, and the more dexterity the task calls for, the more detrimental latency becomes. By better delineating between continuous movements and discrete movements, and supporting the existence of the Staccato movement, the present research may help to detect behavioral differences even when the classic performance measures, such as completion time and errors, fail to show differences.

**Limitations and Future Directions**

This same context dependency implies that the current study design, capped at 1 second of latency, is not capturing the full range of behaviors we might see at higher latencies. As can be seen in Table 8, there is a steep drop-off in Cluster 1 frequency at 1 second of latency. This is the only cluster to display a sharp decrease. Figure 9 shows a similar shift in the overall set of behaviors occurring around .875 seconds. It is possible that this region marks the edge of where the Staccato strategy occurs, in the context of this study. However, it is difficult to make that claim conclusively without extending the data to higher latencies. Fortunately, the analytical approach found here makes it easier to establish equivalencies across contexts with clear, data-driven, definitions of movements and movement strategies. We may see a similar drop-off in cluster frequency when extending this methodology to higher latencies and across contexts.

This last point hints at additional limitations of the study. The movements and derived strategies were generated from a relatively constrained task. Movements were generated from a discrete controller, a keyboard that worked from a combination of six different on/off key presses, rather than more continuous controllers such as a mouse cursor or a joystick. Additionally, the course was a constant for all participants across all trials and left little room for
deviation from the primary route. It is possible that some (or all) clusters are influenced by the control modality, using a keyboard instead of a joystick, or course design such that participants may produce a different pattern of results if they drive a rover along a continuous curve with a joystick, such as in McClelland and Campbell’s (2010) study.

The centrality of Cluster 4 in the Pathfinder solutions may have been influenced by the route design, rather than some extensible human behavior. Cluster 4 links Cluster 6 to all other clusters in Figure 8(A). Given that Cluster 6 is the indicator for a continuous movement strategy, this may suggest a role for Cluster 4 as a course correction or a behavior in response to the zigzag movements at the center of the course (see Figure 1). It, again, has a central position in Figure 8(B), connecting all other clusters together. This central position suggests that movement along the course requires the use of movements that would fall under Cluster 4 regardless of the overarching strategy used. To better generalize the results found here, replication across control schemes, routes, and latencies is required. The hybrid GMM-PRONET approach presented here provides a reproducible, data-driven, technique by which the effects of those variables on movement strategies can be investigated.

The results found here support the existence of a Staccato strategy. However, given the qualitative nature of how Pathfinder network cycles were segmented, with names appended to those segments, there may be alternative explanations. These alternative explanations primarily hinge on the role of Cluster 4. Here, we assume the centrality of Cluster 4 is an artifact of the route design. However, if we drop this assumption, it may be argued that Cluster 4 plays a role in different strategies. One argument may be that the 1→4 link does not represent a transition from a Staccato strategy to the strategies represented by 4→5 / 4→4 (Move and Wait) or 4→6 (Continuous Movement). Instead, the 1→4 link (along with the ancillary 2→1 and 3→1 links)
may itself be representative of the Move and Wait strategy, as Cluster 4 has a fairly moderate
move time ($M = 1.05$ sec, $SD = 0.34$) and frequency (28% of observations and 20% of total
time). This would leave 4→6 as a continuous movement strategy and 4→5 would be left as an
artifact from the clustering procedure, as it accounts for 5% of the observations (but 11% of total
time). One last alternative may claim that 4→4 is a strategy onto itself, expanding the strategy
count to four total strategies. These alternative accounts of what is occurring further emphasize
what was stated earlier: To better generalize the results found here, replication across control
schemes, tasks, routes, and latencies is required.

Applications

The PRONET technique is limited to discrete events, as it relies on counts to feed into the
Pathfinder network. A strength of the analytic approach demonstrated here, is that the GMM
(with Baudry, 2010 extension) stage serves as a bridge between continuous data and the
Pathfinder network by turning continuous data into quantitatively supported discrete events.

Consider other areas in Human Factors or User Research where coding continuous data
may be useful. Take, for example, the measurement of Situation Awareness (Endsley, 1995). We
commonly measure situation awareness using a relatively intrusive method, the Situation
Awareness Global Assessment Technique (SAGAT; Endsley, 1998). In the SAGAT, participants
are given a task to complete on a computer. Occasionally, the screen will go blank, and
participants will be asked about the scene, measuring different components of situation
awareness. However, this is relatively intrusive and only measures situation awareness
occasionally, among other issues (see de Winter, Eisma, Cabrall, Hancock, & Stanton, 2019).
The measurement of Situation Awareness would generally benefit from a trace method that
could measure it unobtrusively and dynamically. Eye-tracking methods have been developed to address these measurement faults (Moore & Gugerty, 2010; de Winter, et al., 2019). However, the measurement outcomes -- such as overall dwell time or average fixation length -- are reminiscent of the discussion on the Move and Wait strategy. These measures occur at the trial level but do not account for the moment-to-moment shift in situation awareness. We may be able to apply a similar method to situation awareness: code the individual fixations based on their fixation time using Gaussian Mixture Modeling and then apply the PRONET technique. The existence of Pathfinder network cycles may be indicative of the dynamic state of situation awareness.

Conclusion

Prior to this work, detection of movement strategies occurred primarily at the trial level (i.e. proportionally more time spent waiting) or through observational means. This work demonstrates a method that can dynamically identify the current movement strategy. In doing so, these findings support the existence of a possible third movement strategy which occurs in the intermediary, between continuous movement and the discrete Move and Wait strategy: the Staccato strategy. Future research should look to validate this model across contexts, such as with different control schemes, route designs and/or across a broader swath of latencies.
REFERENCES


Muehling, A. (2018). *Comato: Analysis of concept maps and concept landscapes* (1.1) [Computer software]. https://CRAN.R-project.org/package=comato


APPENDICES
Appendix 1. Data Output for each Variable Set

**Appendix 1.1. Move-Only Results**

Table 11. Mixture Model for Move-Only Solution.

<table>
<thead>
<tr>
<th></th>
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<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>0.11</td>
<td></td>
<td></td>
<td>0.07</td>
<td>0.00</td>
</tr>
<tr>
<td>2</td>
<td>0.09</td>
<td></td>
<td></td>
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Figure 10. Observations with Assigned Clusters (Uncombined) for Move-Only Solution (1/1).
Table 12. Cluster Summary for Move-Only Solution.

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Figure 11. Observations with Assigned Clusters (Combined) for Move-Only Solution (1/1).
### Table 13. Mean Freq. of Cluster for Move-Only Solution.

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\( \chi^2 = 60.11, \ p = 0.02. \)
Figure 12. Observations with Assigned Clusters (Combined) for Move-Only Solution, faceted by Latency (1/1).
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Figure 13. Frequency-Based Pathfinder Network of Cluster Transitions for Move-Only Solution.
Table 15. Linear Mixed-Effects Models for Move-Only Solution.

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<td>20.24 (1.58)***</td>
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<td>0.34 (0.25)***</td>
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<td>-4.35 (7.84)***</td>
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*p < .05, **p < .01, ***p < .001, +p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.2. Move & NASA-TLX Results

**Table 16. Mixture Model for Move & NASA-TLX Solution.**

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Figure 14. Observations with Assigned Clusters (Uncombined) for Move & NASA-TLX Solution (1/1).
Table 17. Cluster Summary for Move & NASA-TLX Solution.

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Figure 15. Observations with Assigned Clusters (Combined) for Move & NASA-TLX Solution (1/1).
### Table 18. Mean Freq. of Cluster for Move & NASA-TLX Solution.

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$\chi^2 = 222.61, p = 0.$
Figure 16. Observations with Assigned Clusters (Combined) for Move & NASA-TLX Solution, faceted by Latency (1/1).

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Figure 17. Frequency-Based Pathfinder Network of Cluster Transitions for Move & NASA-TLX Solution.
### Table 20. Linear Mixed-Effects Models for Move & NASA-TLX Solution.

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| Marg. R²             | 0.61        | 0.41        | 0.50        |
| Cond. R²             | 0.78        | 0.65        | 0.74        |
| ICCnull              | 0.10        | 0.27        | 0.20        |
| # of Trials          | 379         | 379         | 379         |
| # of Participants    | 89          | 89          | 89          |

* p < .05, ** p < .01, ***p < .001, +p<.10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.3. Move, NASA-TLX, & Temporal Sensitivity Results


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Figure 18. Observations with Assigned Clusters (Uncombined) for Move, NASA-TLX, & Temporal Sensitivity Solution (1/3).
**Figure 19.** Observations with Assigned Clusters (Uncombined) for Move, NASA-TLX, & Temporal Sensitivity Solution (2/3).
Figure 20. Observations with Assigned Clusters (Uncombined) for Move, NASA-TLX, & Temporal Sensitivity Solution (3/3).
Table 22. Cluster Summary for Move, NASA-TLX, & Temporal Sensitivity Solution.

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Figure 21. Observations with Assigned Clusters (Combined) for Move, NASA-TLX, & Temporal Sensitivity Solution (1/3).
**Figure 22.** Observations with Assigned Clusters (Combined) for Move, NASA-TLX, & Temporal Sensitivity Solution (2/3).
Figure 23. Observations with Assigned Clusters (Combined) for Move, NASA-TLX, & Temporal Sensitivity Solution (3/3).
### Table 23. Mean Freq. of Cluster for Move, NASA-TLX, & Temporal Sensitivity Solution.

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**Marginal Means** | 2.73 | 2.37 | 4.03 | 4.66 | 5.93 | 7.83 | 8.03 | 9.74 | 12.93 | 6.47 |

Note: Permutation based analysis do not work when there are row frequencies of 0 (see Clusters 10 / 11)
Figure 24. Observations with Assigned Clusters (Combined) for Move, NASA-T LX, & Temporal Sensitivity Solution, faceted by Latency (1/3).
Figure 25. Observations with Assigned Clusters (Combined) for Move, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (2/3).
Figure 26. Observations with Assigned Clusters (Combined) for Move, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (3/3).
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Figure 27. Frequency-Based Pathfinder Network of Cluster Transitions for Move, NASA-TLX, & Temporal Sensitivity Solution.

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Rand. Effects

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Marg. R² 0.61
Cond. R² 0.80
ICCnull 0.13

# of Trials 379
# of Participants 90

* p < .05, ** p< .01, ***p < .001, +p<.10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.4. Move & Temporal Sensitivity Results

Table 26. Mixture Model for Move & Temporal Sensitivity Solution.

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Figure 28. Observations with Assigned Clusters (Uncombined) for Move & Temporal Sensitivity Solution (1/1).
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Figure 29. Observations with Assigned Clusters (Combined) for Move & Temporal Sensitivity Solution (1/1).
Table 28. Mean Freq. of Cluster for Move & Temporal Sensitivity Solution.

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<th>625</th>
<th>750</th>
<th>875</th>
<th>1000</th>
<th>Marginal Means</th>
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Marginal Means 5.54 | 3.63 | 5.3 | 4.77 | 7.71 | 10.04 | 12.23 | 13.85 | 15.44 | 8.72

\(\chi^2 = 220.76, p = 0.\)
Figure 30. Observations with Assigned Clusters (Combined) for Move & Temporal Sensitivity Solution, faceted by Latency (1/1).
Table 29. Count of Cluster Transitions in Test Set for Move & Temporal Sensitivity Solution.

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Figure 31. Frequency-Based Pathfinder Network of Cluster Transitions for Move & Temporal Sensitivity Solution.
**Table 30.** Linear Mixed-Effects Models for Move & Temporal Sensitivity Solution.

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<th># of Errors</th>
<th>Total Distance Traveled</th>
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<td>B (SE)</td>
<td>B (SE)</td>
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<td>153.95 (7.48)**</td>
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<td>Clearance (meters)</td>
<td>-0.32 (0.02)**</td>
<td>-2.92 (0.22)**</td>
<td>-10.24 (1.17)**</td>
</tr>
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<td>Prop. Total Time Moving in Cluster 1</td>
<td>-1.10 (0.26)**</td>
<td>6.76 (2.64)*</td>
<td>76.75 (14.16)**</td>
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<td>9.31 (6.66)</td>
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<td>20.57 (38.52)</td>
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<td>10.40 (6.99)</td>
<td>93.83 (37.51)*</td>
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<td>11.98 (6.89)+</td>
<td>84.74 (36.97)*</td>
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<td>4.10 (6.09)</td>
<td>83.77 (32.68)*</td>
</tr>
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<td>12.14 (4.57)**</td>
<td>64.99 (24.52)**</td>
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<td>17.67 (4.10)**</td>
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<td>77.02 (31.78)*</td>
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<td>8.19 (6.00)</td>
<td>67.36 (32.21)*</td>
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<td>6.07 (6.32)</td>
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<td>11.07 (3.00)**</td>
<td>57.01 (16.08)**</td>
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* p < .05, ** p < .01, *** p < .001, + p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
## Appendix 1.5. Move & Wait Results

Table 31. Mixture Model for Move & Wait Solution.

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</tr>
<tr>
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<td>0.09 (0.02)</td>
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<tr>
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Figure 32. Observations with Assigned Clusters (Uncombined) for Move & Wait Solution (1/1).
Table 32. Cluster Summary for Move & Wait Solution.

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Figure 33. Observations with Assigned Clusters (Combined) for Move & Wait Solution (1/1).
Table 33. Mean Freq. of Cluster for Move & Wait Solution.

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Marginal Means: 5.35, 4.55, 6.42, 5.31, 8.37, 10.37, 12.87, 15.47, 15.65, 9.37

$\chi^2 = 31.6, p = 1$. 
Figure 34. Observations with Assigned Clusters (Combined) for Move & Wait Solution, faceted by Latency (1/1).
Table 34. Count of Cluster Transitions in Test Set for Move & Wait Solution.

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Figure 35. Frequency-Based Pathfinder Network of Cluster Transitions for Move & Wait Solution.
Table 35. Linear Mixed-Effects Models for Move & Wait Solution.

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<td>-14.32 (1.29)**</td>
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<td>6.84 (0.27)**</td>
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<td>6.79 (0.93)**</td>
<td>-27.92 (17.03)</td>
<td>-19.65 (83.22)</td>
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<td>5.41 (1.00)**</td>
<td>-0.57 (18.27)</td>
<td>111.41 (88.42)</td>
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<td>3.51 (0.53)**</td>
<td>-32.78 (9.75)**</td>
<td>-28.09 (47.46)</td>
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<td>3.49 (0.77)**</td>
<td>-50.05 (14.19)**</td>
<td>-176.11 (69.55)*</td>
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<td>-30.92 (16.86)+</td>
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<td>-40.83 (13.25)**</td>
<td>-57.26 (64.31)</td>
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<td>-172.86 (94.13)</td>
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<td>-55.03 (19.03)**</td>
<td>-145.30 (94.13)</td>
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<td>-98.13 (49.61)</td>
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<td>36.10 (57.43)</td>
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<td>1.33 (0.61)*</td>
<td>18.23 (11.19)</td>
<td>163.51 (54.74)**</td>
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<tr>
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<td>0.00 (0.56)</td>
<td>19.99 (10.29)+</td>
<td>153.33 (51.11)**</td>
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<td>-0.10 (0.92)</td>
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<td>122.87 (27.54)**</td>
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<td>1182.52 (34.39)**</td>
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*p < .05, **p < .01, ***p < .001, +p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.6. Move, Wait, & NASA-TLX Results

Table 36. Mixture Model for Move, Wait, & NASA-TLX Solution.

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Figure 36. Observations with Assigned Clusters (Uncombined) for Move, Wait, & NASA-TLX Solution (1/3).
Figure 37. Observations with Assigned Clusters (Uncombined) for Move, Wait, & NASA-TLX Solution (2/3).
Figure 38. Observations with Assigned Clusters (Uncombined) for Move, Wait, & NASA-TLX Solution (3/3).

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Figure 39. Observations with Assigned Clusters (Combined) for Move, Wait, & NASA-TLX Solution (1/3).
Figure 40. Observations with Assigned Clusters (Combined) for Move, Wait, & NASA-TLX Solution (2/3).
Figure 41. Observations with Assigned Clusters (Combined) for Move, Wait, & NASA-TLX Solution (3/3).
Table 38. Mean Freq. of Cluster for Move, Wait, & NASA-TLX Solution.

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Marginal Means: 5.46 | 4.65 | 7.2 | 6.03 | 8.4 | 12.2 | 10.06 | 13.82 | 15.89 | 9.3

\( \chi^2 = 317.37, p = 0. \)
Figure 42. Observations with Assigned Clusters (Combined) for Move, Wait, & NASA-TLX Solution, faceted by Latency (1/3).
Figure 43. Observations with Assigned Clusters (Combined) for Move, Wait, & NASA-TLX Solution, faceted by Latency (2/3).
Figure 44. Observations with Assigned Clusters (Combined) for Move, Wait, & NASA-TLX Solution, faceted by Latency (3/3).
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Figure 45. Frequency-Based Pathfinder Network of Cluster Transitions for Move, Wait, & NASA-TLX Solution.
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<td>-12.91 (1.23)***</td>
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<td>-118.71 (24.15)***</td>
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<td>4.47 (0.90)***</td>
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<td>-19.69 (15.85)</td>
<td>-133.81 (81.85)</td>
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<td>-7.91 (14.45)</td>
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<td>-33.07 (8.59)***</td>
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Marg. R² | 0.87 | 0.51 | 0.49 |
Cond. R² | 0.90 | 0.69 | 0.75 |
ICCnull | 0.06 | 0.37 | 0.23 |
# of Trials | 379 | 379 | 379 |
# of Participants | 90 | 90 | 90 |

* p < .05, ** p < .01, *** p < .001, +p<.10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Table 41. Mixture Model for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution.

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Figure 46. Observations with Assigned Clusters (Uncombined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (1/6).
Figure 47. Observations with Assigned Clusters (Uncombined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (2/6).
Figure 48. Observations with Assigned Clusters (Uncombined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (3/6).
Figure 49. Observations with Assigned Clusters (Uncombined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (4/6).
Figure 50. Observations with Assigned Clusters (Uncombined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (5/6).
Figure 51. Observations with Assigned Clusters (Uncombined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (6/6).
Table 42. Cluster Summary for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution.

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Figure 52. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (1/6).
Figure 53. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (2/6).
Figure 54. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (3/6).
Figure 55. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (4/6).
Figure 56. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-T LX, & Temporal Sensitivity Solution (5/6).
Figure 57. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution (6/6).
Table 43. Mean Freq. of Cluster for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution.

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$\chi^2 = 549.08, p = 0.$
Figure 58. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (1/6).
Figure 59. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-T LX, & Temporal Sensitivity Solution, faceted by Latency (2/6).
Figure 60. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (3/6).
Figure 61. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-T LX, & Temporal Sensitivity Solution, faceted by Latency (4/6).
Figure 62. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (5/6).
Figure 63. Observations with Assigned Clusters (Combined) for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (6/6).
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Figure 64. Frequency-Based Pathfinder Network of Cluster Transitions for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution.
**Table 45. Linear Mixed-Effects Models for Move, Wait, NASA-TLX, & Temporal Sensitivity Solution.**

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<td>B (SE)</td>
<td>B (SE)</td>
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<td>7.24 (1.91)***</td>
<td>685.65 (10.29)***</td>
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<td>34.92 (2.09)***</td>
<td>197.49 (11.20)***</td>
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<td>-4.69 (0.27)***</td>
<td>-12.38 (1.43)***</td>
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<td>2.58 (0.82)**</td>
<td>9.29 (11.81)</td>
<td>58.33 (63.15)</td>
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<tr>
<td>Prop. Total Time Waiting in Cluster 2</td>
<td>3.29 (0.74)***</td>
<td>-35.84 (10.71)***</td>
<td>-43.99 (57.20)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 3</td>
<td>5.05 (0.28)***</td>
<td>-37.69 (4.16)***</td>
<td>-97.02 (22.46)***</td>
</tr>
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<td>Prop. Total Time Waiting in Cluster 4</td>
<td>4.19 (0.86)***</td>
<td>-24.53 (12.46)*</td>
<td>-118.86 (66.70)+</td>
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<tr>
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<td>-21.62 (11.74)+</td>
<td>-17.07 (63.25)</td>
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<td>1.84 (0.74)*</td>
<td>-15.03 (10.56)</td>
<td>-7.72 (56.03)</td>
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<td>-12.35 (10.59)</td>
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<td>-9.32 (12.03)</td>
<td>22.17 (64.28)</td>
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<td>5.06 (0.63)***</td>
<td>-44.28 (9.14)***</td>
<td>-102.38 (48.71)*</td>
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<td>-16.90 (65.65)</td>
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<td>22.73 (59.04)</td>
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<td>2.84 (0.84)***</td>
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<td>6.85 (58.14)</td>
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<td>-14.84 (11.97)</td>
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<td>0.75 (3.33)</td>
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Rand. Effects

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Marg. R²        0.83
Cond. R²        0.86
ICCnull         0.17

# of Trials     379
# of Participants 90

* p < .05, ** p< .01, ***p < .001, +p<.10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.8. Move, Wait, & Temporal Sensitivity Results

Table 46. Mixture Model for Move, Wait, & Temporal Sensitivity Solution.

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<td>0.07</td>
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<td>0.85 (0.42)</td>
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<td>0.04</td>
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<td>0.01</td>
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Figure 65. Observations with Assigned Clusters (Uncombined) for Move, Wait, & Temporal Sensitivity Solution (1/3).
Figure 66. Observations with Assigned Clusters (Uncombined) for Move, Wait, & Temporal Sensitivity Solution (2/3).
Figure 67. Observations with Assigned Clusters (Uncombined) for Move, Wait, & Temporal Sensitivity Solution (3/3).
Table 47. Cluster Summary for Move, Wait, & Temporal Sensitivity Solution.

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Figure 68. Observations with Assigned Clusters (Combined) for Move, Wait, & Temporal Sensitivity Solution (1/3).
Figure 69. Observations with Assigned Clusters (Combined) for Move, Wait, & Temporal Sensitivity Solution (2/3).
Figure 70. Observations with Assigned Clusters (Combined) for Move, Wait, & Temporal Sensitivity Solution (3/3).
### Table 48. Mean Freq. of Cluster for Move, Wait, & Temporal Sensitivity Solution.

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Marginal Means: 5.51, 3.8, 7.39, 5.54, 7.42, 9.47, 11.93, 13.62, 12.1, 8.53

\( \chi^2 = 373.38, p = 0. \)
Figure 71. Observations with Assigned Clusters (Combined) for Move, Wait, & Temporal Sensitivity Solution, faceted by Latency (1/3).
Figure 72. Observations with Assigned Clusters (Combined) for Move, Wait, & Temporal Sensitivity Solution, faceted by Latency (2/3).
Figure 73. Observations with Assigned Clusters (Combined) for Move, Wait, & Temporal Sensitivity Solution, faceted by Latency (3/3).
Table 49. Count of Cluster Transitions in Test Set for Move, Wait, & Temporal Sensitivity Solution.

