AUTOMATED MODELING OF HUMAN-IN-THE-LOOP SYSTEMS

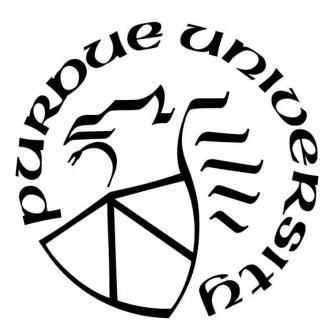
by

Noah Marquand

A Thesis

Submitted to the Faculty of Purdue University In Partial Fulfillment of the Requirements for the degree of

Master of Science in Aeronautics and Astronautics



School of Aeronautics and Astronautics West Lafayette, Indiana December 2021

THE PURDUE UNIVERSITY GRADUATE SCHOOL STATEMENT OF COMMITTEE APPROVAL

Dr. Karen Marais, Chair

School of Aeronautics and Astronautics

Dr. Milind Kulkarni

School of Aeronautics and Astronautics

Dr. Dengfeng Sun

School of Aeronautics and Astronautics

Approved by:

Dr. Gregory A. Blaisdell

Dedicated to the friends and family that trusted me to make it this far

ACKNOWLEDGMENTS

In acknowledgement of Purdue University's contributions of seed funding for this project.

TABLE OF CONTENTS

LIST OF TABLES					
LIST OF FIGURES					
GLOSSA	GLOSSARY 11				
ABSTRA	ABSTRACT12				
1. INT	1. INTRODUCTION				
1.1 N	Iotivation	13			
1.2 C	urrent Approaches	14			
1.3 E	Background and Definitions	14			
1.3.	1 Formal Models	14			
1.3.	2 System Records	15			
1.3.	3 Combined Definitions	16			
1.4 S	ystem Factors	16			
1.4.	1 Factor: Continuity	16			
1.4.2	2 Factor Parallelism	17			
1.4.	3 Factor: Temporality	17			
1.4.4	4 Factor: Boundedness	18			
1.5 B	asic Approach	18			
1.5.	1 Collecting System Traces	19			
1.5.	2 Isolating System States	20			
1.5.	3 Isolating System Paths	20			
1.6 P	robing Potential Methods	21			
1.6.	Application of Theory to a Simple System	21			
1.6.	2 Application of Theory to Complex System	22			
2. APPI	LICATION OF THEORY TO SIMPLE SYSTEM	24			
2.1 S	ystem Overview	24			
2.1.	1 Defining the System	24			
2.1.2	2 Implications of System Factors	24			
2.2 S	ystem Trace	25			
2.2 I	solating System States	26			

2.3.1	The Local Context	27
2.3.2	The Global Context	
2.3.2	The Combination Model	
	ining Known States	
2.4 Ker 2.4.1	Parallel Models	
2.4.2	Correcting State Redundancy	
2.4.2	Path Intersection	
	al State Machines	
	CATION OF THEORY TO COMPLEX SYSTEM	
	stem Overview	
3.1 Sys	Defining the System	
3.1.2		
	Implications of the System	
3.2 Sys	Data Collection	
3.2.1		
3.2.2	Synchronizing Microstates with Microinputs Additional Parameters and Transformations	
3.2.4	Examining System State Frequency	
	te Detection through Unsupervised Machine Learning	
3.3.1	Classifier Selection	
3.3.2	Classifier Optimization	
3.3.3	State Validation against Known Behaviors	
3.3.4	State Validation through Parameter Variation	
3.3.5	State Validation through Sampling Frequency Variation	
	ficulties with Applying Basic Machine Learning in Path Determination	
3.4.1	Path Detection with Basic Machine Learning	
3.4.2	Path Detection with a Multi-Classifier Model	
3.4.3	Path Reading Comparisons	
3.4.4	Path Detection with Microstate Prediction and Complex Interactions	
3.4.5	Inverse Time Scaling	
4. DISCU	SSION AND CONCLUSION	88
4.1 Co	nclusions on the Use of System Factors	88

	4.2 Conclusions on the Use of Logical Tools for Simple Systems	. 88
	4.3 Conclusions on the Use of Machine Learning for Complex Systems	. 89
	4.4 Closing Thoughts	. 89
А	PPENDIX A. CHAPTER 2 SCRIPTS	. 90
А	PPENDIX B. CHAPTER 3 STATE ID SCRIPTS	132
А	PPENDIX C. CHAPTER 3 PATH ID SCRIPTS	149
R	EFERENCES	157

LIST OF TABLES

Table 1: Sample Inputs, IIDS, and Number of Uses in Data Set.	26
Table 2: YS-Flight recorded flight parameters	43
Table 3: Flight paths recorded in trace	46
Table 4: Total parameter set used in trace	52
Table 5: Compass heading 4 Hz normalized parameter means	61
Table 6: Target heading 4 Hz normalized parameter means	63
Table 7: Positionless 4 Hz normalized parameter means	65
Table 8: Compass heading 40 Hz normalized parameter means	67
Table 9: Target heading 40 Hz normalized parameter means	67
Table 10: Positionless 40 Hz normalized parameter means	69

LIST OF FIGURES

Figure 22: Top-down view of 40 Hz positionless optimization using landing runway relative coordinates
Figure 23: K-Nearest Neighbors visualization
Figure 24: Example confusion matrix
Figure 25: Low-speed cruise, direct prediction with standard sampling confusion matrices 74
Figure 26: Low-speed cruise, direct prediction with random sampling confusion matrices 75
Figure 27: High-speed cruise, direct prediction with standard sampling confusion matrices 76
Figure 28: High-speed cruise, direct prediction with random sampling confusion matrices 76
Figure 29: Hazard, direct prediction with standard sampling confusion matrices
Figure 30: Hazard, direct prediction with random sampling confusion matrices
Figure 31: Merged path model for paths out of low-speed cruise
Figure 32: Merged path mdoel for paths outs of high-speed cruise
Figure 33: Merged path model for paths out of hazard
Figure 34: Normalized metrics in paths out of low-speed cruise
Figure 35: Normalized metrics in paths out of high-speed cruise
Figure 36: Normalized metrics in paths out of hazard
Figure 37: Low-speed cruise, microstate prediction confusion matrices
Figure 38: High-speed cruise, microstate prediction confusion matrices
Figure 39: Hazard, microstate prediction confusion matrices

GLOSSARY

Chapter 1

- <u>State:</u> The remembered information in the system that affects how it responds to different conditions, and what it is capable of
- *Input:* The external conditions that could alter system state *Path:* The transition between states due to a provided input

Parameter: A measurable system characteristic that defines system state

- Control: A measurable user action that can affect system state
- *Trace:* A record of parameters and controls taken during system operations

Microstate: A list of parameters recorded at the same time, a specific instantiation of a state

Microinput: A list of controls recorded at the same time, a specific instantiation of an input

Reading: A list of parameters and controls taken at the same time

Factor: A system feature that defines how it can be modeled

- <u>Continuity</u>: The number of continuous parameters and controls a system has relative to its discrete metrics
- Parallelism: The number of controls a user can provide at once

Temporality: The degree to which the system expects users to provide inputs between state updates

<u>Boundedness</u>: The degree an analyst understands the relevant parameters and controls for the system

Chapter 2

Substate: A state that appears to exist in the path between two other states

Chapter 3

True Positive Rate: The rate at which a classifier correctly identifies data

Positive Predictive Value: The rate at which the reported classifications of a classifier are correct

ABSTRACT

Safety in human in the loop systems, systems that change behavior with human input, is difficult to achieve. This difficulty can cost lives. As desired system capability grows, so too does the requisite complexity of the system. This complexity can result in designers not accounting for every use case of the system and unintentionally designing in unsafe behavior. Furthermore, complexity of operation and control can result in operators becoming confused during use or receiving insufficient training in the first place. All these cases can result in unsafe operations. One method of improving safety is implementing the use of formal models during the design process. These formal models can be analyzed mathematically to detect dangerous conditions, but can be difficult to produce without time, money, and expertise.

This document details the study of potential methods for constructing formal models autonomously from recorded observations of system use, minimizing the need for system expertise, saving time, money, and personnel in this safety critical process. I first discuss how different system characteristics affect system modeling, isolating specific traits that most clearly affect the modeling process Then, I develop a technique for modeling a simple, digital, menu-based system based on a record of user inputs. This technique attempts to measure the availability of different inputs for the user, and then distinguishes states by comparing input availabilities. From there, I compare paths between states and check for shared behaviors. I then expand the general procedure to capture the behavior of a flight simulator. This system more closely resembles real-world safety critical systems and can therefore be used to approximate a real use case of the method outlined. I use machine learning tools for statistical analysis, comparing patterns in system behavior and user behaviors. Last, I discuss general conclusions on how the modeling approaches outlined in this document can be improved and expanded upon.

For simple systems, we find that inputs alone can produce state machines, but without corresponding system information, they are less helpful for determining relative safety of different use cases than is needed. Through machine learning, we find that records of complex system use can be decomposed into sets of nominal and anomalous states but determining the causal link between user inputs and transitions between these conditions is not simple and requires further research.

1. INTRODUCTION

Robust, complex systems that interact with humans are difficult to design (Solar-Lezama, Rabbah, Bodik, & Ebicioglu, 2005). Complex systems are typically sensitive to user inputs, and this sensitivity lends itself to more complex interactions between a system's conditions and its inputs. This behavior can result in systems becoming difficult to understand as either a designer or operator, masking how they respond to changing inputs and environmental shock, and making them less safe to use. Current methods of improving the safety of these HITL systems use model checking techniques to analyze behavior under different conditions

These techniques are often bottlenecked behind the need for a system model, which can be difficult to obtain. This research focuses on studying potential methods for autonomously constructing these system models using logical, statistical, and machine learning methods, without expert input.

1.1 Motivation

Many systems can accidentally reach failure modes without any component failures occurring. In the case of Asiana Flight 214, during final approach to the runway, unbeknownst to the pilots, the glide slope was too steep and airspeed too low. Pilots noticed the engines were set to idle, despite the auto-throttle system being in the armed position, and attempted to regain speed, but were unable to avoid a crash into the runway, during which the plane broke apart and claimed three lives.

The NTSB investigation found that the auto-throttle system did not automatically switch on as expected because it required neither or both flight director computers to be on, but only one computer was on during approach. This confusing priority system is credited in the report as being one of the major contributors to the pilots' "faulty mental model", which resulted in the crash (National Transportation Safety Board, 2013). If such a confusing aspect could be caught before the system went into production and use, it could prevent accidents.

1.2 Current Approaches

Formal methods of model checking use mathematical tools to determine whether different conditions allow the system in the model to reach an uncontrolled system state, or whether an anomalous state can be returned to user control (NASA Langley, 2016). Such methods rely on specific types of system models, called formal models. Building these models by hand requires a near exhaustive understanding of the system to achieve a level of detail that is useful for determining specific safety improvements. This expertise is time-consuming to achieve, and comes with great monetary expense, so often the models checked are of a reduced complexity, or of only a specific component of the main system, making them less useful for examining overall safety (Aalto, Husberg, & Varpaaniemi, 2003).

Much of current work focuses on techniques for autonomously identifying and labelling anomalous data (Puranik & Mavris, 2018), while other work focuses on improving autonomous model construction on digital subsystems. Emphasis is placed on mapping the decision-making space for autonomous systems as well, with some demonstration of autonomous model construction for MATLAB models of lane-change decision making systems (Selvaraj, Farooqui, Panahandeh, & Fabian, 2020). Most of this effort is dedicated to learning discrete models or distinguishing two phases of system behaviors in known systems. This work focuses on minimizing the required system knowledge and expanding the modeling process to capture system-wide phenomena.

1.3 Background and Definitions

This work predominantly uses the terminology of formal models that we expand upon to capture complex behavior. To begin our investigation, we define the most basic terms and provide some background on how they are used in industry.

1.3.1 Formal Models

Formal models are precise definitions of system operations. One of the most common and recognizable formal models is the state machine. There are many variants, but most simply, state machines are composed of three parts:

- 1. *States*: The remembered information in the system that affects how it responds to different conditions, and what it is capable of. For example, a light switch has states "On" and "Off"
- 2. *Inputs*: The external conditions that could alter system state. To continue with the previous example, a switch could be flipped to "On" or to "Off". Note that some inputs may not always be available or may not always alter system states.
- 3. *Paths*: The transition between states due to a provided input. Using the same example, a light switch in "On" could be flipped to "Off", after which it would be in "Off."

State machines used for safety applications, like those used in formal safety checks, often label states as nominal or anomalous (Jung, et al., 2021). Nominal states are considered acceptable and part of standard operations. Anomalous states are abnormal, and perhaps hazardous. With these labels, a system designer can examine their system state machine and use formal methods to examine nominal states' proximity and relation to anomalous states, which can be further used to compare the relative safety of each state, and so on.

The relevant states, inputs, and paths of a system may be unknown. It is not always clear when a state transition has occurred, or if a small change is relevant to system operations. Modelers then need to establish definitions for these components that capture various expected nominal behaviors, and how they might transition between themselves and anomalous behaviors; with enough depth that actionable change can be made where needed. This is difficult to do without exact knowledge of the system, and so this document focuses on how to construct such system models with only a recording of system use.

1.3.2 System Records

System records are a collection of measurements of the system and the user during operation. In this document, we will refer to each system characteristic measured as a *parameter*. For example, altitude is a parameter in a flight recording. We refer to a user characteristic measured in a recording as a *control*. One such control in a flight recording is the pilot throttle setting.

We will also use the term *trace* when referring to the system recording itself (IBM, 2017). Most simply, a trace can be represented with a matrix, where columns indicate each unique parameter/control and rows indicate simultaneous measurements.

1.3.3 Combined Definitions

Combining the two sets of terminology then provides some insight into how we may begin to examine systems. Parameters, being measurements of the system characteristics, are indicative of the current system state. For example, altitude, attitude, and velocity, are useful parameters for determining if an aircraft is in a stalled state. We can then view each reading of parameters taken at the same time as merely a specific instantiation of their state classification, which we call a *microstate*.

Similarly, controls are measurements of user characteristics that could be diagnostic of wider input categories. For example, a yoke deflection right and up with left pedal pressure might generally correspond to a bank right input. Control measurements recorded at the same time make up a specific instantiation of their input classification, which we call a *microinput*.

With these concepts in mind, each row in the trace should be useful for predicting the next. I will refer to each row of measurements taken at the same time as a *reading*.

1.4 System Factors

Systems come in a variety of forms and with variety comes different assumptions on system operations. Different assumptions affect how we must collect and extract information and need to be carefully considered. We consider four main aspects of how systems operate:

- 1. Continuity: Are important performance metrics discrete, continuous, or a mixture thereof?
- 2. Parallelism: Does the system accept multiple controls at once?
- 3. Temporality: Does the system continuously update its state without human intervention?
- 4. Boundedness: Are relevant inputs and parameters visible to the user upon use?

In this document, we refer to each of these considerations as the *system factors*. Each of these factors affect how we can effectively collect a trace and how we can detect states and paths, as discussed in further detail in each section below.

1.4.1 Factor: Continuity

Systems with discrete characteristics have clear delineations between different states, with little ambiguity between them. For example, a menu-based digital system has clear distinctions

between states, and inputs are categorical or Boolean. This type of system can be analyzed using logical techniques, checking whether exact inputs are provided, and so on.

By contrast, continuous systems have no clear delineations between states or parameters, making exactitude difficult and any purely logical deductions obscured. For example, flight uses many distinct continuous parameters, so without system knowledge, it is difficult to make exact logical conclusions. Instead, we can analyze this type of system with statistical methods, examining the probability of changes occurring based on a range of values.

In general, we can assume that a system with purely discrete characteristics is simpler to analyze than a system with continuous variables. The most complex of cases being a mix of discrete and continuous variables, which would require a mix of logical and statistical methods to analyze. Most real-world, safety critical systems would be considered part of this last category.

1.4.2 Factor Parallelism

Serial systems accept a singular control as input at any given time. For example, menubased digital systems will often only accept one input at a time. Parallel systems can accept multiple simultaneous controls. For example, each axis of the control yoke of an airplane could be considered a separate control, making flight a parallel system.

In general, serial systems are simpler to analyze than parallel systems for two main reasons. First, the added variability of possible inputs in parallel systems makes it much more difficult to use logical methods to analyze them, because complex microinputs are less likely to be exactly replicated, making it more difficult to determine when the system behaves in the same way in multiple points in the trace. Second, parallel systems can simultaneously accept discrete and continuous controls, requiring more specialized applications of each statistical/logical tool than if only one type were usable at a time. However, most real-world complex systems would be parallel systems.

1.4.3 Factor: Temporality

Atemporal systems do not change their system state without user input. For example, a menu-based digital system might not change state until the user presses a button. Temporal systems update their state without user input, and in some cases, constantly. Many safety critical systems

that rely extensively on physical phenomena, like flight, would fall into this category, as vehicle physics are constantly operating on the system.

Modeling temporal systems is much more complicated than the atemporal type. Atemporal systems can record readings in the trace after every input is provided and that is enough, but temporal systems require that a modeler estimate how quickly they need to be able to detect state transitions and record readings at the corresponding frequency. Different frequencies may not capture all behavior and need to be studied to find consistent system behavior.

1.4.4 Factor: Boundedness

Bounded systems have clear and obvious boundaries for what is a relevant parameter control and what is not. For example, it is clear in a menu-based digital system that the controls used to interact with the system are the button selections made in the menu, and it is clear that the system state has changed when the display updates to a new menu screen. Unbounded systems have non-obvious boundaries. In flight, it is unclear which parameters are meaningful for determining state, and how meaningful they are. For instance, consider that while it is evidently useful to know the aircraft velocity, it is unclear what that velocity needs to be relative to when determining states.

In general, we consider bounded systems to be simpler to analyze, as they require fewer steps to determine state definitions. Unbounded systems require greater system knowledge and still require model comparisons to determine which parameters are relevant for safety.

1.5 Basic Approach

With these terms and characteristics in mind, we can outline a general process for constructing a state machine from a trace:

- 1. Determine system factors
- 2. Record a trace of system operations
- 3. Produce definitions for system states from the trace
- 4. Produce definitions for system paths from the trace

1.5.1 Collecting System Traces

Once we classify with the four factors, we can collect the trace. Each factor presents unique implications for how we need to collect and manipulate a meaningful trace. Continuous systems for instance are less likely to have exact repetitions of readings than discrete counterparts, making it less clear where state boundaries lie. For example, in flight it is unlikely than any two recorded flights will pass through the same point with the same velocity, but the distinction between the start of a stall and nominal flight is subtle. To counteract this effect, we introduced some artificial discretization into continuous data to make microstates more distinct (see Section Implications of the System3.1.2). This process requires some system knowledge, with educated guesses for what is likely to be a meaningful change in parameter and control values.

To record serial systems, we only need a single data channel for tracking performance, with an associated time channel if the system is temporal. Parallel systems by contrast require multiple channels, which can add complexity and time to the trace construction process depending on the measuring techniques used.

When we record atemporal systems, parameters and controls need to be measured after each input. Temporal systems then have multiple options for how they can be recorded, which have different behaviors. First, if the system continuously accepts user inputs, like in flight, where the user is continuously supplying a yoke input, it is efficient to record behavior at a fixed sampling rate to capture behavior. This sampling rate needs to be determined with some degree of system expertise, based on the rate at which states can change. Alternatively, if the system is designed to idle between inputs, like in a digital system such as a computer, readings should be taken when inputs are made, otherwise inputs and timings can be lost in the recording process.

Lastly, recording bounded system traces only requires recording the obvious metrics of the system, whereas unbounded systems require requires any metric that might be relevant, even indirectly. It should also be recognized that many parameters used in unbounded systems may not be used for state identification in their raw state.

After factors are considered, we need to ensure that the trace data captured is enough to determine a system model. This means that the trace should include a variety of typical operating behaviors, capturing mostly nominal behavior with known anomalous behaviors labeled. In general, we assume that deviation from the behavior seen in most of the trace should be considered anomalous. This ideation is used in many similar works for anomaly detection (Puranik & Mavris,

2018), which can be used in conjunction with the methods specified in this document to label states generated in the state machine.

Traces also need to be as close to exhaustive as feasible, including multiple repetitions of all typical procedures that are to be considered part of the system. This reduces the likelihood that any typical procedures are considered anomalous and provides information on how slight variations in execution of procedures can affect the outcome.

1.5.2 Isolating System States

To identify states from the trace, we need to identify common trends in the behavior of microstates. Some questions we might ask are:

- Are specific configurations of parameters distinct from other configurations? For example, a plane transitioning from climb to cruise will, relative to the time scale of the flight, quickly transition from a high pitch, to a neutral one, making the delineation from high to neutral pitch distinct.
- Do specific configurations of parameters occur more frequently than others? For example, high throttle is most often paired with high speed because an aircraft operating at a high throttle tends to accelerate to its top speed.
- 3. Do specific configurations of parameters often result in known anomalous parameters? For example, a rapid descent might commonly correlate with a stall indicator.
- 4. How frequently are specific configurations of parameters paired with each configuration of controls? For example, in menu-based navigation, some inputs are not available always, making them potentially diagnostic of state.

We can use logical and statistical measures to attempt to answer each of these questions for each potential state. Each system may need a different tool to assess these and determine the definition of its relevant states.

1.5.3 Isolating System Paths

Once we have established definitions for states, we can begin to connect them together with paths and inputs, which are conceptually linked together. In a state machine, every path is the result of an input, including paths that return to the initial state. We can therefore extract classes of inputs by first examining the paths observed in the trace.

To identify paths then, we need to identify common trends in the transitions between microstates. As with identifying states, there are several questions we can ask:

- 1. How frequently do states transition between one another?
- In any given state, do specific configurations of controls result in specific state transitions?
 Do they always result in the same state transitions?
- 3. In any given state, do specific changes in microstate result in specific state transitions? Are these changes associated with specific configurations of controls?

As with state identification, these questions can be answered with logical and statistical tools to identify possible inputs from known paths.

1.6 Probing Potential Methods

To further explore the process we have outlined, the rest of this research extrapolates on the application of theory to two systems. The first system is a simple case, an automatic coffee machine with a menu-based, digital interface. This system exhibits discrete, serial inputs, atemporal states, and bounded parameters and controls, allowing for testing of basic theory and logical analysis techniques.

The second system a complex case, a flight simulator in cruise. This case allows for the extension of theory into more "real-world" data with mixed discrete/continuous parameters and controls, temporal states, and unbounded parameters. To analyze it, we need to utilize more complex, statistical methods, making it a good comparison of methods with the logical, simple case.

1.6.1 Application of Theory to a Simple System

In the case of the coffee machine, the trace was recorded prior to our research, and only includes the controls provided. This complicates the process, requiring that states be extracted from inputs alone, but because of its menu-base architecture, this should still be possible if we distinguish states by comparing where inputs are seen in the trace relative to one another.

The system exhibits one of the simplest configurations of factors. Discrete, serial, bounded controls allow us to consider each unique control to be its own input, recorded in sequence. With some basic simplifications, we can consider the system atemporal as well, further simplifying analysis. This allows us to further consider many individual recordings as functionally identical, simplifying the logical processes and increasing our assurance that all common paths are navigated in the trace.

In general, we decompose the trace by first partitioning the trace with states based on how similar each input sequence is to other sequences in the trace. With basic state definitions, we then compare paths between them and ensure that they are mutually consistent to refine the model which concludes model construction.

Overall, this process demonstrates that a simple, menu-based system can be logically decomposed into a state machine model from an input trace using our methodology.

1.6.2 Application of Theory to Complex System

In our flight simulator case, the system factors suggest specific methods of analysis that differ from the simpler case. Mixed discrete/continuous parameters and controls cannot be simply analyzed by logical tools, so we instead reduce the system to its continuous metrics and use statistical tools, as the continuous metrics are likely to be the most informative. Additionally, parallel parameters and controls do not repeat in the trace frequently enough for microstates and microinputs to be directly considered states and inputs in a useful state machine. Here, we use statistical tools to measure similarity in behaviors for different microstate and micropath configurations.

This system is also a continuously updating temporal system, so we explore techniques for finding state and path definitions at different sampling frequencies. The parameters used during this process are also unbounded, so we demonstrate methods for producing new parameters and down-select to a useful set as well.

In general, this exploration begins with state definitions we find by comparing parameter distributions in varying sampling frequencies and parameter configurations. With these state definitions, we explore input identification techniques from the paths now visible in the trace, emphasizing statistical methods. This process demonstrates the complexities of applying

22

statistical techniques without system knowledge. We suggest future exploration into improving methods.

2. APPLICATION OF THEORY TO SIMPLE SYSTEM

This chapter goes into detail on the methods used for constructing a state machine for a simple system, an automatic coffee machine. Discussion will begin with a system overview, where I will describe the system and its basic characteristics. Next, I will cover how we collected and organized the system trace, which will lead into how we isolated preliminary states from the trace and organized them into final state definitions. Last, we will discuss the effectiveness of our methodology for constructing a state machine for the system.

2.1 System Overview

To begin, we sought to study a test case with known, deterministic behavior to simplify analysis and check modeling results, as well as a test case that would be simple to collect trace data for. Here, we elected to test methods on an automatic coffee machine, as existing experimental trace data was available for use, and its functionality is well known.

2.1.1 Defining the System

The coffee machine used in the pre-recorded trace was a unit placed in an office lounge that could be periodically bulk loaded with drink materials, so that any user interactions were limited to loading cups and following a digital menu on the machine face, like digital soda machines. The menu options themselves were available for study in the system manual itself.

We can imagine system states for this case as the steps in the drink setup process, and any unique selections of the user. For instance, one system state might be "Empty cup in tray, coffee drink selected" while another might be "No cup in tray, hot drink selected, hot chocolate selected". System inputs would then be the menu selections from the user and any cup manipulation

2.1.2 Implications of System Factors

Because this system has a limited set of button selections for controls, we can describe the system as having discrete controls. This feature means that each control is distinct and categorical, lending system analysis towards logical methods over statistical. Controls are also input serially,

as the system does not accept multiple menu inputs at once. This further simplifies any logical analysis performed by connecting state changes to a single control input instead of multiple.

This system largely operates without any regard for time between inputs, making system states atemporal. We can then assume that all system state changes are directly related to user inputs, simplifying our analysis to data directly recorded in the initial trace. Two exceptions to this rule exist however, the first being that the user manipulation of their drink cup would not affect whether the machine would pour drinks. As such, a user could potentially place a cup in the tray, and then remove it before the drink was poured, which would not be captured in the trace without timing information on when the cup was moved and when the drink poured. Drink pour times were not recorded, so to simplify analysis, I assumed that this event did not happen in any recorded trace.

The second exception to atemporal states in the system involves the system's internal "timeout condition. If a user didn't make an input in a certain amount of time, the system would reset to the start state (excluding cup positions). This feature was not engaged for most cases, so to simplify analysis, I cut and labeled the trace instance where timeouts occurred as if no future behavior was known.

Lastly, this system is clearly bounded, the only state changes occur directly from the user inputs recorded in the original trace. Most inputs could be found as programmable options in the manual, and the others used in the trace, like "move cup to tray" are obvious. This bounding simplifies analysis, ensuring that everything recorded is relevant for determining states and nothing is missed.

2.2 System Trace

The trace used for this case was originally collected as part of an unrelated study on humandevice interactions and captured interactions with video. The video footage was then transcribed in a spreadsheet with the user behaviors at the video time stamp, with behaviors such as "Grab cup", "Press Coffee Drink 1", and "Think". This transcript included two camera failure incidents labeled as user actions, at which point it was inherited by the current project. Only the spreadsheet transcript was used and available for our demonstration.

To begin processing the transcript into a usable trace, I cleaned the data set of typos, duplicate labels, and "non-interactions". Duplicate labels in this case refer to different input labels

for the same input. For instance, "Grab cup", "Move cup", and "Release cup" were used in some cases and "Place cup in Tray" in others. For this study, I used as few input labels as possible to simplify the analysis. The original trace also included "non-interaction" inputs, such as "Think". These actions were not relevant for our study, as they do not change the system state, and I removed them from the transcript.

To normalize user interactions around performing a task, I considered a user making a single drink as a single interaction. Any user making multiple drinks in a row would then simply have multiple interactions recorded in the final trace. To finish turning the transcript into a usable trace, I inserted input labels for "Start" and "End" into the transcript to demarcate the bounds for each interaction. This process provided a total of 102 separate interactions recorded over the course of two afternoons. This dataset sufficiently maps the system space, as it is not expected that the drinks made day to significantly change, so system use will not vary largely beyond what was seen in the original recording.

With these changes made to the transcript, we now have a usable trace, seen as a series of user inputs to the system, with some inputs marking the beginning and end of a drink being made. To condense this trace, I converted each unique label into a unique numerical ID, so the entire trace can be represented as a column vector. Table 1 shows some of the sample inputs and their corresponding ID values.

Inputs	IID	Number of uses in set
Start	1	102
End	3	102
Place Cup in Tray	4	102
Select Coffee 2	16	24
Select Coffee Drink	19	159
Select Large	25	35
Select Milk	29	2

Table 1: Sample Inputs, IIDS, and Number of Uses in Data Set

2.3 Isolating System States

With this system understanding, we can assume that two systems in identical states receiving different inputs should arrive at different states. An extremely simple model of this behavior could use a flowchart that perfectly copies the recorded behavior, splitting any time a new sequence is recognized. This model would be inadequate though, because it cannot replicate

behaviors that do not exactly follow a use instance in the trace. For example, if users are presented with the option to select between three drink sizes, but users in the trace only select the largest size for a specific drink variant, the simple model would not recognize that there was an option to select other sizes. If we consider all interactions not represented in our model as anomalous, this could result in otherwise nominal behavior appear to be anomalous as interactions grow longer and more complex. Even a simple use case like the "Select Cancel" would appear as a completely unique branch in the simple model, with all subsequent inputs appearing as anomalous.

To begin addressing these issues, we needed to develop a more robust method for identifying changing states rather than differences in user behavior. In a menu-based system, the clearest indicator of states differing is a difference in input availability to the user. Because this system has diverse inputs correlated the menu states, input availability can be observed with two methods or contexts: the local and global contexts. When the trace is then examined under both contexts at once, we can generate lists of available inputs for each step in the trace. When available inputs change, a new state is reached.

2.3.1 The Local Context

The local context focuses on examining what inputs in the trace immediately follow all the other inputs. This context assumes that inputs are only available if they have been seen to immediately follow the previous input in the trace. For example, if "Select Coffee Drink" is only ever followed by "Select Coffee 1", "Select Coffee 2", "Select Coffee 3", and "Select Cancel", no other inputs are considered available following a "Select Coffee Drink" input. This context works well for menu-based systems with a diverse input set that is strongly correlated with previous inputs because it can directly identify those correlations.

However, it struggles to operate on systems with low-diversity inputs because they can be highly repetitive. The frequency of each input in the trace will result in each input being seen to follow each other input and so provide no new information. For example, a menu-based system might operate off yes/no inputs and provide a targeted question following each input. Analysis would suggest that yes/no is always available, but this provides no information on whether yes and no responses were both in the trace for the specific question asked. This can be avoided by carefully labelling inputs to increase input diversity: in the sample case, convert "Yes/No" into "Yes for Q1/ No for Q1". Such conversions would need to be done with some degree of system knowledge and

may not be possible in all cases. Luckily, such low-diversity input systems do not frequently occur in safety critical systems because fewer input options necessitate longer input sequences to transfer the same amount of information to a system. This inefficiency extends the time required to complete any task, making them less capable of resolving time-critical hazards.

The local context will also struggle on systems that do not have a strong correlation between their inputs and their precursor inputs. It would instead favor exactly copying the trace behavior. For example, a menu-based questionnaire system emulating a multiple-choice quiz may not have relations between individual responses, regardless of how diverse the potential inputs are.

Lastly, this context is limited in that it does not meaningfully constrain the number of available inputs for inputs that have diverse following inputs. For example, "Select Cancel" reverts the system to the previous state and can be input to the system in a variety of states. As such, many different inputs immediately follow it, none of which are only available after "Select Cancel" is input to the system.

2.3.2 The Global Context

The global context focuses on examining what inputs always occur before other inputs in the trace. This context assumes that inputs that always occur before other inputs are mandatory for the second input to occur. For example, "Select Cappuccino" is only seen in traces where "Select Gourmet Drink" has already been input to the system, so "Select Cappuccino" is never listed as an available input until at least "Select Gourmet Drink" has been input by the user. This global context complements the local context weakness for inputs with diverse following inputs. In the same example given before, when "Select Cancel" is input to the system, only inputs that have had their mandatory precursors are considered available in the global context, so the field of available inputs in narrowed.

However, this strength makes this context useful only for high-diversity, high-correlation systems. If no inputs have mandatory precursors, this context does not help narrow the inputs available. Additionally, if the system allows itself to return to previous states, the global context becomes less useful for identifying input availability. For instance, a use instance where a user inputs "Select Cancel" after every input until each menu-option is exhausted, would see every mandatory precursor having been input, so the global context would not be useful for narrowing available inputs.

2.3.3 The Combination Model

These contexts focus primarily on input availability, which can be indications that the system is in a different state but is not the sole determining factor for state differentiation. For example, the menu display for selecting drink size presents the same options regardless of what drink is being made. Input availability alone would suggest that all instances of this menu are the same, even though "Select Cancel" would direct to different menus depending on prior inputs. To maintain consistency in paths, we define initial states iteratively using the following process:

- 1. Starting at the Start state for each instance, we can navigate through the trace input by input.
- 2. If our dual context method suggests that multiple inputs are available, a state has been reached.
- 3. If the same input sequence is used to reach a state as in a prior instance, the same state is reached.
- 4. Once a state is reached, navigate to the next instance, until all instances have been examined.
- 5. This process is repeated, navigating from each of the new states as if they were the start state, until the full trace has been examined and no new states can be detected.

This process creates an initial branching tree model, with all instances represented as a sequence of state-to-state paths, reconvening in the end state as shown in Figure 1: Simplified branching tree model.

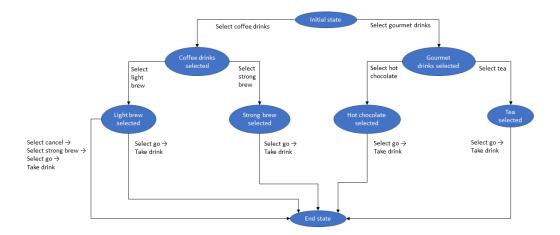


Figure 1: Simplified branching tree model

2.4 Refining Known States

The state definitions generated in this manner are incomplete, often being redundant or inconsistent. Some states are functionally identical, sharing paths, which suggests that some preliminary state definitions are duplicated. Some paths are inconsistent and share some behavior with other behavior that suggests that some states are not being detected in the initial identification pass. Additionally, some true states are likely missing from the model. As shown in Figure 2: Instance dilution with inputs, the total number of people on each path decreases with each input. If paths are selected randomly from a current state, the probability that all paths out of a given system state are seen in the trace is dependent on the number of users that arrive at said state.

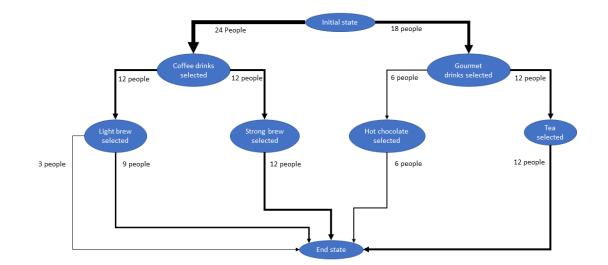


Figure 2: Instance dilution with inputs

These issues can be addressed in three ways:

- 1. Create a second model operating in the reverse order to the trace. This concentrates instances at the end state instead of the start state, making it more likely to catch missing states than the forward order model.
- 2. Create logical rules for identifying when states are functionally similar. This would allow for some state definitions to be combined, simplifying the model.
- 3. Create logical rules for identifying when paths can be broken into segments passing through additional states. This would ensure that inputs and paths are consistent.

2.4.1 Parallel Models

To construct a reverse order model, we ran the same model construction process with the entire trace inverted, starting with the end states, and running to the initial states. This concentrated instances into the end paths as intended. Figure 3: Simplified reverse branching tree model, shown below, demonstrates how a reverse model using the same simplified trace might appear. Now, both a forward and reverse model can be run together to identify states and paths.

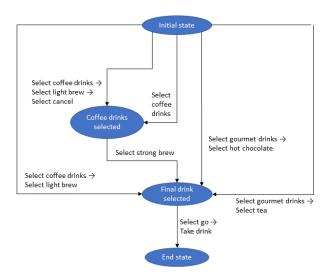


Figure 3: Simplified reverse branching tree model

2.4.2 Correcting State Redundancy

When preliminary states share behavior to operate logically similarly, they can be describing the same state. As such, they should be combined, considering that if we combine states

that are not actually identical, we will add false information to the model. To avoid doing this, we acknowledge that states are largely determined by their paths in this method, so any preliminary states that share paths are functionally identical.

In forward iteration, two preliminary states sharing all their outward paths are functionally identical. Combining said states would not any additional information, making them safe to combine and simplify the model. For example, **Error! Reference source not found.** shows how t he states "Strong brew selected", "Hot chocolate selected", and "Tea selected" can be combined to form the new state "Final drink (Not light brew) selected". Note that "Light brew selected" is not considered functionally identical because it has an additional path that is not seen in the other states.

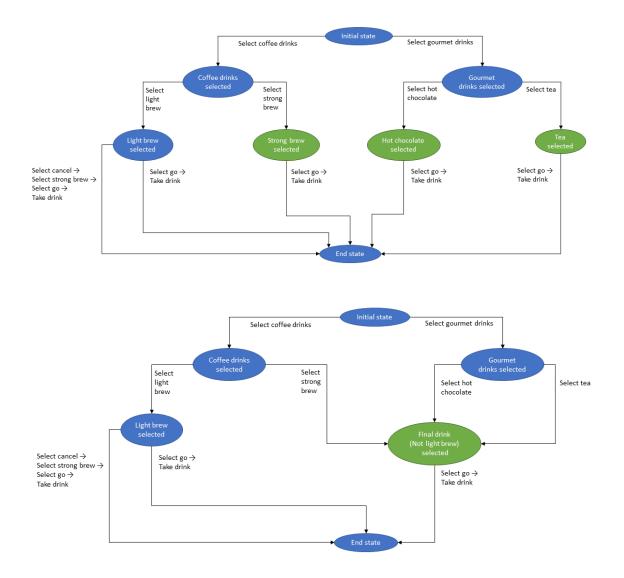


Figure 4: Forward model with redundant behavior merged. Green states in the first diagram are merged into the single green state in the second

Reverse iteration operates in the reverse direction from forward, and so states that can be considered functionally identical are instead those that share inward paths. This direction makes sense, as the same sequence of inputs should always lead to the same state. This fact also implies that states only need to share one inward to be considered the same, whereas forward iteration requires the sharing of all outwards paths to be considered identical. Figure 5 shows how this concept can be applied to a simple case.

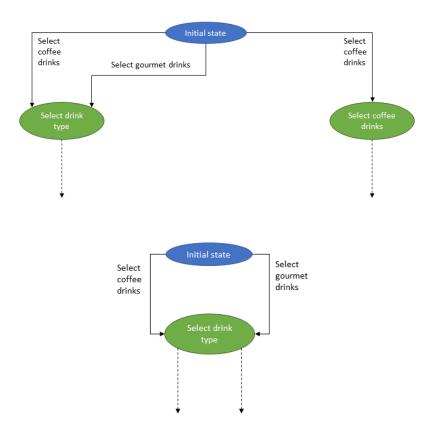


Figure 5: Reverse model with redundant behavior merged. Green states in the first diagram are merged into the single green state in the second

2.4.3 Path Intersection

Some paths may pass through known states without being labeled as such, making the paths and state definitions inconsistent and not match the true performance. For example:

Path 1) Coffee ready to brew \rightarrow Input: Go \rightarrow Input: Remove cup \rightarrow Ready for new drink Path 2) Coffee in cup \rightarrow Input: Remove cup \rightarrow Ready for new drink

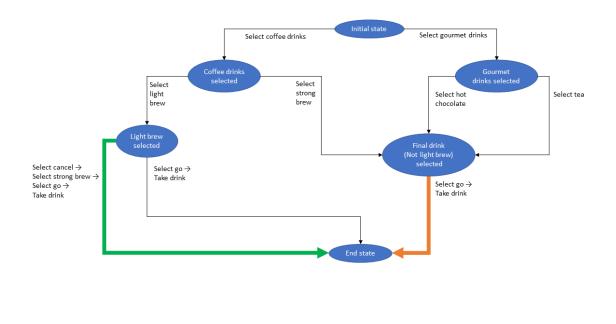
Both paths appear to share behavior. From only this information, we would conclude that path 2 is a subset of path 1, such that it would be more efficient and potentially more accurate to rewrite these paths as follows:

Path 1) Coffee ready to brew \rightarrow Input: Go \rightarrow Coffee in cup Path 2) Coffee in cup \rightarrow Input: Remove cup \rightarrow Ready for new drink We formalize this process of intersecting paths with two different methods, one for forward iteration and one for the reverse. Each direction places different logical demands on how we can conclude that states are passed through. Both iteration directions however share the concept of a *sub-state* to indicate the state inserted into a path between an initial and end state.

In forward iteration, we use the following set of rules to determine the presence of substates:

Rule 1.1) All the potential end states of a sub-state must also be potential end states of the initial state. This rule ensures that no additional connections are made beyond initial to sub.Rule 1.2) All the sub-state to end state paths must be included exactly as part of the existing initial to end state paths. This rule ensures that the component paths from the initial and the sub-states into the end states are shared.

Figure 6 shows how these rules operate. There is a path from "Light brew selected" decomposed to pass through the sub-state "Final drink selected (Not light brew)". For Rule 1.1, both states share end states, namely the "End state" state. Rule 1.2 is then satisfied when the sub-state path "Select go" \rightarrow "Take drink" is included exactly in an initial state path. It is included in both paths, satisfying the rule.



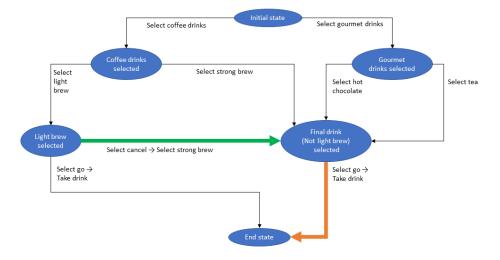


Figure 6: Forward model with path intersection. The orange path is subset to the green in the first diagram, so the green is redirected in the second diagram

This process is modified for reverse iteration:

- Rule 2.1) The sub-state must be an existing end state of the initial state. This rule prevents excess connections being made.
- Rule 2.2) The existing path from initial to sub-state is the beginning of another path from initial to end state. This enforces path determinism.

Figure 7 and Figure 8 show how these rules can be applied twice over, simplifying the model twice. First, "Coffee drinks selected" is made subset to a path from "Initial state" to "Final drink selected". Rule 2.1 is observed, as a path from "Initial state" to "Coffee drinks selected" exists, and this path is also the beginning of the larger path from "Initial state" to "Final drink selected", satisfying Rule 2.2 for path intersection. This process is then repeated, making "Coffee drinks selected" subset to its own path to "Final drink selected". Both applications introduce recursion into the model, which would not be possible without path intersection. While the final reverse iteration model alone does not represent reality completely (Selecting cancel after ordering tea would not allow the user to selected coffee drinks) the model is more accurate in cases where recursion does occur. Additionally, this model is not to be used in isolation, and can be paired with the forward iteration model to better understand the system.

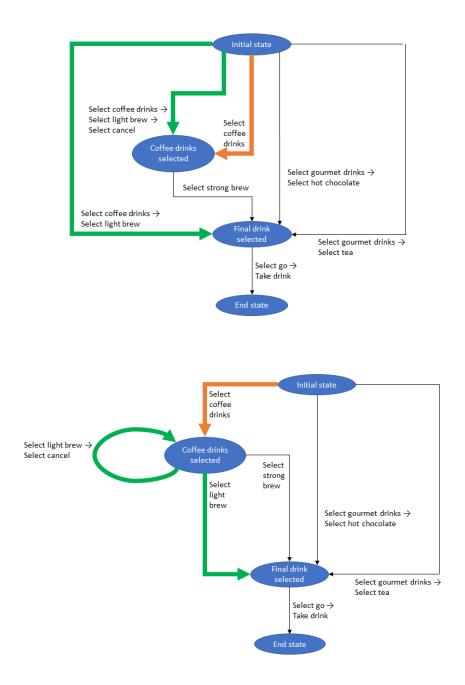


Figure 7: Reverse iteration model with path intersection. Orange is subset to green paths in the first case, so green paths are redirected

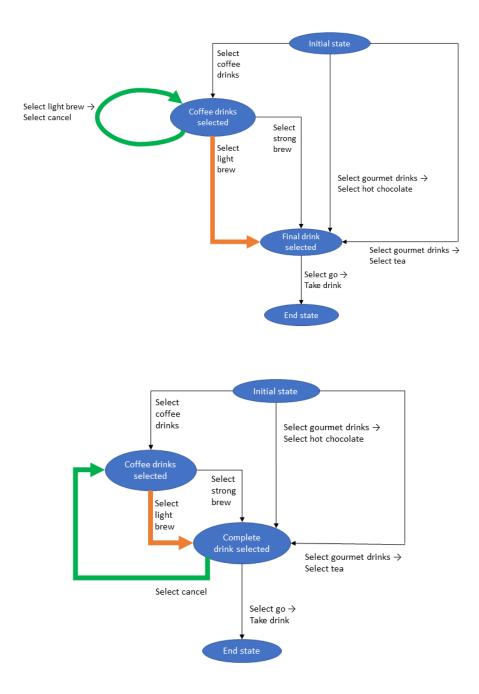


Figure 8: Reverse iteration model with path intersection applied once more. Orange is subset to green in the first case, so green is redirected

2.5 Final State Machines

The steps of state combination and path decomposition can be run iteratively, alternating between steps. Once no further simplifications can be made, the two state machines are complete. Figure 9 and Figure 11Figure 10 show the final state machines we constructed for the coffee maker, shown in forward and reverse iteration respectively. The forward iteration model exactly replicates trace behaviors, such that all paths shown are valid paths through the menu, but it is not exhaustive of all possible paths. The reverse iteration model, by contrast, includes both valid and invalid paths not seen in the trace. For example, one valid path included allowed a user to place a cup in the machine, remove the cup, and then end the interaction. Other paths included allow for recursion, which is a possibility the forward model is not capable of replicating.

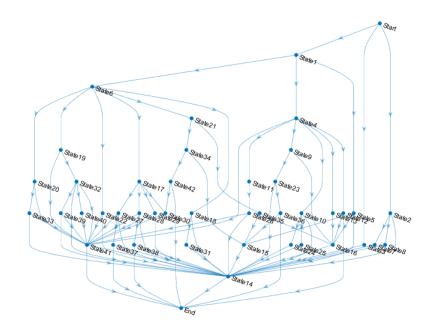


Figure 9: Final cofee maker state machine in forward iteration

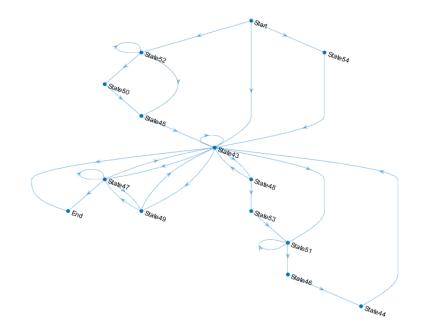


Figure 10: Final cofee maker state machine in reverse iteration

The models can also be analyzed in parallel. Note that in other simple cases, the state machines generated with the method may be very similar, but they will diverge with increased system complexity. While it may be possible to combine these machines together, it may not be efficient to do so. Parallel state machines are used for simplicity in many cases, particularly those with two disjointed tasks being performed at once. For example, we could imagine that it might be efficient to decompose the cup/coffee machine system into two subsystems (cup and coffee machine) with their own state machines, allowing us to avoid considering how the cup might affect the machine in ways beyond catching the drink at the end.

In general, we can see how the basic methodology outlined here can apply to a real system and produce a functional state machine that replicates trace behavior. Further demonstrations could also work to capture more behavior, expanding beyond simply replicating the trace, despite the lack of parameter information.

3. APPLICATION OF THEORY TO COMPLEX SYSTEM

This chapter goes into detail on the methods explored for constructing a state machine for a complex system: a flight simulator. We elected to use such a system for a demonstration of complex systems for its similarity to "real-world" safety critical systems, and for its convenience. Flight simulators provide a safe way to explore a variety of scenarios and are relatively simple to learn to operate, making them excellent candidates for study. Discussion begins with an overview of the simulator's characteristics, and then moves into how we collected and organized our trace of use. The next section centers on how we developed state detection methods with machine learning techniques, and the final section covers how these techniques fare with path and input classification.

3.1 System Overview

3.1.1 Defining the System

To begin, I selected the flight simulator YSFlight for study (Yamakawa, 2021). YSFlight presents a wide variety of benefits, first being that it is free and has low CPU and GPU requirements, making it simple to collect on any computers used, including home computers. Much of this recording needed to be performed at home due to social distancing guidelines, so this was a strong quality to have. The simulator also offers a built-in recording tool for collecting a trace. The recording tool was originally developed for replaying gameplay footage, and outputs a selection of flight data to a text file at the end of each flight. Given that this file is specialized for video replay, it unfortunately features some compression in the form of an irregular recording frequency of approximately 20 Hz that varies depending on accelerations to make video playback smooth. Nevertheless, having a built-in recorder made trace collection convenient. Table 2: YS-Flight recorded flight parametersshows the flight parameters the tool records.

Parameter	Description	Format
Time	The time after simulation start when parameters are recorded	Continuous, recorded in [s]
Inertial position (X/Y/Z)	Aircraft position vector in the simulation map, with the y parameter corresponding to altitude	Continuous vector, recorded in [m]
Attitude	Compass heading, pitch, and yaw	Continuous vector, recorded in [rad]
G-load	Unknown loading parameter	Unknown
Flight status	Categorical parameter indicating if aircraft is in flight, rolling, stalled, on fire, broken, etc.	Discrete, ranging from 1–6
Variable wing geometry	Deflection of any variable wing geometry features	Discrete, ranging from 0–255
Airbrake status	Deflection of any airbrakes	Discrete, ranging from 0–255
Landing gear position	Deflection of landing gear	Discrete, ranging from 0–255
Flap position	Deflection of flaps	Discrete, ranging from 0–255
Brake strength	Strength of brake application	Discrete, ranging from 0–255
Smoke trail status	Features of controllable smoke trail	Unknown
Vapor trail status	Features of controllable vapor trail	Unknown
Vehicle strength	Vehicle health (Used for military simulations)	Discrete, ranging from 0–4
Throttle strength	Throttle setting	Discrete, ranging from 0–99
Control surface deflections	Deflection vector of three main control surfaces	Discrete, ranging from –255– 255
Thrust vector deflection	Deflection vector for thrust vectoring systems	Discrete, ranging from –255– 255
Thrust reverser deflection	Deflection of thrust reverser surfaces	Discrete, ranging from 0–255
Bomb bay deflection	Deflection of bomb bay doors	Discrete, ranging from 0–255
Turret positions	Rotation position of aircraft mounted turrets	Discrete, ranging from 0–255

Table 2: YS-Flight recorded flight parameters

YS-Flight also has many features that allow it to better simulate real-world behaviors, first being a built-in air traffic control system that can provide live directions to a target airport and runway, following typical flight paths. Such directions included target bearing, altitude, and airspeed, making instructions intuitive to follow, and updates the pilot regularly as legs of the flight change or if major deviations occur. This system generally helps pilots fly more consistently and closer to realistic scenarios for safe flight.

This realism is further enabled with the YS-Flight selection aircraft and airports available. Real GA, commercial, and military vehicles are all available for flight in the simulation, as well as many airports, most of which are in Japan, the home of the game developers. Real airports allow our simulated system to mimic real flight paths, making our pilot behavior more like a real, safetycritical system operator's than hypothetical cases. The environment can also be controlled as weather, time, and visibility conditions are all controllable in the simulation, giving additional options for testing in hazardous conditions.

Once we had settled on YS-Flight, we needed to ensure that any trace we recorded would explore the use of a single system in multiple ways, and span as much of the system space as feasible. To span the space, we decided to fix as much of the physical system as possible, beginning with the aircraft itself. I elected to record traces with a Cessna 172-R exclusively, because it is a common GA aircraft, is intuitive to learn, and has little variable geometry that might affect flight behavior, making the trace more consistent. We also elected to fix our system study to cruising flight, allowing our study to avoid the use of flaps and taxiing entirely, simplifying the space we needed to model.

The physical space we navigated could also be constrained to reduce variability in system behavior and make flights shorter and therefore easier to record. I selected two runways near to each other: Misawa airport and Hachinohe airbase in the Aomori prefecture, Japan, with a total flight time of about 15 minutes between the two. This short flight time also had the additional benefit of keeping the vehicle mass from changing significantly during the flight, which would result in aerodynamic forces acting differently on the aircraft with time, making it more difficult to approximate behavior. We reduced this issue further by fixing the initial vehicle fuel load to 75%, making each flight more consistent than a varying starting mass. To constrain the flight path between the two airports to a safe approach, we engaged the automatic ATC system and followed its directions as best as possible during trace recording. These flights were always conducted in full sun and with no wind to ensure that air velocities and inertial velocities matched, simplifying any needed approximations of physics.