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Figure 74. Frequency-Based Pathfinder Network of Cluster Transitions for Move, Wait, & Temporal Sensitivity Solution.
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<th># of Errors</th>
<th>Total Distance Traveled</th>
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<td>B (SE)</td>
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<td>698.60 (10.55)***</td>
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<td>Latency (sec.)</td>
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<td>29.39 (1.99)***</td>
<td>192.45 (10.82)***</td>
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<td>-3.78 (0.24)***</td>
<td>-11.38 (1.28)***</td>
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<td>Prop. Total Time Waiting in Cluster 1</td>
<td>6.24 (0.26)***</td>
<td>-34.97 (4.49)***</td>
<td>-106.63 (24.68)***</td>
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<td>Prop. Total Time Waiting in Cluster 2</td>
<td>3.36 (0.88)***</td>
<td>-26.06 (14.58)+</td>
<td>-43.28 (77.55)</td>
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<td>Prop. Total Time Waiting in Cluster 3</td>
<td>3.37 (0.84)***</td>
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<td>Prop. Total Time Waiting in Cluster 4</td>
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<td>-36.89 (9.20)***</td>
<td>-80.54 (49.43)</td>
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<tr>
<td>Prop. Total Time Waiting in Cluster 6</td>
<td>2.35 (0.52)***</td>
<td>-34.12 (8.80)***</td>
<td>-62.51 (47.31)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 7</td>
<td>3.53 (0.88)***</td>
<td>-42.62 (14.75)***</td>
<td>-75.49 (79.06)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 8</td>
<td>3.65 (0.70)***</td>
<td>-19.41 (11.48)+</td>
<td>-60.27 (60.63)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 9</td>
<td>0.99 (0.86)</td>
<td>-7.31 (14.31)</td>
<td>11.42 (76.26)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 10</td>
<td>2.53 (0.86)**</td>
<td>-7.31 (14.18)</td>
<td>-23.22 (75.33)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 11</td>
<td>3.32 (0.81)**</td>
<td>-21.08 (13.49)</td>
<td>-91.76 (71.65)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 12</td>
<td>2.44 (0.80)**</td>
<td>-24.63 (13.22)+</td>
<td>-57.64 (69.92)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 13</td>
<td>2.93 (0.83)**</td>
<td>-32.92 (13.68)*</td>
<td>-55.26 (72.45)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 14</td>
<td>4.29 (0.47)**</td>
<td>-33.98 (7.75)***</td>
<td>-79.97 (41.20)+</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 1</td>
<td>-1.58 (0.20)***</td>
<td>6.54 (3.30)*</td>
<td>98.60 (17.37)***</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 2</td>
<td>1.39 (0.89)</td>
<td>-13.10 (14.72)</td>
<td>32.98 (78.49)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 3</td>
<td>1.46 (0.86)+</td>
<td>-15.32 (13.97)</td>
<td>-63.92 (73.11)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 4</td>
<td>1.97 (0.87)*</td>
<td>-30.51 (14.40)*</td>
<td>-117.83 (76.74)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 5</td>
<td>0.38 (0.29)</td>
<td>1.34 (4.84)</td>
<td>35.99 (25.56)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 6</td>
<td>1.01 (0.31)**</td>
<td>-4.51 (5.08)</td>
<td>55.82 (26.87)*</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 7</td>
<td>-0.07 (0.86)</td>
<td>12.60 (14.44)</td>
<td>33.91 (77.43)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 8</td>
<td>0.05 (0.71)</td>
<td>-13.17 (11.53)</td>
<td>86.50 (59.96)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 9</td>
<td>2.73 (0.89)**</td>
<td>-27.72 (14.68)+</td>
<td>-12.24 (78.02)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 10</td>
<td>1.15 (0.88)</td>
<td>-24.63 (14.53)+</td>
<td>34.58 (77.42)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 11</td>
<td>0.28 (0.85)</td>
<td>-15.67 (13.96)</td>
<td>85.90 (73.73)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 12</td>
<td>1.61 (0.82)+</td>
<td>-16.52 (13.50)</td>
<td>57.01 (71.19)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 13</td>
<td>1.27 (0.85)</td>
<td>-5.41 (13.98)</td>
<td>6.00 (74.13)</td>
</tr>
<tr>
<td>Prop. Total Time Moving in Cluster 14</td>
<td>0.34 (0.23)</td>
<td>-0.71 (3.83)</td>
<td>46.87 (20.20)*</td>
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</table>

**Rand. Effects**

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<tr>
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<th>Var. (SD)</th>
<th>Var. (SD)</th>
</tr>
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<td>0.06 (0.25)*</td>
<td>29.80 (5.46)***</td>
<td>1395.95 (37.36)***</td>
</tr>
<tr>
<td>Residual</td>
<td>0.22 (0.47)</td>
<td>56.16 (7.49)</td>
<td>1478.69 (38.45)</td>
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</tbody>
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Marg. R² 0.88 0.49 0.51
Cond. R² 0.91 0.66 0.75
ICCnull 0.08 0.36 0.29
# of Trials 379 379 379
# of Participants 90 90 90

* p < .05, ** p < .01, *** p < .001, +p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.9. Wait-Only Results

Table 51. Mixture Model for Wait-Only Solution.

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<td>0.08</td>
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<td>0.10</td>
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<td></td>
<td>0.13</td>
<td>0.15</td>
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<tr>
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<td>1</td>
<td>1.23</td>
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<td></td>
<td>0.19</td>
<td>0.26</td>
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<tr>
<td>10</td>
<td>1</td>
<td>1.57</td>
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<td>0.03</td>
<td>0.03</td>
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<td>11</td>
<td>3.93</td>
<td></td>
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</table>
Figure 75. Observations with Assigned Clusters (Uncombined) for Wait-Only Solution (1/1).
### Table 52. Cluster Summary for Wait-Only Solution.

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<td>0.02 (0.01)</td>
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<td>0.00</td>
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<tr>
<td>2</td>
<td>0.59 (0.49)</td>
<td>0.97</td>
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<tr>
<td>3</td>
<td>4.98 (2.75)</td>
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Figure 76. Observations with Assigned Clusters (Combined) for Wait-Only Solution (1/1).
Table 53. Mean Freq. of Cluster for Wait-Only Solution.

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<th>Cluster</th>
<th>Latency 0</th>
<th>Latency 125</th>
<th>Latency 250</th>
<th>Latency 375</th>
<th>Latency 500</th>
<th>Latency 625</th>
<th>Latency 750</th>
<th>Latency 875</th>
<th>Latency 1000</th>
<th>Marginal Means</th>
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<td>4.92</td>
<td>4.5</td>
<td>3.93</td>
<td>3.58</td>
<td>3.36</td>
<td>3.02</td>
<td>2.98</td>
<td>2.57</td>
<td>2.48</td>
<td>3.48</td>
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<tr>
<td>2</td>
<td>56.4</td>
<td>45.18</td>
<td>50.12</td>
<td>68.7</td>
<td>87.71</td>
<td>154.19</td>
<td>171.36</td>
<td>212.75</td>
<td>183.23</td>
<td>114.41</td>
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<td>0.02</td>
<td>0</td>
<td>0.05</td>
<td>0.05</td>
<td>0.12</td>
<td>0.07</td>
<td>0.23</td>
<td>0.3</td>
<td>0.1</td>
<td>0.1</td>
</tr>
<tr>
<td>Marginal Means</td>
<td>20.45</td>
<td>16.56</td>
<td>18.03</td>
<td>24.11</td>
<td>30.37</td>
<td>52.44</td>
<td>58.14</td>
<td>71.85</td>
<td>62</td>
<td>39.33</td>
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</table>

$\chi^2 = 22.48$, $p = 0.01$. 
Figure 77. Observations with Assigned Clusters (Combined) for Wait-Only Solution, faceted by Latency (1/1).
**Table 54. Count of Cluster Transitions in Test Set for Wait-Only Solution.**

<table>
<thead>
<tr>
<th>First</th>
<th>Second 1</th>
<th>Second 2</th>
<th>Second 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>254</td>
<td>1026</td>
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<tr>
<td>2</td>
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<td>42815</td>
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<td>3</td>
<td>0</td>
<td>37</td>
<td>0</td>
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</table>
Figure 78. Frequency-Based Pathfinder Network of Cluster Transitions for Wait-Only Solution.
Table 55. Linear Mixed-Effects Models for Wait-Only Solution.

<table>
<thead>
<tr>
<th></th>
<th>Completion Time (min.)</th>
<th># of Errors</th>
<th>Total Distance Traveled</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fixed Effects</td>
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<tr>
<td>Intercept</td>
<td>3.16 (0.07)***</td>
<td>12.01 (0.95)***</td>
<td>704.38 (5.55)***</td>
</tr>
<tr>
<td>Latency (sec.)</td>
<td>1.84 (0.14)***</td>
<td>26.00 (1.73)***</td>
<td>192.23 (9.83)***</td>
</tr>
<tr>
<td>Clearance (meters)</td>
<td>-0.20 (0.02)***</td>
<td>-3.57 (0.23)***</td>
<td>-12.07 (1.30)***</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 1</td>
<td>3.08 (0.28)***</td>
<td>-18.44 (3.26)***</td>
<td>-109.24 (18.47)***</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 2</td>
<td>3.58 (0.21)***</td>
<td>-22.16 (2.64)***</td>
<td>-105.22 (15.04)***</td>
</tr>
<tr>
<td>Prop. Total Time Waiting in Cluster 3</td>
<td>3.21 (0.28)***</td>
<td>-18.96 (3.32)***</td>
<td>-96.49 (18.82)***</td>
</tr>
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</table>

<table>
<thead>
<tr>
<th>Rand. Effects</th>
<th>Var. (SD)</th>
<th>Var. (SD)</th>
<th>Var. (SD)</th>
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</thead>
<tbody>
<tr>
<td>Subject</td>
<td>0.10 (0.31)</td>
<td>32.78 (5.73)***</td>
<td>1228.25 (35.05)***</td>
</tr>
<tr>
<td>Residual</td>
<td>0.43 (0.66)</td>
<td>55.93 (7.48)</td>
<td>1763.70 (42.00)</td>
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</tbody>
</table>

|                     |                        |                  |                         |
| Marg. R²            | 0.79                   | 0.45             | 0.49                    |
| Cond. R²            | 0.83                   | 0.65             | 0.70                    |
| ICC_{null}          | 0.06                   | 0.35             | 0.23                    |
| # of Trials         | 379                    | 379              | 379                     |
| # of Participants   | 89                     | 89               | 89                      |

* p < .05, ** p < .01, *** p < .001, + p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.10. Wait & NASA-TLX Results

**Table 56.** Mixture Model for Wait & NASA-TLX Solution.

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<td>0.01</td>
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<td>2</td>
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<td>38.4 (8.58)</td>
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<td>0.05</td>
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<tr>
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<td>0.15 (0.05)</td>
<td>40.02 (5.02)</td>
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<td>73.09 (5.55)</td>
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<td></td>
<td>0.05</td>
<td>0.06</td>
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<tr>
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<td>0.11 (0.04)</td>
<td>54.44 (4.51)</td>
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<td>0.10</td>
<td>0.04</td>
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<tr>
<td>11</td>
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<td>0.83 (0.18)</td>
<td>51.86 (7.70)</td>
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<td>0.07</td>
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<tr>
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<td>1.48 (0.50)</td>
<td>59.03 (5.05)</td>
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<td>0.02</td>
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<tr>
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<td>26.35 (3.77)</td>
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<td>0.06</td>
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<tr>
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<td>70.03 (8.91)</td>
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<td>0.06</td>
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<td>86.45 (8.65)</td>
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<td>0.04</td>
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<tr>
<td>25</td>
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<td>0.04</td>
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<tr>
<td>26</td>
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Figure 79. Observations with Assigned Clusters (Uncombined) for Wait & NASA-TLX Solution (1/1).
Table 57. Cluster Summary for Wait & NASA-TLX Solution.

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<td>0.01</td>
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<td>82.23 (3.92)</td>
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<td>0.01</td>
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<td>0.01</td>
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<td>0.02</td>
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<td>0.00</td>
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<td>12.08 (3.87)</td>
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Figure 80. Observations with Assigned Clusters (Combined) for Wait & NASA-TLX Solution (1/1).
### Table 58. Mean Freq. of Cluster for Wait & NASA-TLX Solution.

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</tr>
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</table>

**Marginal Means**

| Marginal Means | 7.02 | 3.99 | 6.95 | 5.46 | 8.83 | 11.01 | 13.26 | 12.47 | 15.37 | 9.37 |

$\chi^2 = 380.11, p = 0.$
Figure 81. Observations with Assigned Clusters (Combined) for Wait & NASA-TLX Solution, faceted by Latency (1/1).
Table 59. Count of Cluster Transitions in Test Set for Wait & NASA-TLX Solution.

<table>
<thead>
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<th>2</th>
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Figure 82. Frequency-Based Pathfinder Network of Cluster Transitions for Wait & NASA-TLX Solution.

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<th># of Errors</th>
<th>Total Distance Traveled</th>
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<tr>
<td>Intercept</td>
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<td>9.71 (1.50)*****</td>
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<tr>
<td>Latency (sec.)</td>
<td>0.91 (0.12)*****</td>
<td>31.84 (1.95)*****</td>
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<tr>
<td>Clearance (meters)</td>
<td>-0.15 (0.02)*****</td>
<td>-4.05 (0.23)*****</td>
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<td>Prop. Total Time Waiting in Cluster 1</td>
<td>4.66 (0.42)*****</td>
<td>-40.96 (6.55)*****</td>
</tr>
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<td>-36.46 (3.41)*****</td>
</tr>
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<td>-30.85 (6.67)*****</td>
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<td>-35.13 (6.84)*****</td>
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<td>Prop. Total Time Waiting in Cluster 6</td>
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</tr>
<tr>
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<td>Prop. Total Time Waiting in Cluster 13</td>
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<td>-39.16 (6.54)*****</td>
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<th>Var. (SD)</th>
<th>Var. (SD)</th>
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<td>27.46 (5.24)*****</td>
<td>1276.69 (35.73)*****</td>
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<td>55.72 (7.46)</td>
<td>1719.06 (41.46)</td>
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</tbody>
</table>

Marg. $R^2$ 0.87 0.56 0.49
Cond. $R^2$ 0.88 0.70 0.71
ICC null 0.13 0.33 0.25
# of Trials 379 379 379
# of Participants 89 89 89

* $p < .05$, ** $p < .01$, *** $p < .001$, +$p < .10$. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.11. Wait, NASA-TLX, & Temporal Sensitivity Results

Table 61. Mixture Model for Wait, NASA-TLX, & Temporal Sensitivity Solution.

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<td>0.01</td>
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<td>37.94 (15.40)</td>
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<td>0.12</td>
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<td>0.02</td>
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</table>
Figure 83. Observations with Assigned Clusters (Uncombined) for Wait, NASA-TLX, & Temporal Sensitivity Solution (1/3).
Figure 84. Observations with Assigned Clusters (Uncombined) for Wait, NASA-TLX, & Temporal Sensitivity Solution (2/3).
Figure 85. Observations with Assigned Clusters (Uncombined) for Wait, NASA-TLX, & Temporal Sensitivity Solution (3/3).
<table>
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Figure 86. Observations with Assigned Clusters (Combined) for Wait, NASA-TLX, & Temporal Sensitivity Solution (1/3).
Figure 87. Observations with Assigned Clusters (Combined) for Wait, NASA-TLX, & Temporal Sensitivity Solution (2/3).
Figure 88. Observations with Assigned Clusters (Combined) for Wait, NASA-TLX, & Temporal Sensitivity Solution (3/3).
Table 63. Mean Freq. of Cluster for Wait, NASA-TLX, & Temporal Sensitivity Solution.

<table>
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<th>Latency</th>
<th>Marginal Means</th>
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<td>0.84</td>
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</tr>
<tr>
<td>18</td>
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Marginal Means | 3.11 | 2.33 | 2.62 | 4.29 | 5.52 | 6.05 | 9.07 | 11.09 | 10.19 | 6.03 |

Note: Permutation based analysis do not work when there are row frequencies of 0 (see Clusters 10 / 11)
Figure 89. Observations with Assigned Clusters (Combined) for Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (1/3).
Figure 90. Observations with Assigned Clusters (Combined) for Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (2/3).
Figure 91. Observations with Assigned Clusters (Combined) for Wait, NASA-TLX, & Temporal Sensitivity Solution, faceted by Latency (3/3).
| Second | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  | 12  | 13  | 14  | 15  | 16  | 17  |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 2      | 3046| 154 | 126 | 96  | 0   | 31  | 70  | 14  | 12  | 16  | 1071| 103 | 58  | 24  |
| 3      | 154 | 933 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| 4      | 125 | 0   | 423 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| 5      | 99  | 0   | 0   | 4   | 1   | 0   | 1   | 0   | 0   | 4   | 0   | 0   | 0   | 0   | 0   |
| 6      | 0   | 0   | 0   | 0   | 855 | 0   | 0   | 0   | 0   | 56  | 0   | 0   | 0   | 0   | 0   |
| 7      | 30  | 0   | 0   | 0   | 0   | 0   | 26  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| 8      | 70  | 0   | 0   | 2   | 0   | 0   | 111 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| 9      | 14  | 0   | 0   | 0   | 0   | 0   | 0   | 448 | 534 | 0   | 0   | 0   | 0   | 0   | 0   |
| 10     | 11  | 0   | 0   | 1   | 0   | 0   | 0   | 534 | 1402| 0   | 0   | 0   | 0   | 0   | 0   |
| 13     | 18  | 0   | 0   | 0   | 0   | 56  | 0   | 0   | 0   | 81  | 58  | 0   | 0   | 0   | 0   |
| 14     | 1063| 0   | 0   | 3   | 0   | 0   | 0   | 0   | 0   | 0   | 60  | 1596| 0   | 0   | 0   |
| 15     | 103 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 386 | 0   | 0   | 0   | 0   |
| 16     | 57  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 20  | 0   | 0   | 0   |
| 17     | 24  | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 5   |
Figure 92. Frequency-Based Pathfinder Network of Cluster Transitions for Wait, NASA-TLX, & Temporal Sensitivity Solution.
Table 65. Linear Mixed-Effects Models for Wait, NASA-TLX, & Temporal Sensitivity Solution.

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<th># of Errors</th>
<th>Total Distance Traveled</th>
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<td>B (SE)</td>
<td>B (SE)</td>
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<td></td>
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<tr>
<td>Intercept</td>
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<td>12.37 (1.29)***</td>
</tr>
<tr>
<td>Latency (sec.)</td>
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<td>27.58 (2.07)***</td>
</tr>
<tr>
<td>Clearance (meters)</td>
<td>-0.17 (0.02)***</td>
<td>-4.25 (0.27)***</td>
</tr>
<tr>
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<td>3.52 (0.25)***</td>
<td>-24.31 (3.36)***</td>
</tr>
<tr>
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<td>2.58 (0.42)***</td>
<td>-18.03 (5.38)***</td>
</tr>
<tr>
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<td>1.90 (0.42)***</td>
<td>-17.80 (5.43)**</td>
</tr>
<tr>
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<td>-17.00 (5.55)**</td>
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<tr>
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<td>-17.93 (5.29)**</td>
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<td>-28.58 (5.42)**</td>
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<td>-27.02 (5.02)**</td>
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<td>-15.09 (5.41)**</td>
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<td>-13.03 (5.51)*</td>
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<td>-17.19 (5.41)**</td>
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<td>-16.40 (5.46)**</td>
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<td>Rand. Effects</td>
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<td>22.39 (4.73)***</td>
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Marg. $R^2$ 0.76 0.49 0.48
Cond. $R^2$ 0.79 0.61 0.67
ICC $null$ 0.15 0.22 0.19
# of Trials 379 379 379
# of Participants 89 89 89

* p < .05, ** p < .01, *** p < .001, +p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
### Appendix 1.12. Wait & Temporal Sensitivity Results

Table 66. Mixture Model for Wait & Temporal Sensitivity Solution.

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Figure 93. Observations with Assigned Clusters (Uncombined) for Wait & Temporal Sensitivity Solution (1/1).
Table 67. Cluster Summary for Wait & Temporal Sensitivity Solution.

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Figure 94. Observations with Assigned Clusters (Combined) for Wait & Temporal Sensitivity Solution (1/1).
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<th>Latency 375</th>
<th>Latency 500</th>
<th>Latency 625</th>
<th>Latency 750</th>
<th>Latency 875</th>
<th>Latency 1000</th>
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<td>0.68</td>
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</table>

**Marginal Means**


$\chi^2 = 333.89$, $p = 0$. 

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Figure 95. Observations with Assigned Clusters (Combined) for Wait & Temporal Sensitivity Solution, faceted by Latency (1/1).
### Table 69. Count of Cluster Transitions in Test Set for Wait & Temporal Sensitivity Solution.

<table>
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Figure 96. Frequency-Based Pathfinder Network of Cluster Transitions for Wait & Temporal Sensitivity Solution
Table 70. Linear Mixed-Effects Models for Wait & Temporal Sensitivity Solution.