To then ensure that our trace captured significant variation in system use, we recorded flights to and from each airport, using both runways in either direction. This method of capturing the system space provided numerous flight paths to examine how behavior in each path differs, as well as how total system behavior operates. We also decided that some abnormal behavior was necessary in the trace to include such behaviors in a final model. Such behavior could be included by recording the trace with an inexperienced pilot, or by altering the visibility conditions or disabling flight instruments. I had little prior piloting experience, so my unmodified flights seemed sufficient for adding variation. Our attempts to record with disabled instruments resulted in flight conditions that were so abnormal that they were difficult to interpret into a distinct cruise phase, making them too difficult to integrate into the trace to be usable in analysis.

3.1.2 Implications of the System

Flight is defined by a variety of parameters and controls, both discrete and continuous. For instance, flap deflections are set positions, making them discrete, but altitude is a continuous parameter. Controls like the brake toggle are discrete, but yoke deflections are continuous. While the simulator itself is a digital tool, all the measurements taken for the trace are technically discrete but are taken with enough precision to be treated as continuous variables. Truly discrete variables are in the minority here, and we assumed that they had a minimal effect on flight, as we restricted the system to cruising flight only, where brakes and flaps are not in use. The stall indicator remains as a discrete parameter for study, but it is exclusively used for signaling to the pilot and does not affect the system otherwise, so we excluded it from analysis to simplify the study to continuous variables only and reserved it for validation tests. Continuous variables however result in measurements that are difficult to distinguish, and thus should be rounded to a minimum precision that is expected to be relevant. This rounding requires some knowledge from the analyst, and results in a system where purely logical definitions of states and inputs like that seen in Chapter 2 are non-achievable.

Flight is defined by many parameters and controls at once, making it a parallel system. With many continuous variables in use at once, each microstate and microinput will likely see little to exact replication in the trace, removing the possibility of simple logical model. Instead, statistical definitions for states and inputs need to be generated to classify behavior.

These states are also time-dependent, as the system state constantly updates based on physics. This means that an effective system frequency needs to be determined and used as a sampling rate for trace. Different sampling rates might result in different classifications because the difference between consecutive readings decreases at higher sampling rates. So, model construction will require sampling at multiple frequencies and selecting the most effective state definitions that are consistently identify similar states despite varying sampling frequencies and parameters provided.

Lastly, it is unclear what parameters are meaningful for determining the system state. For example, is proximity to a runway meaningful? This question cannot be answered without analysis,

so we can describe the system as being unbounded. Flight is bound by physics, so we can surmise that parameter vectors like position and velocity will be relevant, but reference frames and attitudes are also important to consider. Multiple variations of parameters in different references frames need to be studied and optimized to select the most effective classifiers.

3.2 System Trace

With a system defined, the system space needs to be traversed and recorded into a trace. This process begins with data collection and synchronizing microstates and microinputs. Once they are synced, we can add parameters that could not be initially recorded in the trace and perform any reference frame manipulations we might need to explore to expand the trace. Once an initial trace is completed, we can compute alternate traces with differing sampling frequencies to examine system frequency and begin analyzing the trace.

3.2.1 Data Collection

The system space can be spanned by recording multiple instances of each flight path to explore variations in execution of each path. As previously mentioned, the airports selected (Misawa airport and Hachinohe airbase) each have a single runway, which could be taken off from and landed on in either direction. Table 3: Flight paths recorded in trace shows the configurations of flights used in the final trace, and Figure 11 shows the complete record of flight from engine start to shut down.

Takeoff runway	Landing runway	Instances recorded
Misawa RW28	Hachinohe RW25	4
Misawa RW28	Hachinohe RW07	2
Misawa RW10	Hachinohe RW25	3
Misawa RW10	Hachinohe RW07	3
Hachinohe RW25	Misawa RW10	3
Hachinohe RW25	Misawa RW28	3

Table 3: Flight paths recorded in trace

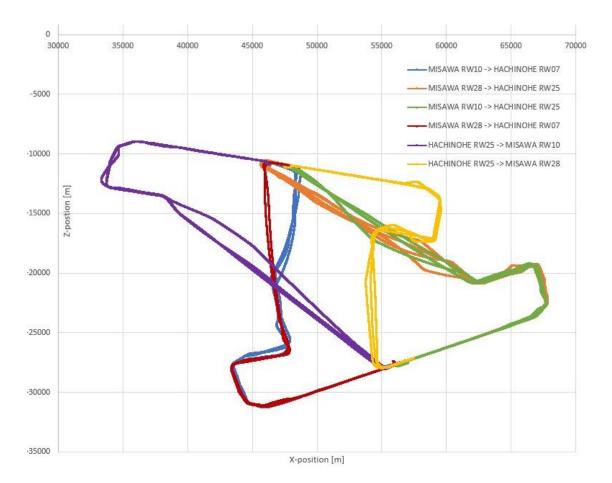


Figure 11: Top down view of flight paths recorded

I piloted the trace myself, using a Logitech Extreme 3D Pro Joystick controller, which I connected to a Simulink recording tool outputting inputs at 40 Hz. We assumed this frequency to be sufficient to capture all but the most aggressive stick inputs, which were not performed in this experiment. Given the sampling frequencies and duration of each flight, many thousands of microstate/microinput conditions were recorded, and while there are only a few instances of each flight path and no exact repetitions of microstates, similarities between each reading are likely to be high, making further repetitions likely to reinforce existing similarities. This behavior also implies that the trace approximately spans the nominal system space. Any additional flights do not seem as if they would add more information on the validity of different flights, beyond the missing flight paths.

To further expand on this trace collection, we could begin by recording more instances of each flight path, which would provide more information about behavior exclusive to the flight path but was not deemed necessary for the system wide study for the aforenoted reasons. We could also capture all runway-to-runway configurations instead of the six in the set used here. Doing so would provide an exhaustive set of flight paths, which would more likely capture the total breadth of anticipated behaviors, but was not expected to significantly improve models, as the flight paths themselves would overlap with much of the existing set. Lastly, the order in which flights were recorded could be better managed, as is, each flight path was recorded with each of its repetitions all in a row, such that the first paths recorded saw the least experience with the system. This could have biased analysis towards finding more hazardous conditions in the vicinity of the early recorded flight paths, but I did not see this bias as a significant enough factor for further study. While the initial flight recorded were slightly more anomalous than the others, the total proportion of stalls decreased only gradually with more practice. Additionally, flight paths often passed through the same flight corridors, demonstrating less that any anomalous flight was due to the physical location.

3.2.2 Synchronizing Microstates with Microinputs

Time between readings needs to be constant and consistent to effectively compare changes in microstate and state. In other words, parameter and control sampling rates should be equivalent to measure the effect of inputs on states. Unfortunately, YS-Flight records at a non-constant sampling frequency close to 20 Hz, which needs to be matched to a constant 40 Hz control sampling frequency. YS-Flight records parameters to approximate the real behavior in as few frames as possible while maintaining smooth transitions between frames. This trait implies that the true behavior can be approximated with linear interpolations between frames, further implying that the final data set can then be up sampled to a fixed 40 Hz frequency without overly distorting system behavior.

We began synchronization by finding an initial reading for both parameters and controls. YS-Flight sims start by selecting conditions and then loads to a starting window that begins recording with any further inputs. As such, recording can then proceed through the following steps:

- 1. Prepare flight weather/vehicle/starting location conditions
- 2. Start control recording
- 3. Set YS-Flight to the simulation start screen
- 4. Input a single, Boolean command via the control stick
- 5. Set up ATC

6. Fly normally

The step four Boolean command was issued through an unused control input on the stick, the trigger. Thus, the first trigger reading in the control recording is simultaneous with the first recorded parameter reading. This establishes a uniform time zero. Once the two data sets had a synchronized start, we linearly interpolated each parameter value to match the control reading time, producing a synchronized 40 Hz record of parameters and controls.

3.2.3 Additional Parameters and Transformations

Each system state may be defined by parameters that are not directly recordable, suggesting that known parameters that fit this description should be added to the trace when possible. In this case, YS-Flight does not record velocities, which presumably affect state, so velocities need to be calculated from the existing trace if possible. Failing to include all the system relevant parameters will result in the system state being undetermined.

In this case, velocity can be extracted from the existing record using position and sampling frequency to calculate a distance moved per unit time. For this analysis, we conceptualized velocity as being determined from the current position and position in the immediately preceding frame. This concept matches with the rest of data presented in the trace as being an instantaneous measurement.

However, frame-by-frame analysis can result in "jitter" due to precision loss in the parameters. For example, a slow-moving aircraft in our system could see zero velocity for several readings and then a sudden spike in velocity for one reading, followed by zero velocity. This cannot be completely corrected, as the true behavior is not recorded in YS-Flight. The best option then to reduce jitter is to smooth velocity, using the average calculated velocity for a given time frame. In this case, we opted for a 0.125 s smoothing window, centered on the reading being updated, that averaged the five readings within the window. Longer smoothing windows would result in a loss of high-frequency velocity changes, which are largely correlated with anomalous behavior because most of the nominal flight is conducted through with low accelerations for safety. Shorter smoothing windows do not meaningfully reduce velocity jitter, making this window size effective for this application. Additionally, because system is in cruise, high speeds will balance out most precision issues in position data, making smoothing less necessary that low-speed applications, but still required to improve performance.

Other parameters may need to be added to the set with reference frame transformations. When applied well, reference frames can be used to produce alternative parameter sets with less variation between flight paths, making them more effective for characterizing overall system behavior. In our existing trace, inertial position alone provides an incomplete view of the system, mostly emphasizing information on system-wide valid flight paths, but it does not provide information on valid flight paths for specific runway configurations, and obscures information on the mechanics of flight itself.

To combat this issue, we transformed the inertial coordinates to runway-relative reference frames. This added two reference frames to the trace, one for takeoff and one for landing, providing a total of five positional parameters. Each frame was centered on the runway of interest, ran one axis in the direction of use, preserved the vertical altitude axis, and ran the third axis in the transverse direction of the runway.

We transformed velocities similarly to match the positional frame, with the additional information that the physics of flight are largely defined by aircraft relative velocities, suggesting that a third frame be used. We then placed this third frame in the aircraft relative orientation, with one axis point along the forward axis of the vehicle, one on the vertical, and one on the horizontal axis. With the three velocity reference frames, two sharing a vertical axis, we brought the total number of velocity parameters up to eight.

Other parameters, like compass heading, similarly lack consistent meaning from one flight path to another. North is held consistent with inertial coordinates and could help with identifying valid flight paths, but in the runway-relative frames, North is not consistent. Instead, I used a targetrelative heading, using the direction to center of the landing runway as "North". This alternative helps enforce cruising generally towards the landing runway.

Attitude in general presents some issues for analysis because it is a vector of angular parameters. Angular parameters that can rotate fully skip from 359 degrees to zero degrees which statistical modeling techniques will have difficulty modeling. Instead, we took the sine and cosine of angular parameters and split compass heading into two parameters, removing the discontinuity.

Some system behaviors may have time-delayed effects, which could require additional parameters to capture. For example, aircraft flaps have several set positions in YS-Flight and can be controlled by pressing a corresponding button to initiate extension or retraction. This change in position does not occur immediately, so a parameter and control set that only captures the current

flap position and current flap control input would be unable to determine what the next flap position would be. This issue would not be corrected with the inclusion of a flap velocity parameter either, because no information on how many times the extend/retract command has been input is stored. Potential fixes would be to use a dedicated parameter for tracking commanded flap position, or in the case of system behaviors that execute after a passage of time, a "time since input x" parameter. Because we are operating exclusively in cruise, where flaps are not in use, such time-delayed effects are not a concern, but the issue could be relevant in other systems.

Once we had selected all the parameters, I encoded each parameter to condense discussion Table 4 shows the final parameter set, including the parameter encodings. Note that the stall indicator parameter is a Boolean variable, and therefore cannot be used in conjunction with the other continuous variables using statistical methods. As previously discussed, its inclusion in the trace was useful for validation of analysis.

When discussing the parameters in this analysis, it is useful to also develop a concept of parameter frequency. Here, I will use this term to qualitatively refer to how quickly a parameter is likely to change its value in a meaningful way. For example, we could consider most position parameters as being low-frequency parameters, because they change their value very little between readings in most cases. On the other end, control surface deflections and throttle strength could be considered high frequency, because even in non-hazardous conditions, they may change their value significantly relative to the recording frequency.

Table 4: Total	parameter	set used	l in trace
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Parameter	Code	Description	Freq.	Unit
SIN(Compass heading or Target heading)	SINCH/ SINTH	Sine of the corresponding bearing variable	High	
COS(Compass heading or	COSCH/SI	Cosine of the corresponding bearing	High	
Target heading)	NTH	variable		
Pitch angle	Angle between the aircraft longitudinal axis and level flight	High	rad	
Bank angle	BA	Angle between the aircraft wing and level flight	High	rad
X-position (Takeoff)	XPT	Distance between the aircraft and the center of the takeoff runway in the direction of takeoff	Low	m
Y-position (Inertial)	YPI	Aircraft altitude relative to sea-level	Low	m
Z-position (Takeoff)	ZPT	Distance between the aircraft and the center of the takeoff runway in the direction of the runway transverse	Low	
X-position (Landing)	XPL	Distance between the aircraft and the center of the takeoff landing in the direction of landing	Low	m
Z-position (Landing)	ZPL	Distance between the aircraft and the center of the landing runway in the direction of the runway transverse	Low	m
X-velocity (Takeoff)	XVT	Aircraft velocity in the direction of takeoff	Low	m/s
Y-velocity (Inertial)	YVI	Aircraft climb velocity	Low	m/s
Z-velocity (Takeoff)	ZVT	Aircraft velocity in the direction of takeoff transverse	Low	m/s
X-velocity (Landing)	XVL	Aircraft velocity in the direction of landing	Low	m/s
Z-velocity (Landing)	ZVL	Aircraft velocity in the direction of landing transverse	Low	m/s
Forward velocity (Plane)	FVP	Aircraft forward velocity	Low	m/s
Vertical velocity (Plane)	VVP	Aircraft vertical velocity	Low	m/s
Horizontal velocity (Plane)	HVP	Aircraft horizontal velocity	Low	m/s
Throttle strength	Т	Throttle setting on a scale of 0-100	High	
Elevator deflection	CSE	Elevator deflection from -256-256	High	
Aileron deflection	CSA	Aileron deflection from -256-256	High	
Rudder deflection	CSR	Rudder deflection from -256-256	High	
Stall indicator	S	Truncation of the original "Flight status" parameter, showing one if stall has occurred and zero otherwise	N/A	

3.2.4 Examining System State Frequency

The rate at which the system changes state is unknown and needs to be explored. Low sampling rates will not capture fast changes in state and will instead overemphasize the effect of high frequency parameters. For example, instantaneous control surface deflections would generally do little to affect the system state, but sustained deflection would. A trace with a low sampling rate recording a pilot rapidly oscillating the elevators would not be effective for matching the elevator deflection to aircraft motion. However, this effect would have the positive outcome of

making microstates behave like random, independent samples, which is necessary for performing statistical analysis.

In the opposite case, high sampling rates can bias state classification methods towards low frequency parameters. At these rates, parameters that change with low frequency will have values that are closer together than those that change at high frequencies because they change value slowly. This makes the trace readings more visibly dependent on each other and less useful for statistical methods of analysis. Additionally, this effect biases classification methods based on group densities, which are common and generally effective tools, towards using the high density and low-frequency parameters, obscuring the true system behavior. Microstates that are close in value are more difficult to separate into mutually exclusive states, making the final classifications less meaningful.

Overall, these effects suggest that multiple sampling frequency traces need to be constructed and examined to determine whether there is consistent behavior across multiple frequencies. This consistent behavior would then indicate a true system frequency. To do this, we elected to test 40 Hz and 4 Hz traces. 40 Hz was the highest possible frequency we could reliably capture data with the recording controls, and 4 Hz is much lower, but not so low as to not catch high-frequency transitions like a dive due to stall. No recovery attempt post stall would result in normal flight parameters at this sampling frequency, so it would still be able to catch basic behavior.

There are two basic methods for converting the baseline 40 Hz to 4 Hz. The first option is to down-sample the set by picking every tenth point of the 40 Hz set, which would result in measurements as if the system had been originally sampled at 4 Hz. The second is to arithmetically average each 10-reading segment of the trace into a single reading. This process would lower the apparent frequency of all parameters by averaging values but would affect high frequency parameters the most. Overall, this would bring parameter frequencies closer together, reducing the high-frequency bias, and making it the preferable choice for downsampling.

3.3 State Detection through Unsupervised Machine Learning

With a complete trace, we can analyze microstates to produce state descriptions. Several methods already exist to classify vector data into classes, which we can use to approximate state

descriptions. Methods that seek to produce the ground truth we are seeking are called "unsupervised" methods.

Most simple classifiers treat the microstate as spatial coordinates for points in the state space (Boonchoo, et al., 2019). Such coordinates would have n dimensions, with n being the number of parameters. The raw parameters in the trace have dramatically different magnitudes and need to be normalized to ensure that each parameter is weighted evenly in our statistical methods. With a normalized trace, the classifier can then examine the distribution of points and use different methods to partition the space into states.

In general, classifiers require some tuning to produce meaningful results, so they often require several attempts at classification before a final model is achieved (IBM, 2020). For this case, we will not only need to tune the classifier variables to our system, but we also need to determine which parameters are useful for describing states. I constructed an optimizer tool described in the next section to tune these settings and produce the most reasonable state descriptions possible. Once we had state descriptions, I validated them against known conditions like stall and other clear transitions in behavior, variations in trace reference frames, and variations in sampling frequency.

3.3.1 Classifier Selection

We considered three classifiers that are commonly used for generating states: DBSCAN, K-means, and Gaussian-Mixed-Models (IBM, 2020).

DBSCAN (Density-based spatial clustering of applications with noise) operates by clustering microstates by proximity, using two metrics: minPts and search radius (Mathworks, 2021). We can describe it as following this set of rules to determine states:

- 1. Each parameter is normalized to weight changes in magnitude as equivalently as possible
- 2. All microstates within the search radius of each other are neighbors
- 3. Each microstate counts the number of neighbors
- 4. Microstates with at least minPts neighbors become core points, starting a new state
- 5. If a microstate is neighbors with a microstate in a state, it can also be said to be in a state
- 6. Microstates with no neighbors are considered to be outliers

Figure 12 shows these rules graphically, where red indicates core points, yellow indicates non-core points in the same state as red, and blue indicates outlier points that not classified.

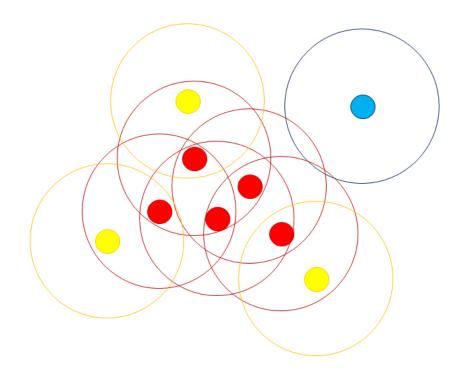


Figure 12: DBSCAN visualization

DBSCAN offers two main advantages (Boonchoo, et al., 2019). First, unlike other classifiers, DBSCAN does not require an analyst to specify the number of states to classify data into. This reduces the amount of system knowledge required to optimize, and the two tuning variables have established techniques for estimation. Second, DBSCAN can classify states that have arbitrarily shaped perimeters. Many classification methods struggle with state definitions that create concave shapes, especially when they leave the centroid of the structure outside the perimeter. Figure 13 shows a potential real-world case of this concavity in data sets, where coordinates are being using to classify flight into a safe zone and an unsafe mountainous zone. If a classification method that cannot handle concavity is used, it might generate state boundaries like the ellipsoids marking the map. Such definitions can lead to ambiguity over whether the intersection is a safe flight zone, and in this case, the centroid of the safe flight state definition is completely outside the true border.

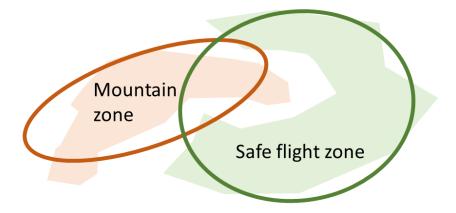


Figure 13: Demonstration of how concavity can affect classification. Here, the green and orange filled areas are being defined using a technique based around ellipsoids (GMM)

On the other hand, DBSCAN is less effective than other methods with higher-dimensional data sets, finding more arbitrary definitions than other methods in high dimensions (Boonchoo, et al., 2019). This is due to an effect referred to as the curse of dimensionality, where adding a new dimension to data exponentially increases the hyperspace of the set (Köppen, 2000). This increases the random odds that any point is within a given distance of any other, increasing the likelihood of random "order" appearing in data defined by proximity. Some alternative measures of distance, like city-block, can help with the issue, but in general DBSCAN handles this perceived order worse than other classifiers. Additionally, each parameter is weighted the same for each point in each state, which has the side effect of making each state tend towards having the same minimum density. In general, despite the established techniques for tuning, finding optimized values for the tuning metrics can be difficult to approach, given that they affect each state uniformly.

For our specific application, DBSCAN is also unsuited for our task because it requires all points to be independent samples. Any dependence leads to separate readings being very geometrically close, and hence difficult to distinguish. Random sampling readings from the trace can combat this but given that we expect traces to sample states unevenly, this can lead to complications. Lastly, DBSCAN only classifies specific sets of points together into states, and requires further analysis to produce state definitions, while other classifiers do not.

The K-means classifier works to define k states, with new microstates being classified into states based on which states they are closest to the mean value of all its constituent points. This is done by assuming that microstates can be separated partitioning the hyperspace with hyperplanes, drawing a clear boundary between states (IBM, 2020). To place these planes, first the analyst must provide one tuning metric: the number of states to establish. Then, they place hyperplanes in the state space, attempting to maximize the density of each state, by minimizing the total variance of the microstates in each state. Figure 14: K-means visualizationFigure 14 shows how a K-means classifier might separate 12 microstates into three states, with each color indicating the final state of classification.

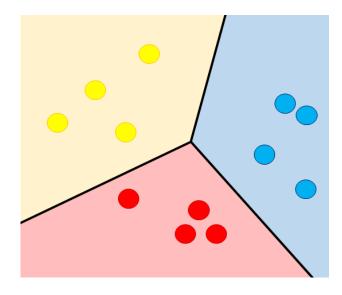


Figure 14: K-means visualization

This classifier offers several advantages over DBSCAN, first and most obviously, that only a single tuning metric is needed. K-means can also interpret dependent data better than DBSCAN, because it does not classify all similar states as identical, reducing the effect of the curse of dimensionality. This method also establishes clear, geometric definitions of states, allowing new readings to be classified easily without additional interpretation.

However, DBSCAN is slightly preferable in some regards. Placing the hyper-planes is computationally difficult and requires many iterations. K-means state definitions tend to trend towards spherical states that are roughly equal in size, as hyperspheres generally have the lowest variance. This geometry is not necessarily how states are structured and distributed however, we can expect that a trace will exhibit states at different rates and shapes.

The last method we considered was the Gaussian-Mixed-Model (GMM) classifier. It is often considered as a direct improvement on K-means classification, as they both used iterative methods to minimize variance in classifications, but they approach the problem differently (McGonagle, Pilling, & Dobre, 2021). As with K-means, GMM uses state count as its sole tuning variable. GMM then follows the following set of rules:

- 1. Each parameter is normalized to weight changes in magnitude as equivalently as possible.
- 2. Within each state, each parameter is assumed to follow a normal distribution.
- 3. Each state can then be described with a set of mean, variance, and covariance values for each parameter.
- 4. Statistical tools can estimate reasonable values for each metric from the trace.
- 5. Microstates can then be assumed to be randomly produced by each state model, with a probability of generation provided.
- 6. Each microstate in the trace can be classified to the highest probability state.

Figure 15 then shows how we could visualize probability curves for different states and how those curves could plausibly generate corresponding microstates.

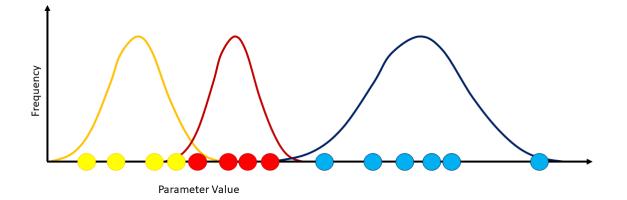


Figure 15: Gaussian Mixed Model visualization

This final method is preferable for our application, because it can manipulate dependent data sets well, like K-means, but has more flexible geometric constraints for states. While it still cannot produce concave state perimeters, it lacks some of the major downsides of K-means, namely its restrictions on size and shape. Additionally, GMM provides confidence ratings for each

classification, providing another value for an analyst to compare states and microstates on the periphery of each state.

3.3.2 Classifier Optimization

While Gaussian Mixed Modeling can classify microstates into states, it still requires tuning, with the additional need to compare importance for determining states with different parameters. I considered tuning the GMM to be an optimization problem, where differently tuned models could be compared to maximize the quality of classifications produced.

We can think of classification quality as being composed primarily of two metrics: distance between states, and density of states. Classifications that produce states that are generally wellseparated show that their states are well-defined and distinct. Classifications that then produce states that are dense, show that their states show many readings with similar behavior, and are well represented in the data set.

Classification methods then use at least one of three criteria to measure the combined effects of distance and density: silhouette, Davies-Bouldin, and Calinski-Harabasz (MathWorks, 2021). The silhouette criterion is defined with mean distances between microstates in a state compared to the mean distances of microstates in the next closest state. This method produces a metric that is bounded, making it easy to interpret, but it is computationally complex, because it requires distance calculations between each point in the set.

The Davies-Bouldin index is akin to the average similarity between states, primarily relying on the state centroids. This process is less computationally expensive than silhouette but restricts analysis to Euclidean space. This can be an issue if classifiers use non-Euclidean distances to determine classifications. This is not the case here, but it can be restrictive for some classifiers. The Calinski-Harabasz index by comparison, uses matrix comparisons of microstate dispersions inside states and between states, avoiding using the centroid and distance, making it preferable to both other options.

To then optimize models compared with the Calinski-Harabasz index, I used genetic optimization. In general, we can think of this method as using different optimization variables as genes for many separate model tunings. In this case, these variables would be our state count, since we are using GMM, and Booleans indicating which parameters should be considered relevant for determining state, each encoded as a gray binary number. The optimizer then generates many

random configurations of genes and evaluates them with a fitness criterion (in our case, the Calinski-Harabasz index). Individual configurations that performed worse in the bottom 50% are culled from the population, and the surviving configurations are randomly paired to swap gene values, with some degree of random mutation. Each pairing produces four "child" configurations, establishing a new population for a second iteration. In this way, we produce an artificially evolving system, with genes for configurations that perform well being retained in the population. Once 90% of the genes in the population are identical, the optimization finishes, and the best performing configuration is output as the optimized solution.

This optimization scheme works well in our case, as many optimization techniques are restricted to continuous variables, whereas our variables are all discrete or categorical. It also works well if even if there are multiple local minimums in the optimization space. We can assume multiple local minimums exist in this set, as it is plausible that certain parameter inclusions will have different optimized state counts, especially with the high dimensionality of the trace, so this is a trait that is desirable for our optimization.

To set up this optimization, each variable used must be bounded and encoded into binary. I bounded the state count from 3 to 18, deeming that fewer than three states would provide no more information than existing anomalous state identification techniques, and more than 18 states would result in definitions so fine-grained that they may not be intuitive to distinguish, and therefore difficult to validate. This range then holds 16 possible values, keeping the number of binary digits required to represent the data as small as possible to reduce the volume of data needed to optimize, improving turn-around rates for diagnostics.

Parameter inclusion was represented as a gene by assigning each parameter a gene of value zero or one, indicating its inclusion in the GMM model. However, allowing all parameters to be enabled and disabled in the optimization could result in well-defined states that had little to do with the safety critical performance. For example, we would imagine that a state classifier that does not consider the rate of climb/descent for the aircraft would not be meaningfully considering the system safety and could instead be classifying irrelevant parameters. This issue is a direct result of the system being unbounded.

To adapt to this problem, we assumed that some parameters are relevant for determining states, so they are not included as genes in the optimization but are always used in the classifier.

These parameters, Y-velocity (Inertial), plane relative velocity, and the throttle setting, are strongly correlated with the physics of flight and flight safety.

With these pieces in place, we began optimization. Our initial test case used 4 Hz sampled data and compass heading as the bearing variable and provided three coherent states. Table 5 lists the means for each normalized parameter included in the optimization. Most parameters show a clear separation of means for one state, providing some simple information on what distinguishes each state from the others. For example, none of the mean parameter values of the first state are outliers, suggesting that this is close to a baseline, and can be primarily defined by its contrast with the other states. The second state has high SINCH, ZVL, FVP, VVP, and T means, and a low ZPL mean. With many high velocity parameter means as well as a high throttle setting, we can assume that this state will largely be characterized by its high speed. The third and final state can then be contrasted with low YVI and HVP means, suggesting that this is a dive state, and likely an uncontrolled dive given the HVP value. Overall, we can now view each state as the low-speed, high-speed, and hazard state respectively.

Name	SINCH	COSCH	ZPL	YVI	ZVT	ZVL	FVP	VVP	HVP	Т
Low-	-0.10	0.14	0.13	0.03	-0.01	-0.12	-0.38	-0.37	0.02	-0.36
speed										
High-	0.28	-0.35	-0.40	0.02	0.03	0.34	1.04	1.05	0.02	1.02
speed										
Hazard	-0.17	-0.15	0.31	-0.74	0.07	-0.23	-0.16	-0.40	-0.41	-0.38

Table 5: Compass heading 4 Hz normalized parameter means

3.3.3 State Validation against Known Behaviors

With a state model in place, we can classify microstates in the trace and examine their behavior to see if the state definitions result in coherent behavior. Figure 16 shows the top-down view of the recorded flights in the landing-runway relative frame. There is a clear delineation of the low-speed and high-speed flight states as the aircraft transitions from flying towards the runway to lining up for approach. Figure 17 then shows the recorded altitudes in order of instance, with the hazard state showing up disproportionately in areas of rapid descent. Both inspections suggest that our definitions are coherent.

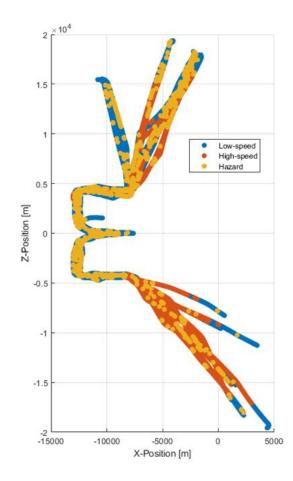


Figure 16: Top-down view of initial classification using landing runway relative coordinates

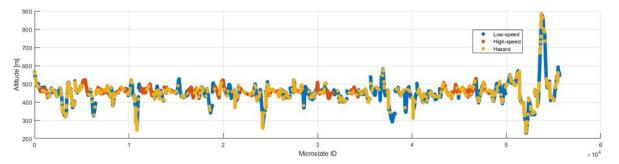


Figure 17: Altitude readings of initial classification in order of appearance in trace with state indication

As an additional check, we compared the distribution of hazard states to the distribution of stalled microstates. 75% of stalled microstates appeared in the hazard state, with the remaining 25% appearing exclusively immediately before state transitions into the hazard state, with about a half second lag time. This makes sense, as short periods of stall will not dramatically affect flight

parameters, but sustained stall will. Overall, checking the initial data set against the perceived behavior and the stall characteristics supports that our states have some grounding in reality.

3.3.4 State Validation through Parameter Variation

To provide further grounding, we assume that true system states will have definitions that can be found with this optimization process even when the initial parameters available are changed. To then test if our initial definitions exhibit this property, we altered the initial parameter set and reoptimized the system in two separate ways.

First, we altered the reference frame of the compass heading. As is, the compass heading variable is somewhat arbitrary outside the inertial reference frame. In a runway relative frame, North is inconsistent from flight to flight, so instead, we rotated the compass reference frame to always point North towards the center of the target landing runway, producing the target heading parameter, which is converted with sine and cosine as before into SINTH and COSTH respectively.

With compass heading replaced, I optimized the model again, and produced a second set of state definitions. When comparing the states generated, we can look at the parameters shared in both definitions, and their extreme means. Table 6 shows the normalized parameter means as before, and we can see similar trends in behavior, with the shared extrema highlighted, green corresponding to shared high values and red corresponding to shared low values. No extrema disagree, suggesting that these definitions are defining the same states, like we would expect of a true system state.

Name	SINTH	ХРТ	XPL	YVI	XVL	ZVL	FVP	VVP	HVP	Т
Low-	-0.15	0.01	-0.58	0.06	0.21	-0.05	-0.61	-0.58	0.02	-0.59
speed										
High-	0.25	0.01	0.80	-0.01	-0.31	0.09	0.87	0.85	0.02	0.85
speed										
Hazard	-0.16	0.17	0.00	-0.68	0.21	-0.15	-0.13	-0.38	-0.68	-0.32

Table 6: Target heading 4 Hz normalized parameter means

When we examine the states by comparing them to known behaviors as before, we see similar performance to the compass heading case. Figure 18 shows the top-down view, where we can see a similar transition from a mix of all three states to exclusively low-speed and hazard once we transition into approach. Interestingly, some flight paths appear to have been completely reclassified from low-speed to high-speed, while others have been reclassified in the opposite manner. In Figure 19, target heading shows similar behavior to the compass heading for altitude plots, and when we compared stall inclusion, we saw the same 75% in hazardous split, suggesting that these state definitions are describing similar phenomena in the system.

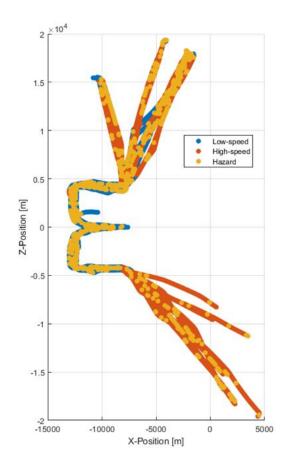


Figure 18: Top-down view of target heading optimization using landing runway relative coordinates

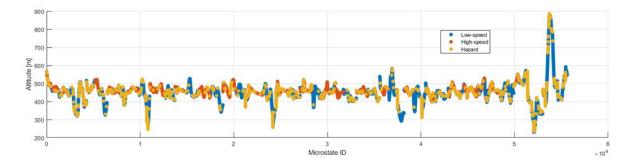


Figure 19: Altitude readings of target heading optimization in order of appearance in trace with state indication

The evidence in both cases suggests however that the parameters included may be masking the true system behavior. Both optimizations included parameters in their definitions that have no clear connections to behavior. For instance, XPL and ZPL are both position parameters indicating proximity to the landing runway. Proximity might affect when a pilot might alter their speed or course, but it would not physically alter the vehicle state, suggesting correlation with state, but not causation. This masking issue is further reinforced when entire flight paths appear to change state from compass to target heading optimizations, but the actual speeds flown remain the same. To then develop a more consistent definition, we excluded position and runway-relative velocities from the optimization and produced a third set of definitions.

As before, the normalized mean values retain their extrema in the parameters used in all three definitions, as seen in Table 7, where green and red once again indicate conserved extrema. Interestingly, without the position parameters, the optimization instead includes pitch angle, bank angle, and elevator deflection to define states. This is technically a less optimized definition, as the Calinski-Harabasz index of the positionless optimization is the lowest of the three performed so far, but these new parameters have much more obvious causal connections to states. For example, the low-speed state has a high pitch angle mean relative to the other states, suggesting that flying at low speeds requires flying at a higher angle of attack to stay in level flight, as we would expect.

Name	PA	BA	YVI	FVP	VVP	HVP	Т	CSE
Low-	0.31	0.00	0.04	-0.41	-0.39	0.02	-0.39	0.36
speed								
High-	-0.74	0.02	0.01	1.06	1.05	0.02	1.03	-0.96
speed								
Hazard	-0.09	-0.19	-0.64	-0.29	-0.51	-0.33	-0.52	0.52

Table 7: Positionless 4 Hz normalized parameter means

The top-down plot in Figure 20 shows that like the other optimizations, the same general regions each state occupies are preserved, with slightly more transitions from low to high-speed states. Overall, we can conclude that despite the new parameters, the state definitions we have reached are consistent in roughly which microstates belong to which state, and how those states look and behave.

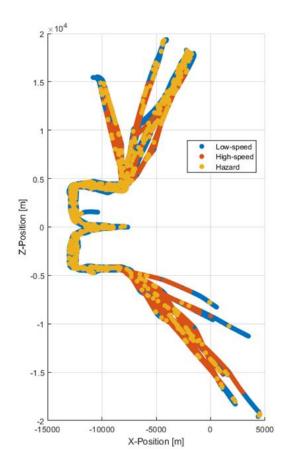


Figure 20: Top-down view of 4 Hz positionless optimization using landing runway relative coordinates

3.3.5 State Validation through Sampling Frequency Variation

We can also assume that true system states will share behavior in multiple sampling frequencies. State definitions that do not have this property are more likely to be artifacts of the recording process or of the specific parameters provided. As such, we performed the same optimization process on a 40 Hz trace to compare results to the 4 Hz optimizations performed previously.

To begin this comparison, we first consider that while the 4 Hz trace has parameter smoothing implemented to reduce the effect of high-frequency parameters, the individual microstates still resemble the original microstates taken from the 40 Hz. As such, a 4 Hz classifier should be able to classify 40 Hz microstates, and vice-versa, but the more visibly dependent

microstates in the 40 Hz trace may affect the tuning of a 40 Hz classifier. When optimizing a GMM classifier to the 40 Hz trace as before, we see varying state definitions because of this dependency.

Compass and target heading state definitions appear like each other, but nothing like their 4 Hz counterparts, as shown in Table 8 and Table 9. Completely different extrema are shared, highlighted in red and green as usual. This issue is likely due to the inclusion of low-frequency, position parameters, as the higher 40 Hz frequency is more biased to low-frequency parameters. We can see this bias by examining the top-down plot in Figure 21, where each state appears to be constrained to specific regions of the map. Overall, it is difficult to extract meaning from these state definitions beyond the local state, which contains all points of stall in the trace, but is also so present in the rest of the trace that it is unhelpful to label it as exclusively a hazard state.

Name	SINCH	COSCH	ХРТ	YVI	ZVT	ZVL	FVP	VVP	HVP	Т
North	-0.63	0.12	-0.49	0.00	-1.01	-0.69	0.67	0.66	-0.01	0.67
cruise										
South	0.84	-0.49	0.71	-0.02	0.74	0.84	0.85	0.82	-0.01	0.85
cruise										
Local	-0.03	0.18	-0.05	0.01	0.26	0.01	-0.85	-0.83	0.01	-0.85

Table 8: Compass heading 40 Hz normalized parameter means

Table 9: Target heading 40 Hz normalized parameter means

Name	SINTH	COSTH	XPL	YVI	ZVL	FVP	VVP	HVP	Т
North	-1.01	0.63	0.00	-0.05	-1.14	0.18	0.14	-0.02	0.17
cruise									
South	0.98	-0.26	0.62	0.05	0.88	0.42	0.40	0.02	0.43
cruise									
Local	-0.03	-0.47	-0.87	-0.00	0.28	-0.83	-0.76	-0.00	-0.83

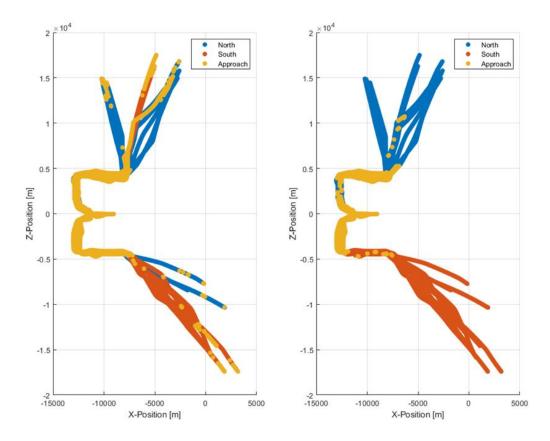


Figure 21: Top-down view of 40 Hz optimizations using landing runway relative coordinates

It follows then that a positionless optimization then would likely have fewer problems with states being fixed in position. Table 10: Positionless 40 Hz normalized parameter meansTable 10 shows the normalized means for such an optimization, which now shares the 4 Hz definitions for states, with one exception, the horizontal plane-relative velocity extrema. In the 40 Hz case, the hazard case is characterized with a high HVP mean, where in 4 Hz, hazard is characterized with a low HVP mean, suggesting that these state definitions may be describing different phenomena. However, consider that the sign of HVP may not be relevant for determining the state of the system. The aircraft system is symmetric, such that any effects recorded for positive HVP would also be possible if the situation was mirrored so the HVP were negative. That would imply that the mean value of HVP in each state should be near zero. This makes the extreme mean HVP values in all hazardous state definitions likely to be more a result of the specific data in the trace, and less meaningful as a description of hazard. If we instead inspect the standard deviation of HVP in both positionless models however, we can see that it is much higher in the hazard definition than those for other states, as we would expect. This shows consistency in definition beyond just the

normalized means, suggesting that the state definitions proposed here are describing real system states.

Name	PA	YVI	FVP	VVP	HVP	Т	CSE
Low-speed	0.32	0.02	-0.41	-0.40	-0.01	-0.40	0.37
High-speed	-0.65	-0.00	0.84	0.83	-0.01	0.84	-0.78
Hazard	0.42	-0.12	-0.60	-0.61	0.10	-0.66	0.61

Table 10: Positionless 40 Hz normalized parameter means

To confirm that the position-fixated states are no longer present, consider the top-down view in Figure 22, where we see a distribution much more akin to the 4 Hz states.

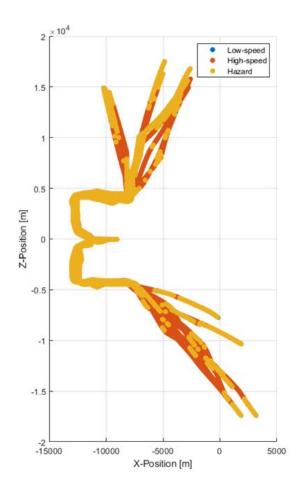


Figure 22: Top-down view of 40 Hz positionless optimization using landing runway relative coordinates

3.4 Difficulties with Applying Basic Machine Learning in Path Determination

With state definitions determined, the trace can now be analyzed for paths. If the states determined are to be considered the ground truth for system behavior, we can generate a ground truth for paths from them by looking at the current and then the next state for each microstate. In the system's operations, these paths are determined by the combination of the microstate and the microinput, so the task becomes determining a method for producing a path from the readings.

Unfortunately, our analysis suggests that basic machine learning techniques are not sufficient to determine path from current microstate and microinput. This could be a result of any of three factors:

- 1. Paths do not necessarily have distinguishable characteristics in readings
- 2. Inverse time scaling of the trace makes paths difficult to observe
- 3. Parameter connections are complex, making the true prediction of the system complex

3.4.1 Path Detection with Basic Machine Learning

In theory, we could train a simple machine learning (ML) classifier to distinguish paths in a similar way to how we determined states. This would be slightly different however, as we would have a ground truth, making any classifier we developed able to use supervised learning techniques. These classifiers tend to be simpler, because they can check their accuracy against the ground truth to determine success rather than optimizing against an abstract classification index like the Calinski-Harabasz index. To do this, we must:

- 1. Use the known states to generate path IDs for each reading in the trace. For example, a reading starting from S1 and followed by S1 would be path 1, a reading in S1 and followed by S2 would be path 2, and so on.
- 2. Train a supervised ML classifier to interpret readings into path IDs, using the generated path IDs as ground truth.
- 3. Decompose the most effective ML classifier to determine characteristics of each path.

This process can be further improved by training a ML classifier for each initial state, instead of a general classifier for distinguishing paths. This reduces the number of paths that need to be distinguished by a single classifier from n^2 to n, where n is the number of states, and would

take advantage of the existing state classifier we have already developed. It would also have the additional benefit of narrowing the data which the classifier needs to account for to only that in its initial state, making it theoretically simpler to distinguish.

MATLAB natively supports many ML classifiers but given the many successive classifiers I needed to construct, I opted to only train classifiers from the list that could produce a result quickly in parallel to other training. With this option, I was able to train many different variations of classifiers at once and select the result that produced the greatest accuracy for classifying paths when using a five-fold cross validation, with one-fifth of the training data is reserved for checking accuracy. The classifiers then considered in this approach were variations on decision trees and *K*-Nearest Neighbors (KNN).

Decision trees classify readings by sequentially passing them through Boolean checks, for instance, checking if pitch angle is above a given threshold to determine if the aircraft if going to stall and transition into the hazardous state. They can be trained to have a varying degree of fidelity, measured in the number and specificity of checks, but were most frequently selected in high fidelity variants, suggesting that the paths between states are difficult to distinguish.

KNN classifies readings by instead comparing new readings directly to the training set, placing the readings in a hyperspace as done before with the classifiers used for state definition. Then, it determines the k nearest readings to the unknown reading and determines which path ID has the highest count in the k selected. If the same number of points are randomly sampled from each state to train the classifier, it is probable that this path ID is also the ID for the new reading, so KNN outputs this path ID as its classification. For instance, Figure 23 shows how a varying k value might change the classification of the central point, with each successive circle enclosing a corresponding k nearest neighbors. Further variations on this method include altering the distance metric, which can improve KNN performance on higher dimensional data, and enabling distance-based weighting, where classification is biased towards readings that are closer to the unknown point, which can improve performance but requires further training to tune.

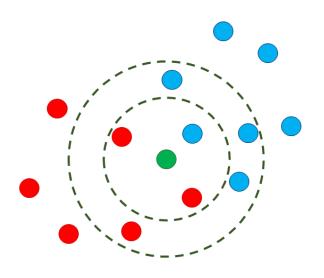


Figure 23: K-Nearest Neighbors visualization

KNN highly values density of points. This in itself is not a problem, as an indicator of a clear distinction between definitions is the density of readings matching each description in the state space—higher densities suggest consistent behavior. This emphasis however results in KNN being heavily biased in training towards paths with the highest number of readings in the training set. Given that we expect that most paths are *stable* paths (paths that return to the current state) a training set that includes all the paths out of our state of interest will be biased towards identifying stable paths if KNN classifiers are selected. To reduce this bias, we randomly selected the same number of readings for each path when training classifiers. We compared both training methods to determine whether any consistent gaps persist despite random sampling.

Unfortunately, this technique of using simple ML classifiers is not sufficient for finding definitions for path behaviors. No classifier was able to successfully parse paths from the coherent state definitions, with consistent issues regardless of the parameters included. In general, paths that return to their original state, which we will call *stable* paths, are the most consistently identified, but other path identifiability varies state to state.

We used confusion matrices, like the example shown in Figure 24, to visualize the effectiveness of each classifier clearly. Once paths are classified, we compare the ground truth path we generated by the state definitions, and the predicted path from the trained classifier. Starting with the central matrix, rows indicate the ground truth path ID, and columns indicate

predicted path ID, and the value in the corresponding element indicates the total number paths found in the trace with those IDs. For example, element (1,2) in our example matrix has a value of 83, telling us that 83 paths were labeled as paths to high-speed cruise, but were actually paths to low-speed cruise. Ideally this, main matrix would be a diagonal matrix, as this would indicate that all paths were classified correctly. Elements that are closer to this ideal number are color-coded in darker blues, while elements that are farther away are colored in orange.

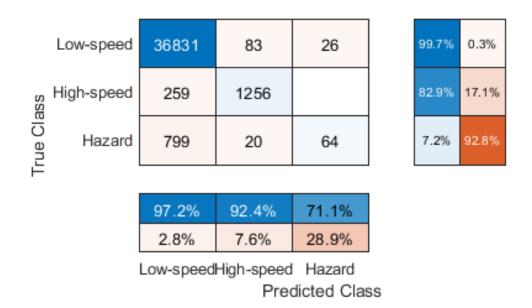


Figure 24: Example confusion matrix

The submatrices correspond to measurements of the true positive rate (TPR) and positive predictive value (PPV) respectively. TPR, measured in the left column of the right matrix, indicates the rates at which each path was correctly identified, mathematically measured as what percentage of the row is in the diagonal. PPV is then measured in the top row of the bottom matrix, and indicates the rates at which prediction is correct, mathematically measured as the percentage of each column that is in the diagonal. Higher percentages in the diagonal indicate a more effective classifier, so higher TPR and PPV also indicate better performance. Each submatrix is color-coded to match the main matrix, with blue indicating higher performance, and orange suggesting lower.

Classification of Paths out of Low-Speed Cruise

In general, both methods of classifying paths out of low-speed cruise showed bias towards predicting stable paths, and paths into the hazard state were generally the most difficult to correctly identify. Even accounting for bias, paths to hazard are disproportionately classified as stable paths, suggesting that the path to hazard and the stable path are very similar, more so than paths to high-speed, which has fewer misclassifications, despite occurring more frequently. As shown in Figure 25 and Figure 26, the standard sampling method of providing all paths as training data appears to have resulted in classifiers with a higher PPV, while random sampling resulted in a higher TPR.

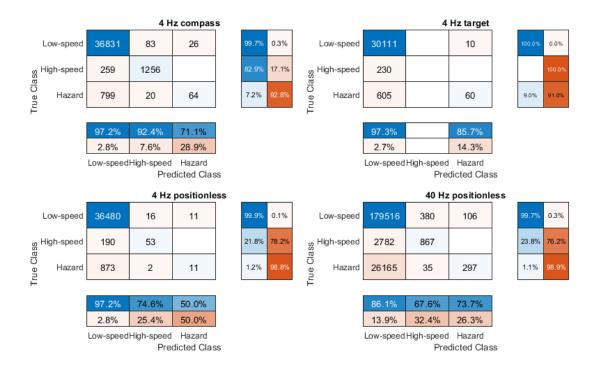


Figure 25: Low-speed cruise, direct prediction with standard sampling confusion matrices

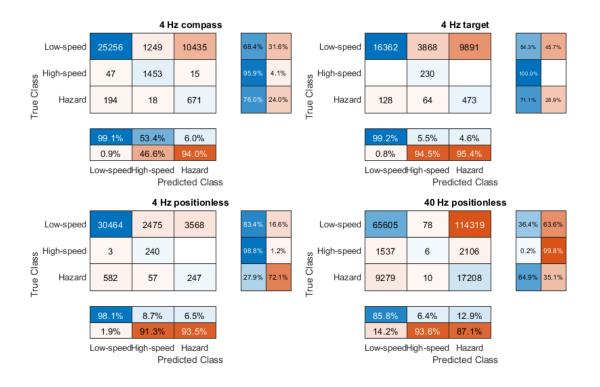


Figure 26: Low-speed cruise, direct prediction with random sampling confusion matrices

40 Hz random data shows the largest amount of misclassifications of the stable path as the hazard path, suggesting that this high frequency shows the most similarity between the two paths.

Classification of Paths out of High-Speed Cruise

Similar trends to those seen in the paths out of low-speed cruise are visible in high-speed cruise. Standard sampling shows biasing towards the stable path, has a higher PPV, and lower TPR as shown in Figure 27 and Figure 28. Note that paths from high-speed to hazard and low-speed are not being confused in the same way that paths to hazard and low-speed were when they originate in low-speed. This suggests that these paths look more different than they did in low-speed, but the relative infrequency of paths to hazard from high-speed mask behavior.

Additionally, note that the total number of paths to hazard is smaller in the 40 Hz model than in all others. If this were a true path, this value would likely be conserved, or at least remain a similar magnitude. Instead, it seems plausible that the increased sampling rate captured low-speed readings between high-speed to hazard readings in 4 Hz, suggesting that to navigate from high-speed to hazard, the aircraft quickly passes through low-speed in our trace data.

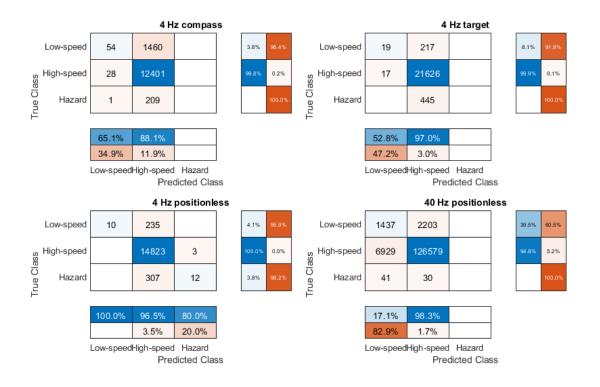


Figure 27: High-speed cruise, direct prediction with standard sampling confusion matrices

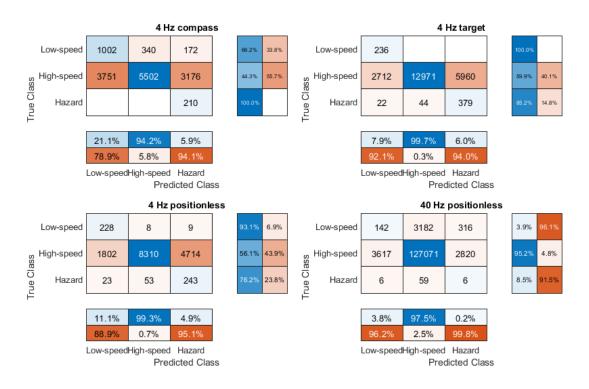


Figure 28: High-speed cruise, direct prediction with random sampling confusion matrices

Classification of Paths out of Hazard

Of the paths from the three initial states, paths out of hazard are the most consistently identifiable. In all three 4 Hz classifiers, regardless of training method, the lowest TPR and PPV is 73.6%. Figure 29 and Figure 30 once again show that paths to hazard and low-speed are often misclassified as the other, but in lower rates than in other states. Paths to low-speed are more frequently misclassified as paths to high-speed than paths to hazard are to high-speed, suggesting that paths to low-speed are more similar to high-speed than the stable path is. As in the previous case, 40 Hz sees dramatically fewer paths to high-speed than the other models, suggesting a similar path to low-speed is necessary first in all but the most specific cases. Otherwise, the 40 Hz data performs much worse than the other models however, with many more misclassifications.