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<tr>
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<th>Completion Time (min.)</th>
<th># of Errors</th>
<th>Total Distance Traveled</th>
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<td>B (SE)</td>
<td>B (SE)</td>
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<td>14.92 (1.25)***</td>
<td>715.33 (6.70)***</td>
</tr>
<tr>
<td>Latency (sec.)</td>
<td>1.44 (0.13)***</td>
<td>29.21 (1.84)***</td>
<td>180.75 (9.12)***</td>
</tr>
<tr>
<td>Clearance (meters)</td>
<td>-0.17 (0.02)***</td>
<td>-4.19 (0.25)***</td>
<td>-12.38 (1.24)***</td>
</tr>
<tr>
<td>Prop. Total Time Waiting</td>
<td>2.95 (0.37)***</td>
<td>-21.88 (5.06)***</td>
<td>-53.54 (25.31)*</td>
</tr>
<tr>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Prop. Total Time Waiting</td>
<td>4.03 (0.22)***</td>
<td>-28.49 (3.15)***</td>
<td>-88.85 (16.08)***</td>
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<tr>
<td>in Cluster 2</td>
<td>2.81 (0.42)***</td>
<td>-19.60 (5.70)***</td>
<td>-55.64 (27.86)*</td>
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<tr>
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<td>-13.53 (5.97)***</td>
<td>-36.56 (29.17)</td>
</tr>
<tr>
<td>in Cluster 4</td>
<td>2.50 (0.43)***</td>
<td>-12.31 (5.80)***</td>
<td>-54.50 (28.43)+</td>
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<tr>
<td>Prop. Total Time Waiting</td>
<td>2.80 (0.38)***</td>
<td>-10.06 (5.35)+</td>
<td>-41.53 (26.91)</td>
</tr>
<tr>
<td>in Cluster 6</td>
<td>2.19 (0.42)***</td>
<td>-15.80 (5.76)**</td>
<td>-36.18 (28.52)</td>
</tr>
<tr>
<td>Prop. Total Time Waiting</td>
<td>2.56 (0.44)***</td>
<td>-11.81 (5.98)*</td>
<td>-106.43 (29.56)***</td>
</tr>
<tr>
<td>in Cluster 8</td>
<td>2.72 (0.41)***</td>
<td>-17.89 (5.60)**</td>
<td>-66.18 (27.89)*</td>
</tr>
<tr>
<td>Prop. Total Time Waiting</td>
<td>2.52 (0.39)***</td>
<td>-22.07 (5.43)***</td>
<td>-55.65 (27.15)</td>
</tr>
<tr>
<td>in Cluster 10</td>
<td>2.75 (0.42)***</td>
<td>-4.14 (5.73)</td>
<td>-3.47 (28.30)</td>
</tr>
<tr>
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<td>3.30 (0.38)***</td>
<td>-21.45 (5.38)***</td>
<td>-109.39 (27.22)***</td>
</tr>
<tr>
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<td>-15.76 (5.71)**</td>
<td>-74.94 (28.06)***</td>
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<tr>
<td>Prop. Total Time Waiting</td>
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<td>-18.60 (5.82)**</td>
<td>-40.15 (28.73)</td>
</tr>
<tr>
<td>in Cluster 14</td>
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<td></td>
<td></td>
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<td>Var. (SD)</td>
<td>Var. (SD)</td>
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<td>32.37 (5.69)***</td>
<td>1380.26 (37.15)***</td>
</tr>
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<td>1619.75 (40.25)</td>
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<td>Cond. $R^2$</td>
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<td># of Participants</td>
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</tr>
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</table>

* p < .05, ** p < .01, *** p < .001, + p < .10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect.
Appendix 2. R Scripts

Appendix 2.1 – Data Cleaning

athome<-T
recalculateErrorSet<-T

if(athome){
gdrive<-"D:/"
} else{
gdrive<-"C:/Users/fscho/"
}

beep <- function(n = 6){
  for(i in seq(n)){
    system("rundll32 user32.dll,MessageBeep -1")
    Sys.sleep(.5)
  }
}

fileURL<-"Google Drive/Graduate School/Research/Dissertation/Data Analysis"
setwd(paste(gdrive,fileURL,sep=""))
BAMF<-read.csv("BAMF_01_03_2020.csv")

frameDecision<-0
p<-levels(as.factor(BAMF$PNum))
tri<-as.numeric(levels(as.factor(BAMF$Trial)))
k<-1

#Z < 10 & X < 80
#Z > 70 & X < 80
BAMF$NoGoZone<-0
BAMF$NoGoZone[which( (BAMF$position_Z < 10 | BAMF$position_Z >70 ) &
BAMF$position_X<80)]<-1
BAMF$TrialSummaryRow<-0

#Function is going be used in the loop below
#Function is going to take two things: Name of new data set, the current trial data, and a vector
#of starts and stops
#Output a data set
eventMaker<-function(setName, trial, marker){
st<-marker[c(TRUE, FALSE)]
stp<-marker[c(FALSE, TRUE)]
for(i in 1:length(st)){
currEvent <- trial[st[i]:stp[i],]
currEvent$startTime <- currEvent$currentTime[1]
currEvent$endTime <- currEvent$currentTime[nrow(currEvent)]
currEvent$dist <- sum(currEvent$PythDist)
currEvent$tot_rot <- sum(abs(currEvent$rotation_Y))
currEvent$startTime <- currEvent$endTime - currEvent$startTime
currEvent$start_position_X <- currEvent$position_X[1]
currEvent$start_position_Y <- currEvent$position_Y[1]
currEvent$start_position_Z <- currEvent$position_Z[1]
currEvent$start_rotation_X <- currEvent$rotation_X[1]
currEvent$start_rotation_Y <- currEvent$rotation_Y[1]
currEvent$start_rotation_Z <- currEvent$rotation_Z[1]
currEvent$end_position_X <- currEvent$position_X[nrow(currEvent)]
currEvent$end_position_Y <- currEvent$position_Y[nrow(currEvent)]
currEvent$end_position_Z <- currEvent$position_Z[nrow(currEvent)]
currEvent$end_rotation_X <- currEvent$rotation_X[nrow(currEvent)]
currEvent$end_rotation_Y <- currEvent$rotation_Y[nrow(currEvent)]
currEvent$end_rotation_Z <- currEvent$rotation_Z[nrow(currEvent)]
currEvent$NoGoZone <- sum(currEvent$NoGoZone)
if(sum(currEvent$NoGoZone) != 0){
    currEvent$NoGoZone <- 1
}

if(exists(setName)){
    assign(setName, rbind(get(setName), currEvent[1,]), envir=.GlobalEnv)
}else{
    assign(setName, currEvent[1,], envir=.GlobalEnv)
}

for(i in p){
    for(j in tri){
        currSet <- BAMF[which(BAMF$PNum==i & BAMF$Trial==j),]
        currSet <- currSet[which(currSet$Input==1)[1]:nrow(currSet),]
        #Drops anything before they press a button
        currSet$rot <- currSet$rotation_Y[-c(0,currSet$rotation_Y[-nrow(currSet)])]
        #Change in rotation for trial
        currSet$PythDist[1] <- 0
        #Fix PythDist for first frame of each data set
        currSet$rowIndex <- 1:nrow(currSet)
        #Renumber the rows
        currSet$currentTime <- currSet$currentTime - currSet$currentTime[1]
        #Current Time for Trial start <- currSet$currentTime[1]
end <- currSet$currentTime[nrow(currSet)]
currSet$SCT <- as.numeric(end) - as.numeric(start)
currSet$maxIndex <- max(currSet$currentIndex)
currSet$tot_dist <- sum(currSet$PythDist)
currSet$tot_rot <- sum(abs(currSet$rot))
currSet$error[which(currSet$Collision != "No Collision")]<-1
currSet$noError[which(currSet$Collision == "No Collision")]<-1

# Identify transition rows
# There is a unique edge case that will make this crash, 
# where if the first and last frames are transition frames
ISD <- sort(c(1, which(diff(currSet$Input, lag=1)!=0), which(diff(currSet$Input, lag=1)!=0)+1, nrow(currSet)))

# ExSD <- sort(c(1, which(diff(currSet$Executing, lag=1)!=0), which(diff(currSet$Executing, lag=1)!=0)+1, nrow(currSet)))

ErSD <- sort(c(1, which(diff(currSet$error, lag=1)!=0), which(diff(currSet$error, lag=1)!=0)+1, nrow(currSet))) # This one is calculated differently

eventMaker("InputSet", currSet, ISD)

# eventMaker("ExecutingSet", currSet, ExSD) # Executive decision that the executing Set doesn't add anything about the input set
if(recalculateErrorSet){
  eventMaker("ErrorSet", currSet, ErSD)
}

# BAMF[which(BAMFS$PNum==i & BAMFS$Trial==j),]$TrialSummaryRow[nrow(currSet)]<1 # Is wrong, InputSet is the summary row guy

k <- k + 1
# progress(grep(i, p)[1], length(p), TRUE)
cat("\n\n Just finished: ", i, " trial ", j)
flush.console()
}

beep()

# Picks the last row for each trial as the summary row
InputSet$TrialSummaryRow <- c(diff(InputSet$Trial), 1)

trials <- InputSet[which(InputSet$TrialSummaryRow != 0),]
# Fixes the single frame undercount issue
fix <- InputSet$startTime[-1] - InputSet$startTime[-nrow(InputSet)]
fix[which(fix <= 0)] <- InputSet$endTime[which(fix <= 0)] - InputSet$startTime[which(fix <= 0)] + 1/InputSet$currentFPS[which(fix <= 0)]
fix[length(fix) + 1] <- InputSet$endTime[nrow(InputSet)] - InputSet$startTime[nrow(InputSet)] + 1/InputSet$currentFPS[nrow(InputSet)]
InputSet$timeOfEvent <- fix

# Fixes the single frame undercount issue
fix <- ErrorSet$startTime[-1] - ErrorSet$startTime[-nrow(ErrorSet)]
fix[which(fix <= 0)] <- ErrorSet$endTime[which(fix <= 0)] - ErrorSet$startTime[which(fix <= 0)] + 1/ErrorSet$currentFPS[which(fix <= 0)]
fix[length(fix) + 1] <- ErrorSet$endTime[nrow(ErrorSet)] - ErrorSet$startTime[nrow(ErrorSet)] + 1/ErrorSet$currentFPS[nrow(ErrorSet)]
ErrorSet$timeOfEvent <- fix

trials$errors <- 0
trials$tot_wait_time <- 0
for (i in 1:nrow(trials)) {
  a <- ErrorSet$PNum == trials$PNum[i]
  b <- ErrorSet$Latency == trials$Latency[i]
  c <- ErrorSet$error == 1
  trials$errors[i] <- nrow(ErrorSet[which(a & b & c),])
  a <- InputSet$PNum == trials$PNum[i]
  b <- InputSet$Latency == trials$Latency[i]
  c <- InputSet$Input == 0
  trials$tot_wait_time[i] <- sum(InputSet$timeOfEvent[which(a & b & c)])
  a <- InputSet$PNum == trials$PNum[i]
  b <- InputSet$Latency == trials$Latency[i]
  c <- InputSet$Input == 1
  trials$tot_move_time[i] <- sum(InputSet$timeOfEvent[which(a & b & c)])
}

trials$CTMin <- trials$CT / 60
trials$num_button_presses <- round(trials$maxIndex / 2, digits = 0) # Rounding incase the last press is a move.
trials$num_button_pressesPerSec <- trials$num_button_presses / trials$CT
trials$num_button_pressesPerDist <- trials$num_button_presses / trials$tot_dist
trials$ErrorsPerMin <- trials$errors / (trials$CT / 60)
trials$ErrorsPerDist <- trials$errors / trials$tot_dist
trials$num_button_pressesPerDistPerSec <- trials$num_button_presses / (trials$tot_dist / trials$CT)
trials$ErrorsPerDistPerSec <- trials$errors / (trials$tot_dist / trials$CT)
trials$sabs_a_len <- abs(trials$a_len - 1)
trials$sabs_a_time <- abs(trials$a_time - 1)
trials$DistPerMin <- trials$tot_dist / trials$CTMin
trials$Wait_Per_Min <- trials$tot_wait_time / trials$CTMin

# Clean up data set
trials$Lat1000 <- trials$Latency / 1000
ErrorSet$Lat1000 <- ErrorSet$Latency / 1000
# executingSet$Lat1000 <- executingSet$Latency / 1000
InputSet$Lat1000 <- InputSet$Latency / 1000
trials$Lat1000 <- trials$Latency / 1000

trials$CTMin <- trials$CT / 60
trials$c_atime <- trials$a_time - mean(trials$a_time)
trials$c_Lat1000 <- trials$Lat1000 - .5
trials$c_Clearance <- trials$Clearance - 7

InputSet$c_atime <- InputSet$a_time - mean(InputSet$a_time)
InputSet$c_Lat1000 <- InputSet$Lat1000 - .5
InputSet$c_Clearance <- InputSet$Clearance - 7

# Now I have to essentially make a second InputSet, that pairs each item with its post move and post wait
# First, lets shrink.

keep <- c("PNum", "Experimenter", "Trial", "Latency", "Clearance", "Computer","a_time","a_time_medSplit","Input","Input_Movement","Input_Rotating","tot_rot","dist","CT","tot_dist","NoGoZone","TrialSummaryRow","startTime","endTime","timeOfEvent","Lat1000","c_atime","c_Lat1000","c_Clearance")

InputSet <- InputSet[,keep]

# repeats <- c(dist, timeOfEvent)
InputSet$PM_Move_Time <- 0
InputSet$PM_Move_dist <- 0
InputSet$PM_Move_rot <- 0
InputSet$PM_Move_NoGoZone <- 0

InputSet$PM_Wait_Time <- 0
InputSet$Index<-1:nrow(InputSet)

p<levels(as.factor(InputSet$PNum))
tris<levels(as.factor(InputSet$Trial))
for(i in p){
  for(j in tris){
    currSet<-InputSet[which(InputSet$PNum==i & InputSet$Trial==j),]
    #For each item in the set, check if its (1) a move, then (2) for the existence of a post wait, and
    # (3) for a post move
    for(k in 1:nrow(currSet)){
      if(currSet$Input[k]){#I'm dealing with a move
        if(k+1<=nrow(currSet)){#There's a wait!
          currSet$PM_Wait_Time[k]<-currSet$timeOfEvent[k+1]
        }else{#There's no wait :(
          currSet$PM_Wait_Time[k]<-NA
        }
      }
      if(k+2<=nrow(currSet)){#There's a move!
        currSet$PM_Move_Time[k]<-currSet$timeOfEvent[k+2]
        currSet$PM_Move_dist[k]<-currSet$dist[k+2]
        currSet$PM_Move_rot[k]<-currSet$tot_rot[k+2]
        currSet$PM_Move_NoGoZone[k]<-currSet$NoGoZone[k+2]
      }else{#There's no move :(
        currSet$PM_Move_Time[k]<-NA
        currSet$PM_Move_dist[k]<-NA
        currSet$PM_Move_rot[k]<-NA
        currSet$PM_Move_NoGoZone[k]<-NA
      }
    }
    #Its in this space where I go from currSet back to InputSet
    InputSet[currSet$Index[1]:currSet$Index[nrow(currSet)],]<-currSet
  }
}
InputSet<-InputSet[which(InputSet$Input==1),]

save.image(file = paste( getwd(), "/01_03_2020.RData", sep=""))
#Store data sets in case of a mistake
if(recalculateErrorSet){
  write.csv(ErrorSet, file = paste( getwd(), "/errorSet_01_03_2020.csv", sep=""),
            row.names=FALSE)
}

write.csv(trials, file = paste( getwd(), "/trials_02_27_2020.csv", sep=""), row.names=FALSE)
write.csv(InputSet, file = paste( getwd(), "/inputSet_01_03_2020.csv", sep=""),
row.names=FALSE)
Appendix 2.2 – Cluster Generation

# Load data into script
# Cluster ~50 times per variable set. Finds the best match between data and variable combo.
# Save after each cluster attempt
# Historically, running each variable set for MLE and MAP took 14 hours per iteration
# This is my attempt at parallelization, such that each iteration takes 14 hours, but I’ve got
# multiple going at once
# I.e., if I have "num_parallel" = 3 AND at least 3 cpu cores, then I can run 3 iterations over a 14
# hour period... a gain of 300%
# Note: I'm like 80/20 that R doesn't use hyperthreading, so its actual cores and not logical cores.
# :(
rm(list=ls())
athome<-T
maxG<-T # If True, maxG is n^0.3, if a number, then it calculates that number of clusters (i.e.
"maxG<-10", old run had it set to 10)
num_iterations <-50
num_parallel <-6

if(athome){
  gdrive<-"D:/"
}else{
  gdrive<-"C:/Users/fscho/
}

fileURL<-"Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

ProcessID<- Sys.getpid()
# print(ProcessID)

library(mclust) #note, this also needs to be called after the sockets are made
library(parallel)
library(gtools)
library(doParallel)

### THIS LOADS UP THE DATA AND APPENDS THE WORKLOAD SCORES I FORGOT TO APPEND###
InputSet<-read.csv(file = "inputSet_01_03_2020.csv", stringsAsFactors=FALSE)
InputSet$SampleWeight <- InputSet$timeOfEvent / InputSet$CT # Used for HC sampling
InputSet$rowIndex <- 1:nrow(InputSet) # Same
InputSet$U_ID<-paste(InputSet$Latency, InputSet$Clearance, sep="_")
InputSet$U_ID_P2<-paste(InputSet$Latency, InputSet$Clearance, InputSet$PNum, sep="_")
trials<-read.csv("trials_01_03_2020.csv", stringsAsFactors = F)
InputSet$TLX<-1
#Append TLX things
for(i in 1:nrow(trials)){
  pnum<-trials$PNum[i]
  tri<-trials$Trial[i]

  InputSet[which(InputSet$PNum==pnum & InputSet$Trial==tri),]$TLX <-
  trials$weightedRating[i]
}

InputSet$jitter_timeOfEvent <- InputSet$timeOfEvent + runif(nrow(InputSet), -.5/60, .5/60)
#Adds some jitter
InputSet$jitter_PM_Wait_Time <- InputSet$PM_Wait_Time + runif(nrow(InputSet), -.5/60, .5/60) #Adds some jitter

#Drop incomplete cases
varOfInt<-c("jitter_timeOfEvent", "jitter_PM_Wait_Time", "TLX", "a_time")
InputSet<-InputSet[complete.cases(InputSet[,varOfInt]),]

#Clustering Variables
#All 1D variable sets of interest
M_N<-c("jitter_timeOfEvent")
W_N<-c("jitter_PM_Wait_Time")

#All 2D variable sets of interest
M_W_N<-c("jitter_timeOfEvent", "jitter_PM_Wait_Time")
M_TLX<-c("jitter_timeOfEvent", "TLX")
M_TS<-c("jitter_timeOfEvent", "a_time") #

W_TLX<-c("jitter_PM_Wait_Time", "TLX") #
W_TS<-c("jitter_PM_Wait_Time", "a_time")

#All 3D variable sets of interest
M_TLX_TS<-c("jitter_timeOfEvent", "TLX", "a_time") #
M_W_TS<-c("jitter_timeOfEvent", "jitter_PM_Wait_Time", "a_time") #
M_W_TLX<-c("jitter_timeOfEvent", "jitter_PM_Wait_Time", "TLX") #
W_TLX_TS<-c("jitter_PM_Wait_Time", "TLX", "a_time") #

#All 4D variable sets of interest
M_W_TLX_TS<-c("jitter_timeOfEvent", "jitter_PM_Wait_Time", "TLX", "a_time") #
varSet<-list(M_N, W_N, M_W_N, M_TLX, M_TS, W_TLX, W_TS, M_TLX_TS, M_W_TS, M_W_TLX, W_TLX_TS, M_W_TLX_TS)


#Make a function to split the data set into test and train
randTrain<-function(dataSet){
    combos<-levels(as.factor(dataSet$U_ID))
    trainVec<-c()
    for(i in 1:length(combos)){
        trainVec<-c(trainVec,sample(levels(as.factor(dataSet$U_ID_P2[which(dataSet$U_ID==combos[i])]), 5))
    }
    test<-InputSet[which(!is.element(InputSet$U_ID_P2, trainVec)),] #Remember to report demographics for test and train data sets
    return(which(is.element(dataSet$U_ID_P2, trainVec)))
}

if(maxG == T){
    maxG <- ceiling((nrow(InputSet)/2)^.3) #Largest integer greater than n^.3...
    #but training sets are approx half the data, so /2
}

megaModels<-rep(varSet, num_iterations)

#Run randTrain num_model times, where num_model is the TOTAL number of models to be fit
#number of variable sets * number of iterations
num_models<-length(megaModels)
randModels<-list()
for(i in 1:num_models){
    randModels[[i]]<-randTrain(InputSet)
# Feed it randModels[[i]], megaModels[[i]]

clusterProcess <- function(Data, Gsize=1:maxG, varSet, iter, trainVec ){

  nameOfVarSet <- names(varSet)
  varSet <- unlist(varSet)
  # trainData <- Data[trainVec,]
  write(timestamp(), paste("Clusters/Jitter/___", nameOfVarSet,"_", iter, ",",Sys.getpid(), "_____started.txt", sep=""))

  if(length(varSet)==1){
    MN <- c("V")
  }else{
    MN <- c("VVV")
  }

  # save(trainVec, file=paste(wd,"/Clusters/",nameOfVarSet,"_DATA_", iter_varSet,"_", Sys.getpid(), "_RNG", sample(1:999999)[1], ",.RData", sep=""))
  MixtureFit <- Mclust(data = Data[trainVec, varSet],modelNames=MN, G=Gsize,
                        prior=priorControl())
  ret <- list(iter, varSet, MixtureFit, trainVec)
  names(ret) <- c("iter", "Variables_Used", "Results", "trainVec")
  fileName <- paste(wd,"/Clusters/Jitter/",nameOfVarSet,"_", iter, ",", Sys.getpid(), "_RNG", sample(1:999999)[1], ",.RData", sep=""))
  save(ret, file = fileName)
  set.seed(seed=NULL)
  write(timestamp(), paste("Clusters/Jitter/___", nameOfVarSet,"_", iter, "_",Sys.getpid(), "_____finished.txt", sep=""))

  return(ret)
}

# Need to make a socket cluster
# Make num_parallel sockets
sock <- makeCluster(num_parallel)
Sys.sleep(3) # Wait 3 seconds in case sockets take a while
# Send stuff to put in each socket
wd <- getwd()
feet <- c("wd")
clusterExport(sock, feet)
clusterEvalQ(sock, library(mclust)) # Loads MClust into my sockets
registerDoParallel(sock)
gatheredClusters<- foreach(j=1:num_models.,verbose = T) %dopar% clusterProcess(Data = InputSet, varSet = megaModels[j], trainVec = randModels[[j]], iter = j )
stopCluster(sock)
# save(gatheredClusters, file= paste("Clusters/doPar/Script_2_doPar.RData", sep=""))
save(gatheredClusters, file= paste("Script_2_jitter_doPar.RData", sep=""))
Appendix 2.3 – Cluster Combiner (Baudry, et al. 2010 Procedure)

rm(list=ls())
athome<-T
num_parallel <-4 #dopar is inefficient w/RAM relative to parLapply.... but I've figured out a way to manage
    #it using a chunking strategy that works around it. It does possibly cause some bottlenecking issues
chunk_size<12 #The larger this is, the more memory I'm required to have, but the fewer bottlenecking events I'll run into.
    #Bottlenecking should be minimal when chunk_size / num_parallel is an integer
num_piecewise<- 2 #This is sorta arbitrary, but the article that suggested it used both 2 and 3. The more changepoint, the more conservative.

if(athome){
    gdrive<"D:"
}else{
    gdrive<"C:/Users/fscho/
}

fileURL<"Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

library(mclust)
library(parallel)
library(doParallel)

script2<list.files(pattern="Script_2")
if(length(script2) > 1){
    stop("Too many scripts")
}

load(script2)

#Using this to generate a list to do stuff on
clust<list()
iterName<"c()"
for(i in 1:length(gatheredClusters)){
    clust[[i]]<-gatheredClusters[[i]]$Results
    iterName[i]<-paste(gatheredClusters[[i]]$Iter, paste(gatheredClusters[[i]]$Variables_Used, collapse ="-"), collapse="-"
#Clust is too big, so I'm going to chunk it into a bunch of smaller, memory friendly chunks, and then bring them all together.

```r
start <- seq(1, length(clust), by=chunk_size)
stop <- seq(0, length(clust), by=chunk_size)[-1]
for(i in 1:length(start)){
  #This is really annoying, but I have to start and then kill the clusters after every chunk
  sock2 <- makeCluster(num_parallel)
 Sys.sleep(3)
  wd <- getwd()
  feet <- c("wd")
  clusterExport(sock2, feet)
  clusterEvalQ(sock2, library(mclust))
  registerDoParallel(sock2)
  #This is me doing the chunking
  chunk <- clust[start[i]:stop[i]]
  combiClust <- foreach(j=1:length(chunk),.verbose = T, .inorder = T) %dopar%
  clustCombi(chunk[[j]])
  names(combiClust) <- names(chunk)
  stopCluster(sock2)
  save(combiClust, file = paste("Clusters/Jitter/Dissertation Combined Clusters/Script_3_Jitter_CombiClust_Start_", start[i], ", Stop_", stop[i], ", _PID_", Sys.getpid(), "_RData", sep=" "))
}
```

#Find the "optimal" cluster size
#They're almost too big to load in memory all at once, so I'm going to have to chunk again

```r
combis <- list.files(path="Clusters/Jitter/Dissertation Combined Clusters/", pattern="Script_3_Jitter_CombiClust_Start", full.names = T)
```