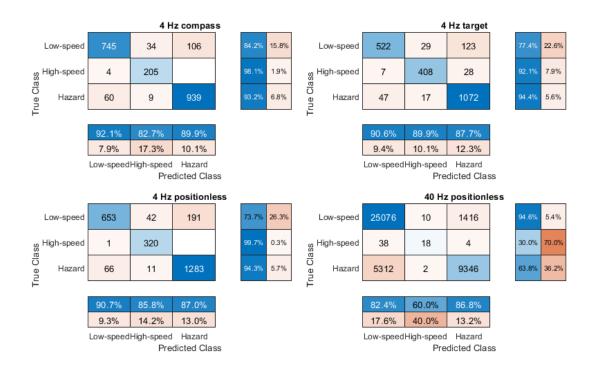


Figure 29: Hazard, direct prediction with standard sampling confusion matrices

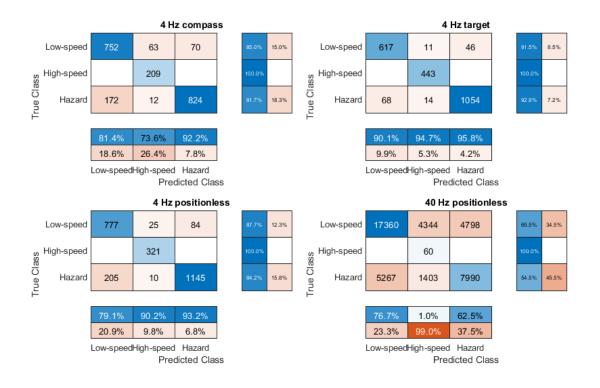


Figure 30: Hazard, direct prediction with random sampling confusion matrices

3.4.2 Path Detection with a Multi-Classifier Model

In theory, all the classifiers created in this exercise have been attempting to capture the same behavior, just defined slightly differently. This includes the descriptions of state we have generated. With this concept in mind, it seems plausible that a joint definition can be reached, where multiple classifiers can be applied at once and results compared.

To do this, we first constructed a combined state model using all three consistent 4 Hz models. Each model classified the trace as before, and classifications were weighted by their probability of being generated in their respective GMM function. This resulted in an equally biased classifier, generating as close to all three models as possible. Then, we passed each trace reading through the standard, direct path classifiers based on their combined state. We weighted these paths predictions by the confusion matrix PPV values, including the other terms in the matrix column as other weighted towards other path IDs.

This approach did not result in any improvement over other methods. Figures Figure 31– Figure 33 shows how the bias towards the stable path was consistent as in other cases, and how paths out of hazard remained the most consistently simple to identify, with the caveat that this method proved the least effective at locating these paths.

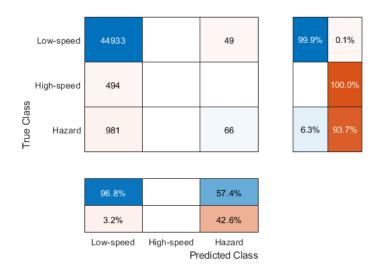


Figure 31: Merged path model for paths out of low-speed cruise

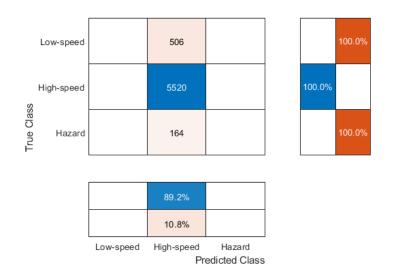


Figure 32: Merged path mdoel for paths outs of high-speed cruise

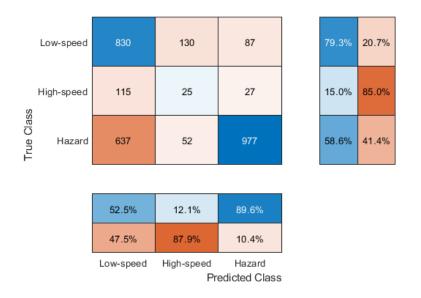


Figure 33: Merged path model for paths out of hazard

3.4.3 Path Reading Comparisons

Generally, we expect that ML classifiers will fail when each path has similar values in each parameter and control. To visualize where classifiers may see this issue, we normalize parameter and control means for path and compare them, similarly to how we compared state definitions. Paths that show similar metric means and standard deviations will be more difficult to distinguish, with more metrics sharing behavior being more difficult to distinguish.

Figure 34 shows each of these comparisons of paths out of low-speed cruise, examining each of the four consistent models found. As expected from the classifier performances in the confusion matrices, paths to high-speed cruise are consistently showing different metrics, particularly FVP, VVP, T, elevators, and throttle. Each of these metrics have a clear mean outside the standard deviations of the other paths and have a generally smaller standard deviation. The stable path and hazard path then show little differentiation at all, explaining why path to hazard is difficult to identify.

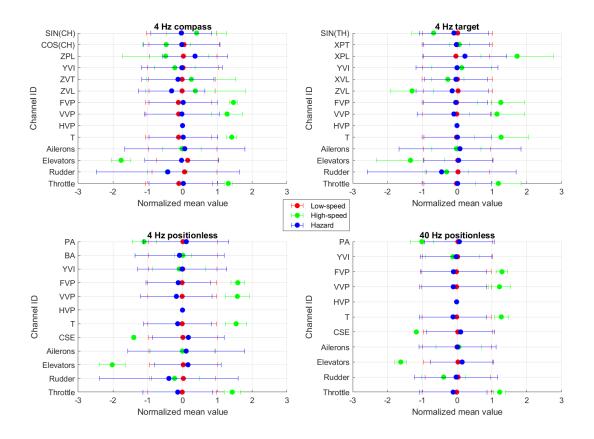


Figure 34: Normalized metrics in paths out of low-speed cruise

Paths out of high-speed cruise, shown in Figure 35, are much more difficult to distinguish based on mean and standard deviation. Mean values are generally much more tightly packed, and almost exclusively within one standard deviation of one another. Note that the wide standard deviation of 4 Hz positionless hazard decreases in 40 Hz, while low-speed increases. This suggests that paths seen as high-speed to hazard in 4 Hz are indeed high-speed to low-speed to hazard paths at higher sampling rates, confirming behavior in the confusion matrices.

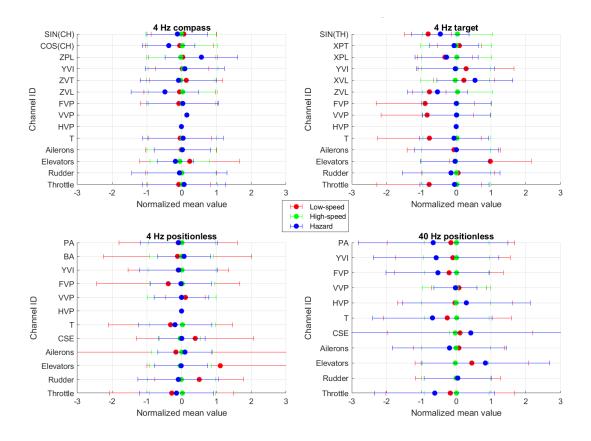


Figure 35: Normalized metrics in paths out of high-speed cruise

Interestingly, paths out of hazard much more distinct than those from low-speed. In Figure 36, we can see the same trend of high-speed paths being isolated and easily identifiable, while low-speed and stable paths are more tightly packed. However, the mean values of these two paths are slightly more distinct than those seen in low-speed, which is apparently enough to consistently distinguish paths as shown in the confusion matrices.

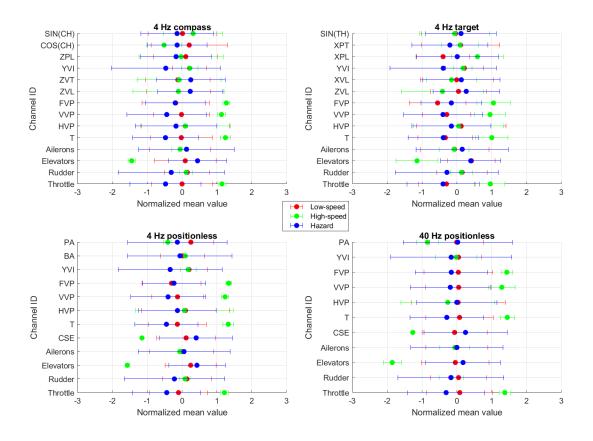


Figure 36: Normalized metrics in paths out of hazard

Overall, we can consider many of the issues visible in the confusion matrices as being direct results of system metrics behaving similarly. Under the right conditions, these paths can be distinguished, even when mean metric values are closer, but without consistency in difference, a classifier examining a single reading and direct predicting behavior will not be able to differentiate paths.

3.4.4 Path Detection with Microstate Prediction and Complex Interactions

An alternative to predicting path directly from readings is to predict the next microstate, classify the result into a state, and use the predicted state and the initial state to label the path. In this way, we could predict path without having to rely on direct classifiers, avoiding the issues with metrics appearing similar.

To predict microstate, we elected to construct linear regression models for each parameter. To ensure that the regressions were trained to predict any behavior unique to the state, we produced unique regression sets for each initial state. Thus, path labeling from readings follows the following procedure:

- 1. Normalize the readings parameters and controls against the entire trace.
- 2. Classify the normalized readings into a state.
- 3. Normalize the original readings parameters and controls against the readings with the same state in the trace.
- 4. Predict the value of each parameter in the next microstate using the linear regression models specific to the current state.
- 5. Normalize the resultant microstate parameters against the entire trace.
- 6. Classify the normalized predicted microstate into a state.
- 7. Classify the original readings with the corresponding path ID for the current and predicted subsequent state.

Once again however, this method was no more accurate at producing correct path identifications than the last. Although, the confusion matrices are different in behavior, showing faults for different paths. In Figures Figure 37–Figure 39, we can see that performance has declined relative to the previous method. Paths from hazard still appear the simplest to identify, but both TPR and PPV are affected negatively in all cases.

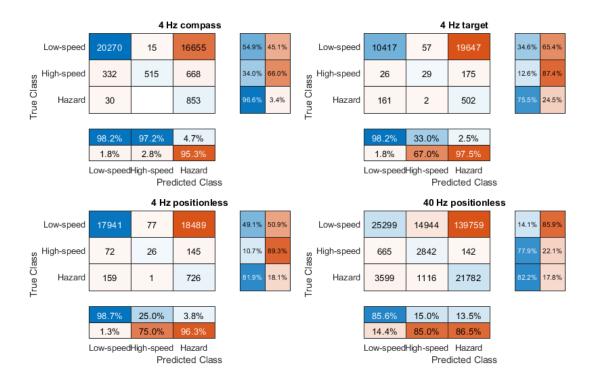


Figure 37: Low-speed cruise, microstate prediction confusion matrices

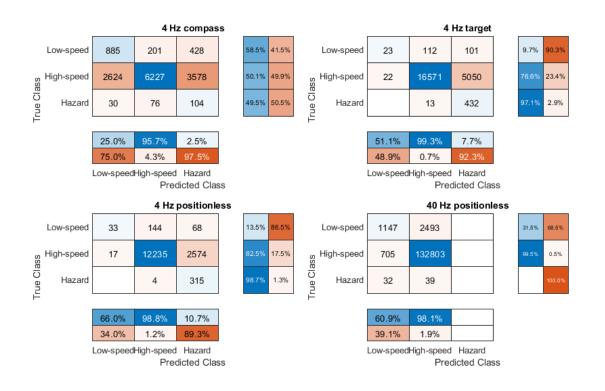


Figure 38: High-speed cruise, microstate prediction confusion matrices

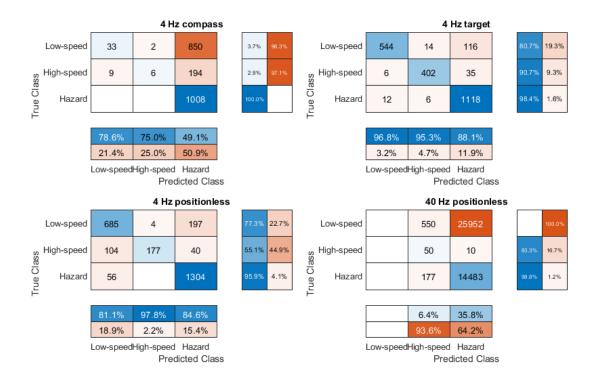


Figure 39: Hazard, microstate prediction confusion matrices

These issues are likely due to difficulties with extracting effective parameter predictors, as the metrics in the data set showed little correlation to one another. RMSE in these models could often exceed one, making many metrics poor predictors of parameters. Such behavior is likely due to unknown, or complex linkages between these metrics. Linear regressions alone appear not to be capable of predicting parameters with enough precision unless extensive tuning is done.

To then improve on this method, we could develop more sophisticated prediction tools, relying on neural networks or other ML methods to automate the process. Alternatively, a designer could manually include known physics models for different parameters, for example, calculating next position from position and velocity, but this requires knowledge of the metrics which may not always be available. It is also plausible that parameter prediction cannot be done from the microstate used to identify state alone, and other information from the complete set in the trace is necessary. However, the larger number of dimensions included in a model expand the *n*-dimensional space, making it more difficult to ensure that enough data is collected to verify behaviors (Köppen, 2000). Careful inclusion and exclusion testing would need to be performed to avoid implying false connections between metrics.

3.4.5 Inverse Time Scaling

As noted previously, it is apparent that some paths occur to quickly to be correctly labeled in the 4 Hz model and are likely more visible in 40 Hz. This suggests that detecting these paths requires high sampling rates, despite their worse performance in path identification.

High sampling rates alone increase the proportion of paths taken up by stable paths, as unstable paths then take up a smaller proportion of the total time. This first biases classifiers towards the largest represented sets in the training data, the stable path, which can be difficult to correct for as seen in the random sampled tests. It also forces state transitions to occur over a shorter period of time as path lengths decrease. This makes readings more similar by giving less time to change, which makes them more difficult to distinguish. It also expands state definitions by shortening time spent on an unstable path "between states". This makes state boundaries less distinct, and less differentiable for most applications.

Multiple potential solutions exist. First, 40 Hz behavior could potentially be integrated into 4 Hz traces by adjusting metric smoothing windows, preventing metric values from being over smoothed by wide windows. Alternatively, the window could be applied non-uniformly to emphasize current value or deemphasize future values to draw a harsher line between one reading and the next. Another option would be to include the standard deviation of measurements in the smoothing window as new metrics. This could take into account how variable the true reading is at any given point in the trace but would double the number of metrics in the trace, causing performance and dimensionality issues as previously discussed.

Another method for distinguishing behavior would be to compare where different classifiers succeed at making predictions, and selectively applying classifiers only when they have a higher degree of accuracy. This transition between classifiers could also consider the standard deviations of metrics in the smoothing window as a method of measuring imminent variability. Overall, this would be difficult to implement without bias as seen in the multi-classifier model attempted here but could be effective.

An extreme option would be to modify the trace to allow for multi-frequency sampling, but this seems to be the most complex to implement correctly.

4. DISCUSSION AND CONCLUSION

Overall, this document demonstrates that a basic approach for constructing state machines from a trace can be extrapolated across multiple systems and capture their respective behaviors with some success. For systems with simple system factors, entirely autonomous methods can construct basic state machines from a trace, but some work is still needed to expand on the method.

The basic methodology functions adequately for constructing complex factor state machines. With it, we can find state definitions which appear consistently in the trace, but we cannot determine how users can alter state enough to construct useful path definitions.

4.1 Conclusions on the Use of System Factors

System factors remain a useful tool for separating and understanding system behaviors, if only qualitatively. Each factor of continuity, parallelism, temporality, and boundedness has strong implications on what needs to be done to decompose the system trace into a state machine. In general, we can expect that systems with more continuity, parallelism, and temporality will be more difficult to study, and those with less boundedness to be less so.

Continuity implies a lack of distinction between system conditions, and therefore system states. Parallelism increases the total number of ways the system can be interacted with, and obscures operations. Temporality behaves similarly to continuity, by blending obscuring state definitions in continuous time. Boundedness decreases the number of unknown characteristics that need to be defined and checked in the process.

These definitions provide a basis for beginning to model a system and force the analyst to consider system behavior before recording a trace.

4.2 Conclusions on the Use of Logical Tools for Simple Systems

Logical tools operate well on simple factor systems but can result in state machines that make no implications beyond replicating exact behavior in the trace. The exception to this is the state machine constructed in reverse order, which, because of its looser path combination rules, can introduce recursion into the model. However, it can also result in paths that are not traversable in all cases, making it less effective as a tool for analysis.

4.3 Conclusions on the Use of Machine Learning for Complex Systems

Complex factors result in many additional complexities in the analysis procedure. Using statistical tools, we were able to isolate state definitions that were consistent in several different parameter schemes and sampling rates and matched up with perceived real-world behavior, as well as known anomalous behaviors. Overall, these states are helpful for demonstrating that we can extract trends in trace data, but the states themselves are not particularly sophisticated. Given the curse of dimensionality, it seems plausible that the only method for developing more informative states with this technique is to reduce the total number of parameters used in the state generation process. In doing so, an analyst could iterate through many parameters sets and tune many separate classifiers, comparing results between them to find classifications consistent despite extremely different parameters provided.

Path description is even less developed, as some paths were unable to be defined by the classification methods attempted. Direct path classification attempts failed to identify meaningful distinguishing behaviors in parameters and controls due to the similarity of these values between paths. More sophisticated supervised ML tools may be able to distinguish paths, but given the metric similarities, it seems unlikely that such tools will be more effective. Alternatively, microstate prediction could be improved using more advanced prediction techniques given the wealth of ML tools available. This approach seems the most plausible area for improvement.

4.4 Closing Thoughts

Overall, the methods examined in this document for constructing a state machine from a trace proved to be sufficient for generating simple state definitions in multiple systems with dramatically different qualities, but more work is needed to expand on these methods.

APPENDIX A. CHAPTER 2 SCRIPTS

Setup

To construct system state machines for the simple test case, first compile each of the scripts in this appendix into separate files, named exactly as their heading.

CoffeeMiner.mat

Next, run CoffeeMiner.mat with all of the other scripts in this appendix in the same folder. This will extract trends in the matrix stored in CoffeeMachine_03.dat. The user should define string and integer labels for this file in CoffeeActLabels_s.dat and CoffeeActLabels i.dat respectively.

To interpret forward iteration results, open the paths_pre variable, which stores a path in the state machine in each index. Each path is stored as a sequence of integers, led by the initial state ID and concluded by the final state ID. For example, [1;4;30] corresponds to a path starting in state 1, accepting input 4, and ending in state 30. Intermediate values indicate user inputs provided during the state transition, with each integer corresponding to the input of the same index in the labeling file. Similar formatting for reverse iteration results can be found in paths_pos. Note that inputs and states use the same labeling set, so the first new states beyond "Start", "Data Fault", and "End", will index to values greater than the number of inputs plus three.

This script also includes some additional functionalities not used in the final research, tracking the frequency of use of different paths, only tracking instances of use that include specific inputs, and so on. To track frequency of use, set toggle_ana to one. Variables concen_state_pre and concen_path_pre provide the percentage of use instances that included said state or path in forward iteration respectively. Variables probs_state_pre and probs_path_pre contain the respective probability of navigating to a given state or path respectively given an initial state. Rows in the cell array correspond to initial state and contain a two-column matrix. The first column of this matrix includes the corresponding end state. These

variables also have corresponding variables storing the reverse iteration information but utilize the _pos suffix instead of the _pre.