#Load chunk, optim the chunk, save the new optim stuff
for(i in 1:length(combis)){
  sock2 <- makeCluster(num_parallel)
  Sys.sleep(3)
  wd <- getwd()
  feet <- c("wd")
  clusterExport(sock2, feet)
  clusterEvalQ(sock2, library(mclust))
registerDoParallel(sock2)
go(gc(verbose = F))

chunk <- combis[i]
start <- as.numeric(strsplit(chunk, " ")[[1]][grep("Start", strsplit(chunk, " ")[[1]])+1])
stop <- as.numeric(strsplit(chunk, " ")[[1]][grep("Stop", strsplit(chunk, " ")[[1]])+1])
load(chunk)

combiOptimClust <- foreach(j = 1:length(combiClust), .verbose = T, .inorder = T) %dopar% clustCombiOptim(combiClust[[j]], reg = num_piecewise)
names(combiOptimClust) <- names(combiClust)
stopCluster(sock2)
save(combiOptimClust, file = paste("Clusters/Jitter/Optim/Script_3_Jitter_Output_CombiClustOptim_", "PcwReg_", num_piecewise, "_Start_", start, "_Stop_", stop, "_PID_", Sys.getpid(), "RData", sep = ""))
}
Appendix 2.4 – Cluster File Reorganizer

rm(list=ls())
athome<-T
num_parallel <- 4 # dopar is inefficient w/RAM relative to parLapply,... but I've figured out a way to manage
# it using a chunking strategy that works around it. It does possibly cause some bottlenecking issues
chunk_size<-12 # The larger this is, the more memory I'm required to have, but the fewer bottlenecking events I'll run into.
# Bottlenecking should be minimal when chunk_size / num_parallel is an integer

if(athome){
  gdrive<-"D:/"
} else{
  gdrive<-"C:/Users/fscho/"
}

fileURL<-"Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

library(mclust)
library(parallel)
library(doParallel)

mclustFL<-list.files("Clusters/Jitter/MClust Output", pattern="RNG")
combiFL<-list.files("Clusters/Jitter/Dissertation Combined Clusters", pattern="Script")
optimFL<-list.files("Clusters/Jitter/Optim", pattern="Script")
optimFL_PCW2 <- grep("PcwReg_2", optimFL, value = T)
optimFL_PCW3 <- grep("PcwReg_3", optimFL, value = T)

# Clustering Variables
# All 1D variable sets of interest
M_N<-c("timeOfEvent")
W_N<-c("PM_Wait_Time")

# All 2D variable sets of interest
M_W_N<-c("timeOfEvent", "PM_Wait_Time")
M_TLX<-c("timeOfEvent", "TLX")
M_TS<-c("timeOfEvent", "a_time") #

W_TLX<-c("PM_Wait_Time", "TLX") #
W_TS<-c("PM_Wait_Time", "a_time")
All 3D variable sets of interest

```r
M_TLX_TS <- c("timeOfEvent", "TLX", "a_time") #
M_W_TS <- c("timeOfEvent", "PM_Wait_Time", "a_time") #
M_W_TLX <- c("timeOfEvent", "PM_Wait_Time", "TLX") #
W_TLX_TS <- c("PM_Wait_Time", "TLX", "a_time") #
```

All 4D variable sets of interest

```r
M_W_TLX_TS <- c("timeOfEvent", "PM_Wait_Time", "TLX", "a_time") #
```

```r
varSet <- list(M_N, W_N, M_W_N, M_TLX, M_TS, W_TLX, W_TS, M_TLX_TS, M_W_TS, M_W_TLX, W_TLX_TS, M_W_TLX_TS)
```

```r
```

Process:

```r
for(i in 1:length(varSet)){ #Top level is my varSet
    cat("\n")
    cat(paste("Starting ", i, " - ", names(varSet)[i], " at...\n", sep=""))
    timestamp()
    flush.console()
    mclustFLVarSet <- grep(paste("^", names(varSet)[i], ",\", ",\", sep=""), mclustFL, value =T)
    #List structure:
    #TOP LEVEL: ITERATION (length(list) == 50)
    #VarSet, iter, trainVec, clustCombi, Optim
    ##VarSet: Just the variable set (no further depth)
    ##Iter: Just the iteration (no further depth)
    ##TrainVec: Just the trainVec (no further depth)
    ##clustCombi: ClustCombi Stuff / Mclust Stuff
    ###Mclust Stuff
    ##Optim: Just the optim stuff
    varSetList <- list()
    for(j in 1:length(mclustFLVarSet)){ #This level is for the iteration
        load(paste("Clusters/Jitter/MClust Output/", mclustFLVarSet[j], sep=""))
        varSetList[j]$varSet <- ret[1]
        varSetList[[j]][2:3] <- ret[c(2,4)]
        names(varSetList[[j]]) <- c("Iteration", "VariableSet", "trainVec")
        #Identify the start/stop coordinates that the current iter belongs to
        #Need to make sure three cases work: At the beginning (i.e. = start), at the end (i.e. = stop),
        #and the middle (start < value < stop)
        #If I take the [ 1+ iter - (iter % length(varSet)) ], I get the "start" value that it belongs to
        CarmenSandiego <- varSetList[[j]]$Iteration
        if( (CarmenSandiego % length(varSet) == 0){ #This is a stop
```
stopHere<- CarmenSandiego
} else{ #If it isn't a stop, round it up
stopHere<- CarmenSandiego + (12 - CarmenSandiego %% (length(varSet) ))
}

loadCombi<-grep(paste("Stop_", stopHere, ",PID", sep=""), combiFL, value = T)
load(paste("Clusters/Jitter/Dissertation Combined Clusters/", loadCombi, sep=""))
position<-ifelse(CarmenSandiego %% 12 == 0, 12, CarmenSandiego %% 12 )
cc<-combiClust[[position]]
varSetList[[j]][4]<-list(cc)
names(varSetList[[j]])[4]<-"clustCombi"

loadOptim2<-grep(paste("Stop_", stopHere, ",PID", sep=""), optimFL_PCW2, value = T)
load(paste("Clusters/Jitter/Optim/", loadOptim2, sep=""))
co<-combiOptimClust[[position]]
varSetList[[j]][5]<-list(co)
names(varSetList[[j]])[5]<-"clustCombiOptim_pcwReg2"

loadOptim3<-grep(paste("Stop_", stopHere, ",PID", sep=""), optimFL_PCW3, value = T)
load(paste("Clusters/Jitter/Optim/", loadOptim3, sep=""))
co<-combiOptimClust[[position]]
varSetList[[j]][6]<-list(co)
names(varSetList[[j]])[6]<-"clustCombiOptim_pcwReg3"

}
save(varSetList, file= paste(getwd(), "/Clusters/Jitter/varSetOrganization/", names(varSet)[i], ".RData", sep=""))
cat("n\n")
cat(paste("Stopping ", i, " - ", names(varSet)[i], " at...\n", sep=""))
timestamp()
flush.console()
Appendix 2.5 – Cluster Summary Plots and Piecewise Regression

rm(list=ls())
athome<-'T'
num_parallel <-4 #dopar is inefficient w/RAM relative to parLapply.... but I've figured out a way to manage
#it using a chunking strategy that works around it. It does possibly cause some bottlenecking issues
chunk_size<-12 #The larger this is, the more memory I'm required to have, but the fewer bottlenecking events I'll run into.
#Bottlenecking should be minimal when chunk_size / num_parallel is an integer

if(athome){
  gdrive<-'D:/'
}else{
  gdrive<-'C:/Users/fscho/
}

fileURL<-'Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

library(mclust)
library(parallel)
library(doParallel)
library(ggplot2)
#library(colorbrewer)
library(gridExtra)
library(colorspace)
library(gtable)

ExtractEntropy<-function(combinedCluster){
  #This function comes from a statsexchange page.
  #It looks like it uses an internal clustCombi function.... but the extracted entropy makes identical graphs
  #So it works!
  #https://stats.stackexchange.com/a/244974
  combiM <- combinedCluster$combiM
  Kmax <- ncol(combinedCluster$MclustOutput$z)
  z0 <- combinedCluster$MclustOutput$z
  ent <- numeric()

  for (K in Kmax:1) {
    z0 <- t(combiM[[K]] %*% t(z0))
  }
ent[K] <- -sum(mclust::xlog(z0))
}

ENT <- data.frame(`Number of clusters` = 1:Kmax, `Entropy` = round(ent, 3))

ENT$Diff.In.Ent <- ENT$Entropy - ENT$Entropy[c(NA, 1:(nrow(ENT)-1))]

# Learned from the above function, and I dug right into the entPlot code... I'm changing it up a
# smidge
mergedn <- numeric()
z0 <- combinedCluster$MclustOutput$z
Kmax <- ncol(combinedCluster$MclustOutput$z)
for (K in (Kmax - 1):1) {
z0 <- t(combiM[[K + 1]] %*% t(z0))
mergedn[K] = sum(sapply(map(z0), function(x)
any(which(as.logical(combiM[[K]][rowSums(combiM[[K]]) == 2, j]) == x)))
)
}
return(ENT)
}

# Build the data frame
vs <- list.files("Clusters/Jitter/varSetOrganization", pattern="RData", full.names = T)
makeFrame <- function(vsSingle){
load(vsSingle)
BICFrame <- as.data.frame(matrix(nrow =
length(varSetList[[1]]$clustCombi$MclustOutput$BIC) * length(varSetList),
ncol = 3))
names(BICFrame)<-c("Iteration", "Mixtures", "BIC")
BICFrame$Iteration<- -99
BICFrame$Mixtures<- rep(1:length(varSetList[[1]]$clustCombi$MclustOutput$BIC), length(varSetList))
BICFrame$BIC <- -999999999999999999
BICFrame$Entropy <- NA
BICFrame$Normed_Entropy <- NA
BICFrame$Optimal_Number_2 <- NA
BICFrame$Optimal_Number_3 <- NA

for(i in 1:length(varSetList)){
start<- 1 + (length(varSetList[[i]]$clustCombi$MclustOutput$BIC) * (i - 1))
stop<- start + length(varSetList[[i]]$clustCombi$MclustOutput$BIC) -1
BICFrame$Iteration[start:stop] <- varSetList[[i]]$Iteration
BICFrame$Mixtures[start:stop] <-
l: length(unlist(varSetList[[i]]$clustCombi$MclustOutput$BIC))
BICFrame$BIC[start:stop] <-
unlist(varSetList[[i]]$clustCombi$MclustOutput$BIC)[1:length(unlist(varSetList[[i]]$clustCombi$MclustOutput$BIC))]

ent <- ExtractEntropy(varSetList[[i]]$clustCombi)
stop_ent <- start + nrow(ent) - 1

BICFrame$Entropy[start:stop_ent] <- ent$Entropy
BICFrame$Optimal_Number_2[start:stop_ent] <-
varSetList[[i]]$clustCombiOptim_pcwReg2$numClusters.combi
BICFrame$Optimal_Number_3[start:stop_ent] <-
varSetList[[i]]$clustCombiOptim_pcwReg3$numClusters.combi

for(i in 1:length(vs)){
cat("n
nStarting", i, "n")
timestamp()
flush.console()

dfTemp<-makeFrame(vs[i])
ifelse(i==1, bigFrame <- dfTemp, bigFrame<-rbind(bigFrame, dfTemp))
}
save(bigFrame, file="Jitter_Script5_DF.RData")

hasMove<- grepl("M", bigFrame$VarSet)
hasWait <- grepl("W", bigFrame$VarSet)
hasBothM <- hasMove & hasWait
onlyMove <- as.logical(hasMove - hasBothM)
onlyWait <- as.logical(hasWait - hasBothM)

bigFrame$Move<-
bigFrame$Move[which(hasBothM)]<-"Both"
bigFrame$Move[which(onlyMove)]<-"Move"
bigFrame$Move[which(onlyWait)]<-"Wait"

#TLX, TS, None, Both
hasTLX <- grepl("TLX", bigFrame$VarSet)
hasTS <- grepl("TS", bigFrame$VarSet)
hasBothC <- hasTLX & hasTS
onlyTLX <- as.logical(hasTLX - hasBothC)
onlyTS <- as.logical(hasTS - hasBothC)

bigFrame$Context <- "None"
bigFrame$Context[which(hasBothC)] <- "Both"
bigFrame$Context[which(onlyTLX)] <- "NASA-TLX"
bigFrame$Context[which(onlyTS)] <- "Temporal Sensitivity"

bigFrame$Context <- factor(bigFrame$Context, levels = c("None", "NASA-TLX", "Temporal Sensitivity", "Both"))
bigFrame$Move <- factor(bigFrame$Move, levels = c("Move", "Wait", "Both"))

BICPlots <- function(){
bicPlotRibbon <- ggplot(bigFrame, aes(x=Mixtures, y=BIC, col = Iteration))+
  stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1/2),
  color="black")+
  # stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 2/3),
  #  color="black", alpha = 7/10 )+
  stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1),
  color="black", alpha = 5/10 )+
  scale_x_continuous(breaks = seq(0,max(bigFrame$Mixtures), 5)[-1],
  limits=c(1,max(bigFrame$Mixtures)) ) +
  xlab("Number of Mixture Components") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    legend.text = element_text(size=12))+
  theme(legend.position = "none") +
  facet_grid(Move~Context, scales="fixed") +
  theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

#Drop NASA-TLX and both context, look at moves
bigFrameNoTLXBoth <- bigFrame[ -which(hasTLX | hasBothC),]

bicPlotRibbonLessContext <- ggplot(bigFrameNoTLXBoth, aes(x=Mixtures, y=BIC, col = Iteration)) +
  stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1/2),
  color="black") +
  # stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 2/3),
  #  color="black", alpha = 7/10 ) +

```r
stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10 ) +
scale_x_continuous(breaks = seq(0,max(bigFrameNoTLXBoth$Mixtures), 5)[-1], limits=c(1,max(bigFrameNoTLXBoth$Mixtures))) +
xlab("Number of Mixture Components") +
theme_minimal() +
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
axis.title.x = element_text(size = 12),
axis.title.y = element_text(size = 12),
legend.text = element_text(size=12)) +
theme(legend.position = "none") +
facet_grid(Move~Context, scales="fixed") +
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

bicPlotRibbonLessContext_Flip<- ggplot(bigFrameNoTLXBoth, aes(x=Mixtures, y=BIC , col = Iteration)) +
stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1/2), color="black" ) +
# stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10 ) +
stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10 ) +
scale_x_continuous(breaks = seq(0,max(bigFrameNoTLXBoth$Mixtures), 5)[-1], limits=c(1,max(bigFrameNoTLXBoth$Mixtures))) +
xlab("Number of Mixture Components") +
theme_minimal() +
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
axis.title.x = element_text(size = 12),
axis.title.y = element_text(size = 12),
legend.text = element_text(size=12)) +
theme(legend.position = "none") +
facet_grid(Context~Move, scales="fixed") +
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

bigFrame_minimal<- bigFrame[ -which(hasTLX | hasBothC | hasBothM),]
bicPlotRibbon_minimal<- ggplot(bigFrame_minimal, aes(x=Mixtures, y=BIC , col = Iteration)) +
stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1/2), color="black" ) +
# stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10 ) +
stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10 ) +
```
scale_x_continuous(breaks = seq(0,max(bigFrame_minimal$Mixtures), 5)[-1],
limits=c(1,max(bigFrame_minimal$Mixtures))) +
  xlab("Number of Mixture Components") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    legend.text = element_text(size=12))+
  theme(legend.position = "none") +
  facet_grid(Context~Move, scales="fixed")+
  theme(strip.text.x = element_text(size=12), strip.text.y = element_text(size=12))

bicPlotRibbon_minimal_flip <- ggplot(bigFrame_minimal, aes(x=Mixtures, y=BIC, col = Iteration)) +
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
    color="black") +
  # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
  # color="black", alpha = 7/10 ) +
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
    color="black", alpha = 5/10 ) +
  scale_x_continuous(breaks = seq(0,max(bigFrame_minimal$Mixtures), 5)[-1],
limits=c(1,max(bigFrame_minimal$Mixtures))) +
  xlab("Number of Mixture Components") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    legend.text = element_text(size=12)) +
  theme(legend.position = "none") +
  facet_grid(Move~Context, scales="fixed")+
  theme(strip.text.x = element_text(size=12), strip.text.y = element_text(size=12))

saveThese=list(bicPlotRibbon,
  bicPlotRibbonLessContext,
  bicPlotRibbonLessContext_Flip,
  bicPlotRibbon_minimal,
  bicPlotRibbon_minimal_flip)
names(saveThese)<-c("bicPlotRibbon",
  "bicPlotRibbonLessContext",
  "bicPlotRibbonLessContext_Flip",
  "bicPlotRibbon_minimal",
  "bicPlotRibbon_minimal_flip")
"bicPlotRibbon_minimal",
"bicPlotRibbon_minimal_flip")
for(i in 1:length(saveThese)){
ggsave(paste(names(saveThese)[i],".png",sep=""), plot=saveThese[[i]], path=paste(getwd(), "/Plots",sep=""), dpi=800, height=9, width=16, units="in")
}

# return(bigFrame)

BICPlots()

ENTPlots<-

entPlotRibbon<- ggplot(bigFrame, aes(x=Mixtures, y=Entropy , col = Iteration))+
   stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
   color="black") +
   # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
   # color="black", alpha = 7/10 ) +
   stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
   color="black", alpha = 5/10 ) +
   scale_x_continuous(breaks = seq(0,max(bigFrame$Mixtures), 5)[-1],
   limits=c(1,max(bigFrame$Mixtures))) +
   xlab("Number of Mixture Components") +
   theme_minimal() +
   theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
   axis.title.x = element_text(size = 12),
   axis.title.y = element_text(size = 12),
   legend.text = element_text(size=12)) +
   theme(legend.position = "none") +
   facet_grid(Move~Context, scales="fixed") +
   theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

#Drop NASA-TLX and both context, look at moves

bigFrameNoTLXBoth<- bigFrame[ -which(hasTLX | hasBothC),]

entPlotRibbonLessContext<- ggplot(bigFrameNoTLXBoth, aes(x=Mixtures, y=Entropy , col = Iteration)) +
   stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
   color="black") +
   # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
   # color="black", alpha = 7/10 ) +
   stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
   color="black", alpha = 5/10 ) +
scale_x_continuous(breaks = seq(0,max(bigFrameNoTLXBoth$Mixtures), 5)[-1],
limits=c(1,max(bigFrameNoTLXBoth$Mixtures))) +
xlab("Number of Mixture Components") +
theme_minimal() +
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    legend.text = element_text(size=12)) +
theme(legend.position = "none") +
facet_grid(Move~Context, scales="fixed") +
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size=12))

entPlotRibbonLessContext_Flip <- ggplot(bigFrameNoTLXBoth, aes(x=Mixtures, y=Entropy, col = Iteration)) +
stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
color="black") +
# stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
color="black", alpha = 7/10 ) +
stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
color="black", alpha = 5/10 ) +
scale_x_continuous(breaks = seq(0,max(bigFrameNoTLXBoth$Mixtures), 5)[-1],
limits=c(1,max(bigFrameNoTLXBoth$Mixtures))) +
xlab("Number of Mixture Components") +
theme_minimal() +
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
    axis.title.x = element_text(size = 12),
    axis.title.y = element_text(size = 12),
    legend.text = element_text(size=12)) +
theme(legend.position = "none") +
facet_grid(Context~Move, scales="fixed") +
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size=12))

bigFrame_minimal <- bigFrame[ -which(hasTLX | hasBothC | hasBothM),]
entPlotRibbon_minimal <- ggplot(bigFrame_minimal, aes(x=Mixtures, y=Entropy, col = Iteration)) +
stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
color="black") +
# stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
color="black", alpha = 7/10 ) +
stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
color="black", alpha = 5/10 ) +
scale_x_continuous(breaks = seq(0,max(bigFrame_minimal$Mixtures), 5)[-1],
limits=c(1,max(bigFrame_minimal$Mixtures))) +
xlab("Number of Mixture Components") +
theme_minimal() +
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
axis.title.x = element_text(size = 12),
axis.title.y = element_text(size = 12),
legend.text = element_text(size=12)) +
theme(legend.position = "none") +
facet_grid(Context~Move, scales="fixed") +
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size=12))

entPlotRibbon_minimal_flip <- ggplot(bigFrame_minimal, aes(x=Mixtures, y=Entropy , col = Iteration)) +
stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
color="black") +
# stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
color="black", alpha = 7/10 ) +
stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
color="black", alpha = 5/10 ) +
scale_x_continuous(breaks = seq(0,max(bigFrame_minimal$Mixtures), 5)[-1],
limits=c(1,max(bigFrame_minimal$Mixtures))) +
xlab("Number of Mixture Components") +
theme_minimal() +
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
axis.title.x = element_text(size = 12),
axis.title.y = element_text(size = 12),
legend.text = element_text(size=12)) +
theme(legend.position = "none") +
facet_grid(Move~Context, scales="fixed") +
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size=12))

saveThese<-
list(entPlotRibbon,
entPlotRibbonLessContext,
entPlotRibbonLessContext_Flip,
entPlotRibbon_minimal,
entPlotRibbon_minimal_flip)
names(saveThese)<-c("entPlotRibbon",
"entPlotRibbonLessContext",
"entPlotRibbonLessContext_Flip",
"entPlotRibbon_minimal",
"entPlotRibbon_minimal_flip")
for(i in 1:length(saveThese)){
ggsave(paste(names(saveThese)[i],".png",sep=""), plot=saveThese[[i]], path=paste(getwd(), "/Plots",sep=""), dpi=800, height=9, width=16, units="in")
}

# return(bigFrame)

}  

ENTPlots()

normed_ENTPlots<-function(){
  normed_entPlotRibbon<- ggplot(bigFrame, aes(x=Mixtures, y=Normed_Entropy, col = Iteration))+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2), color="black")+
  # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10)+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10)+
  scale_x_continuous(breaks = seq(0,max(bigFrame$Mixtures), 5)[1:15], limits=c(1,max(bigFrame$Mixtures))) +
  xlab("Number of Mixture Components") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1,"lines"),
  axis.title.x = element_text(size = 12),
  axis.title.y = element_text(size = 12),
  legend.text = element_text(size=12))+
  theme(legend.position = "none") +
  facet_grid(Move~Context, scales="fixed") +
  theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size=12))

#Drop NASA-TLX and both context, look at moves

bigFrameNoTLXBoth<- bigFrame[ -which(hasTLX | hasBothC),]

  normed_entPlotRibbonLessContext<- ggplot(bigFrameNoTLXBoth, aes(x=Mixtures, y=Normed_Entropy, col = Iteration))+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2), color="black")+
  # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10)+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10)+
  scale_x_continuous(breaks = seq(0,max(bigFrameNoTLXBoth$Mixtures), 5)[1:15], limits=c(1,max(bigFrameNoTLXBoth$Mixtures))) +
normed_entPlotRibbonLessContext_Flip<- ggplot(bigFrameNoTLXBoth, aes(x=Mixtures, y=Normed_Entropy , col = Iteration))+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2), color="black")+
  # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10 )+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10 )+
  scale_x_continuous(breaks = seq(0,max(bigFrameNoTLXBoth$Mixtures), 5)[-1], limits=c(1,max(bigFrameNoTLXBoth$Mixtures))) +
  xlab("Number of Mixture Components") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
        axis.title.x = element_text(size = 12),
        axis.title.y = element_text(size = 12),
        legend.text = element_text(size=12))+
  theme(legend.position = "none") +
  facet_grid(Move~Context, scales="fixed")+
  theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

bigFrame_minimal<- bigFrame[-which(hasTLX | hasBothC | hasBothM),]

normed_entPlotRibbon_minimal<- ggplot(bigFrame_minimal, aes(x=Mixtures, y=Normed_Entropy , col = Iteration))+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2), color="black")+
  # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10 )+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10 )+
  scale_x_continuous(breaks = seq(0,max(bigFrame_minimal$Mixtures), 5)[-1], limits=c(1,max(bigFrame_minimal$Mixtures))) +
  xlab("Number of Mixture Components") +
  theme_minimal()
```r
theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
      axis.title.x = element_text(size = 12),
      axis.title.y = element_text(size = 12),
      legend.text = element_text(size=12))+
theme(legend.position = "none") +
facet_grid(Context~Move, scales="fixed")+
theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

normed_entPlotRibbon_minimal_flip <- ggplot(bigFrame_minimal, aes(x=Mixtures, y=Normed_Entropy , col = Iteration))+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1/2),
               color="black" )+
  # stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 2/3),
  #              color="black", alpha = 7/10 )+
  stat_summary(geom="ribbon", fun.data ="median_hilow", fun.args = list(conf.int = 1),
               color="black", alpha = 5/10 )+
  scale_x_continuous(breaks = seq(0,max(bigFrame_minimal$Mixtures), 5)[-1],
                     limits=c(1,max(bigFrame_minimal$Mixtures))) +
  xlab("Number of Mixture Components") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
       axis.title.x = element_text(size = 12),
       axis.title.y = element_text(size = 12),
       legend.text = element_text(size=12))+
  theme(legend.position = "none") +
  facet_grid(Move~Context, scales="fixed")+
  theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

saveThese<-list(normed_entPlotRibbon,
                 normed_entPlotRibbonLessContext,
                 normed_entPlotRibbonLessContext_Flip,
                 normed_entPlotRibbon_minimal,
                 normed_entPlotRibbon_minimal_flip)
names(saveThese)<-c("normed_entPlotRibbon",
                   "normed_entPlotRibbonLessContext",
                   "normed_entPlotRibbonLessContext_Flip",
                   "normed_entPlotRibbon_minimal",
                   "normed_entPlotRibbon_minimal_flip")
for(i in 1:length(saveThese)){
```

```r
ggsave(paste(names(saveThese)[i], ".png", sep=""), plot=saveThese[[i]], path=paste(getwd(), "/Plots", sep=""), dpi=800, height=9, width=16, units="in" )

}

# return(bigFrame)

}
normed_ENTPlots()

prop_cluster_pcwReg2 <- table(bigFrame$VarSet, bigFrame$Optimal_Number_2) / rowSums(table(bigFrame$VarSet, bigFrame$Optimal_Number_2))
prop_cluster_pcwReg3 <- table(bigFrame$VarSet, bigFrame$Optimal_Number_3) / rowSums(table(bigFrame$VarSet, bigFrame$Optimal_Number_3))

write.csv(prop_cluster_pcwReg2, file="Output/jitter_prop_cluster_pcwReg2.csv")
write.csv(prop_cluster_pcwReg3, file="Output/jitter_prop_cluster_pcwReg3.csv")
```
Appendix 2.6 – Pairwise Adjusted Rand Index

rm(list=ls())
athomex<-T
num_parallel <- 2 #doPar is inefficient w/RAM and if I'm on my laptop, I can only run 1 instance :

if(athomex){
  gdrive<="D://"
} else{
  gdrive<="C://Users/fscho/"
}

fileURL<-"Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive, fileURL, "/Data Analysis", sep=""))

library(mclust)
library(parallel)
library(doParallel)
library(reshape2)
# library(ggplot2)
# library(reshape2)
# library(colorbrewer)
# library(gridExtra)
# library(colorspace)
# library(gtable)

vs <- list.files("Clusters/Jitter/varSetOrganization", pattern="RData", full.names = T)

###FROM SCRIPT

####THIS LOADS UP THE DATA AND APPENDS THE WORKLOAD SCORES I FORGOT TO APPEND####
InputSet<-read.csv(file = "inputSet_01_03_2020.csv", stringsAsFactors=FALSE)
InputSet$SampleWeight <- InputSet$timeOfEvent / InputSet$CT #Used for HC sampling
InputSet$rowIndex <- 1:nrow(InputSet) #Same
InputSet$U_ID<-paste(InputSet$Latency, InputSet$Clearance, sep="_")
InputSet$U_ID_P2<-paste(InputSet$Latency, InputSet$Clearance, InputSet$PNum, sep="_")
trials<-read.csv("trials_02_27_2020.csv", stringsAsFactors = F)
InputSet$TLX<- -1
#Adds jitter to non-jittered input
InputSet$jitter_timeOfEvent <- InputSet$timeOfEvent + runif(nrow(InputSet), -.5/60, .5/60)
#Adds some jitter
InputSet$jitter_PM_Wait_Time <- InputSet$PM_Wait_Time + runif(nrow(InputSet), -.5/60, .5/60) #Adds some jitter
# Append TLX things
for(i in 1:nrow(trials)){
  pnum<-trials$PNum[i]
  tri<-trials$Trial[i]

  InputSet[which(InputSet$PNum==pnum & InputSet$Trial==tri),]$TLX <- trials$weightedRating[i]
}

# Drop incomplete cases
varOfInt<-c("jitter_timeOfEvent", "jitter_PM_Wait_Time", "TLX", "a_time")
InputSet<-InputSet[complete.cases(InputSet[,varOfInt]),]

# Custom function to apply the clustCombi results to an out-of-sample prediction
combiCollapse<-function(combiM, mcAssign, collapseTo){
  for(i in (length(combiM)-1):collapseTo){
    cMat<- combiM[[i]]
    for(k in 1:ncol(cMat)){
      for(j in 1:nrow(cMat)){
        if(j!=k & cMat[j,k] == 1){
          # Carefully check, but I got it working. :)
          mcAssign$classification[which(mcAssign$classification==k)]<-j
          # Note, the z's are wrong... but I'm not using them nor returning them so the only way to know that are if you read this comment.
        }
      }
    }
  }

  return(mcAssign$classification)
}

ARITable <- function(fl, dat = InputSet){
  load(fl)

  matNames <- c()
  for(i in 1:length(varSetList)){
    matNames[i]<-varSetList[[i]]$Iteration
ARIMat <- matrix(data = NA, nrow = length(varSetList), ncol = length(varSetList), 
dimnames = list(matNames, matNames))
ARIMat_2 <- ARIMat
ARIMat_3 <- ARIMat
BICMat <- ARIMat
# Shrink dat to only use the variables of interest
Input <- dat[varSetList[[1]]$VariableSet]  # If crash, check here
for(i in 1:nrow(ARIMat)){
cat("n", i, "of", fl, "n")
timestamp()
flush.console()
for(j in 1:ncol(ARIMat)){
iSample <- Input[varSetList[[i]]$trainVec,]
if(i == j){
  ARIMat_2[i,j] <- NA
  ARIMat_3[i,j] <- NA
}
mod <- varSetList[[j]]$clustCombi$MclustOutput
ee <- estep(mod$modelName, iSample, mod$parameters, warn = T)
BICMat[i,j] <- bic(ee$modelName, ee$loglik, ee$n, ee$d, ee$G)
} else{
  # Generate a sample (same as model i)
  # Get ARI between models i and j
  # In this case, row means are similarity due to sample
  # And column means are model performance
  i_predict_mixtures <- predict.Mclust(varSetList[[i]]$clustCombi$MclustOutput, iSample)
  j_predict_mixtures <- predict.Mclust(varSetList[[j]]$clustCombi$MclustOutput, iSample)

  i_predict_clusters_2 <- combiCollapse(varSetList[[i]]$clustCombi$combiM, 
  i_predict_mixtures, 
  varSetList[[i]]$clustCombiOptim_pcwReg2$numClusters.combi)
  j_predict_clusters_2 <- combiCollapse(varSetList[[j]]$clustCombi$combiM, 
  j_predict_mixtures, 
  varSetList[[j]]$clustCombiOptim_pcwReg2$numClusters.combi)
  ARIMat_2[i,j] <- adjustedRandIndex(i_predict_clusters_2, j_predict_clusters_2)

  i_predict_clusters_3 <- combiCollapse(varSetList[[i]]$clustCombi$combiM, 
  i_predict_mixtures, 
  varSetList[[i]]$clustCombiOptim_pcwReg3$numClusters.combi)
  j_predict_clusters_3 <- combiCollapse(varSetList[[j]]$clustCombi$combiM, 
  j_predict_mixtures, 
  varSetList[[j]]$clustCombiOptim_pcwReg3$numClusters.combi)
  ARIMat_3[i,j] <- adjustedRandIndex(i_predict_clusters_3, j_predict_clusters_3)
mod <- varSetList[[j]]$clustCombi$MclustOutput
ee <- estep(mod$modelName, iSample, mod$parameters, warn=T)
BICMat[i,j] <- bic(ee$modelName, ee$loglik, ee$n, ee$d, ee$G)

} colnames(ARIMat_2)[j] <- paste("Iteration_{", varSetList[[j]]$Iteration, sep="")
colnames(ARIMat_3)[j] <- paste("Iteration_{", varSetList[[j]]$Iteration, sep=""

colnames(BICMat)[j] <- paste("Model_Iteration_{", varSetList[[j]]$Iteration, sep="")

} rownames(ARIMat_2)[i] <- paste("Sample_Iteration_{", varSetList[[i]]$Iteration, sep=""
rownames(ARIMat_3)[i] <- paste("Sample_Iteration_{", varSetList[[i]]$Iteration, sep=""

rownames(BICMat)[i] <- paste("Sample_Iteration_{", varSetList[[i]]$Iteration, sep=""

} write.csv(ARIMat_2, file = paste("Output/Jitter/AdjustedRandIndex/","ARI_2_
    names(varSetList[[i]]$VariableSet)[1], ".csv", sep=""))
write.csv(ARIMat_3, file = paste("Output/Jitter/AdjustedRandIndex/","ARI_3_
    names(varSetList[[i]]$VariableSet)[1], ".csv", sep=""))
write.csv(BICMat, file = paste("Output/Jitter/AdjustedRandIndex/","BICMat_
    names(varSetList[[i]]$VariableSet)[1], ".csv", sep=""))

ret <- list(ARIMat_2, ARIMat_3, BICMat)

names(ret) <- c("ARI_PcwReg2", "ARI_PcwReg3", "BICMat")

return(ret)

}

sock2 <- makeCluster(num_parallel)
Sys.sleep(3)
wd <- getwd()
feet <- c("wd", "combiCollapse")
clusterExport(sock2, feet)
clusterEvalQ(sock2, library(mclust))
registerDoParallel(sock2)

AllARI <- foreach(j=vs,.verbose = T, .inorder = T) %dopar% ARITable(j, dat = InputSet)

stopCluster(sock2)
names(AllARI) <- vs
save(AllARI, file=paste("Output/Jitter/AdjustedRandIndex/AllARI.RData"))

# Now I want to go through each table and find the "best" one for each varSet / pcwReg
ARI_Descrips_2 <- list()
ARI_Descrips_3 <- list()
BIC_Descrips <- list()
for(i in 1:length(AllARI)){
    # ARI[[i]][1] PCW 2
    # ARI[[i]][2] PCW 3
    cat("\n\n", names(AllARI)[i])

    for(j in 1:3){
        suppressWarnings( rm("ARI_SUM"))

        for(k in 1:ncol(AllARI[[i]][[j]])){
            desc<-psych::describe(AllARI[[i]][[j]][,k], IQR = T)
            rownames(desc)<-colnames(AllARI[[i]][[j]][,k])

            ifelse(exists("ARI_SUM"),
                ARI_SUM <- rbind (ARI_SUM, desc),
                ARI_SUM <- desc)

            }
        ARI_SUM$isMaxMedian<-0
        ARI_SUM$isMaxMedian[which(ARI_SUM$median== max(ARI_SUM$median))]<-1
        ifelse(j==1,
            ARI_Descr_2[i]<-list(ARI_SUM),
            ifelse(j==2,
                ARI_Descr_3[i]<-list(ARI_SUM),
                BIC_Descr[i]<-list(ARI_SUM)
            )
        )
    }
}

# Same as above, but for BIC

names(ARI_Descr_2)<-names(AllARI)
names(ARI_Descr_3)<-names(AllARI)
names(BIC_Descr)<-names(AllARI)

# Combine the pcw2 and pcw3 models

ARI_Descr_23 <- list()
for(i in 1:length(ARI_Descr_2)){
    two<-ARI_Descr_2[[i]]
names(two) <- paste(names(two),"_2", sep="")

three<-ARI_Descrips_3[[i]]
names(three) <- paste(names(three), ","_3", sep="")

ARI_Descrips_23[i] <- list(cbind(two, three))
ARI_Descrips_23[[i]]$isMaxMedian_Both <- ARI_Descrips_23[[i]]$isMaxMedian_2 &
ARI_Descrips_23[[i]]$isMaxMedian_3
}

names(ARI_Descrips_23) <- names(ARI_Descrips_2)
save(ARI_Descrips_23, file=paste("Output/Jitter/AdjustedRandIndex/ARI_Descrips_23.RData") )
save(BIC_Descrips, file=paste("Output/Jitter/AdjustedRandIndex/BIC_Descrips.RData") )
Appendix 2.7 – Run Selection

# This script identifies the "most similar" and "best" run for each model type, using the highest median ARI/BIC
# Then it loads up each run, and saves it in a single file which I've named "The Dirty Dozen"
# Although, looking at the movie, I might rename it after the Cylons from BSG
rm(list=ls())
athomex<-T
num_parallel <- 2 # doPar is inefficient w/RAM :

if(athomex){
    gdrive<="D:/"
}else{
    gdrive<="C:/Users/fscho/"
}

fileURL<="Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

load("Output/Jitter/AdjustedRandIndex/ARI_Descrips_23.RData")
load("Output/Jitter/AdjustedRandIndex/BIC_Descrips.RData")
pickMax<-function(comparisonSet, same){
    names(comparisonSet) <- substring(names(comparisonSet), 35, nchar(names(comparisonSet)) - 6) # Makes names prettier
    maxMedian<-list()
    for(i in 1:length(comparisonSet)){
        if(same){
            maxMedian[i] <- row.names(comparisonSet[[i]])[which(comparisonSet[[i]]$isMaxMedian_2==1)]
        }else{
            maxMedian[i] <- row.names(comparisonSet[[i]])[which(comparisonSet[[i]]$isMaxMedian==1)]
        }
    }
    names(maxMedian)<-names(comparisonSet)
}

if(same){
    theDirtyDozenIters <- unlist(strsplit(unlist(maxMedian), "."))[c(F,T)] # Uses wizardry to get just the iteration number for my dirty dozen
}
else {
    theDirtyDozenIters <- unlist(strsplit(unlist(maxMedian), "_"))[c(T,F,F)] # Uses wizardry to get just the iteration number for my dirty dozen
}

names(theDirtyDozenIters) <- substr(names(theDirtyDozenIters), 1, nchar(names(theDirtyDozenIters))-1)
theDirtyDozen <- list()
for (i in 1:length(theDirtyDozenIters)) {
    load(paste("Clusters/Jitter/varSetOrganization/", names(theDirtyDozenIters)[i], ".RData", sep=""))
    iter <- theDirtyDozenIters[i]
    iterCount <- 0
    for (j in 1:length(varSetList)) {
        if (iter == varSetList[[j]]$Iteration) {
            theDirtyDozen[[i]] <- varSetList[[j]]
            iterCount <- iterCount + 1 # This is here to check for logic errors. If the count is anything BUT 1, I screwed up somewhere
        }
    }
    print(names(theDirtyDozenIters)[i])
    print(iterCount)
    flush.console()
}
return(theDirtyDozen)

mostSimilar <- pickMax(ARI_Descrips_23, same=T)
mostBIC <- pickMax(BIC_Descrips, same=F)

save(mostSimilar, file= "Clusters/Jitter/TheFinalTwelve/mostSimilar.RData")
save(mostBIC, file= "Clusters/Jitter/TheFinalTwelve/mostBIC.RData")
Appendix 2.8 – Apply Clusters to Test Data

# Get descriptives of each cluster solution
rm(list=ls())
athome<-T
num_parallel <-2 # doPar is inefficient with RAM :( 

if(athome){
    gdrive<-"D:/"
}else{
    gdrive<-"C:/Users/fscho/"
}

fileURL<-"Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

library(ggplot2)
load("Clusters/Jitter/TheFinalTwelve/mostSimilar.RData")
load("Clusters/Jitter/TheFinalTwelve/mostBIC.RData")

##### FROM SCRIPT
2###############################################################
### THIS LOADS UP THE DATA AND APPENDS THE WORKLOAD SCORES I FORGOT
### TO APPEND####
InputSet<-read.csv(file = "inputSet_01_03_2020.csv", stringsAsFactors=FALSE)
InputSet$SampleWeight <- InputSet$timeOfEvent / InputSet$CT # Used for HC sampling
InputSet$rowIndex <- 1:nrow(InputSet) # Same
InputSet$U_ID<-paste(InputSet$Latency, InputSet$Clearance, sep="_")
InputSet$U_ID_P2<-paste(InputSet$Latency, InputSet$Clearance, InputSet$PNum, sep="_")

trials<-read.csv("trials_01_03_2020.csv", stringsAsFactors = F)
InputSet$TLX<- -1
# Append TLX things
for(i in 1:nrow(trials)){
    pnum<-trials$PNum[i]
    tri<-trials$Trial[i]
    InputSet[which(InputSet$PNum==pnum & InputSet$Trial==tri),]$TLX <- trials$weightedRating[i]
}

# Drop incomplete cases
varOfInt<-c("timeOfEvent", "PM_Wait_Time", "TLX", "a_time")
InputSet<-InputSet[complete.cases(InputSet[,varOfInt]),]
InputSet$jitter_timeOfEvent <- InputSet$timeOfEvent + runif(nrow(InputSet), -.5/60, .5/60)  # Adds some jitter
InputSet$jitter_PM_Wait_Time <- InputSet$PM_Wait_Time + runif(nrow(InputSet), -.5/60, .5/60)  # Adds some jitter

# Having changed selection criteria, I have to tinker...
doScript8 <- function(theDirtyDozen, additive) {

# Make BIC and ENT plots for the individuals

modelPerformance_plots <- function() {
    # A lot of this is a repeat of Script 5, but for my final models
    ExtractEntropy <- function(combinedCluster) {
        # This function comes from a statsexchange page.
        # It looks like it uses an internal clustCombi function... but the extracted entropy makes identical graphs
        # So it works!
        # https://stats.stackexchange.com/a/244974
        combiM <- combinedCluster$combiM
        Kmax <- ncol(combinedCluster$MclustOutput$z)
        z0 <- combinedCluster$MclustOutput$z
        ent <- numeric()
        for (K in Kmax:1) {
            z0 <- t(combiM[[K]] %*% t(z0))
            ent[K] <- -sum(mclust:::xlog(z0))
        }
        ENT <- data.frame(`Number of clusters` = 1:Kmax, `Entropy` = round(ent, 3))
        ENT$Diff.In.Ent <- ENT$Entropy - ENT$Entropy[c(NA, 1:(nrow(ENT)-1))]
    }

    # Learned from the above function, and I dug right into the entPlot code... I'm changing it up a smidge
    mergedn <- numeric()
    z0 <- combinedCluster$MclustOutput$z
    Kmax <- ncol(combinedCluster$MclustOutput$z)
    for (K in (Kmax - 1):1) {
        z0 <- t(combiM[[K + 1]] %*% t(z0))
        mergedn[K] = sum(sapply(map(z0), function(x) any(which(as.logical(combiM[[K]])[rowSums(combiM[[K]]) ==

238
return(ENT)

# Build the data frame

makeFrame <- function(){

  BICFrame <- as.data.frame(matrix(nrow =
    length(theDirtyDozen[[1]]$clustCombi$MclustOutput$BIC) * length(theDirtyDozen),
    ncol = 3))
  names(BICFrame) <- c("Iteration", "Mixtures", "BIC")
  BICFrame$Iteration <- -99999999999999999999
  BICFrame$Mixtures <- rep(1:length(theDirtyDozen[[1]]$clustCombi$MclustOutput$BIC),
    length(theDirtyDozen))
  BICFrame$BIC <- -99999999999999999999
  BICFrame$Entropy <- NA
  BICFrame$Normed_Entropy <- NA
  BICFrame$Optimal_Number_2 <- NA
  BICFrame$Optimal_Number_3 <- NA

  for(i in 1:length(theDirtyDozen)){

    start <- 1 + (length(theDirtyDozen[[i]]$clustCombi$MclustOutput$BIC) * (i - 1))
    stop <- start + length(theDirtyDozen[[i]]$clustCombi$MclustOutput$BIC) - 1

    BICFrame$Iteration[start:stop] <- theDirtyDozen[[i]]$Iteration
    BICFrame$Mixtures[start:stop] <-
    1:length(unlist(theDirtyDozen[[i]]$clustCombi$MclustOutput$BIC))
    BICFrame$BIC[start:stop] <-
    unlist(theDirtyDozen[[i]]$clustCombi$MclustOutput$BIC)[1:length(unlist(theDirtyDozen[[i]]$clustCombi$MclustOutput$BIC))]
    BICFrame$VarSet[start:stop] <- names(theDirtyDozen[[i]]$VariableSet)[1]
    ent <- ExtractEntropy(theDirtyDozen[[i]]$clustCombi)
    stop_ent <- start + nrow(ent) - 1

    BICFrame$Entropy[start:stop_ent] <- ent$Entropy
    BICFrame$Optimal_Number_2[start:stop_ent] <-
    theDirtyDozen[[i]]$clustCombiOptim_pcwReg2$numClusters.combi
    BICFrame$Optimal_Number_3[start:stop_ent] <-
    theDirtyDozen[[i]]$clustCombiOptim_pcwReg3$numClusters.combi
    # print(start)