To force the entire model to include a given input, set targ_node_AID to have a value corresponding to the mandatory input ID.

```
%% Coffee Model Miner Version 19
% Constructs path-based model of coffee machine operation based on trace
% data collected from video.
% Requires:
% - CoffeeMachine 03.dat
        - CoffeeActLabels s.dat
00
       - CoffeeActLabels i.dat
00
8
       - globalPathPre
00
       - globalPathPos

loca...
terminalSeek
stateIterator
stateEnforce
stateJoin (09
``teSubset

00
00
         - terminalSeek (02)
90
00
00
       - stateJoin (09)
8
% - pathAnalyze (02)
% Changes from 18:
% - Utilizes split stateJoin/stateSubset
00
        - Removes validate
clc
clear
%% Input target data
toggle_plot_pre = 1; % Plot previous path
toggle_plot_pos = 1; % Plot following path
toggle_txt_labels = 1; % Use text labels in plots
toggle_mand = 0; % Utilize mandatory action plotting
toggle_ana = 1; % Collect concentration, timing, and
toggle ana = 1;
                                % Collect concentration, timing, and probability
data
                               % Designate mandatory action in path
targ node AID = 0;
%% Instance Data
threshold = 0;
                                                                % Threshold for data
exclusion
data master = load('CoffeeMachine 03.dat');
                                                               % Data set
                                                               % Action ID for Start
start AID = 1;
action
dataF AID = 2;
                                                                % Action ID for Data
Failure action
end AID = 3;
                                                                % Action ID for End
action
act num master = max(data master(:, 2));
                                                               % Number of individual
actions
if toggle txt labels
                                                                % Action Labels
     labelFID = fopen('CoffeeActLabels s.dat');
```

```
stateLabel = 'State';
else
    labelFID = fopen('CoffeeActLabels i.dat');
    stateLabel = 'S';
end
labels = textscan(labelFID, '%s', 'Delimiter', '\n');
labels master = labels{1};
fclose(labelFID);
fprintf('Begin analysis:\n');
%% Iterate from sample start
fprintf(' Forward iteration commencing...\n');
% Iterate
data pre = stateIterator(start AID, targ node AID, dataF AID, end AID,
data master, act num master, threshold, 1);
% Join and subset states
[data pre, paths pre] = stateEnforce(start AID, dataF AID, end AID, data pre,
act num master, 1);
act_num_pre = max(data_pre(:, 2));
% Calculate state paths
state paths store = [];
for path1 ID = 1:length(paths pre)
   path1 = paths pre{path1 ID};
    state strt = path1(1);
    state_end = path1(end);
    % Append state path to set
    if isempty(state paths store)
        state_paths_store = [state_strt, state end];
        path map store = [path1 ID, 1];
    else
        path2 ID = 1;
        while path2 ID <= size(state paths store, 1)</pre>
            path2 = state paths store(path2 ID, :);
            if isequal([state strt, state end], path2)
                break
            end
            path2 ID = path2 ID + 1;
        end
        if path2 ID > size(state paths store, 1)
            state paths store = [state paths store; state strt, state end];
        end
        path map store = [path map store; path1 ID, path2 ID];
    end
end
state paths pre = sortrows(state paths store);
path map pre = path map store;
for path1 ID = 1:size(state paths pre, 1)
   path1 = state paths pre(path1 ID, :);
   path2 ID = 1;
```

```
while path2 ID <= size(state paths store, 1)</pre>
        path2 = state paths store(path2 ID, :);
        if isequal(path1, path2)
            break
        end
        path2 ID = path2 ID + 1;
    end
    for path3 ID = 1:size(path map store)
        if path map store(path3 ID, 2) == path2 ID
            path map pre(path3 ID, 2) = path1 ID;
        end
    end
end
fprintf('
            Forward iteration complete\n');
% Update labels
act num = act num pre;
for state1 = 1:(act num - act num master)
    NLabel = stateLabel;
    NLabel = strcat(NLabel, num2str(state1));
    labels master = [labels master{:}, {NLabel}]';
end
%% Visualize Pre Iteration
if toggle plot pre
    %% Reset data
    % Instance storage
    strt node AID = start AID;
    end node AID = end AID;
    strt seq IDs = [];
                                                       % Sequence ID for start
nodes
                                                       % Sequence ID for end
    end seq IDs = [];
nodes
    act cnt = zeros(act num, 1);
    % Remove actions
    data store = data pre;
    seq1_ID = 1;
    while seq1 ID <= size(data pre, 1)</pre>
        if ismember(data pre(seq1 ID, 2), [dataF AID, (end AID +
1):act num master])
            data pre(seq1 ID, :) = [];
        else
            seq1 ID =seq1 ID + 1;
        end
    end
    % Scan for sample terminals
    [strt seq IDs, end seq IDs, act cnt] = terminalSeek(data pre,
strt node AID, targ node AID, end node AID, end AID, act num);
    % Determine actions with low measurable behavior
```

```
skip AIDs = [];
    for act1 = (act num master + 1):act num
        if (act cnt(act1) <= threshold) && not(ismember(act1, skip AIDs)) &&
not(act1 == dataF AID)
            skip AIDs = [skip AIDs, act1];
        end
    end
    skip AIDs = sort(skip AIDs);
    % Add states to labels
    labels = \{\};
    for act1 = 1:act_num_pre
        if not(ismember(act1, [skip AIDs, dataF AID, (end AID +
1):act num master]))
            labels = [labels(:)', labels master(act1)];
        end
    end
    labels = labels';
    figure(1)
    if toggle mand
        title1 = 'Mandatory Previous States';
        % Set edges
        act path pre = globalPathPre(data pre, act num, strt seq IDs,
end_seq_IDs, dataF_AID, skip AIDs);
        act mand pre = act path pre(:, 2);
        % Mandatory previous action model
        disp path1 = []; % Construct edges
        for act1 = 1:act num pre
            for act2 = act mand pre{act1}
                disp path1 = [disp path1; act1, act2];
            end
        end
    else
        title1 = 'State Diagram as Determined by Forward Iteration';
        % Set edges
        disp path1 = [];
        for seq1 ID = 1:(size(data pre, 1) - 1)
            state1 = data_pre(seq1_ID, 2);
            if not(state1 == end AID)
                state2 = data pre((seq1 ID + 1), 2);
                if isempty(disp path1)
                     disp path1 = [state1, state2];
                else
                    match = 0;
                    edge ID = 1;
                    while (edge ID <= size(disp path1, 1)) && not(match)</pre>
                        if isequal(disp path1(edge ID, :), [state1, state2])
                            match = 1;
                        end
                        edge ID = edge ID + 1;
                    end
                    if not(match)
                        disp path1 = [disp path1; state1, state2];
                    end
```

```
end
            end
        end
        disp path1 = sortrows(disp path1);
    end
    diagram1 = digraph(disp path1(:, 1), disp path1(:, 2));
    diagram1 = rmnode(diagram1, [skip AIDs, dataF AID, (end AID +
1):act num master]);
   NLabels = labels;
    plot(diagram1, 'Layout', 'layered', 'NodeLabel', NLabels);
   title(title1);
    % Reset
    data pre = data store;
end
%% Iterate from sample end
          Reverse iteration commencing...\n');
fprintf('
% Iterate
data pos = stateIterator(start AID, targ node AID, dataF AID, end AID,
data master, act num master, threshold, -1);
% Join and subset states
[data pos, paths pos] = stateEnforce(start AID, dataF AID, end AID, data pos,
act num master, -1);
act_num_pos = max(data_pos(:, 2));
% Calculate state paths
state paths store = [];
for path1 ID = 1:length(paths pos)
    path1 = paths pos{path1 ID};
    state strt = path1(1);
    state end = path1 (end);
    % Append state path to set
    if isempty(state paths store)
        state paths store = [state strt, state end];
        path map store = [path1 ID, 1];
    else
        path2 ID = 1;
        while path2 ID <= size(state_paths_store, 1)</pre>
            path2 = state paths store(path2 ID, :);
            if isequal([state strt, state end], path2)
                break
            end
            path2_ID = path2_ID + 1;
        end
        if path2 ID > size(state paths store, 1)
            state paths store = [state paths store; state strt, state end];
        end
        path map store = [path map store; path1 ID, path2 ID];
    end
end
```

```
state paths pos = sortrows(state paths store);
path map pos = path map store;
for path1 ID = 1:size(state paths pos, 1)
    path1 = state paths pos(path1 ID, :);
    path2 ID = 1;
    while path2 ID <= size(state paths store, 1)</pre>
        path2 = state paths store(path2 ID, :);
        if isequal(path1, path2)
           break
        end
        path2 ID = path2 ID + 1;
    end
    for path3 ID = 1:size(path map store)
        if path map store (path\overline{3} ID, 2) == path2 ID
            path map pos(path3 ID, 2) = path1 ID;
        end
    end
end
          Reverse iteration complete\n');
fprintf('
% Correct State IDs
act num = act num pos + act num pre - act num master;
for seq1 ID = find(data pos(:, 2) > act num master)'
    data pos(seq1 ID, 2) = data pos(seq1 ID, 2) - act num master +
act num pre;
end
for path ID = 1:size(paths pos, 1)
    path = paths_pos{path ID};
    if not(path(1) == start AID)
        path(1) = path(1) - act num master + act num pre;
    end
    if not(path(end) == end AID)
        path(end) = path(end) - act_num_master + act_num_pre;
    end
    paths pos{path ID} = path;
end
% Update labels
for state1 = 1:(act num pos - act num master)
    NLabel = stateLabel;
    NLabel = strcat(NLabel, num2str(state1 + act num pre - act num master));
    labels master = [labels master{:}, {NLabel}]';
end
%% Visualize Post Iteration
if toggle plot pos
    %% Reset data
    % Instance storage
    strt node AID = start AID;
```

```
end node AID = end AID;
```

```
strt seq IDs = [];
                                                      % Sequence ID for start
nodes
    end seq IDs = [];
                                                      % Sequence ID for end
nodes
    act cnt = zeros(act num, 1);
    % Remove actions
    data store = data pos;
    seq1 ID = 1;
    while seq1 ID <= size(data pos, 1)</pre>
        if ismember(data_pos(seq1_ID, 2), [dataF_AID, (end AID +
1):act num master])
           data pos(seq1 ID, :) = [];
        else
            seq1 ID =seq1 ID + 1;
        end
    end
    % Scan for sample terminals
    [strt seq IDs, end seq IDs, act cnt] = terminalSeek(data pos,
strt node AID, targ node AID, end node AID, end AID, act num);
    % Determine actions with low measurable behavior
    skip AIDs = [];
    for act1 = (act num master + 1):act num
        if (act cnt(act1) <= threshold) && not(ismember(act1, skip AIDs)) &&
not(act1 == dataF AID)
            skip AIDs = [skip AIDs, act1];
        end
    end
    skip AIDs = sort(skip AIDs);
    % Add states to labels
    labels = {};
    for act1 = 1:act num
        if not(ismember(act1, [skip_AIDs, dataF_AID, (end_AID +
1):act num pre]))
            labels = [labels(:)', labels master(act1)];
        end
    end
    labels = labels';
    figure(2)
    if toggle mand
        title2 = 'Mandatory Post States';
        % Set edges
        act_path_pos = globalPathPos(data_pos, act_num, strt_seq_IDs,
end_seq_IDs, dataF_AID, skip_AIDs);
        act mand pos = act path pos(:, 2);
        % Mandatory post action model
        disp path2 = []; % Construct edges
        for act1 = 1:act num
            for act2 = act mand pos{act1}
                disp path2 = [disp path2; act1, act2];
            end
```

```
end
    else
        title2 = 'State Diagram as Determined by Reverse Iteration';
        % Set edges
        disp path2 = [];
        for seq1 ID = 1: (size(data pos, 1) - 1)
            state1 = data pos(seq1 ID, 2);
            if not(state1 == end AID)
                state2 = data pos((seq1 ID + 1), 2);
                if not(isequal([state1, state2], [start_AID, end_AID]))
                    if isempty(disp path2)
                        disp path2 = [state1, state2];
                    else
                        match = 0;
                        edge ID = 1;
                        while (edge ID <= size(disp path2, 1)) && not(match)</pre>
                             if isequal(disp path2(edge ID, :), [state1,
state2])
                                match = 1;
                             end
                             edge ID = edge ID + 1;
                        end
                        if not(match)
                             disp_path2 = [disp_path2; state1, state2];
                        end
                    end
                end
            end
        end
        disp path2 = sortrows(disp path2);
    end
    diagram2 = digraph(disp path2(:, 1), disp path2(:, 2));
    diagram2 = rmnode(diagram2, [skip AIDs, dataF AID, (end AID +
1):act num pre]);
    NLabels = labels;
    plot(diagram2, 'Layout', 'layered', 'NodeLabel', NLabels);
    title(title2);
    % Reset
    data pos = data store;
end
if toggle ana
    %% Analyze path user behavior
    for direction = [-1, 1]
        switch direction
            case -1
                paths dir = paths pos;
                data dir = data pos;
                state list = [start AID, end AID, (act num pre +
1):act num pos];
                path map dir = path map pos;
            case 1
                paths dir = paths pre;
                data dir = data pre;
```

```
state list = [start AID, end AID, (act num master +
1):act num pre];
                path map dir = path map pre;
        end
        % Analyze data
        [concen_p_dir, time_p_dir, prob_p_dir, concen_s_dir, time_s_dir,
prob s dir] = pathAnalyze(data dir, paths dir, path map dir, start AID,
dataF AID, end AID, act num master);
        switch direction
            case -1
                concen paths pos = concen p dir;
                time paths pos = time p dir;
                prob paths pos = prob p dir;
                concen state pos = concen s dir;
                time state pos = time s dir;
                prob state_pos = prob_s_dir;
            case 1
                concen paths pre = concen p dir;
                time paths pre = time p dir;
                prob paths pre = prob p dir;
                concen state pre = concen s dir;
                time state pre = time s dir;
                prob state pre = prob s dir;
        end
    end
    fprintf('
                User data collection complete\n');
end
fprintf('Analysis complete\n');
```

collectPaths.mat

This function collects a list of all the path seen in the data set, outputting a cell array containing all the paths as described in the CoffeeMiner.mat section.

```
function paths = collectPaths(dataF_AID, end_AID, act_num_master, data)
%% collectPaths 01
% Collects list of paths in data set
%% Prep storage
paths = {};
%% Iterate through data
seq1_ID = 1;
while seq1_ID < size(data, 1)
    state1 = data(seq1_ID, 2);
    if state1 == end_AID
        seq1_ID = seq1_ID + 1;
    end
    % Find end of path</pre>
```

```
seq2 ID = seq1 ID + 1;
    state2 = 0;
    while not(state2) && (seq2_ID <= size(data, 1))</pre>
        state2 = data(seq2 ID, 2);
        if not(state2 == end AID) && not(state2 > act num master)
            state2 = 0;
            seq2 ID = seq2 ID + 1;
        end
    end
   path = data(seq1 ID:seq2 ID, 2);
    if not(ismember(dataF AID, path))
        % Store path
        if isempty(paths)
            paths = \{path\};
        else
            % Check inclusion in paths
            match = 0;
            path1 ID = 1;
            while not(match) && (path1 ID <= length(paths))</pre>
                path1 = paths{path1_ID};
                if isequal(path, path1)
                    match = 1;
                else
                    path1 ID = path1 ID + 1;
                end
            end
            if not(match)
                paths = sortPaths([paths; {path}]);
            end
        end
    end
   seq1 ID = seq2 ID;
end
```

```
end
```

globalPathPre.mat

This script collects the inputs and states that are mandatory for other inputs. The output, act_mand_pre, is a cell array with each row index corresponding to an input ID. The first column includes a list of inputs and states that occur prior to the row ID input in every use instance, and the second indicates those that always occur after the row ID input.

```
function act_mand_pre = globalPathPre(data, act_num, smpl_strt_IDs,
smpl_end_IDs, dataF_AID, skip_AIDs)
    %% Analyze global mandatory path
    % Outputs complete paths as well as reduced paths
    % Instance storage
```

```
act cnt = zeros(act num, 1);
    path glob pre = zeros(act num) + 1; % Switches for mandatory
inclusion in previous path
    absent = zeros(act num, 1);
    % Scan path
    for smpl ID = 1:length(smpl strt IDs)
        start ID = smpl strt IDs(smpl ID);
        end ID = smpl end IDs(smpl ID);
        smpl = data(start ID:end ID, :);
        for act1 = 1:act num
            if not(ismember(act1, smpl))% Mark if not present
                absent(act1) = absent(act1) + 1;
            end
        end
        for act1 ID = 1:size(smpl, 1)
            act1 = smpl(act1 ID, 2);
            if (act1 == dataF AID) || ismember(act1, skip AIDs)
                continue
            end
            path prev = smpl(1:(act1 ID - 1), 2);
            if not(ismember(dataF AID, path prev))
                for act2 = 1:act num
                    if not(ismember(act2, path prev)) || ismember(act2,
skip AIDs)
                        path glob pre(act1, act2) = 0;
                    end
                end
            end
        end
    end
    for act1 = 1:act num % Convert absent to boolean
        if absent(act1) == length(smpl strt IDs)
             absent(act1) = 1;
        else
            absent(act1) = 0;
        end
    end
    %% Collect mandatory actions
    % Instance storage
    act mand pre = \{\};
    % Begin iteration
    for act1 = 1:act num
        act_mand_pre = [act_mand_pre(:)', {[]}];
        if not(absent(act1))
            for act2 = 1:act num
                if path glob pre(act1, act2) == 1
                    act mand pre{act1} = [act mand pre{act1}, act2];
                end
            end
        end
    end
```

```
act mand_pre = act_mand_pre';
    %% Reduce Routes
    % Prep cells
    act pre = cell(act num, 2);
    for act1 = 1:act num
        act pre{act1, 1} = act mand pre{act1};
    end
    act mand pre = act pre;
    % Reduce mandatory actions (Previous)
    for act1 = 1:act num % Collect actions which act1 is a component of
        state1 pre = [act mand pre{act1}, act1];
        for act2 = 1:act num
            state2_pre = [act_mand_pre{act2}, act2];
            if all(ismember(state1 pre, state2 pre)) && not(act2 == act1)
                act mand pre{act1, 2} = [act mand pre{act1, 2}, act2];
            end
        end
    end
    for act1 = 1:act num % Reduce component actions to direct routes
        comp1 = act mand pre{act1, 2};
        remove = zeros(1, length(comp1));
        for act2 ID = 1:length(comp1) % Seek through component actions
            act2 = comp1(act2 ID);
            comp2 = act mand pre{act2, 2};
            act2 ID store = act2 ID;
            for act3 = comp2 % Seek through component actions component
actions
                for act2 ID = 1:length(comp1) % Seek matching component
actions
                    act2 = comp1(act2 ID);
                    if act3 == act2
                        remove(act2 ID) = 1;
                    end
                end
            end
            act2 ID = act2 ID store;
            act2 = compl(act2 ID);
        end
        comp1 store = comp1;
        comp1 = []; % Remove redudant actions
        for act2 ID = 1:length(remove)
            if not(remove(act2 ID))
               comp1 = [comp1, comp1 store(act2 ID)];
            end
        end
        act mand pre{act1, 3} = comp1;
    end
    act mand pre = act mand pre(:, [1, 3]);
```

globalPathPos.mat

This script functions identically to globalPathPre.mat but operates on data sets in reverse iteration.

```
function act mand pos = globalPathPos(data, act num, smpl strt IDs,
smpl end IDs, dataF AID, skip AIDs)
    %% globalPathPos 01
          Combines paths at sample end
    2
    act cnt = zeros(act num, 1);
    path glob pos = zeros(act num) + 1;
                                         % Switches for mandatory
inclusion in following path
    absent = zeros(act_num, 1);
    % Scan path
    for smpl ID = 1:length(smpl strt IDs)
        start ID = smpl strt IDs(smpl ID);
        end ID = smpl end IDs(smpl ID);
        smpl = data(start ID:end ID, :);
        for act1 = 1:act num
            if not(ismember(act1, smpl))% Mark if not present
                absent(act1) = absent(act1) + 1;
            end
        end
        for act1 ID = 1:size(smpl, 1)
            act1 = smpl(act1 ID, 2);
            if (act1 == dataF_AID) || ismember(act1, skip_AIDs)
                continue
            end
            path_pos = smpl((act1_ID + 1):size(smpl, 1), 2);
            if not(ismember(dataF AID, path pos))
                for act2 = 1:act num
                    if not(ismember(act2, path pos)) || ismember(act2,
skip AIDs)
                        path glob pos(act1, act2) = 0;
                    end
                end
            end
        end
    end
    for act1 = 1:act num % Convert absent to boolean
        if absent(act1) == length(smpl strt IDs)
             absent(act1) = 1;
        else
```

end

```
absent(act1) = 0;
        end
    end
    %% Collect mandatory actions
    % Instance storage
    act mand pos = \{\};
    % Begin iteration
    for act1 = 1:act num
        act mand pos = [act mand pos(:)', {[]}];
        if not(absent(act1))
            for act2 = 1:act num
                if path glob pos(act1,act2) == 1
                    act mand pos{act1} = [act mand pos{act1}, act2];
                end
            end
        end
    end
    act mand pos = act mand pos';
    %% Reduce Routes
    % Prep cells
    act pos = cell(act num, 2);
    for act1 = 1:act num
        act pos{act1, 1} = act mand pos{act1};
    end
    act mand pos = act pos;
    % Reduce mandatory actions (Post)
    for act1 = 1:act num % Collect actions which act1 is a component of
        state1 pos = [act mand pos{act1}, act1];
        for act2 = 1:act num
            state2 pos = [act mand pos{act2}, act2];
            if all(ismember(state1 pos, state2 pos)) && not(act2 == act1)
                act mand pos{act1, 2} = [act mand pos{act1, 2}, act2];
            end
        end
    end
    for act1 = 1:act num % Reduce component actions to direct routes
        comp1 = act mand pos{act1, 2};
        remove = zeros(1, length(comp1));
        for act2 ID = 1:length(comp1) % Seek through component actions
            act2 = compl(act2 ID);
            comp2 = act mand pos{act2, 2};
            act2 ID store = act2 ID;
            for act3 = comp2 % Seek through component actions component
actions
                for act2 ID = 1:length(comp1) % Seek matching component
actions
                    act2 = compl(act2 ID);
                    if act3 == act2
```

```
remove(act2 ID) = 1;
                    end
                end
            end
            act2 ID = act2 ID store;
            act2 = compl(act2 ID);
        end
        comp1 store = comp1;
        comp1 = []; % Remove redudant actions
        for act2 ID = 1:length(remove)
            if not(remove(act2 ID))
               comp1 = [comp1, comp1 store(act2 ID)];
            end
        end
        act mand pos{act1, 3} = comp1;
    end
    act mand pos = act mand pos(:, [1, 3]);
end
```

localPath.mat

This function produces simple Markov chain analysis of the trace behavior. Variable path_T1_pos stores the probabilities of an input being made given the previous input. This information is stored in a matrix, with each potential sequence of inputs stored in a separate row, such that the first index in the row stores the probability, the second index stores the second input, and the third index stores the initial input.

Variable path_T2_pos stores information similarly, only calculating probabilities given two known inputs instead of one. Each row of the matrix is the probability, final input, initial input, and second input.

```
function [path_T1_pos, path_T2_pos] = localPath(data, strt_seq_IDs,
end_seq_IDs, dataF_AID, skip_AIDs)
    %% Analyze Local Path
    % Iterates through local path in specified sample data
    % Instance storage
    path_T1_pos = []; % Probability (3) of action (2) following given
actions (1)
    path_T2_pos = []; % Probability (4) of action (3) following given
actions (1-2)
    %% Scan path
    % Iterate through samples
    for smpl_ID = 1:length(strt_seq_IDs)
        strt_seq_ID = strt_seq_IDs(smpl_ID);
        end_seq_ID = end_seq_IDs(smpl_ID);
```

```
for seq ID = strt seq ID:end seq ID
            act1 = data(seq ID, 2);
            if (seq ID == end seq ID) || (act1 == dataF AID) ||
ismember(act1, skip AIDs)
                continue
            elseif seq ID == (end seq ID - 1)
                act2 = data((seq ID + 1), 2);
                if (act2 == dataF AID) || ismember(act2, skip AIDs)
                    act2 = 0;
                end
                act3 = 0;
            else
                act2 = data(seq ID + 1, 2);
                if (act2 == dataF AID) || ismember(act2, skip AIDs)
                    act2 = 0;
                end
                act3 = data(seq ID + 2, 2);
                if (act3 == dataF AID) || ismember(act3, skip AIDs)
                    act3 = 0;
                end
            end
            % Append to first order path
            if act2
                if not(isempty(path T1 pos))
                    match = 0;
                    for check index = 1:size(path T1 pos, 1)
                        path = path_T1_pos(check_index, :);
                        if (path(1) == act1) && (path(2) == act2)
                            path T1 pos(check index, 3) =
path T1 pos(check index, 3) + 1;
                            match = 1;
                            break
                        end
                    end
                    if not(match)
                        path T1 pos = [path T1 pos; [act1, act2, 1]];
                    end
                else
                    path T1 pos = [act1, act2, 1];
                end
            end
            % Append to second order path
            if act3
                if not(isempty(path T2 pos))
                    match = 0;
                    for check index = 1:size(path T2 pos, 1)
                        path = path_T2_pos(check_index, :);
                        if (path(1) == act1) && (path(2) == act2) && (path(3)
== act3)
                            path T2 pos(check index, 4) =
path T2 pos(check index, 4) + 1;
                            match = 1;
                            break
                        end
```

```
end
                    if not(match)
                         path T2 pos = [path T2 pos; [act1, act2, act3, 1]];
                    end
                else
                    path T2 pos = [act1, act2, act3, 1];
                end
            end
        end
    end
    %% Sort and convert to probability
    path T1 pos = sortrows(path T1 pos);
    path T2 pos = sortrows(path T2 pos);
    path ID = 1;
    while path ID <= size(path T1 pos, 1)</pre>
        path = path_T1_pos(path_ID, :);
        sum = 0;
        match path ID = path ID;
        match path = path T1 pos(match_path_ID, :);
        while path(1) == match path(1)
            sum = sum + match path(3);
            match path ID = match path ID + 1;
            if match path ID > size(path T1 pos, 1)
                break
            end
            match_path = path_T1_pos(match_path_ID, :);
        end
        path T1 pos(path ID:(match path ID - 1), 3) =
path_T1_pos(path_ID:(match_path_ID - 1), 3) / sum;
        path_ID = match_path_ID;
    end
    path ID = 1;
    while path ID <= size(path T2 pos, 1)</pre>
        path = path T2 pos(path ID, :);
        sum = 0;
        match path ID = path ID;
        match_path = path_T2_pos(match_path_ID, :);
        while path(1:2) == match path(1:2)
            sum = sum + match path(4);
            match path ID = match path ID + 1;
            if match path ID > size(path T2 pos, 1)
                break
            end
            match path = path T2 pos(match path ID, :);
        end
        path_T2_pos(path_ID:(match_path_ID - 1), 4) =
path T2 pos(path ID: (match path ID - 1), 4) / sum;
        path ID = match path ID;
    end
end
```

stateSubset.mat

This function reads the trace, determines if paths subset each other, modifies path definitions to remove subsetting, and then outputs a trace with the updated state palcements.

```
function data = stateSubset(start AID, dataF AID, end AID, data, paths,
act num master, direction)
    %% stateSubset 01
    % Detects when paths between states overlap
    %% Prep data
    % Find sample terminals
    strt smpl seq IDs = find(data(:, 2) == start AID);
    end_smpl_seq_IDs = find(data(:, 2) == end_AID);
    if direction == 1
        %% Find new paths for forward iterated states
        % Collect paths by state
        paths by state = {};
        strt states = [];
        end states = \{\};
        path1 ID = 1;
        while path1_ID <= length(paths)</pre>
            path1 = paths{path1 ID};
            strt_state1 = path1(1);
            path2 ID = path1 ID + 1;
            state match = 1;
            while state match && (path2 ID < length(paths))</pre>
                path2 = paths{path2 ID};
                strt state2 = path2(1);
                if not(strt state1 == strt state2)
                    state match = 0;
                else
                    path2 ID = path2 ID + 1;
                end
            end
            % Isolate paths
            paths out = paths(path1 ID:(path2 ID - 1));
            end states sub = [];
            for path3_ID = 1:length(paths out)
                path3 = paths out{path3 ID};
                end_state3 = path3(end);
                if not(ismember(end state3, end states sub))
                    end states sub = [end states sub; end state3];
                end
            end
            % Store paths
            strt states = [strt states; strt_state1];
            end states = [end states; {end states sub}];
            paths by state = [paths by state; {paths out}];
```

```
path1 ID = path2 ID;
        end
        % Compare paths between states
        rem_paths = {};
        for state sub ID = 1:length(strt states)
            state_sub = strt_states(state_sub_ID);
            end states sub = end states{state sub ID};
            paths sub = paths by state{state sub ID};
            for state sup ID = 1:length(strt states)
                if not(state sub ID == state sup ID) % Skip self subsetting
                    state sup = strt states(state sup ID);
                    end states sup = end states{state sup ID};
                    paths_sup = paths_by_state{state_sup_ID};
                    if all(ismember(end states sub, end states sup)) &&
(length (paths sup) >= length (paths sub)) % Check possibility of inclusion
                        % Collect remainder paths
                        rem paths1 = \{\};
                        rem_reach sub = {};
                        for path sub ID = 1:length(paths sub)
                            path_sub = paths_sub{path_sub_ID};
                            len sub = length(path sub);
                            for path sup ID = 1:length(paths sup)
                                path sup = paths sup{path sup ID};
                                 len sup = length(path sup);
                                 if len sup > len sub
                                     path comp = path sup((end - len sub +
2):end);
                                     if isequal(path comp, path sub(2:end))
                                         rem path1 = path sup(1:(end - len sub
+ 1));
                                         rem path ID = 1;
                                         while rem path ID <=
length(rem paths1)
                                             rem path =
rem paths1{rem path ID};
                                             if isequal(rem path, rem path1)
                                                 break
                                             end
                                             rem path ID = rem path ID + 1;
                                         end
                                         if rem path ID > length(rem paths1)
                                             rem paths1 = [rem paths1;
{rem path1}];
                                             rem reach sub = [rem reach sub;
{[]}];
                                         end
                                         rem reach sub{rem path ID} =
[rem reach sub{rem path ID}; path sub ID];
                                     end
                                 end
                            end
                        end
```

```
% Determine remainder path utility
                         rem paths1 store = rem paths1;
                         rem_paths1 = \{\};
                         for rem path1 ID = 1:length(rem paths1 store)
                             rem path1 = rem paths1 store{rem path1 ID};
                             rem reach sub1 = rem reach sub{rem path1 ID};
                             if all(ismember(1:length(paths sub),
rem reach subl)) % Check if remainder path reaches all sub paths
                                 in path sups = [];
                                 for path sup ID = 1:length(paths sup)
                                     path sup = paths sup{path sup ID};
                                     if length(path sup) > length(rem path1)
                                         if isequal(rem path1,
path sup(1:length(rem path1)))
                                              in path sups = [in path sups;
path sup ID];
                                         end
                                     end
                                 end
                                 if length(in path sups) ==
length(paths sub) % Check if remainder path does not lead to non-sub paths
                                     rem paths1 = [rem paths1; {rem path1}];
                                 end
                             end
                         end
                         % Store results
                         for rem path1_ID = 1:length(rem_paths1)
                             rem path1 = [rem paths1{rem path1 ID};
state sub];
                             rem paths = [rem paths; {rem path1}];
                         end
                     end
                end
            end
        end
        %% Merge with paths
        paths store = sortPaths([paths; rem paths]);
        paths = \{\};
        path1 ID = 1;
        while path1 ID < length(paths store)</pre>
            path1 = paths_store{path1 ID};
            state1 = path1(1);
            path2 ID = path1 ID + 1;
            while path2 ID <= length(paths store)</pre>
                path2 = paths store{path2 ID};
                state2 = path2(1);
                if not(state1 == state2)
                    break
                else
                     path2 ID = path2 ID + 1;
                end
```

```
110
```

end

```
bound1 = path1 ID;
        bound2 = path2 ID - 1;
        for path1 ID = bound1:bound2
            do not inc = 0;
            path1 = paths store{path1 ID};
            for path3 ID = bound1:bound2
                path3 = paths store{path3 ID};
                 len3 = length(path3);
                 if len3 < length(path1)</pre>
                     path comp = path1(1:(len3 - 1));
                     if isequal(path comp, path3(1:(end - 1)))
                         do not inc = 1;
                         break
                     end
                 end
            end
            if not(do not inc)
                paths = [paths; {path1}];
            end
        end
        path1 ID = path2 ID;
    end
end
% Collect paths by state
paths_by_state = {};
strt states = [];
end states = \{\};
path1 ID = 1;
while path1 ID <= length(paths)</pre>
    path1 = paths{path1 ID};
    strt state1 = path1(1);
    path2 ID = path1 ID + 1;
    state match = 1;
    while state match && (path2 ID < length(paths))</pre>
        path2 = paths{path2 ID};
        strt state2 = path2(1);
        if not(strt state1 == strt state2)
            state match = 0;
        else
            path2 ID = path2 ID + 1;
        end
    end
    % Isolate paths
    paths out = paths(path1 ID:(path2 ID - 1));
    end states out = [];
    for path3 ID = 1:length(paths out)
        path3 = paths out{path3 ID};
        end_state3 = path3(end);
        if not(ismember(end state3, end states out))
            end states out = [end states out; end state3];
```

```
end
        end
        % Store paths
        strt_states = [strt_states; strt_state1];
        end states = [end states; {end states out}];
        paths by state = [paths by state; {paths out}];
        path1 ID = path2 ID;
    end
    %% Store data
    % Iterate through samples
    data store = data;
    data = [];
    for smpl ID = 1:length(strt smpl seq IDs)
        strt smpl seq ID = strt smpl seq IDs(smpl ID);
        end smpl seq ID = end smpl seq IDs(smpl ID);
        smpl data = data store(strt smpl seq ID:end smpl seq ID, :);
        smpl = smpl data(:, 2);
        % Iterate through single sample
        path strt ID = 1;
        smpl end ID = length(smpl);
        while path strt ID < smpl end ID
            path strt AID = smpl(path strt ID);
            % Collect current path
            path_end_ID = path_strt_ID + 1;
            path_end_AID = smpl(path_end_ID);
            while not(path_end_AID == end_AID) && not(path_end_AID >
act num master)
                path end ID = path end ID + 1;
                path end AID = smpl(path end ID);
            end
            path curr = smpl(path strt ID:path end ID);
            % Collect known paths from start state
            if path strt AID == start AID
                path set = paths by state{1};
            else
                path set = paths by state{path strt AID - act num master +
1};
            end
            % Iterate through current path
            match = 0;
            seq1 ID = 1;
            while (seq1_ID < length(path_curr)) && not(match)</pre>
                path seg = path curr(1:seq1 ID);
                % Match current path segment against known paths
                path kno ID = 1;
                while (path kno ID <= length(path set)) && not(match)</pre>
                    path kno = path set{path kno ID};
```

```
if (isequal(path seg, path kno(1:(end - 1)))) &&
not(length(path kno) == length(path curr))
                        match = 1;
                    else
                        path kno ID = path kno ID + 1;
                    end
                end
                if not(match)
                    seq1 ID = seq1 ID + 1;
                end
            end
            % Update sample
            if match
                path_strt_ID = path_strt ID + seq1 ID;
                smpl data store = smpl data;
                smpl data = smpl data store(1:(path strt ID - 1), :);
                smpl data = [smpl data; smpl data(end, :)];
                smpl data(end, 2) = path kno(end);
                smpl_data = [smpl_data;
smpl_data_store(path_strt_ID:end, :)];
                smpl = smpl_data(:, 2);
                smpl end ID = length(smpl);
                capture = 1;
            else
                path strt ID = path end ID;
            end
        end
        % Store data
        if isempty(data)
            data = smpl data;
        else
            data = [data; smpl data];
        end
    end
end
```

stateEnforce.mat

This function merges preliminary states and subsets paths iteratively until paths are consistent and no further simplifications can be made to the state machine. Output data1 is the updated trace with new state definitions, and paths1 is the new path set extracted from the trace.

```
%% Iterate
              State enforcement commencing...\n');
    fprintf('
    % Prep iterators
    complete = 0;
    data1 = data master;
   paths1 = collectPaths(dataF AID, end AID, act num master, data1);
    % Begin enforcement
    while not(complete)
        [data2, paths2] = stateJoin(start AID, dataF AID, end AID, data1,
act num master, direction);
       data3 = stateSubset(start AID, dataF AID, end AID, data2, paths2,
act num master, direction);
       paths3 = collectPaths(dataF AID, end AID, act num master, data3);
        if direction == -1
           capture = 1;
        end
        if isequal(data3, data1)
            complete = 1;
        else
            data1 = data3;
            paths1 = paths3;
        end
    end
    fprintf('
                   State enforcement complete\n');
end
```

stateIterator.mat

This function examines the trace and detects states with the global and local contexts and appends detected states to the trace. This trace is then the output.

```
function data = stateIterator(start AID, targ node AID, dataF AID, end AID,
data master, act num master, threshold, direction)
    %% Prep Path Iterator
    % Detect states iteratively and add to data set
    % Changes from 01
          - Changed how states were stored to require matching paths in
    8
           - Requires that next node not be start node when creating states
    8
    % Start conditions
    act num = act num master;
    complete = [0];
    switch direction
        case 1
            end node AID = end AID;
            data = data master;
            new state AIDs = [start AID];
```

```
case -1
            end node AID = start AID;
            data = flipud(data master);
            new state AIDs = [end AID];
    end
    %% Iterate
    while not(all(complete))
          fprintf(' New States %d\n', length(new state AIDs));
00
        strt_node_list = new state AIDs;
        end node list = end node AID;
        new_state AIDs = [];
        path list = [];
        for strt node AID = strt node list
            for end node AID = end node list
                path list = [path list; strt node AID, end node AID];
            end
        end
        complete = zeros(size(path list, 1), 1);
        path ID = 1;
        while path ID <= length(complete)</pre>
            %% Initial Scan
            % Instance action IDs
            strt node AID = path list(path ID, 1);
            end node AID = path list(path ID, 2);
            state AIDs = (act num master + 1):act num;
            % Scan for sample terminals
            switch direction
                case 1
                    [strt seq IDs, end seq IDs, act cnt] = terminalSeek(data,
strt node AID, targ node AID, end node AID, end AID, act num);
                case -1
                    [strt seq IDs, end seq IDs, act cnt] = terminalSeek(data,
strt node AID, targ node AID, end node AID, start AID, act num);
            end
            % Determine actions with low measurable behavior
            skip_AIDs = [];
            for act1 = 1:act num
                if (act_cnt(act1) <= threshold) && not(ismember(act1,</pre>
skip AIDs)) && not(act1 == dataF AID)
                    skip_AIDs = [skip_AIDs, act1];
                end
            end
            skip_AIDs = sort(skip_AIDs);
            if isempty(strt seq IDs)
    8
                 fprintf('
                                  ERROR: Path %s does not exist\n',
labels master{strt node AID});
            elseif length(skip AIDs) > (act num - 2)
    00
                 fprintf(' ERROR: Not enough data to characterize
behavior on %s\n', labels master{strt node AID});
            else
                %% Analyze global mandatory path
```

```
90
                  fprintf('
                                   Path %s\n', labels master{strt node AID});
                % Determine mandatory preceding actions and find states
                act path pre = globalPathPre(data, act num, strt seq IDs,
end seq IDs, dataF AID, skip AIDs);
                act mand pre = act path pre(:, 2);
                act num pre = size(act mand pre, 1);
                act mand pre root = cell(act num pre, 1);
                for act1 = 1:act num pre
                    branch1 = act mand pre{act1};
                    for act2 = branch1
                        root1 = act_mand_pre_root{act2, 1};
                        if not(ismember(act1, root1))
                             act mand pre root{act2, 1} = [root1, act1];
                        end
                    end
                end
                %% Analyze local mandatory path
                [act avail pos T1, ~] = localPath(data, strt seq IDs,
end_seq_IDs, dataF_AID, skip_AIDs);
                %% Update data set
                data store = data;
                data = [];
                seq1 ID = 1;
                states = \{\};
                while seq1 ID <= size(data store, 1)</pre>
                    data = [data; data store(seq1 ID, :)];
                    if ismember(seq1 ID, strt seq IDs)
                        end seq ID = end seq IDs(strt seq IDs == seq1 ID);
                        while seq1_ID <= end_seq_ID</pre>
                             if ismember(seq1 ID, strt seq IDs)
                                 smpl = [];
                             else
                                 data = [data; data store(seq1 ID, :)];
                             end
                             smpl = [smpl; data store(seq1 ID, :)];
                            if size(smpl, 1) > 1 % Only add states after
first action
                                 act avail IDs = act avail pos T1(:, 1) ==
data(end, 2);
                                 act out local =
act avail pos T1(act avail IDs, 2)';
                                 act out = [];
                                 for act1 = act out local
                                     if all(ismember(act path pre{act1, 1},
smpl))
                                         act out = [act out, act1];
                                     end
                                 end
                                 switch direction
                                     case 1
                                         end exclude = not(ismember(end AID,
smpl(:, 2)));
```

```
case -1
                                         end exclude = not(ismember(start AID,
smpl(:, 2)));
                                 end
                                 if not(ismember(dataF AID, smpl(:, 2))) &&
end exclude && (length(act out) > 1) && not(ismember(data store((seq1 ID +
1), 2), [start AID, end AID]))
                                     state1 ID = 1;
                                     while state1 ID <= length(states)</pre>
                                         if isequal(smpl(:, 2),
states{state1 ID})
                                             break
                                         end
                                         state1 ID = state1 ID + 1;
                                     end
                                     if state1 ID > length(states)
                                         states = [states(:)', smpl(:, 2)];
                                         act num pre = act num pre + 1;
                                         state1_AID = act_num_pre;
                                     else
                                         state1 AID = state1 ID + act num;
                                     end
                                     data = [data; data store(seq1 ID, 1),
state1 AID, data store(seq1 ID, 3)];
                                     data = [data; data store((seq1 ID +
1):end seq ID, :)];
                                     seq1 ID = end seq ID + 1;
                                 else
                                     seq1 ID = seq1 ID + 1;
                                 end
                             else
                                 seq1 ID = seq1 ID + 1;
                             end
                        end
                    else
                        seq1 ID = seq1 ID + 1;
                    end
                end
                new state num = act num pre - act num;
                % Update states
                if new state num
                    for state1 = 1:new state num
                        new state AIDs = [new state AIDs, (act num +
state1)];
                    end
                end
                act num = max(data(:, 2));
            end
            %% Iterate
            if (length(skip AIDs) > (act_num - 1)) || isempty(strt_seq_IDs)
```

```
|| (new_state_num == 0)
```

```
complete(path_ID) = 1;
end
path_ID = path_ID + 1;
end
if direction < 0
data = flipud(data);
end
end
```

stateJoin.mat

This function detects when states share identical paths, and relabels them to the same state ID. This updated trace is then output data and the updated path set is output paths.

```
function [data, paths] = stateJoin(start AID, dataF AID, end AID, data,
act num master, direction)
    %% stateJoin 09
    % Detects when states share identical action paths to future state
    % and relabels them as the same state
    % Requires:
    8
      - sortPaths
    % Changes from 08
    00
       - Removes subsetting
    %% Prep data
    act num = max(data(:, 2));
    switch direction
       case 1
            strt node AID = start AID;
            end node AID = end AID;
        case -1
            strt node AID = end AID;
            end node AID = start AID;
            data = flipud(data);
    end
    %% Find state to state paths
    % Iterate until all possible states merged
    reduce states = 1;
    while reduce states
        % Instance storage
       branches = cell(act_num - act_num_master + 2, 1);
       paths = cell(act num - act num master + 2);
       % Iterate through start states
       states = [start AID, end_AID, (act_num_master + 1):act_num];
        for state1 = states
            branches1 = [];
```

```
paths1 = cell(act num - act num master + 2, 1);
if not(state1 == end node AID)
    for state1_seq_ID = find(data(:, 2) == state1)'
        state2 seq ID = state1 seq ID + 1;
        state2 = data(state2 seq ID, 2);
        while not(ismember(state2, states))
            state2 seq ID = state2 seq ID + 1;
            state2 = data(state2 seq ID, 2);
        end
        path = data((state1 seq ID + 1):state2 seq ID, 2);
        if not(ismember(dataF AID, path))
            if not(ismember(state2, branches1))
                branches1 = [branches1, state2];
            end
            % Check if path recorded
            include = 0;
            path ID = 1;
            if state2 > act num master
                paths1 2 = paths1{state2 - act num master + 2};
            elseif state2 == start_AID
                paths1 2 = paths1{1};
            else
                paths1_2 = paths1{2};
            end
            if isempty(paths1 2)
                paths1 2 = \{path\};
            else
                while path ID <= length(paths1 2)</pre>
                    if isequal(path, paths1 2{path ID})
                        include = 1;
                        break
                    end
                    path ID = path ID + 1;
                end
                if not(include)
                    paths1 2 = [paths1 2(:)', path];
                end
            end
            if state2 > act num master
                paths1{state2 - act num master + 2} = paths1 2;
            elseif state2 == start AID
                paths1{1} = paths1 2;
            else
                paths1{2} = paths1 2;
            end
        end
    end
end
branches1 = sort(branches1);
% Store data
state1 ID = find(states == state1);
branches{state1 ID} = branches1;
```

```
for state2 ID = 1:length(states)
                paths list = paths1{state2 ID};
                % Sort paths
                if not(isempty(paths list))
                   paths list = sortPaths(paths list')';
                end
               paths(state1 ID, state2 ID) = {paths list};
           end
       end
       %% Detect shared paths
       % Prep iteration
       checked = zeros(act num - act num master + 2, 1);
       convert_sink = [];
       convert source = {};
       % Iterate through states
       for state1_ID = 1:length(states)
           state1 = states(state1_ID);
           branches1 = branches{state1 ID};
           % Find matching future states
           match states = [];
           state2 ID = state1 ID + 1;
           while state2 ID <= length(states)</pre>
                if not(checked(state2 ID))
                   branches2 = branches{state2 ID};
                    if (isequal(branches1, branches2) && (direction == 1)) ||
(any(ismember(branches1, branches2)) && (direction == -1))
                        match states = [match states, states(state2 ID)];
                    end
                end
                state2 ID = state2 ID + 1;
           end
            % Check if paths match
           if not(isempty(match states))
               paths1 = paths(state1 ID, :);
               match states store = match states;
               match states = [];
                if direction == -1
                    % Compile ongoing list of paths in possible super state
                   match paths = {};
                    for state3 ID = 1:length(states)
                        paths1 3 = paths1{state3 ID};
                        for path_ID = 1:length(paths1_3)
                            match_paths = [match_paths, {paths1_3{path_ID}}];
                        end
                    end
                end
                % Iterate through states
                d len = 1;
                while d len > 0
                                   % Iterate until no change is match states
                    curr len = length(match states);
```

```
for state2 = match states store
                         if ismember(state2, match states)
                             continue
                         elseif state2 > act num master
                             state2 ID = state2 - act num master + 2;
                         elseif state2 == start AID
                             state2 ID = 1;
                         else
                             state2 ID = 2;
                         end
                         paths2 = paths(state2 ID, :);
                         if isequal(paths1, paths2) && (direction == 1)
                             match states = [match states, state2];
                             checked(state2 ID) = \overline{1};
                         elseif direction == -1
                             for state3 ID = 1:length(states)
                                 paths2_3 = paths2{state3_ID};
                                 path1 ID = 1;
                                 match check = 0;
                                  % Find match
                                 while (path1 ID <= length(match paths)) &&</pre>
not(match check)
                                      path2 ID = 1;
                                      while path2 ID <= length(paths2 3) &&</pre>
not(match check)
                                          if isequal(match paths{path1 ID},
paths2 3{path2 ID})
                                              match check = 1;
                                          end
                                          path2 ID = path2 ID + 1;
                                      end
                                      path1 ID = path1 ID + 1;
                                  end
                                  if match check
                                      match states = [match states, state2];
                                      for path3_ID = 1:length(paths2_3)
                                          path2^{-}3 = paths2 3 \{path3 ID\};
                                          path_include = 0;
                                          for path1 ID = 1:length(match paths)
                                              path1 = match paths{path1 ID};
                                              if isequal(path1, path2 3)
                                                   path include = 1;
                                                   break
                                              end
                                          end
                                          if not(path include)
                                              match_paths = [match_paths,
path2_3];
                                          end
                                      end
                                      checked(state2 ID) = 1;
                                 end
                             end
                         end
```

```
end
                    match states = sort(match states);
                    d len = length(match states) - curr len;
                end
            end
            % Update match data
            checked(state1 ID) = 1;
            if not(isempty(match states))
                convert sink = [convert sink, state1];
                convert source = [convert source(:)', match states];
            end
        end
        convert source = convert source';
        %% Join states
        % Prep convert detection
        convert sources = [];
        for state1 ID = 1:length(convert source)
            convert sources = [convert sources, convert source{state1 ID}];
        end
        convert sources = sort(convert sources);
        % Convert
        for seq1 ID = find(ismember(data(:, 2), convert sources))'
            state1 = data(seq1 ID, 2);
            state2 ID = 1;
            while state2 ID <= length(convert source)</pre>
                if ismember(state1, convert source{state2 ID})
                    data(seq1 ID, 2) = convert sink(state2 ID);
                    break
                end
                state2 ID = state2 ID + 1;
            end
        end
        %% Reduce states
        if not(isempty(convert_sources))
            % Reduce
            for seq1 ID = find(data(:, 2) > convert sources(1))'
                state1 = data(seq1 ID, 2);
                reduce = nnz((convert sources - state1) < 0); % Count number</pre>
of states removed
                data(seq1 ID, 2) = state1 - reduce;
            end
            % Reset trackers
            act num = max(data(:, 2));
        else
            reduce states = 0;
        end
    end
```

```
%% Correct output
    % Reverse data
    if direction == -1
        data = flipud(data);
        paths = paths';
    end
    % Reorganize paths
    paths store = paths;
    paths = \{\};
    for state1 ID = 1:size(paths store, 1)
        for state2 ID = 1:size(paths store, 2)
            paths1 2 = paths store{state1 ID, state2 ID};
            if not(isempty(paths1 2))
                for path ID = 1:length(paths1 2)
                    path = paths1 2{path ID};
                    if not(ismember(dataF_AID, path))
                         if direction == -1
                            path = flipud(path);
                             % Append end action ID
                             if state2 ID == 2
                                 path = [path; end AID];
                             else
                                 path = [path; (act num master + state2 ID -
2)];
                             end
                         else
                             % Append start action ID
                             if state1 ID == 1
                                 path = [start_AID; path];
                             else
                                 path = [(act num master + state1 ID - 2);
path];
                             end
                         end
                         % Store
                        paths = [paths; path];
                    end
                end
            end
        end
    end
    % Sort paths
    paths = sortPaths(paths);
end
```

pathAnalyze.mat

This function provides the concentration analysis data for CoffeeMiner.mat. Variables concen_state_pre and concen_path_pre provide the percentage of use instances that included said state or path in forward iteration respectively. Variables probs_state_pre and probs_path_pre contain the respective probability of navigating to a given state or path respectively given an initial state. Rows in the cell array correspond to initial state and contain a two-column matrix. The first column of this matrix includes the corresponding end state or path ID, and the second column then includes the probability of navigation given the initial state. These variables also have corresponding variables storing the reverse iteration information but utilize the pos suffix instead of the pre.

```
function [concens p, timings p, probs p, concens s, timings s, probs s] =
pathAnalyze (data, paths, path map, start AID, dataF AID, end AID,
act num master)
    %% pathAnalyze 02
    % Collects concentration, timing, and probability data
    % Changes from 01
         - Computes data from states to state as well as path specifically
    2
    00
          - State based probability calculation
    %% Prep storage
    state cnt = zeros(max(data(:, 2)), 1);
    smpl_cnt = 0;
    state path cnt = max(path map(:, 2));
    concens p = zeros(length(paths), 1);
    timings p = cell(length(paths), 1);
    probs p = cell(max(data(:, 2)), 1);
    concens s = zeros(state path cnt, 1);
    timings s = cell(state path cnt, 1);
    probs s = cell(max(data(:, 2)), 1);
    %% Iterate through data
    % Find sample terminals
    strt seq IDs = find(data(:, 2) == start AID);
    end seq IDs = find(data(:, 2) == end AID);
    % Iterate through samples
    for smpl ID = 1:length(strt seg IDs)
        strt seq ID = strt seq IDs(smpl ID);
        end seq ID = end seq IDs(smpl ID);
        smpl data = data((strt seq ID:end seq ID), :);
        smpl path = smpl data(:, 2);
        if not(ismember(dataF AID, smpl path))
```

```
smpl cnt = smpl cnt + 1;
            concen p smpl = zeros(length(paths), 1);
            concen_s_smpl = zeros(state path cnt, 1);
            % Isolate paths in sample
           path strt IDs = [1; find(smpl path(:) > act num master)];
            for path1 ID = 1:length(path strt IDs)
                if path1 ID == 1 && smpl ID == 7
                    gotcha = 1;
                end
                path1_strt_ID = path_strt_IDs(path1_ID);
                if path1 ID == length(path strt IDs)
                    path1 end ID = length(smpl path);
                else
                    path1_end_ID = path_strt_IDs(path1_ID + 1);
                end
                path1 = smpl path(path1 strt ID:path1 end ID);
                strt state = path1(1);
                state cnt(strt state) = state cnt(strt state) + 1;
                end state = path1(end);
                % Match sub path to listed paths
                path2 ID = 1;
                while path2 ID <= length(paths)</pre>
                    path2 = paths{path2 ID};
                    if isequal(path1, path2)
                        break
                    end
                    path2 ID = path2 ID + 1;
                end
                path ID s = path map(path2 ID, 2);
                % Store path data
                concen p smpl(path2 ID) = concen p smpl(path2 ID) + 1;
                timings p{path2 ID} = [timings p{path2 ID},
(smpl data(path1 end ID, 3) - smpl data(path1 strt ID, 3))];
                path probs = probs p{strt state};
                if isempty(path probs)
                    path_probs = [path2_ID, 1];
                else
                    row ID = find(path probs(:, 1) == path2 ID);
                    if isempty(row ID)
                        path probs = sortrows([path probs; path2_ID, 1]);
                    else
                        path probs(row ID, 2) = path probs(row ID, 2) + 1;
                    end
                end
                probs p{strt state} = path probs;
                % Store state path data
                concen s smpl(path ID s) = concen s smpl(path ID s) + 1;
                timings s{path ID s} = [timings s{path ID s},
(smpl data(path1 end ID, 3) - smpl data(path1 strt ID, 3))];
                state probs = probs_s{strt_state};
                if isempty(state probs)
                    state probs = [end state, 1];
                else
```

```
row ID = find(state probs(:, 1) == end state);
                    if isempty(row ID)
                        state probs = sortrows([state probs; end state, 1]);
                    else
                        state probs(row ID, 2) = state probs(row ID, 2) + 1;
                    end
                end
                probs s{strt state} = state probs;
            end
            % Store concentration data
            concens p = concens p + (concen p smpl > 0);
            concens s = concens s + (concen s smpl > 0);
        end
    end
    %% Adjust values
    % Concentrations
    concens p = concens p / smpl cnt;
    concens s = concens s / smpl cnt;
    % Timings
    timings store p = timings p;
    timings p = [];
    for path1 ID = 1:length(paths)
        path timings = timings store p{path1 ID};
        timings p = [timings p; mean(path timings), std(path timings, 1)];
    end
    timings store s = timings s;
    timings s = [];
    for state AID = 1:state path cnt
        path timings = timings store s{state AID};
        timings s = [timings s; mean(path_timings), std(path_timings, 1)];
    end
    % Probabilities
    for state AID = 1:max(data(:, 2))
        if not(isempty(probs p{state AID}))
            probs p{state AID}(:, 2) = probs p{state AID}(:, 2) /
state cnt(state AID);
        end
        if not(isempty(probs_s{state_AID}))
            probs s{state AID}(:, 2) = probs_s{state_AID}(:, 2) /
state cnt(state AID);
        end
    end
end
```

pathClimber.mat

This is a supplementary script which simulates state machine navigation in both machines at once. Available inputs are provided to the user in sequence, who is then presented with the option to select between said inputs, which is then entered to the state machine.

```
%% Path Climber 01
% Climbs the path tree for a system and provides available actions
% Requires:
clc
clear
%% Set toggles
toggle txt labels = 1;
%% Instance data
data master = load('CoffeeMachine_03.dat'); % Data set
start AID = 1;
                                                      % Action ID for Start
action
dataF AID = 2;
                                                      % Action ID for Data
Failure action
                                                      % Action ID for End
end AID = 3;
action
                                                      % Number of individual
act num master = max(data master(:, 2));
actions
load('paths pre.mat');
                                                      % Paths in forward
iteration
load('paths pos.mat');
                                                      % Paths in reverse
iteration
if toggle txt labels
                                                      % Action Labels
   labelFID = fopen('CoffeeActLabels s.dat');
    stateLabel = 'State';
else
    labelFID = fopen('CoffeeActLabels i.dat');
    stateLabel = 'S';
end
labels = textscan(labelFID, '%s', 'Delimiter', '\n');
labels master = labels{1};
fclose(labelFID);
%% Climb tree
% Instance iteration variables
state pre = 1;
state pos = state_pre;
act path pre = [state pre];
act_path_pos = [state_pos];
% Iterate through complete path
fprintf('Start:\n');
while not(state pre == end AID) && not(state pos == end AID)
    % Check if new paths needed
```

```
for dir = [-1, 1]
        switch dir
            case -1
                act path dir = act path pos;
                paths dir = paths pos;
                state dir = state pos;
            case 1
                act_path_dir = act path pre;
                paths dir = paths_pre;
                state dir = state pre;
        end
        if (act path dir(end) > act_num_master) || (act_path_dir(end) ==
start AID)
            % Seek paths with current start state
            start path ID = 0;
            end path ID = 0;
            path ID = 1;
            while path ID <= length(paths dir)</pre>
                curr path = paths dir{path ID};
                if (curr path(1) == state dir) && not(start path ID)
                    start path ID = path ID;
                elseif start path ID && not(curr path(1) == state dir)
                    end path ID = path ID - 1;
                    break
                end
                path ID = path ID + 1;
            end
            if not(end path ID) % If no end detected
                end path ID = length(paths dir);
            end
            % Store paths
            paths avail = cell(end path ID - start path ID + 1, 1);
            for path ID = start path ID:end path ID
                paths avail{path ID - start path ID + 1} =
paths dir{path ID};
            end
            switch dir
                case -1
                    paths avail pos = paths avail;
                    curr path pos = [state pos];
                    seq ID pos = 2;
                case 1
                    paths avail pre = paths avail;
                    curr path pre = [state pre];
                    seq ID pre = 2;
            end
        end
    end
    % Determine available actions
    for dir = [-1, 1]
        switch dir
            case -1
                seq_ID_dir = seq_ID_pos;
```

```
paths avail dir = paths avail pos;
        case 1
            seq ID dir = seq ID pre;
            paths avail dir = paths avail pre;
    end
    act avail dir = [];
    for path ID = 1:length(paths avail dir)
        act AID = paths avail dir{path ID} (seq ID dir);
        if not(ismember(act AID, act avail dir))
            act avail dir = [act avail dir; act AID];
        end
    end
    act avail dir = sort(act avail dir);
    switch dir
        case -1
            act_avail_pos = act_avail_dir;
        case 1
            act avail pre = act avail dir;
    end
end
act avail = [];
for act AID = act avail pos'
    if ismember(act AID, act avail pre')
        act avail = [act avail; act AID];
    end
end
% Display actions
fprintf('
          Available actions: ');
if toggle txt labels
    fprintf('\n');
end
for act_ID = 1:length(act_avail)
    act_AID = act_avail(act_ID);
    if toggle txt labels
        act label = labels master{act AID};
        fprintf('
                         %d) %s\n', act ID, act label);
    else
        fprintf('%d, ', act AID);
    end
end
if toggle txt labels
    fprintf('
                   %d) %s\n', (act ID + 1), 'Other');
else
    fprintf('%d\n', (act AID + 1));
end
% Select action
act sel = input('
                         Select input: ');
if not(act sel)
    fprintf('Devitation from model\n');
    break
end
```

```
if toggle txt labels
        act AID sel = act avail(act sel);
    else
        act AID sel = act sel;
    end
    % Append data
    act path pre = [act path pre; act AID sel];
    curr path pre = [curr path pre; act AID sel];
    act_path_pos = [act_path_pos; act AID sel];
    curr path pos = [curr path pos; act AID sel];
    % Update paths available
    for dir = [-1, 1]
        switch dir
            case -1
                paths avail = paths avail pos;
                curr path = curr path pos;
            case 1
                paths avail = paths avail pre;
                curr path = curr path pre;
        end
        % Check paths against current path
        paths_avail_store = paths_avail;
        paths avail = {};
        for path ID = 1:length(paths avail store)
            path comp = paths avail store{path ID}(1:length(curr path));
            if all(isequal(path comp, curr path))
                paths avail = [paths avail; paths avail store{path ID}];
            end
        end
        switch dir
            case -1
                paths avail pos = paths avail;
                if (length(paths avail) == 1) && (length(paths avail{1}) ==
length(curr path) + 1)
                    state pos = paths avail{1}(end);
                    act path pos = [act path pos; state pos];
                else
                    seq ID pos = seq ID pos + 1;
                end
            case 1
                paths avail pre = paths avail;
                if (length(paths avail) == 1) && (length(paths avail{1}) ==
length(curr_path) + 1)
                    state pre = paths avail{1}(end);
                    act path pre = [act path pre; state pre];
                else
                    seq ID pre = seq ID pre + 1;
                end
        end
    end
end
```

```
if act_sel
    fprintf('Drink complete\n');
end
```

APPENDIX B. CHAPTER 3 STATE ID SCRIPTS

Setup

To extract states with genetic optimization, first compile each of the scripts in this appendix into separate files, named exactly as their heading.