  }
}
\[ \text{BICFrame} \leftarrow \text{makeFrame()} \]

\[
\begin{align*}
\text{hasMove} & \leftarrow \text{grepl("M", BICFrame$VarSet)} \\
\text{hasWait} & \leftarrow \text{grepl("W", BICFrame$VarSet)} \\
\text{hasBothM} & \leftarrow \text{hasMove} \& \text{hasWait} \\
\text{onlyMove} & \leftarrow \text{as.logical}(\text{hasMove} - \text{hasBothM}) \\
\text{onlyWait} & \leftarrow \text{as.logical}(\text{hasWait} - \text{hasBothM}) \\
\end{align*}
\]

\[
\begin{align*}
\text{BICFrame$Move} & \leftarrow \\
\text{BICFrame$Move}[\text{which(hasBothM)]} & \leftarrow \text{"Both"} \\
\text{BICFrame$Move}[\text{which(onlyMove)]} & \leftarrow \text{"Move"} \\
\text{BICFrame$Move}[\text{which(onlyWait)]} & \leftarrow \text{"Wait"} \\
\end{align*}
\]

\[
\begin{align*}
\text{hasTLX} & \leftarrow \text{grepl("TLX", BICFrame$VarSet)} \\
\text{hasTS} & \leftarrow \text{grepl("TS", BICFrame$VarSet)} \\
\text{hasBothC} & \leftarrow \text{hasTLX} \& \text{hasTS} \\
\text{onlyTLX} & \leftarrow \text{as.logical}(\text{hasTLX} - \text{hasBothC}) \\
\text{onlyTS} & \leftarrow \text{as.logical}(\text{hasTS} - \text{hasBothC}) \\
\end{align*}
\]

\[
\begin{align*}
\text{BICFrame$Context} & \leftarrow \text{"None"} \\
\text{BICFrame$Context}[\text{which(hasBothC)]} & \leftarrow \text{"Both"} \\
\text{BICFrame$Context}[\text{which(onlyTLX)]} & \leftarrow \text{"NASA-TLX"} \\
\text{BICFrame$Context}[\text{which(onlyTS)]} & \leftarrow \text{"Temporal Sensitivity"} \\
\end{align*}
\]

\[
\begin{align*}
\text{BICFrame$Context} & \leftarrow \text{factor(BICFrame$Context, levels =c("None", "NASA-TLX", "Temporal Sensitivity", "Both"))} \\
\text{BICFrame$Move} & \leftarrow \text{factor(BICFrame$Move, levels=c("Move", "Wait", "Both"))} \\
\end{align*}
\]

\[
\begin{align*}
\text{bicPlotCylons} & \leftarrow \text{ggplot(BICFrame, aes(x=Mixtures, y=BIC))} + \\
& \quad \text{stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1/2), color="black")} + \\
& \quad \text{stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 2/3), color="black", alpha = 7/10 )} + \\
& \quad \text{stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1), color="black", alpha = 5/10 )} + \\
& \quad \text{scale_x_continuous(breaks = seq(0,max(BICFrame$Mixtures), 5)[-1], limits=c(1,max(BICFrame$Mixtures)))} + \\
& \quad \text{geom_line(size=1)+}
\end{align*}
\]
normedEntPlotCylons <- ggplot(BICFrame, aes(x=Mixtures, y=Normed_Entropy)) +
  # stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1/2),
  # color="black") +
  # stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 2/3),
  # color="black", alpha = 7/10) +
  # stat_summary(geom="ribbon", fun.data="median_hilow", fun.args = list(conf.int = 1),
  # color="black", alpha = 5/10) +
  scale_x_continuous(breaks = seq(0,max(BICFrame$Mixtures), 5)[-1],
  limits=c(1,max(BICFrame$Mixtures))) +
  # geom_line(size=1)+
  geom_point(size=1.5)+
  geom_vline(aes(xintercept=Optimal_Number_2), size=1)+
  # geom_vline(aes(xintercept=Optimal_Number_3), size=1, linetype="dashed")+
  xlab("Number of Mixture Components") +
  ylab("Normed Entropy") +
  theme_minimal() +
  theme(panel.background = element_rect(fill = NA, color = "black"), panel.spacing.x = unit(1, "lines"),
  axis.title.x = element_text(size = 12),
  axis.title.y = element_text(size = 12),
  legend.text = element_text(size=12))+
  theme(legend.position = "none") +
  facet_grid(Move~Context, scales="fixed") +
  theme(strip.text.x = element_text(size = 12), strip.text.y = element_text(size= 12))

ggsave(paste(additive,"_CylonPlots_NormedENT.png", sep=""), plot=normedEntPlotCylons,
path=paste(getwd(), "/Plots",sep=""), dpi=800, height=9, width=16, units="in")
}

#Its a functin because it looks nicer in my development environment
modelPerformance_plots()

#Variables I want to eventually look at:
vOfInt<-c("Latency", "Clearance","timeOfEvent","PM_Wait_Time", "a_time", "TLX",
"Input_Movement", "Input_Rotating", "tot_rot", "dist")

#Take cluster solution, make massive data frame
#Then, get means, median, and SD for each vOfInt

###FROM SCRIPT 6###
#Custom function to apply the clustCombi results to an out-of-sample prediction
#Added a change to also calculate Zs
combiCollapse<-function(combiM,mcAssign, collapseTo){
  for(i in (length(combiM)-1):collapseTo ){
cMat <- combiM[[i]]
for(k in 1:ncol(cMat)){
  for(j in 1:nrow(cMat)){
    if(j!=k & cMat[j,k] == 1){
      # Carefully check, but I got it working. :)
      mcAssign$classification[which(mcAssign$classification==k)] <- j # This is fine from the old script
      if(rowSums(cMat)[j]==2){  # i.e. if they're being combined
        newZ <- mcAssign$z[,k] + mcAssign$z[,j]
      } else{
        newZ <- mcAssign$z[,k]
      }
      mcAssign$z[,j] <- newZ
    }
  }
}
mcAssign$z <- as.data.frame(mcAssign$z[, 1:collapseTo])
mcAssign$z$Uncertainty <- -99
for(i in 1:nrow(mcAssign$z)){
  mcAssign$z$Uncertainty[i] <- 1-max(mcAssign$z[i,1:(ncol(mcAssign$z)-1)])
}
retFrame <- cbind(as.data.frame(mcAssign$classification), as.data.frame(mcAssign$z))
names(retFrame)[1]<-"classification"
names(retFrame)<- paste("combi_",names(retFrame), sep="")
return(retFrame)
}
### END SCRIPT 6###
for(i in 1:length(theDirtyDozen)){
  cName<-names(theDirtyDozen[[i]]$VariableSet)
  mclustAssign <- predict.Mclust(theDirtyDozen[[i]]$clustCombi$MclustOutput, InputSet[,theDirtyDozen[[i]]$VariableSet])
  class <- mclustAssign$classification
  probs <- mclustAssign$z
  train <- 1:nrow(InputSet) %in% theDirtyDozen[[i]]$trainVec
boop <- cbind(class, probs, train)
colnames(boop)<-paste(cName, "Mclust", colnames(boop), sep=" ")

combi_boop<-combiCollapse(theDirtyDozen[[i]]$clustCombi$combiM,
mclustAssign,
theDirtyDozen[[i]]$clustCombiOptim_pcWReg2$numClusters.combi )

names(combi_boop) <-paste(cName, names(combi_boop), sep=" ")

#Checks to make sure I'm doing combiZ correctly
# print(i)
# print(max(rowSums(combi_boop[,2:ncol(combi_boop)])))
# print(min(rowSums(combi_boop[,2:ncol(combi_boop)])))
# flush.console()
attache <- cbind(boop, combi_boop)

InputSet <- cbind(InputSet, attache)

write.csv(InputSet, file = paste("megaInputSet", additive,".csv", sep=""))
}
doScript8(mostSimilar, "similar")
doScript8(mostBIC, "BIC")
Appendix 2.9 – Calculate Trial Summaries

#### IF MAKING CHANGES IN THE FUTURE, THERE IS SOME MANUAL HARD CODING IN THIS SCRIPT THAT NEEDS TO BE ADJUSTED####
#### SEE COMMENTS####

```r
library(psych)
# Get descriptives of each cluster solution
rm(list=ls())
athome<-T
num_parallel <- 2 # doPar is inefficient w/RAM :

if(athome){
  gdrive<="D:"
} else{
  gdrive<="C:/Users/fscho/
}

fileURL<="Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

# load("Clusters/Jitter/TheFinalTwelve/Cylons.RData")

load("Clusters/Jitter/TheFinalTwelve/mostSimilar.RData")
load("Clusters/Jitter/TheFinalTwelve/mostBIC.RData")

InputsBIC<read.csv("megaInputSetBIC.csv", stringsAsFactors = F)
InputsSimilar<read.csv("megaInputSetsimilar.csv", stringsAsFactors = F)
Trials <-read.csv("trials_02_27_2020.csv", stringsAsFactors = F)

doScript9<-function(theDirtyDozen, Inputs, appended){

  # The names in "Inputs" have a number ("M_TLX1_Mclust_Class" has a 1)
  # This causes issues downstream that I didn't expect, so I'm fixing it here.
  longString <-strsplit(names(Inputs)[37:ncol(Inputs)], ".") # The first 36 items are from the original input set. THIS IS MANUALLY CODED
  maxCombi<-1
  for(i in 1:length(longString)){
    for(j in 1:length(longString[[i]])){
      if(grepl("[MWTLXNTS]",longString[[i]][j]) & grepl("[:digit:]",longString[[i]][j])){ # Only changes things with both a letter and number
```

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longString[[i]][j] <- substr(longString[[i]][j], 1, nchar(longString[[i]][j])-1)

#Find my max
if(!is.na(suppressWarnings(as.numeric(longString[[i]][length(longString[[i]])])))){#Is a number
  if(as.numeric(longString[[i]][length(longString[[i]])]) > maxCombi){ #Is a bigger number
    if(sum(grepl("combi", longString[[i]]))){ #Also has to be a "combi" number
      maxCombi <- as.numeric(longString[[i]][length(longString[[i]])])
    }
  }
}
longString[[i]] <- paste(longString[[i]], collapse =" ")

names(Inputs) <- c(names(Inputs)[1:36], unlist(longString)) #The first 36 items are from the original input set. THIS IS MANUALLY CODED
#Finished fixing names

#Add lots of columns to trials, which I'm then going to "melt"
Trials$FullyIneligibleTrial<- !paste(Trials$Latency, Trials$Clearance, Trials$PNum, sep=" ") %in% unique(Inputs$U_ID_P2)
Trials$E_CT<- 0
Trials$Ineligible_CT<- 0
Trials$Prop_Ineligible_CT <- 0
Trials$U_ID_P2<-paste(Trials$Latency, Trials$Clearance, Trials$PNum, sep=" ")

longTri <- expand.grid(Trials$U_ID_P2, 1:length(theDirtyDozen), 1:maxCombi )
names(longTri)<-c("U_ID_orig", "varSet", "clustNum")

longTri[names(Trials)]<-0
longTri$hasMove<-F
longTri$hasWait <-F
longTri$hasTLX <-F
longTri$hasTempSen<-F
for(i in 1:max(longTri$varSet)){
  witches<-which(longTri$varSet==i)
  #names(theDirtyDozen[[i]]$VariableSet) is screwy
  newName <- names(theDirtyDozen[[i]]$VariableSet)[1]
  newName<- substr(newName, 1, nchar(newName)-1)
  if(nchar(newName)==2){

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newName <- paste(newName, "N", sep="")
}

longTri$varSet[witches] <- newName

ifelse("jitter_timeOfEvent" %in% theDirtyDozen[[i]]$VariableSet,
  longTri$hasMove[witches]<-T,
  longTri$hasMove[witches]<-F)

ifelse("jitter_PM_Wait_Time" %in% theDirtyDozen[[i]]$VariableSet,
  longTri$hasWait[witches]<-T,
  longTri$hasWait[witches]<-F)

ifelse("a_time" %in% theDirtyDozen[[i]]$VariableSet,
  longTri$hasTempSen[witches]<-T,
  longTri$hasTempSen[witches]<-F)

ifelse("TLX" %in% theDirtyDozen[[i]]$VariableSet,
  longTri$hasTLX[witches]<-T,
  longTri$hasTLX[witches]<-F)

print(newName)
flush.console()

for(i in 1:nrow(Trials)){ #Now this dumps Trials into longTri
  longTri[which(longTri$U_ID_orig == Trials$U_ID_P2[i]), names(Trials)] <- Trials[i,names(Trials)]
  cat(i, " of ", nrow(Trials), " ", i/nrow(Trials), "\n")
  flush.console()
}

longTri$Uncertainty <- 0
longTri$Train <- F
longTri$Tot_Move_in_Clust <- 0
longTri$Tot_Move_in_Clust <- NA
longTri$Tot_Wait_in_Clust <- 0
longTri$Tot_Wait_in_Clust <- NA
longTri$Tot_Ineligible <- 0
longTri$Tot_Ineligible <- NA
longTri$UncertaintyPerSec <- 0
longTri$UncertaintyPerSec <- NA
longTri$count <- 0
for(i in 1:nrow(longTri)){
    ID <- longTri$U_ID_P2[i]
    strat <- paste(longTri$varSet[i], "_combi_classification", sep="")
    uncert <- paste(longTri$varSet[i], "_combi_Uncertainty", sep="")
    strat_clust <- longTri$clustNum[i]
    clust_used <- Inputs[which(Inputs$U_ID_P2 == ID), strat] #Begin fixing here. Remember: Each longTri row is very specific

    #Now select the appropriate clust_used columns to get the subset going
    if(strat_clust %in% clust_used){#If they used the strategy
        Tot_Move_in_Clust <- sum(Inputs$timeOfEvent[which(Inputs$U_ID_P2 == ID & Inputs[strat]== strat_clust)],na.rm=F)
        Tot_Wait_in_Clust <- sum(Inputs$PM_Wait_Time[which(Inputs$U_ID_P2 == ID & Inputs[strat]== strat_clust)],na.rm=F)
        count <- length(Inputs$timeOfEvent[which(Inputs$U_ID_P2 == ID & Inputs[strat]== strat_clust)])

        # Inputs$M_N_combi_Uncertainty
        # sum((move time + wait time )* uncertainty for each) / total eligible
        weighted_uncerta <- sum((Inputs$timeOfEvent[which(Inputs$U_ID_P2 == ID & Inputs[strat]== strat_clust)]
                                  + Inputs$PM_Wait_Time[which(Inputs$U_ID_P2 == ID & Inputs[strat]== strat_clust)]))
                                * Inputs[which(Inputs$U_ID_P2 == ID & Inputs[strat]== strat_clust),uncert])

        longTri$Tot_Move_in_Clust[i] <- Tot_Move_in_Clust
        longTri$Tot_Wait_in_Clust[i] <- Tot_Wait_in_Clust
        longTri$UncertaintyPerSec[i] <- weighted_uncerta / (Tot_Move_in_Clust + Tot_Wait_in_Clust)
        longTri$count[i] <- count
    }
}
longTri$Ineligible_CT[i] <- longTri$CT[i] -
    sum(Inputs$timeOfEvent[which(Inputs$U_ID_P2==ID) ]) -
    sum(Inputs$PM_Wait_Time[which(Inputs$U_ID_P2==ID) ])

    cat(i, " of ", nrow(longTri), ", ", i/nrow(longTri), 

} 

longTri$Mean_Move_In_Clust<- longTri$Tot_Move_in_Clust / longTri$count
longTri$Mean_Wait_In_Clust<- longTri$Tot_Wait_in_Clust / longTri$count
save(longTri, file= paste(appended, "longTri.RData", sep=" "))

} 

doScript9(mostBIC, InputsBIC, "BIC")
doScript9(mostSimilar, InputsSimilar, "Similar")

#Run this to test:
# table(longTri$varSet, longTri$clustNum)
Appendix 2.10 – Inferential Statistics and Plots

library(psych)
library(ggplot2)
library(factoextra)
library(mclust)
library(cluster)
library(ggforce)
library(RColorBrewer)
library(reshape2)
library(lmerTest)
library(doParallel)
library(sjstats)
library(piecewiseSEM)

rm(list=ls())
athome<-T
num_parallel <-2 #doPar is inefficient w/RAM :(

if(athome){
  gdrive<-"D:/"
}else{
  gdrive<-"C:/Users/fscho/"
}

fileURL<-"Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive,fileURL, "/Data Analysis", sep=""))

Inputs<-read.csv("megaInputSetSimilar.csv")
load("longTri.RData")
load("Clusters/Jitter/TheFinalTwelve/mostSimilar.RData")
load("Output/Jitter/AdjustedRandIndex/ARI_Descrips_23.RData")

# #Did some looks, these three are the simplest to explain
# theHolyTrinity<-list(mostSimilar[[1]], mostSimilar[[9]], mostSimilar[[5]])
# save(theHolyTrinity, file="theHolyTrinity.RData")

longTri$FullyIneligibleTrial <- !(longTri$U_ID_P2 %in% unique(Inputs$U_ID_P2))
longTri$Prop_Eligible_CT<- 1 - (longTri$Ineligible_CT / longTri$CT)
longTri$Prop_Ineligible_CT <- 1 - longTri$Prop_Eligible_CT
longTri$E_CT <- longTri$CT * longTri$Prop_Eligible_CT

longTri$Tot_Move_in_Clust[ is.na(longTri$Tot_Move_in_Clust)]<-0
longTri$Tot.Wait_in_Clust[ is.na(longTri$Tot.Wait_in_Clust)]<-0
longTri$prop.eligible.move_in_clust <- longTri$Tot_Move_in_Clust / (longTri$E_CT)
longTri$prop.eligible.wait_in_clust <- longTri$Tot.Wait_in_Clust / (longTri$E_CT)
longTri$count[is.na(longTri$count)]<-0

longTri<-longTri[which(longTri$FullyIneligibleTrial == F),]

#Fixes the DD varset names
vsDD<-c()
for(i in 1:length(mostSimilar)){
  if(length(mostSimilar[[i]]$VariableSet)>1){
    #Chop off last number
    vsDD[i]<- substr(names(mostSimilar[[i]]$VariableSet)[1], 1, nchar(names(mostSimilar[[i]]$VariableSet))-1)
  }else{
    vsDD[i]<-names(mostSimilar[i]$VariableSet)
  }
}
names(mostSimilar)<-vsDD
varSet<-vsDD

#bla bla for each

#############################################FOR FINAL MODELS#########################################################

###Step 1: chi Sq

sock2<-makeCluster(num_parallel)
Sys.sleep(3)
wd<-getwd()
# feet <- c( "wd")
# clusterExport(sock2, feet)
# clusterEvalQ(sock2, library(psych))
registerDoParallel(sock2)
chisqstep<-function(longTriSS, Inputs, varSet, clustSet){
  ##Identify training trials
  csSet<-longTriSS[which(longTriSS$varSet==varSet & !(longTriSS$U_ID_P2 %in% unique(Inputs$U_ID_P2[clustSet$trainVec]))),]
# csSet<-longTriSS[which(longTriSS$varSet==varSet ),]
maxClust<-clustSet$clustCombiOptim_pcwReg2$numClusters.combi
csSet<-csSet[which(csSet$clustNum <= maxClust),]

# Get average frequency of each strategy
castMe<-describeBy(csSet$count, csSet[,c("Latency", "clustNum" )], mat=T)
# castMe<-castMe[which(castMe$mean>0),]
chiSqTable1<-dcast(castMe, group2~group1, value.var="mean")
row.names(chiSqTable1)<-chiSqTable1$group2
chiSqTable<-chiSqTable1[,2:ncol(chiSqTable1)]
# Run chi sq on counts
chi<-chisq.test(chiSqTable, simulate.p.value = T, B=10000000)
ret<-list(chiSqTable, chi)
names(ret) <-c("ChiSqTable", "ChiSq")
return(ret)
}

chisq<-foreach(i=1:length(mostSimilar),
       .verbose=T, .inorder=T, .packages = c("psych", "reshape2")) %dopar%
   chisqstep(longTri, Inputs, varSet[i], mostSimilar[[i]])
stopCluster(sock2)

names(chisq)<-varSet

chiSqGuy<-list()
for(i in 1:length(chisq)){
   formattedChisq<-round(chisq[[i]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1]][[1][...
formattedChisq[nrow(formattedChisq)+1,]<-
round(c(colMeans(chisq[[i]]$ChiSqTable[c(as.character(sort(as.numeric(rownames(chisq[[i]]$ChiSq$residuals))))),c(as.character(sort(as.numeric(colnames(chisq[[i]]$ChiSq$residuals))))))],
mean(rme)),2)
rownames(formattedChisq)[nrow(formattedChisq)]<"Marginal Means"
write.csv(formattedChisq, #May god have mercy on my soul for this line of code
file=paste("Output/Jitter/contingencyTables/chisq _, names(chisq)[i], ".csv", sep=""))
chiSqGuy[[i]]<formattedChisq
}
names(chiSqGuy)<-names(chisq)

#Step 2: Describe

#I was trying to use cast to turn the long set to a wide set,
#but that formula is so frustrating to use, that I'm giving up and
#doing it myself
sock2<-makeCluster(num_parallel)
Sys.sleep(3)
wd<-getwd()
# feet <- c ("wd")
# clusterExport(sock2, feet)
# clusterEvalQ(sock2, library(psych))
registerDoParallel(sock2)
makeWide<-function(DV, IV1, IDCol, dataS, keep){
  # dataS<-longTriSS[which(longTriSS$varSet=="M_N"),]
  # DV<"prop_eligible_move_in_clust"
  # IV1<"clustNum"
  # IDCol<"U_ID_P2"
  # keep< c("CTMin", "Lat1000", "a_time", "Clearance", "CT", "errors", "tot_dist") #Use eligible?
  newDF<-as.data.frame(unique(dataS[,IDCol]), ncol=1, stringsAsFactors = F)
names(newDF)<-IDCol
newDF[,keep]<-NaN

  for(i in 1:length(DV)){
    newCols1<- unique(dataS[, IV1])
    newCols2<-paste(DV[i], newCols1, sep="\_")
    newDF[,newCols2] <- NaN

  }

for(i in 1:nrow(newDF)){
  #Keep columns
  currPT<- newDF$U_ID_P2[i]
  newDF[i,keep] <-dataS[which(dataS[, IDCol]==currPT)[1], keep]
propCols<-(length(keep)+2):ncol(newDF)
for(j in propCols ){
    #String split the name of J, that gets DV and the clust num
    thisGuy<-strsplit(names(newDF)[j], "__")
    #Plop into column

    newDF[i,j]<-dataS[which(dataS[IV1]==thisGuy[[1]][2] & dataS[IDCol] == currPT), thisGuy[[1]][1]]
}
}

#Drops columns that are hold-overs from mass using describeBy larger cluster solutions
dropThese<-which(colSums(newDF[,propCols])==0)
newDF<-newDF[,propCols[dropThese]]
return(newDF)
}
sets<-foreach(i=1:length(mostSimilar), .verbose=T, .inorder=T, .packages = c("psych", "reshape2")) %dopar%
    makeWide(DV=c("prop_eligible_move_in_clust","prop_eligible_wait_in_clust"),
        IV1="clustNum",
        IDCol="U_ID_P2",
        dataS=longTri[which(longTri$varSet==varSet[i] &
        !(longTri$U_ID_P2 %in% unique(Inputs$U_ID_P2[mostSimilar[[i]]$trainVec]) ) ),],
        keep = c("PNum", "CTMin", "E_CT", "c_Lat1000",
        "a_time", "Clearance", "weightedRating", "CT", "errors", "tot_dist", "Prop_Ineligible_CT"))
stopCluster(sock2)
names(sets)<-varSet

#Generate table of summary stuff
rm(tabl)
for(i in 1:length(mostSimilar)){
    rowV<-c()
    rowV[1]<-names(mostSimilar[[i]]$VariableSet)[1]
    rowV[2]<-mostSimilar[[i]]$Iteration
    rowV[3]<-mostSimilar[[i]]$clustCombiOptim_pcwReg2$numClusters.combi
    rowV[4]<-mostSimilar[[i]]$clustCombi$MclustOutput$G
    rowV[5]<-mostSimilar[[i]]$clustCombi$MclustOutput$bic
    rowV[6]<-mostSimilar[[i]]$clustCombi$MclustOutput$loglik
    rowV[7]<-mostSimilar[[i]]$clustCombi$MclustOutput$df
    rowV[8]<-length(mostSimilar[[i]]$trainVec)
rowV[9]<-ARI_Descrips_23[[i]]$paste("Iteration_", mostSimilar[[i]]$Iteration, sep=""), "median_2"]

if(exists("tabl")){
  tabl<-rbind(tabl, rowV)
}else{
  tabl<-(rowV)
}

rownames(tabl)<-NULL
tabl<-as.data.frame(tabl, stringsAsFactors=FALSE)
tabl$BIC<-round(as.numeric(tabl$BIC),2)
tabl$Median ARI<-round(as.numeric(tabl$Median ARI), 2)
write.csv(tabl, file = "Output/Jitter/SummaryOfFinal12.csv")

#Step 3: Plot

#Flip prop eligible... to just overall
#Get prop ineligible
for(i in 1:length(sets)){
  sets[[i]]$Prop_Ineligible_CT[which(sets[[i]]$Prop_Ineligible_CT<0)]<-0  #Some are negative due to a rounding error, smallest is -0.000273, so its a really small rounding error
  newStuff<-(1-sets[[i]]$Prop_Ineligible_CT) * sets[[i]][, grep("_eligible_", names(sets[[i]]))]
  names(newStuff)<-gsub("_eligible_", "_total_", names(newStuff))
  sets[[i]]<-cbind(sets[[i]], newStuff)
}

#Center the total props
for(i in 1:length(sets)){
  ms<-sets[[i]]
  mss<-ms[, grep("_total_",names(ms))]
  mss_c<-mss - colMeans(mss)
  names(mss_c)<-paste("c_", names(mss_c), sep="")
  sets[[i]]<-cbind(sets[[i]], mss_c)
}
#Step 4: Lmer

doStats<-function(dv, ds, vList){

do_Waits<-sum(grepl("W", vList))
do_Moves<-sum(grepl("M", vList))

W<""
M<""
if(sum(do_Waits)>0){
  W<-grep("c_prop_total_wait", names(ds), value = T)
}
if(sum(do_Moves)>0){
  M<-grep("c_prop_total_move", names(ds), value = T)
}

func<-formula(
  paste(dv, "~",
    "c_Lat1000+c_cle+",paste(W, collapse="+"),"+",paste(M, collapse="+"), "+(1|PNum)
    ,collapse="+")
ct<-lmer(func, data=ds)
null_ct<-lmer(formula(paste(dv, ~(1|PNum), sep="")), data=ds)

rNM<-rand(null_ct)
iccM<-icc(null_ct)
r2<-rsquared(ct)
corMat<-vcov(ct)
ret<-list(ct,summary(ct), null_ct, rNM, iccM, r2, corMat)
names(ret)<-c("mod", "summ", "null_mod", "rand-p", "ICC", "R2", "corrMat")
return(ret)
}
lotsOfModStats<-function(sets, vs){
  ds<-sets
ds$c_cle <- ds$Clearance - mean(ds$Clearance)
dvList<-list("CTMin", "errors", "tot_dist")
vList<-list()
if(grepl("M", vs)){
  vList[length(vList)+1]<-c("M")
}
if(grepl("W", vs)){
  vList[length(vList)+1]<-c("W")
}
vList<-unlist(vList)
aaa<-lapply(dvList, doStats, ds, vList)
names(aaa)<-unlist(dvList)
return(aaa)
}
analysis<-list()
for(i in 1:length(sets)){
    analysis[[i]]<-try(lotsOfModStats(sets[[i]], names(sets)[i]))
}
# warnings()
names(analysis)<-varSet
for(i in 1:length(analysis)){
    sink(file=paste("Output/Jitter/lmer/sink_", names(analysis)[i], ".txt", sep=""))
    print(analysis[[i]])
    sink()
}
# themStats<-lapply(sets, lotsOfModStats)

###FROM HRI3###
#Format
formatFunc<-function(H8){
try({
    summ<-H8$summ
    coefDF<-as.data.frame(summ$coefficients)
    coefDF$newCol<-paste(format(round(coefDF$Estimate, 2), nsmall=2),
                        " (", format(round(coefDF$`Std. Error`,2),nsmall=2), ",", sep=""
    coefDF$stars<- (coefDF$`Pr(>|t|)`<.001) + (coefDF$`Pr(>|t|)`<.01) + (coefDF$`Pr(>|t|)`<.05)
    coefDF$newCol2<-"
    for(i in 1:nrow(coefDF)){
        coefDF$newCol2[i]<-paste( coefDF$newCol[i], paste(rep("*", coefDF$stars[i]), collapse=""), sep=""
    }
    coefDF$newCol2[which(coefDF$`Pr(>|t|)`<.1 & coefDF$stars==0)]<-
paste(coefDF$newCol2[coefDF$`Pr(>|t|)`<.1 & coefDF$stars==0], "+", sep="")
    newRows<- (nrow(coefDF)+1) : (nrow(coefDF)+4)
    coefDF[newRows,]<=""nrow(coefDF)+4"
    coefDF$newCol2[newRows[2]]<="Var. (SD)"
    ranDF<-as.data.frame(summ$varcor)
    ranDF$newCol<-paste(format(round(ranDF$vcov, 2), nsmall=2),
                           " (", format(round(ranDF$sdcor,2),nsmall=2), ",")", sep=""
    row.names(coefDF)[newRows]<-c("","Rand. Effects", "Subject", "Residual")
    nullM<-H8$null_mod
}
```r
srNM <- H8$ rand-p'
if(F){
(rsrNM$rand.table[3]<.05))
} else{
  stars2 <- as.numeric((srNM$Pr(>Chisq)[2]<.001) + (srNM$Pr(>Chisq)[2]<.01) +
(srNM$Pr(>Chisq)[2]<.05))
}

# coefDF$newCol2[9] <- paste(ranDF$newCol[1], paste(rep("*", stars1), collapse=""), sep=" ")
coefDF$newCol2[newRows[length(newRows)-1]] <- paste(ranDF$newCol[1], paste(rep("*", stars2), collapse=""), sep=" ")
coefDF$newCol2[newRows[length(newRows)]] <- ranDF$newCol[2]

extRows <- (newRows[length(newRows)]+1):(newRows[length(newRows)]+4)
coefDF[extRows,] <- ""
row.names(coefDF)[extRows] <- c(" ", "Marg.", "Cond.", "ICCnull")

r2 <- H8$R2
coefDF$newCol2[extRows[2]] <- format(round(r2$Marginal, 2), nsmall=2)
coefDF$newCol2[extRows[3]] <- format(round(r2$Conditional, 2), nsmall=2)
# rNM <- rand(nullM)
iccM <- H8$ICC
coefDF$newCol2[extRows[4]] <- format(round(as.numeric(iccM[1]), 2), nsmall=2)

names(coefDF)[8] <- as.character(H8$R2$Response)
# Add N and # Trials
coefDF[nrow(coefDF)+1,] <- summ$devcomp$dims[1] # N-obs
coefDF[nrow(coefDF)+1,] <- summ$devcomp$dims[5] # N-people
l2 <- (nrow(coefDF)-1):nrow(coefDF)
rownames(coefDF)[l2] <- c("# of Trials", "# of Participants")

# gV(full, dv, ylimL, ylimH, ylabel, dpiS)
# gV2(full, dv, ylimL, ylimH, ylabel, dpiS)
blank <- coefDF[1,]
blank[1,] <- "B (SE)"
rownames(blank) <- "Fixed Effects"
coefDF <- rbind(blank, coefDF)
return(coefDF[ncol(coefDF)])
}
}
lmerDudes <- list()
for(i in 1:length(analysis)){
  formatted <- lapply(analysis[[i]], formatFunc)
  for(j in 1:length(formatted)){
    if(j == 1){
      newGuy <- formatted[[j]]
    } else{
    }
  }
}
```
newGuy<-cbind(newGuy, formatted[[j]])
}
}
	ryCatch(write.csv(newGuy,
    file=paste("Output/Jitter/lmer/lmer_{", names(analysis)[i], ", csv", sep="")), error=function(i) print(i))

lmerDudes[[i]]<-newGuy
}
names(lmerDudes)<-names(analysis)

######FROM HR13######

#Useful 2D plots

#Area Plot
ggplot(data=Inputs, aes(x=log(timeOfEvent), y=log(PM_Wait_Time), color=as.factor(W_N_combi_classification)))+
scale_color_manual(values=c(brewer.pal(12, "Paired"), "#000000")) +
geom_point() +
theme(legend.title = element_blank())

#Density Plot
graphs<-function(clust, ds, trainVec, vX,vY, scalex, scaley, namex, namey, xlim, ylim,
density=F, pTitle=NULL){
  ds<- ds[-trainVec,]
  ds$newX<-ds[,vX]
  ds$newY<-ds[,vY]
  ds$clust <- as.factor(ds[,clust])
  # if(length(unique(ds$clust)) >12){
  #  color<-scale_fill_discrete()
  # }else{
  #  color<-scale_fill_brewer(type = "qual", palette="Paired")
  # }
  base<- ggplot(data=ds, aes(x=newX, y=newY ,fill=clust))+
    # stat_bin_2d( aes(alpha=..count..)) +
    stat_bin_2d()+
    # scale_alpha_continuous(range=c(.3,1), trans='log10')+ 
    # +
    theme_minimal()+

theme(axis.text.x = element_text(angle = 90), panel.spacing.x=unit(1.5, "lines")) +
  labs(fill = "Cluster", x = namex, y=namey) +
  color+
  xlim(xlim) +
  ylim(ylim)

if(scalex){
  base<-base +scale_x_continuous(trans='log10', labels=function(x) format(x, scientific = F),
    limits=xlim)
}
if(scaley){
  base<-base+scale_y_continuous(trans='log10', labels=function(x) format(x, scientific = F),
    limits=ylim)
}
if(!is.null(pTitle)){
  base<-base+
    labs(title= pTitle)+
    theme(plot.title = element_text(hjust=.5))
}

lat_facet <- base +
  facet_wrap(~Latency) +
  labs(caption = "Faceted by Latency")+
  theme(plot.caption = element_text(hjust = .5))

cle_facet<- base +
  facet_wrap(~Clearance) +
  labs(caption = "Faceted by Clearance")+
  theme(plot.caption = element_text(hjust = .5))

if(density){
  base<- base +geom_density_2d()
  lat_facet<-lat_facet+geom_density_2d()
  cle_facet<-cle_facet+geom_density_2d()
}

ret<-list(base, lat_facet, cle_facet)
names(ret)<-c("Base", "Lat_fac", "Cle_fac")
return(ret)
}

formatInfo<-function(var, scale, axisName, lim){
  ret<-list(var, scale, axisName, lim)
names(ret) <- c("var", "scale", "axisName", "lim")
return(ret)

M <- formatInfo("timeOfEvent", T, "Move Time (sec.)", lim=c(.01, 100))
W <- formatInfo("PM_Wait_Time", T, "Wait Time (sec.)", lim=c(.01, 30))
TLX <- formatInfo("TLX", F, "NASA-TLX Rating", lim=c(0, 100))
TS <- formatInfo("a_time", F, "Temporal Sensitivity", lim=c(.25, 1.75))
formattedVs <- list(M, W, TLX, TS)
names(formattedVs) <- c("M", "W", "TLX", "TS")
pairings <- combn(c("W", "M", "TLX", "TS"), 2) # Note, row 1 is Y, row 2 is X

# plotCity <- list()
for(k in varSet){
  for(i in c("Mclust", "combi")){
    for(j in 1:ncol(pairings)){
      dire <- paste("Plots/AppendixPlots/", k, sep="")
dir.create(dire, showWarnings = F) # Makes folders
c1C <- grep("class", names(Inputs), value=T)
c1A <- grep(i, names(Inputs), value = T)
c1B <- grep(k, names(Inputs), value = T)

plotTitle <- c()
counter <- 0
if(grepl("M", k)){
  plotTitle[length(plotTitle)+1] <- "Move"
counter <- counter + 1
}
if(grepl("W", k)){
  plotTitle[length(plotTitle)+1] <- "Wait"
counter <- counter + 1
}
if(grepl("TLX", k)){
  plotTitle[length(plotTitle)+1] <- "NASA-TLX"
counter <- counter + 1
}
if(grepl("TS", k)){
  plotTitle[length(plotTitle)+1] <- "Temporal Sensitivity"
counter <- counter + 1
}
if(counter == 1){
  plotTitle <- paste(plotTitle, "Only", sep = " ")
} else {
  plotTitle <- paste(plotTitle, collapse = ", ")
}
filt1 <- clC[clC %in% clA]  
filt2 <- filt1[filt1 %in% clB]  
shrink <- grep(paste("^", k, sep=""), filt2, value = T)  
# Its always going to be the smaller one  
clu <- shrink[which(nchar(shrink) == min(nchar(shrink)))]

x <- formattedVs[[which(names(formattedVs) == pairings[2,j])]]  
y <- formattedVs[[which(names(formattedVs) == pairings[1,j])]]

thisPlot <- graphs(clust = clu,  
  ds = Inputs,  
  trainVec = mostSimilar[[which(names(mostSimilar) == k)]]$trainVec,  
  vX = x$var,  
  vY = y$var,  
  scalex = x$scale,  
  scaley = y$scale,  
  namex = x$axisName,  
  namey = y$axisName,  
  xlim = x$lim,  
  ylim = y$lim,  
  density = F,  
  pTitle = plotTitle)

FN <- paste(k, i, sep="-", paste(pairings[,j], collapse="_")  
for(M in 1:length(thisPlot)){  
  FNC <- paste(FN,"-", names(thisPlot)[M], ".png", sep="")  
ggsave(FNC, plot = thisPlot[[M]], path = dire, dpi = 800)  
  plotCity[length(plotCity)+1] <- thisPlot[[M]]  
  names(plotCity)[length(plotCity)] <- paste(dire, FNC, sep="/")
}

mixGuy <- list()  
combiGuy <- list()  
for(i in 1:length(mostSimilar)){  
  clu <- mostSimilar[i]  
  vs <- names(mostSimilar)[i]  
  ds <- Inputs

  baseTable <- as.data.frame(matrix(nrow = clu$clustCombi$MclustOutput$G, ncol = 8))
names(baseTable) <- c("Cluster", "Mixture Comp.", "jitter_timeOfEvent", "jitter_PM_Wait_Time", "TLX", "a_time", "Prop. Obs. in Training", "Prop. Time in Training")

mclu <- grep("Mclust_class", grep(paste("^", vs, sep=""), names(ds), val=T), val=T)[1]
cco <- grep("combi_class", grep(paste("^", vs, sep=""), names(ds), val=T), val=T)[1]
mixT <- table(ds[,mclu], ds[,cco]) > 0

# I want to append Prop Times into basetable and comTable
dsTrain <- ds[clu$trainVec,]
tri <- longTri[which(longTri$varSet==vs & longTri$U_ID_P2 %in% dsTrain$U_ID_P2 ),]

baseTable$`Mixture Comp.` <- 1:nrow(baseTable)

for(j in 1:nrow(baseTable)){
  baseTable$Cluster[j] <- which(mixT[j,]==T)
}

chickenParm <- clu$clustCombi$MclustOutput$parameters
baseTable$`Prop. Obs. in Training` <- format(round(chickenParm$pro,2), nsmall=2)

# max(dim(chickenParm$mean))
# ifelse(is.null(dim(chickenParm$mean)), maxIter <- length(chickenParm$mean), maxIter <- ncol(chickenParm$mean))

# This works for any var set with >1 variable, but doesn't work for M_N or W_N...
# Consider adjusting by flipping the loop (k/val first, specify differently if M_N, then do j baseTable)

# Identify the variables
val <- clu$VariableSet
if(length(val)<2){
  meanies <- t(t(chickenParm$mean))
  colnames(meanies) <- val
} else{
  meanies <- t(chickenParm$mean)
}

baseTable[,val] <- round(meanies[,val],2)

# Now round things so they look good
# Gotta handle variance totally differently :

for(j in 1:nrow(baseTable)){
  if(length(val)>1){
    va<-round(sqrt(diag(chickenParm$variance$sigma[,j])),2) # According to the mclust documentation, this is the variance (but they call it sigma)... gave me a heart attack
  }else{
    va<-round(sqrt(diag(chickenParm$variance$sigmasq[j])),2)
  }
  for(k in names(va)){
    baseTable[j, k]<-paste(format(baseTable[j,k], nsmall=2), " (",format(va[k], nsmall=2), ")",
  sep="")
  }
}

# baseTable[is.na(baseTable)]<-
baseTable<-baseTable[order(baseTable$Cluster, baseTable$`Mixture Comp.`),]
# baseTable$Cluster[diff(baseTable$Cluster)==0]<-
# names(baseTable)<-c("Cluster", "Mixture Comp.", "Move (sec)", "Wait (sec)", "NASA-TLX", "Temporal Sen.", "Prop. Obs. in Trainig")
# write.csv(baseTable, file=paste("Output/Jitter/MixComp/", vs, ".csv", sep=""), row.names = F)

# Now make a cluster table
comTable<-baseTable
comTable<-.comTable[which(diff(comTable$Cluster)==0),]
comTable$`Mixture Comp.`<-NA
comTable$`Prop. Obs. in Trainig`<-NA

for(L in 1:nrow(comTable)){
  for(M in 2:ncol(comTable)){
    if(!is.na(comTable[L,M])){
      varName<-names(comTable)[M]
      meanie<- mean(dsTrain[which(dsTrain[cco]== comTable$Cluster[L] ), varName])
      std <- sqrt(var(dsTrain[which(dsTrain[cco]== comTable$Cluster[L] ), varName]))
      m2<-format(round(meanie,2), nsmall=2)
      s2<-format(round(std, 2), nsmall=2)
      comTable[L,M] <- paste(m2, " (", s2, ")", sep="")
    }
  }
}

prop <- format(round( (nrow(dsTrain[which(dsTrain[cco]== comTable$Cluster[L] ), ])) / nrow(dsTrain)),2 ), nsmall=2)
comTable$`Prop. Obs. in Trainig`[L] <-prop
firstOccurrence <- match(unique(paste(dsTrain$U_ID_P2, dsTrain$CT, sep="_")), paste(dsTrain$U_ID_P2, dsTrain$CT, sep="_"))

# Use Move
uM <- grepl("M", cco)
# Use Wait
uW <- grepl("W", cco)

# I did something clever. :)  
# If it didn't use Move (or Wait), it multiplies their times by 0, so it adds a bunch of 0s (i.e., nothing gets added)!
propTime <- sum((dsTrain[which(dsTrain[cco] == comTable$Cluster[L]), "jitter_timeOfEvent"] * uM) +
                (dsTrain[which(dsTrain[cco] == comTable$Cluster[L]), "jitter_PM_Wait_Time"] * uW)) / sum(dsTrain$CT[firstOccurrence])
comTable$`Prop. Time in Training`[L] <- format(round(propTime, 2), nsmall=2)

# Do the propTime for mixtures
for(L in 1:nrow(baseTable)) {
  firstOccurrence <- match(unique(paste(dsTrain$U_ID_P2, dsTrain$CT, sep="_")), paste(dsTrain$U_ID_P2, dsTrain$CT, sep="_"))

  # Use Move
  uM <- grepl("M", mclu)
  # Use Wait
  uW <- grepl("W", mclu)

  # I did something clever. :)  
  # If it didn't use Move (or Wait), it multiplies their times by 0, so it adds a bunch of 0s (i.e., nothing gets added)!
  propTime <- sum((dsTrain[which(dsTrain[mclu] == baseTable$`Mixture Comp.`[L]), "jitter_timeOfEvent"] * uM) +
                  sum(dsTrain[which(dsTrain[mclu] == baseTable$`Mixture Comp.`[L]), "jitter_PM_Wait_Time"])) * uW / sum(dsTrain$CT[firstOccurrence])
  baseTable$`Prop. Time in Training`[L] <- format(round(propTime, 2), nsmall=2)

}

# For a while, I considered combining comTable and baseTable
# However, the mean/var in baseTable refers to the mixture mean/var
# While clustCombi/comtable mean/var refers to the mean/var of the observations in those clusters
# And while they're likely close to equivalent... I don't want to give the impression that they are.
# So I'm keeping them as separate, and will probably want a note for this somewhere
comTable$`Mixture Comp.`<-NULL
baseTable$Cluster[which(c(FALSE,diff(baseTable$Cluster)==0))]<-"
baseTable[is.na(baseTable)]<-
comTable[is.na(comTable)]<-
# comTable$Cluster[diff(comTable$Cluster)==0]<-
write.csv(baseTable, file=paste("Output/Jitter/MixComp/", vs, ".csv", sep=""), row.names = F)

mixGuy[[i]]<baseTable
names(mixGuy)[i]<-vs

write.csv(comTable, file=paste("Output/Jitter/ClustComp/", vs, ".csv", sep=""), row.names = F)
combiGuy[[i]]<-comTable
names(combiGuy)[i]<-vs

}

# For each total run,
# Average number of mixture components, avg number of clusters collapsed to
# median BIC

clustChunks<list.files("Clusters/Jitter/varSetOrganization", pattern="RData", full.names = T)
chunkyGuy<-list()
for(i in 1:length(clustChunks)){
  load(clustChunks[i])

  mixComps<-c()
nClust<-c()
  medBIC<-c()
  for(j in 1:length(varSetList)){
    mixComps[j]<-varSetList[[j]]$clustCombi$MclustOutput$G
    nClust[j]<-varSetList[[j]]$clustCombiOptim_pcwReg2$numClusters.combi
    medBIC[j]<-varSetList[[j]]$clustCombi$MclustOutput$bic
  }

  vs<-names(varSetList[[j]]$VariableSet)[1]
  clustSum <- c(quantile(mixComps, c(.25,.5,.75)),
               quantile(nClust, c(.25,.5,.75)),
               quantile(medBIC, c(.25,.5,.75)))
  clustSum<-c(vs, clustSum)
  names(clustSum)<-c("Variable Set",

"# of Mixture Components (25th %ile)", "# of Mixture Components (50th %ile)",
"# of Mixture Components (75th %ile)",
"# of Clusters (25th %ile)","# of Clusters (50th %ile)","# of Clusters (75th %ile)",
"BIC (25th %ile)","BIC (50th %ile)","BIC (75th %ile)"
if(!exists("partyRock")){
  partyRock<-as.data.frame(t(clustSum))
}else{
  partyRock<-rbind(partyRock, t(clustSum) )
}
write.csv(partyRock, "Output/Jitter/SummaryOfAllModels.csv")
chunkyGuy[[i]]<-partyRock
}

#Makes all the data easier to access in the future. This contains everything.
moveForward<-list( chunkyGuy, chisq, chiSqGuy, mixGuy, combiGuy, lmerDudes, #plotCity,
  analysis, Inputs, longTri, mostSimilar, ARI_Descrips_23)
names(moveForward)<-c("chunkyGuy", "chisq", "chiSqGuy", "mixGuy", "combiGuy",
  "lmerDudes", "#plotCity",
  "all_lmer_analysis", "Inputs", "longTri", "mostSimilar","ARI_Descrips_23")
save(moveForward, file="finalDataChunks.RData")

#Do somethign else with plot
library(psych)
library(ggplot2)
library(factoextra)
library(mclust)
library(cluster)
library(ggforce)
library(RColorBrewer)
library(reshape2)
library(lmerTest)
library(doParallel)
library(sjstats)
library(piecewiseSEM)
library(imager)
library(rtf)
library(igraph)
library(comato)
library(grid)
library(gridExtra)

rm(list=ls())
athome<-T
num_parallel <- 2 #doPar is inefficient w/RAM :

if(athome){
  gdrive<="D:/"
}else{
  gdrive<="C:/Users/fscho/"
}

fileURL<="Google Drive/Graduate School/Research/Dissertation"
setwd(paste(gdrive.fileURL, "/Data Analysis", sep=""))

load("finalDataChunks.RData")
attach(moveForward)
# currWidth<-getOption("width")
# options(width=900)
rtfFile<-RTF("Output/Jitter/maybeAppendix.doc")
vsNames<-c("Move-Only",
            "Move & NASA-TLX",
            "Move, NASA-TLX, & Temporal Sensitivity",
            "Move & Temporal Sensitivity",
            "Move & Wait",
            "Move, Wait, & NASA-TLX",
            "Move, Wait, NASA-TLX, & Temporal Sensitivity",
            "Move, Wait, & Temporal Sensitivity",
            "Wait-Only",
            "Wait & NASA-TLX",
            "Wait, NASA-TLX, & Temporal Sensitivity",
            "Wait & Temporal Sensitivity")

#Use vsNames to figure out plot

plotChooser<-function(fl, type, varss){
  #If solo, use M/W
  if(grepl("N", varss)){
    varss<-"M_W_N"
  }

  shrunkFL<-grep(type, fl, val=T)
splits<-unlist(strsplit(shrunkFL, type))[c(F,T)]

  varList<-unlist(strsplit(varss, ","))
counter<-vector(length = length(varList), mode="list")

  for(i in 1:length(varList)){
    counter[[i]]<-grep(varList[i], splits)
  }

  #If its duplicated, that means its got two of my variables... so I want the plot
  numbers<-unlist(counter)[duplicated(unlist(counter))]

  return(shrunkFL[numbers])}
#This function does all the pronet stuff I want
PRONET<-function(condMat, margins=0, fnt=.8, jp=F, condProb=F, weight=F){

    if(condProb){#Gets conditional probabilities
        condMat <- condMat / rowSums(condMat)
    }

    #Take a frequency matrix (like you would pass to jpathfinder), transform it into a weighted
dissimilarity matrix
    testMat<-abs(condMat/max(condMat) - 1)
    testMat<-as.matrix.data.frame(testMat)

    #Believe it or not, to get something that looks like JPathFinder, you gotta flip it twice and drop
the negative Infs...
    wMat<-1-JPathFinder(testMat, nrow(testMat)-1, Inf)
    wMat[which(wMat<0)]<-0

    #This gets you a Pathfinder matrix, ranging from 0 to 1. 0 means no link exists, 1 is the
"strongest" link,
    #and anything inbetween is a weight. Smaller number = longer distance
    heck<-graph.adjacency(wMat, mode="directed", weighted=TRUE)

    if(weight){
        maxWidth<-max(E(heck)$weight)
        E(heck)$width<-5*E(heck)$weight / maxWidth
    }

    if(jp){
        return(heck)
    }

}else{
    x<-plot(heck, layout=layout.graphopt, rescale=T, edge.arrow.size=.5, vertex.color="white",
vertex.size = 30,
        vertex.frame.color="white", vertex.label.color="black", vertex.label.cex=fnt,
vertex.label.dist=0, edge.curved=0,
        margin=margins)
    x<-recordPlot()
ret <- list(wMat, heck, x)
names(ret) <- c("Pathfinder", "igraph", "plot")
return(ret)
}

# Generate pathfinder stuff
condProb <- list()
lat <- sort(unique(moveForward$Inputs$Lat1000))
for(j in 1:length(chiSqGuy)){
  latGuy <- list()
  for(i in 1:length(lat)+1){
    vs <- names(chiSqGuy)[j]
    classCol <- intersect(grep(paste("^", vs, sep=""), names(Inputs), value = T),
                         grep("combi_class", names(Inputs), value=T))[1]
    trainCol <- intersect(grep(paste("^", vs, sep=""), names(Inputs), value = T),
                          grep("Mclust_train", names(Inputs), value=T))[1]
    if(length(classCol)!=1 | length(trainCol)!=1){
      stop("Something screwy happened")
    }
    if(i == length(lat)+1){ # I want one without the latency subset, because I'm doing them all
      trainputs <- Inputs[which(Inputs[trainCol]==0 ),]
    } else{
      trainputs <- Inputs[which(Inputs[trainCol]==0 & Inputs$Lat1000==lat[i]),]
    }
  }
  lastItem <- c(diff(as.numeric(trainputs$U_ID_P2)) != 0, T) # This is the transition item
  testVec <- trainputs[,classCol]
  laggedTestVec <- c(testVec[-1], NA)
  laggedTestVec[lastItem] <- NA

  First <- testVec
  Second <- laggedTestVec
  transitions <- table(First, Second)

  latGuy[[i]] <- transitions
names(latGuy)<-c(lat, "Overall")
condProb[[j]]<-latGuy
}
names(condProb)<-names(chiSqGuy)
freqPath<-condProb #Just to make it clear that I'm using raw frequencies and not conditional probabiilies

# names(transTables)<-names(chiSqGuy)

###NOTE###
#MUST RUN JPATHFINDER TO GET IMAGES BETWEEN HERE AND THE STUFF BELOW
#Just kidding, I can do this much cooler and automatically with R
#######
for(i in 1:12){

vsCode<-names(mixGuy[i])
ap<-list.files(paste("./Plots/AppendixPlots/", vsCode, sep=""))

addParagraph(rtffile, paste("Appendix ", i, ". ", vsNames[i], " Results\n", sep=""))

addParagraph(rtffile, paste("Table ##. Mixture Model for ", vsNames[i], " Solution."), sep=""))
addTable(rtffile, mixGuy[[i]], row.names=F)
addPageBreak(rtffile)

pls<-plotChooser(ap, "Mclust", vsCode)
basePls<-grep("Base", pls, val=T)
for(j in 1:length(basePls)){
    addPng(rtffile, paste("./Plots/AppendixPlots/", vsCode, "/", basePls[j], sep=""), height=4.36, width=6.5)
    addParagraph(rtffile, paste("Figure ##. Observations with Assigned Clusters (Uncombined) for ", vsNames[i], " Solution (", j, "/", length(basePls), ").", sep=""))
    addPageBreak(rtffile)
}
addParagraph(rtffile, paste("Table ##. Cluster Summary for ", vsNames[i], " Solution.", sep=""))
addTable(rtffile, combiGuy[[i]], row.names=F)
addPageBreak(rtffile)

pls<-plotChooser(ap, "combi", vsCode)
basePls<-grep("Base", pls, val=T)
for(j in 1:length(basePls)){
    addPng(rtffile, paste("./Plots/AppendixPlots/", vsCode, "/", basePls[j], sep=""), height=4.36, width=6.5)
    addParagraph(rtffile, paste("Figure ##. Observations with Assigned Clusters (Combined) for ",vsNames[i], " Solution (", j, "/", length(basePls), ").", sep=""))
    addPageBreak(rtffile)
}

addParagraph(rtffile, paste("Table ##. Mean Freq. of Cluster for ", vsNames[i], " Solution.", sep=""))
#Toss residuals, tables look hideous
for(j in 1:nrow(chiSqGuy[[i]])){
    for(k in 1:ncol(chiSqGuy[[i]])){
        chiSqGuy[[i]][j,k]<-strsplit(as.character(chiSqGuy[[i]][j,k]), " ")[1][1]
    }
}
addTable(rtffile, chiSqGuy[[i]], row.names=T)
# addParagraph(rtffile, past"n")
addParagraph(rtffile, paste("#CHISQUARE = ", round(chisq[[i]]$ChiSq$statistic, digits=2), ", ", ", #p = ", round(chisq[[i]]$ChiSq$p.value, digits=2), ", ", sep=""))
addPageBreak(rtffile)

pls<-plotChooser(ap, "combi", vsCode)
basePls<-grep("Lat_fac", pls, val=T)
for(j in 1:length(basePls)){
    addPng(rtffile, paste("./Plots/AppendixPlots/", vsCode, "/", basePls[j], sep=""), height=4.36, width=6.5)
    addParagraph(rtffile, paste("Figure ##. Observations with Assigned Clusters (Combined) for ",vsNames[i], " Solution, faceted by Latency (", j, "/", length(basePls), ").", sep=""))
    addPageBreak(rtffile)
}
addParagraph(rtffile, paste("Table ##. Count of Cluster Transitions in Test Set for ", vsNames[i], " Solution.", sep=""))
addTable(rtffile, freqPath[[i]]$Overall, row.names=T)
addPageBreak(rtffile)

# png(filename = "Plots/tempPathfinder.png", height=4.36, width=6.5, units="in", res=1600)
# pf<-PRONET(freqPath[[i]]$Overall,margins=0, condProb = T)
# dev.off()

addPng(rtffile, "Plots/tempPathfinder.png", height=4.36, width=6.5)
addParagraph(rtffile, paste("Figure ##. Frequency-Based Pathfinder Network of Cluster Transitions for ",vsNames[i], " Solution.", sep=""))
addPageBreak(rtffile)

addParagraph(rtffile, paste("Table ##. Linear Mixed-Effects Models for ", vsNames[i], " Solution.", sep=""))
addTable(rtffile, lmerDudes[[i]], row.names=T)
addParagraph(rtffile, "* p < .05, ** p< .01, ***p < .001, +p<.10. Mean-centered coefficients are reported. Reported ICC is for the within-person intercept-only random effect. ")
addPageBreak(rtffile)

# #I'm only doing this for 0, 500, and 1000 or else I'll be at this forever
# addPng(rtffile, paste("./Pathfinder Stuff/pf_TRANSITIONS_", vsCode, "0_pathfinder.png", sep=""), height=4.36, width=6.5)
# addParagraph(rtffile, paste("Figure ##. Pathfinder Network of Cluster Transitions for ",vsNames[i], " Solution.", sep=""))
# addPageBreak(rtffile)
Below is just random stuff I needed to put in the dissertation

```r
regTest<-function(b1, b2, SE1, SE2){
  top <- b1 - b2
  bottom <- sqrt( b1^2 + b2^2)
  return(top/bottom)
}

#CTMin Clust 5 & 6
regTest(moveForward$all_lmer_analysis$M_NSCTMin$summ$coefficients[8,1],
       moveForward$all_lmer_analysis$M_NSCTMin$summ$coefficients[9,1],
       moveForward$all_lmer_analysis$M_NSCTMin$summ$coefficients[8,2],
       moveForward$all_lmer_analysis$M_NSCTMin$summ$coefficients[9,2])

#Tot_Dist 5 & 6
regTest(moveForward$all_lmer_analysis$M_NTot_dist$summ$coefficients[8,1],
       moveForward$all_lmer_analysis$M_NTot_dist$summ$coefficients[9,1],
       moveForward$all_lmer_analysis$M_NTot_dist$summ$coefficients[8,2],
       moveForward$all_lmer_analysis$M_NTot_dist$summ$coefficients[9,2])
```
moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[9,2])

# Tot_Dist 1 & 6
regTest(moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[4,1],
         moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[9,1],
         moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[4,2],
         moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[9,2])

# Tot_Dist 5 & 1
regTest(moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[8,1],
         moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[4,1],
         moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[8,2],
         moveForward$all_lmer_analysis$M_N$tot_dist$summ$coefficients[4,2])

# Error clust, 5 & 6
regTest(moveForward$all_lmer_analysis$M_N$errors$summ$coefficients[8,1],
         moveForward$all_lmer_analysis$M_N$errors$summ$coefficients[9,1],
         moveForward$all_lmer_analysis$M_N$errors$summ$coefficients[8,2],
         moveForward$all_lmer_analysis$M_N$errors$summ$coefficients[9,2])

# Similarity Plot
SimPl <- read.csv("Pathfinder Stuff/M_N Similarity Plot.csv")
levels(SimPl$XLab) <- c("0\nto\n.125", ".125\nto\n.250", ".250\nto\n.375", ".375\nto\n.500", ".500\nto\n.625", ".625\nto\n.750", ".750\nto\n.875", ".875\nto\n1")

simPlPlot <- ggplot(data=SimPl, aes(x=XLab, y=Ylab, group=1)) +
    geom_point(size=4) +
    geom_path(size=1) +
    theme_minimal() +

    theme(axis.text.x = element_text(angle = 0), panel.spacing.x=unit(1.5, "lines"), plot.title =
         element_text(hjust=.5)) +
    ylim(0,1)+
    labs(title = "Change in Network Similarity by Latency", x = "Change in Latency (sec)",
         y="Network Similarity")

ggsave("Plots/PathfinderSimilarity_Freq.png", plot=simPlPlot, height=4.36, width=6.5,
          units="in")
# png(filename = "Plots/PathfinderFacet.png", height=4.36, width=6.5, units="in", res=360)
# Faceted M_N pf plot
pf_move_Lat<-list()
par(mfrow=c(1,3))
set.seed(12345)
for(i in c(1,5,9)) {
    x<-PRONET(freqPath$M_N[[i]], margins=0, fnt=2, condProb = F, weight=F)$plot
title(paste(names(freqPath$M_N[i], " sec", sep=""))
    # pf_move_Lat[[i]]<-recordPlot()
}
set.seed(NULL)
par(mfrow=c(1,1))
# dev.off()

# NOTE: Opened this in the RStudio viewer and tinkered with things until it looked good and saved from there. The dev.off() route was giving me weird sizes on things

# # Faceted M_N cond pf plot
# pf_move_Lat<-list()
# par(mfrow=c(1,3))
# set.seed(123456)
# for(i in c(1,5,9)) {
#     x<-PRONET(freqPath$M_N[[i]], margins=0, fnt=2, condProb = T, weight=T)$plot
#     title(paste(names(freqPath$M_N[i], " sec", sep=""))
#     # pf_move_Lat[[i]]<-recordPlot()
# }
# set.seed(NULL)
# # dev.off()
# # NOTE: Opened this in the RStudio viewer and tinkered with things until it looked good and saved from there. The dev route was giving me weird sizes on things
#

# Comp<-list()
# for(i in 1:9){
#     Comp[[i]]<-PRONET(freqPath$M_N[[i]], margins=0, fnt=2, condProb = T, weight=T)
# edge<-list()
# for(i in 1:length(Comp)){
#   edge[[i]]<-paste(as_edgelist(Comp[[i]]$igraph)[,1], as_edgelist(Comp[[i]]$igraph)[,2], sep="-
">
# }  

# #Cond Prob Sim Plot
# similarity<-matrix(ncol=9, nrow=9)
# for(i in 1:9){
#   for(j in 1:9){
#     common<- sum(edge[[i]] %in% edge[[j]])
#     similarity[i,j] <- common / (length(edge[[i]]) + length(edge[[j]]) - common)
#   }  
# }  

# vals<-matrix( nrow = 8, ncol=2)
# for(i in 1:8){
#   vals[i, 1]<-similarity[i, i+1]
# }  
# vals[,2]<-c("0\nto\n.125", ".125\nto\n.250", ".250\nto\n.375", ".375\nto\n.500", ".500\nto\n.625", ".625\nto\n.750", ".750\nto\n.875", ".875\nto\n1")
# vals<-as.data.frame(vals, stringsAsFactors=F)
# names(vals)<-c( "Similarity", "Lag")
# vals[,3]<1:8
# names(vals)[3]<"trick"
# vals$Lag<-as.factor(vals$Lag)
# vals$Similarity <- as.numeric(vals$Similarity)
# levels(vals$Lag)<-c("0\nto\n.125", ".125\nto\n.250", ".250\nto\n.375", ".375\nto\n.500", ".500\nto\n.625", ".625\nto\n.750", ".750\nto\n.875", ".875\nto\n1")
# condPlot<-ggplot(data=vals, aes(x=trick, y=Similarity , group=1))+
# geom_point(size=4)+
# geom_path(size=1)+
# scale_x_continuous(breaks = 1:8, labels=c("0\nto\n.125", ".125\nto\n.250", ".250\nto\n.375", ".375\nto\n.500", ".500\nto\n.625", ".625\nto\n.750", ".750\nto\n.875", ".875\nto\n1"))+
# theme_minimal() +
# theme(axis.text.x = element_text(angle = 0), panel.spacing.x=unit(1.5, "lines"), plot.title =
# element_text(hjust=.5)) +
# ylim(0,1)+
# labs(title = "Change in Network Similarity by Latency", x = "Change in Latency (sec)",
y="Network Similarity")
#
# ggsave("Plots/PathfinderSimilarity_Cond.png", plot=condPlot, height=4.36, width=6.5,
# units="in")

# Gonna make a pretty PF plot for Move_Only
basePF<-PRONET(freqPath$M_N$Overall)
# E(basePF$igraph)
# + 12/12 edges from 85e3e3c:  
# [1] 1->1 1->4 2->1 3->1 4->1 4->2 4->3 4->4 4->5 4->6 5->4  
# [12] 6->4  

# From dissertation manuscript:
# 6->4 Continuous  
# 5->4 M&W  
# 2/3->1 / 4->4 / 1->1 / 1->4 Staccato  
# 2/3->1 (acceleration for Staccato?)
# 4->2  
# e_col<-c("s", "s", "s/a", "s/a", "s", "s/a", "s/a", "mw", "mw", "c", "mw", "c")  
e_col[which(e_col=="s")]<-brewer.pal(3, "Set1")[1]
e_col[which(e_col=="s/a")]<-brewer.pal(3, "Set1")[1]
e_col[which(e_col=="mw")]<-brewer.pal(3, "Set1")[2]
e_col[which(e_col=="c")]<-brewer.pal(3, "Set1")[3]
E(basePF$igraph)$color<-e_col
E(basePF$igraph)$width<-3

set.seed(12345)
plot(basePF$igraph, layout=layout.graphopt, rescale=T, edge.arrow.size=1,
vertex.color="white", vertex.size = 30,
vertex.frame.color="white", vertex.label.color="black", vertex.label.cex=2, vertex.label.dist=0, edge.curved=0, margin=0)
set.seed(NULL)
legend("topleft", legend=c("Continuous", "Move & Wait", "Staccato"), fill = brewer.pal(3, "Set1")[3:1], title= "Movement Strategy", cex=1.1, box.lty=0)
legend("left", title = "Cluster | M (SD)", cex=1.1, box.lty=0, legend=c("1 | 0.12 (0.04)", "2 | 0.28 (0.04)", "3 | 0.46 (0.07)", "4 | 1.05 (0.34)", "5 | 3.10 (0.80)", "6 | 9.62 (6.60)")

#Note: Have to save this by hand too

#Link weights:
#Non-faceted
basePF$Pathfinder

#Faceted M_N pf plot
# pf_move_Lat<-list()
# par(mfrow=c(1,3))
# set.seed(12345)
facW<-list()
for(i in c(1,5,9)){

    facW[[length(facW)+1]]<-PRONET(freqPath$M_N[[i]], margins=0, fnt=2, condProb = F, weight=F)$Pathfinder
    # title(paste(names(freqPath$M_N)[i], " sec", sep=""))
    # pf_move_Lat[[i]]<-recordPlot()
}

# set.seed(NULL)
# par(mfrow=c(1,1))
Appendix 3. An Extended Introduction to Gaussian Mixture Modeling: the Expectation-Maximization Algorithm, Model Hyperparameterization, and the number of Mixtures

To approximate the maximum likelihood estimate for Gaussian Mixture Models, the EM algorithm goes through two steps: the Expectation (E) step and the Maximization (M) step. The E step calculates the probability that each observation belongs to each mixture component. The M step then uses these probabilities to calculate new parameterizations for each mixture component, which maximizes the likelihood estimate for the given mixture. The E step is then repeated with these updated mixture components. The E and M steps are repeated until the change in the likelihood function is small (Melnykov & Maitra, 2010), with a change smaller than $10^{-5}$ being the default for some major software packages (Scrucca, Fop, Murphy, & Raftery, 2016).

The M step updates the covariance matrix of each mixture. The covariance matrix for the G-th mixture ($\Sigma_G$) can be decomposed through eigenvalue decomposition into three elements: a matrix of eigenvectors ($D_G$), a diagonal matrix of normalized eigenvalues ($A_G$), and a scalar equal to the first eigenvalue of the covariance matrix ($\lambda_G$) (Banfield & Raftery, 1993). The formula for the covariance matrix below is from Celeux and Govaert (1995):

$$\Sigma_G = \lambda_G D_G A_G D'_G$$

Each component controls a different element for each mixture. $\lambda_G$ is the volume for the G-th mixture (in dimensions, not number of observations), $D_G$ is its orientation relative to the axis, and $A_G$ controls its shape, whether its a sphere or an ellipsoid. These parameters can vary from mixture to mixture or can be restricted to be equal across mixtures. Table 71 lists the common model names for each variation, whether the components are assumed to be equal or allowed to vary between mixture components. Additionally, $D_G$ can be parameterized such that the mixture orientations are equal and aligned to the axis, allowed to vary in orientation relative to the axis.
but not each other, or allowed to vary in orientation relative to each other. In the case that all
three parameters are free to vary, this means that the M-step of the EM algorithm may change the
volume, shape, and orientation of each mixture to find the maximum likelihood estimate.

Restricted models are less computationally intensive, give a more parsimonious solution and are
therefore easier to interpret (Celeux & Govaert, 1995). However, restricted models also risk
erroneous assumptions. For example, restricting orientation to be axis-aligned treats each
clustering variable as independent (i.e. $r = 0$).

**Table 71. Gaussian Mixture Model Hyperparameters**

<table>
<thead>
<tr>
<th>Model</th>
<th>Volume</th>
<th>Shape</th>
<th>Orientation</th>
<th>MAP Available</th>
</tr>
</thead>
<tbody>
<tr>
<td>EII / E</td>
<td>Equal</td>
<td>Spherical</td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>VII / V</td>
<td>Variable</td>
<td>Spherical</td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>EEI</td>
<td>Equal</td>
<td>Equal</td>
<td>Axis-Aligned</td>
<td>✓</td>
</tr>
<tr>
<td>VEI</td>
<td>Variable</td>
<td>Equal</td>
<td>Axis-Aligned</td>
<td>✓</td>
</tr>
<tr>
<td>EVI</td>
<td>Equal</td>
<td>Variable</td>
<td>Axis-Aligned</td>
<td>✓</td>
</tr>
<tr>
<td>VVI</td>
<td>Variable</td>
<td>Variable</td>
<td>Axis-Aligned</td>
<td>✓</td>
</tr>
<tr>
<td>EEE</td>
<td>Equal</td>
<td>Equal</td>
<td>Equal</td>
<td>✓</td>
</tr>
<tr>
<td>VEE</td>
<td>Variable</td>
<td>Equal</td>
<td>Equal</td>
<td></td>
</tr>
<tr>
<td>EVE</td>
<td>Equal</td>
<td>Variable</td>
<td>Equal</td>
<td></td>
</tr>
<tr>
<td>EEV</td>
<td>Equal</td>
<td>Equal</td>
<td>Variable</td>
<td>✓</td>
</tr>
<tr>
<td>VVE</td>
<td>Variable</td>
<td>Variable</td>
<td>Equal</td>
<td></td>
</tr>
<tr>
<td>VEV</td>
<td>Variable</td>
<td>Equal</td>
<td>Variable</td>
<td>✓</td>
</tr>
<tr>
<td>EVV</td>
<td>Equal</td>
<td>Variable</td>
<td>Variable</td>
<td></td>
</tr>
<tr>
<td>VVV</td>
<td>Variable</td>
<td>Variable</td>
<td>Variable</td>
<td>✓</td>
</tr>
</tbody>
</table>

Note: Table adapted from Table 2.1 of McNicholas (2017) and Fraley, Raftery, Murphy, & Scrucca (2012)

To derive the number of components, the same mixture fitting process used for $G$-many mixtures
is repeated for $G+1$ mixtures. The mixtures are initialized and then passed through the EM
algorithm. Once the G+1 model converges, it is compared to the G model using BIC. If there is a sufficiently large improvement in BIC, G+1 mixtures are compared to G+2 mixtures, up to a maximum of $N^{0.3}$ (see Biernacki, Celeux, Govaert, & Langronet, 2006). Typically, the maximum number of mixture components should stay as small as possible (Fraley & Raftery, 1998). Once models are fit across the range, there are a handful of selection rules: the elbow-rule heuristic (Thorndike, 1953), selecting the overall highest BIC (Fraley & Raftery, 1998), the first maxima in BIC (Fraley et al., 1998), or forward selection rules such as a sufficiently large change in BIC (Fraley & Raftery, 1998; Kass & Raftery, 1995) and the Lo-Mendell-Rubin Likelihood Ratio Test (Lo, Mendell, & Rubin, 2001).