ClassMicro.mat

To define optimized state descriptions, run ClassMicro.mat. This can take some time. Running this script will prompt a user input of "Run type" which determines which suffix of trace file will be used to produce state definitions. This should be done in parallel to updating para_inc to label the specific parameters which should be included as consideration for the state definition. Note that para_fixed will require the optimization to include the specific parameters listed.

To interpret results, x_star outputs the optimized configuration, model_GMM outputs the corresponding optimized model, classes_GMM, the corresponding labels for each microstate, and spred includes the relative inclusion rates of each gene during optimization. For diagnostics, stats includes information on generational behaviors, GA550.mat includes the specific information.

```
%% classMicro 04
% This script classifies microstates using the targeted eps method
% Changes from 03
     - Added channel filtering
2
     - Updated x star to output channel IDs
00
clc
clear
%% Program settings
run type = input('Input run type: ', 's');
para inc = [3; 4; 11; [15:21]'];
% Load data
data master = load(strcat('trainingStates trimmed ', run type, '.mat'));
data master = data master.trainingStates trimmed(:, para inc);
[micro cnt, chan cnt] = size(data master);
```

```
% Prep settings
class cnt bounds = [3, 18];
para fixed = [11; [15:18]']; % Must be included in para inc
[~, para fixed] = ismember(para fixed, para inc);
chan var cnt = chan cnt - length(para fixed);
para bounds = zeros(chan var cnt, 2);
para bounds(:, 2) = 1;
bounds = [class cnt bounds; para bounds];
bits = zeros((1 + chan var cnt), 1);
bits(1) = 4;
bits (2:end) = 1;
% Optimization settings
gen para = sum(bits);
pop size = 4 * gen para;
cross freq = 0.5;
mut_freq = (gen_para + 1) / (2 * pop_size * gen_para);
options = goptions([]);
options(11) = pop size;
options(12) = cross freq;
options(13) = mut freq;
options (14) = 300\overline{;}
%% Normalize data
% Prep storage
data norm = data master;
stdDev vals = zeros(chan cnt, 1);
mean vals = stdDev vals;
% Iterate through channels
for chan ID = 1:chan cnt
    stdDev vals(chan ID) = std(data master(:, chan ID));
    mean vals(chan ID) = mean(data master(:, chan ID));
end
% Iterate through dataset
for chan ID = 1:chan cnt
    stdDev_val = stdDev_vals(chan_ID);
    mean_val = mean_vals(chan_ID);
    if stdDev val == 0
        data norm(:, chan ID) = mean val;
    else
        for micro ID = 1:micro cnt
            data norm(micro ID, chan ID) = (data norm(micro ID, chan ID) -
mean_val) / stdDev val;
        end
    end
end
%% Classify data
fprintf('Initializing GMM...\n');
% Construct modeling function
```

```
opt func = @(opt vars) calc obj(opt vars, data norm, para fixed);
% Optimize
[x star, f star, stats, nfit, fgen, lgen, lfit, spred] = GA550(opt func, [],
options, bounds(:, 1)', bounds(:, 2)', bits');
class cnt = round(x star(1), 0);
para bool = x star(2:end);
para include = para_fixed;
para bool ID = 1;
for para_ID = 1:(chan cnt - 2)
    if not(ismember(para ID, para include))
        if para bool (para bool ID)
            para include = [para include; para ID];
        end
        para bool ID = para bool ID + 1;
    end
end
para include = sort(para include);
data train = data norm(:, para include);
x star = [class cnt; para inc(para include)];
model GMM = fitgmdist(data train, class cnt, 'RegularizationValue', 0.0001,
'Options', statset('Display', 'off', 'MaxIter', 500));
classes GMM = cluster(model GMM, data train);
% Save data
save(strcat('lgen ', run type, '.mat'), 'lgen');
save(strcat('stats_', run_type, '.mat'), 'stats');
save(strcat('x_star_', run_type, '.mat'), 'x_star');
save(strcat('model_GMM_', run_type, '.mat'), 'model_GMM');
save(streat('classes_GMM_', run_type, '.mat'), 'classes_GMM');
save(strcat('spred ', run type, '.mat'), 'spred');
fprintf('Done!\n');
```

GA550.mat

This is a modified variant of Dr. Crossley's genetic optimization function as presented in Purdue University's "Multidisciplinary Design Optimization in Aerospace Engineering" course (Crossley, 2020). It outputs the variables defined in ClassMicro.mat. The modifications to the original script allow the system to store and output statistics on the relative presence of different genes with each generation, allowing for some further verification of success and study of how different genes may be related to success.

```
function [xopt,fopt,stats,nfit,fgen,lgen,lfit] = GA550(fun, ...
x0,options,vlb,vub,bits,P1,P2,P3,P4,P5,P6,P7P,P8,P9,P10)
%GA550 minimizes a fitness function using a simple genetic algorithm.
%
X=GA550('FUN',X0,OPTIONS,VLB,VUB) uses a simple
```

```
genetic algorithm to find a minimum of the fitness function
2
90
        FUN. FUN can be a user-defined M-file: FUN.M, or it can be a
90
    string containing the function itself. The user may define all
90
        or part of an initial population XO. Any undefined individuals
%
    will be randomly generated between the lower and upper bounds
00
    (VLB and VUB). If X0 is an empty matrix, the entire initial
0
    population will be randomly generated. Use OPTIONS to specify
%
    flags, tolerances, and input parameters. Type HELP GOPTIONS
0/0
        for more information and default values.
%
    X=GA550('FUN',X0,OPTIONS,VLB,VUB,BITS) allows the user to
00
0/0
    define the number of BITS used to code non-binary parameters
90
    as binary strings. Note: length(BITS) must equal length(VLB)
%
    and length(VUB). If BITS is not specified, as in the previous
%
    call, the algorithm assumes that the fitness function is
8
    operating on a binary population.
%
    X=GA550('FUN', X0, OPTIONS, VLB, VUB, BITS, P1, P2, ...) allows up
%
00
    to ten arguments, P1, P2, ... to be passed directly to FUN.
90
    F=FUN(X, P1, P2, ...). If P1, P2, ... are not defined, F=FUN(X).
%
90
    [X, FOPT, STATS, NFIT, FGEN, LGEN, LFIT] = GA550 (<ARGS>)
90
                   - design variables of best ever individual
           Х
%
                   - fitness value of best ever individual
           FOPT
%
           STATS
                   - [min mean max stopping criterion] fitness values
00
                     for each generation
00
           NFIT - number of fitness function evalations
                  - first generation population
00
           FGEN
00
                   - last generation population
           LGEN
00
           LFIT
                   - last generation fitness
00
00
        The algorithm implemented here is based on the book: Genetic
8
        Algorithms in Search, Optimization, and Machine Learning,
%
        David E. Goldberg, Addison-Wiley Publishing Company, Inc.,
%
        1989.
%
    Originally created on 1/10/93 by Andrew Potvin, Mathworks, Inc.
00
00
    Modified on 2/3/96 by Joel Grasmeyer.
00
    Modified on 11/12/02 by Bill Crossley.
    Modified on 7/20/04 by Bill Crossley.
00
% Make best feas global for stopping criteria (4/13/96)
global best feas
global gen
global fit hist
% Load input arguments and check for errors
if nargin<4,
    error('No population bounds given.')
elseif (size(vlb,1)~=1) | (size(vub,1)~=1),
    % Remark: this will change if algorithm accomodates matrix variables
    error('VLB and VUB must be row vectors')
elseif (size(vlb,2)~=size(vub,2)),
    error('VLB and VUB must have the same number of columns.')
elseif (size(vub,2)~=size(x0,2)) & (size(x0,1)>0),
    error('X0 must all have the same number of columns as VLB and VUB.')
elseif any(vlb>vub),
    error('Some lower bounds greater than upper bounds')
```

```
else
    x0 row = size(x0, 1);
    for i=1:x0 row,
        if any(x0(x0 row,:)<vlb) | any(x0(x0 row,:)>vub),
            error('Some initial population not within bounds.')
        end % if initial pop not within bounds
    end % for initial pop
end % if nargin<4</pre>
if nargin<6,
    bits = [];
elseif (size(bits,1)~=1) | (size(bits,2)~=size(vlb,2)),
    % Remark: this will change if algorithm accomodates matrix variables
    error('BITS must have one row and length(VLB) columns')
elseif any(bits~=round(bits)) | any(bits<1),</pre>
    error('BITS must be a vector of integers >0')
end % if nargin<6</pre>
% Form string to call for function evaluation
if ~( any(fun<48) | any(fun>122) | any((fun>90) & (fun<97)) | ...
        any((fun>57) & (fun<65)) ),
    % Only alphanumeric characters implies that 'fun' is a separate m-file
    evalstr = [fun '(x'];
    for i=1:nargin-6,
        evalstr = [evalstr, ', P', int2str(i)];
    end
else
    % Non-alphanumeric characters implies that the function is contained
    % within the single quotes
    evalstr = ['(',fun];
end
% Determine all options
% Remark: add another options index for type of termination criterion
if size(options,1)>1,
    error('OPTIONS must be a row vector')
else
    % Use default options for those that were not passed in
    options = goptions(options);
end
PRINTING = options(1);
BSA = options(2);
fit tol = options(3);
nsame = options(4) - 1;
elite = options(5);
% Since operators are tournament selection and uniform crossover and
% default coding is Gray / binary, set crossover rate to 0.50 and use
% population size and mutation rate based on Williams, E. A., and Crossley,
% W. A., "Empirically-derived population size and mutation rate guidelines
% for a genetic algorithm with uniform crossover," Soft Computing in
% Engineering Design and Manufacturing, 1998. If user has entered values
% for these options, then user input values are used.
if options(11) == 0,
    pop size = sum(bits) * 4;
else
```

```
pop size = options(11);
end
if options(12) == 0,
    Pc = 0.5;
else
    Pc = options(12);
end
if options(13) == 0,
    Pm = (sum(bits) + 1) / (2 * pop size * sum(bits));
else
    Pm = options(13);
end
\max gen = options(14);
% Ensure valid options: e.q. Pc,Pm,pop_size,max_gen>0, Pc,Pm<1</pre>
if any([Pc Pm pop size max gen]<0) | any([Pc Pm]>1),
    error('Some Pc, Pm, pop size, max gen<0 or Pc, Pm>1')
end
% Encode fitness (cost) function if necessary
ENCODED = any(any(([vlb; vub; x0]~=0) & ([vlb; vub; x0]~=1))) | ....
    ~isempty(bits);
if ENCODED,
    [fgen,lchrom] = encode(x0,vlb,vub,bits);
else
    fgen = x0;
    lchrom = size(vlb,2);
end
% Display warning if initial population size is odd
if rem(pop size,2) == 1,
    disp('Warning: Population size should be even. Adding 1 to population.')
    pop size = pop size +1;
end
% Form random initial population if not enough supplied by user
if size(fgen,1)<pop size,</pre>
    fgen = [fgen; (rand(pop size-size(fgen,1),lchrom)<0.5)];</pre>
end
xopt = vlb;
nfit = 0;
new gen = fgen;
isame = 0;
bitlocavg = mean(fgen,1); % initial bit string affinity
BSA pop = 2 \times \text{mean}(\text{abs}(\text{bitlocavg} - 0.5));
fopt = Inf;
stats = [];
% Header display
if PRINTING>=1,
    if ENCODED,
        disp('Variable coding as binary chromosomes successful.')
        disp('')
        fgen = decode(fgen,vlb,vub,bits);
    end
                              Fitness statistics')
    disp('
    if nsame > 0
```

```
disp('Generation Minimum
                                      Mean
                                                   Maximum
                                                                  isame')
    elseif BSA > 0
        disp('Generation Minimum
                                      Mean
                                                    Maximum
                                                                  BSA')
    else
        disp('Generation Minimum
                                                    Maximum
                                                                  not used')
                                      Mean
    end
end
% Set up main loop
STOP FLAG = 0;
for generation = 1:max gen+1,
    old gen = new gen;
    % Decode binary strings if necessary
    if ENCODED,
        x pop = decode(old gen,vlb,vub,bits);
    else
       x_pop = old_gen;
    end
    % Get fitness of each string in population
    for i = 1:pop size,
        x = x pop(i,:);
        fitness(i) = eval([evalstr,')']);
        nfit = nfit + 1;
    end
    % Store minimum fitness value from previous generation (except for
    % initial generation)
    if generation > 1,
       min fit prev = min fit;
       min gen prev = min gen;
       min x prev = min x_i
    end
    % identify worst (maximum) fitness individual in current generation
    [max fit,max index] = max(fitness);
    % impose elitism - currently only one individual; this replaces worst
    % individual of current generation with best of previous generation
    if (generation > 1 & elite > 0),
        old gen(max index,:) = min gen prev;
        x pop(max index,:) = min x prev;
        fitness(max index) = min fit prev;
    end
    % identify best (minimum) fitness individual in current generation and
    % store bit string and x values
    [min fit,min index] = min(fitness);
    min gen = old gen(min index,:);
    min x = x pop(min index,:);
    % Store best fitness and x values
    if min fit < fopt,</pre>
        fopt = min fit;
```

```
xopt = min x;
    end
    % Compute values for isame or BSA pop stopping criteria
    if nsame > 0
        if generation > 1
            if min fit prev == min fit
                isame = isame + 1;
            else
                isame = 0;
            end
        end
    elseif BSA > 0
        bitlocavg = mean(old gen, 1);
        BSA pop = 2 \times \text{mean}(\text{abs}(\text{bitlocavg} - 0.5));
    end
    % Calculate generation statistics
    if nsame > 0
        stats = [stats; generation-1,min(fitness),mean(fitness), ...
            max(fitness), isame];
    elseif BSA > 0
        stats = [stats; generation-1,min(fitness),mean(fitness), ...
            max(fitness), BSA pop];
    else
        stats = [stats; generation-1,min(fitness),mean(fitness), ...
            max(fitness), 0];
    end
    % Display if necessary
    if PRINTING>=1,
        disp([sprintf('%5.0f %12.6g %12.6g %12.6g %12.6g',
stats(generation,1), ...
                stats(generation, 2), stats(generation, 3),
stats(generation, 4), ...
                stats(generation, 5))]);
    end
    % Check for termination
    % The default termination criterion is bit string affinity. Also
    % available are fitness tolerance across five generations and number of
    % consecutive generations with same best fitness. These can be used
    % concurrently.
    if fit tol>0,
                     % if fit tol > 0, then fitness tolerance criterion used
        if generation>5,
            % Check for normalized difference in fitness minimums
            if stats(generation,1) ~= 0,
                 if abs(stats(generation-5,1)-stats(generation,1))/ ...
                         stats(generation,1) < fit tol</pre>
                     if PRINTING >= 1
                         fprintf(' \ n')
                         disp('GA converged based on difference in fitness
minimums.')
                     end
                     lfit = fitness;
```

```
if ENCODED,
                        lgen = x pop;
                    else
                        lgen = old gen;
                    end
                    return
                end
            else
                if abs(stats(generation-5,1)-stats(generation,1)) < fit tol
                    if PRINTING >= 1
                        fprintf('\n')
                        disp('GA converged based on difference in fitness
minimums.')
                    end
                    lfit = fitness;
                    if ENCODED,
                        lgen = x pop;
                    else
                        lgen = old gen;
                    end
                    return
                end
            end
        end
    elseif nsame > 0, % consecutive minimum fitness value criterion
            if isame == nsame
                if PRINTING >= 1
                    fprintf('\n')
                    disp('GA stopped based on consecutive minimum fitness
values.')
                end
                lfit = fitness;
                if ENCODED,
                    lgen = x pop;
                else
                    lgen = old gen;
                end
                return
            end
    elseif BSA > 0, % bit string affinity criterion
        if BSA pop >= BSA,
            if PRINTING >=1
                fprintf('\n')
                disp('GA stopped based on bit string affinity value.')
            end
            lfit = fitness;
            if ENCODED,
                lgen = x_pop;
            else
                lgen = old gen;
            end
            return
        end
    end
    % Tournament selection
    new gen = tourney(old gen,fitness);
```

```
% Crossover
    new gen = uniformx(new gen, Pc);
    % Mutation
    new gen = mutate(new gen, Pm);
    % Always save last generation. This allows user to cancel and
    % restart with x0 = lgen
    if ENCODED,
        lgen = x pop;
    else
        lgen = old gen;
    end
end % for max gen
% Maximum number of generations reached without termination
lfit = fitness;
if PRINTING>=1,
    fprintf('\n')
    disp('Maximum number of generations reached without termination')
    disp('criterion met. Either increase maximum generations')
    disp('or ease termination criterion.')
end
% end genetic
function [gen,lchrom,coarse,nround] = encode(x,vlb,vub,bits)
%ENCODE Converts from variable to binary representation.
2
    [GEN, LCHROM, COARSE, nround] = ENCODE (X, VLB, VUB, BITS)
8
       encodes non-binary variables of X to binary. The variables
00
       in the i'th column of X will be encoded by BITS(i) bits. VLB
00
       and VUB are the lower and upper bounds on X. GEN is the binary
       representation of these X. LCHROM=SUM(BITS) is the length of
00
       the binary chromosome. COARSE(i) is the coarseness of the
00
%
        i'th variable as determined by the variable ranges and
8
       BITS(i). ROUND contains the absolute indices of the
8
       X which where rounded due to finite BIT length.
%
% Copyright (c) 1993 by the MathWorks, Inc.
2
  Andrew Potvin 1-10-93.
% Remark: what about handling case where length(bits)~=length(vlb)?
lchrom = sum(bits);
coarse = (vub-vlb)./((2.^{bits})-1);
[x row, x col] = size(x);
gen = [];
if ~isempty(x),
```

```
temp = (x-ones(x row, 1) *vlb)./ ...
          (ones(x row, 1) *coarse);
   b10 = round(temp);
   % Since temp and b10 should contain integers 1e-4 is close enough
   nround = find(b10-temp>1e-4);
   qen = b10to2(b10, bits);
end
% end encode
function [x,coarse] = decode(gen,vlb,vub,bits)
%DECODE Converts from binary Gray code to variable representation.
    [X,COARSE] = DECODE(GEN,VLB,VUB,BITS) converts the binary
8
0
       population GEN to variable representation. Each individual
00
       of GEN should have SUM(BITS). Each individual binary string
00
       encodes LENGTH(VLB)=LENGTH(VUB)=LENGTH(BITS) variables.
00
       COARSE is the coarseness of the binary mapping and is also
2
       of length LENGTH(VUB).
0/0
% this *.m file created by combining "decode.m" from the MathWorks, Inc.
  originally created by Andrew Potvin in 1993, with "GDECODE.FOR" written
2
% by William A. Crossley in 1996.
2
00
  William A. Crossley, Assoc. Prof. School of Aero. & Astro.
% Purdue University, 2001
2
% gen is an array [population size , string length], each row is one
individual's chromosome
% vlb is a row vector [number of parameters], each entry is the lower bound
for a variable
% vub is a row vector [number of parameters], each entry is the upper bound
for a variable
% bits is a row vector [number of parameters], each entry is number of bits
used for a variable
no para = length(bits); % extract number of parameters using number of rows
in bits vector
npop = size(gen,1); % extract population size using number of rows in gen
array
x = zeros(npop, no para); % sets up x as an array [population size, number
of parameters]
coarse = zeros(1, no para); % sets up coarse as a row vector [number of
parameters]
for J = 1:no para, % extract the resolution of the parameters
    coarse(J) = (vub(J)-vlb(J))/(2^bits(J)-1); % resolution of parameter J
end
for K = 1:npop, % outer loop through each individual (there may be a more
efficient way to operate on the
                 % gen array) BC 10/10/01
    sbit = 1;
                   % initialize starting bit location for a parameter
                  % initialize ending bit location
    ebit = 0;
```

```
for J = 1:no para, % loop through each parameter in the problem
    ebit = bits(J) + ebit; % pick the end bit for parameter J
        accum = 0.0;
                                    % initialize the running sum for
parameter J
     ADD = 1;
                                    % add / subtract flag for Gray code; add
if (ADD), subtract otherwise
      for I = sbit:ebit,
                                    % loop through each bit in parameter J
        pbit = I + 1 - sbit;
                                    % pbit determines value to be added or
subtracted for Gray code
                                        % if "1" is at current location
        if (gen(K,I))
            if (ADD)
                                            % add if appropriate
               accum = accum + (2.0^{(bits(J)-pbit+1)} - 1.0);
               ADD = 0;
                                        % next time subtract
            else
               accum = accum - (2.0^{(bits(J)-pbit+1)} - 1.0);
               ADD = 1;
                                        % next time add
            end
         end
      end
                                        % end of I loop through each bit
      x(K,J) = accum * coarse(J) + vlb(J);
                                                    % decoded parameter J for
individual K
      sbit = ebit + 1;
                                                             % next parameter
starting bit location
   end
                            % end of J loop through each parameter
end
                        % end of K loop through each individual
%end gdecode
function [new gen,mutated] = mutate(old gen,Pm)
%MUTATE Changes a gene of the OLD GEN with probability Pm.
%
    [NEW GEN, MUTATED] = MUTATE(OLD GEN, Pm) performs random
0
       mutation on the population OLD POP. Each gene of each
8
       individual of the population can mutate independently
00
       with probability Pm. Genes are assumed possess boolean
00
        alleles. MUTATED contains the indices of the mutated genes.
00
90
   Copyright (c) 1993 by the MathWorks, Inc.
0
   Andrew Potvin 1-10-93.
mutated = find(rand(size(old gen))<Pm);</pre>
new gen = old gen;
new gen(mutated) = 1-old gen(mutated);
% end mutate
function [new gen,nselected] = tourney(old gen,fitness)
%TOURNEY Creates NEW GEN from OLD GEN, based on tournament selection.
    [NEW GEN, NSELECTED] = TOURNEY (OLD GEN, FITNESS) selects
8
         individuals from OLD GEN by competing consecutive individuals
0
   after random shuffling. NEW GEN will have the same number of
8
   individuals as OLD GEN.
00
9
        NSELECTED contains the number of copies of each individual
```

```
that survived. This vector corresponds to the original order
2
00
     of OLD GEN.
90
     Created on 1/21/96 by Joel Grasmeyer
2
% Initialize nselected vector and indices of old gen
new gen = [];
nselected = zeros(size(old gen, 1), 1);
i old gen = 1:size(old gen,1);
% Perform two "tournaments" to generate size(old gen,1) new individuals
for j = 1:2,
  % Shuffle the old generation and the corresponding fitness values
  [old gen, i shuffled] = shuffle(old gen);
  fitness = fitness(i shuffled);
  i old gen = i old gen(i shuffled);
  % Keep the best of each pair of individuals
  index = 1:2:(size(old gen, 1) -1);
  [min fit, i min] = min([fitness(index); fitness(index+1)]);
  selected = i \min + [0:2:size(old gen, 1)-2];
  new gen = [new gen; old gen(selected,:)];
  % Increment counters in nselected for each individual that survived
  temp = zeros(size(old gen, 1), 1);
  temp(i old gen(selected)) = ones(length(selected),1);
  nselected = nselected + temp;
end
% end tourney
function [new gen, index] = shuffle(old gen)
%SHUFFLE Randomly reorders OLD GEN into NEW GEN.
    [NEW GEN, INDEX] = MATE (OLD GEN) performs random reordering
8
90
         on the indices of OLD GEN to create NEW GEN.
00
     INDEX is a vector containing the shuffled row indices of OLD GEN.
%
     Created on 1/21/96 by Joel Grasmeyer
8
[junk, index] = sort(rand(size(old gen, 1), 1));
new gen = old gen(index,:);
% end shuffle
function [new gen, sites] = uniformx(old gen, Pc)
%UNIFORMX Creates a NEW GEN from OLD GEN using uniform crossover.
      [NEW GEN, SITES] = UNIFORMX (OLD GEN, Pc) performs uniform crossover
8
          on consecutive pairs of OLD GEN with probability Pc.
%
0/0
      SITES shows which bits experienced crossover. 1 indicates
```

```
% allele exchange, 0 indicates no allele exchange. SITES has
```

```
% size(old_gen,1)/2 rows.
% Created 1/20/96 by Joel Grasmeyer
new_gen = old_gen;
sites = rand(size(old_gen,1)/2,size(old_gen,2)) < Pc;
for i = 1:size(sites,1),
    new_gen([2*i-1 2*i],find(sites(i,:))) = old_gen([2*i
2*i-1],find(sites(i,:)));
end
% end uniformx
```

goptions.mat

This function is an unmodified subfunction related to GA550.mat (Crossley, 2020). This function defines the constraints of operation for genetic optimization.

```
function OPTIONS=goptions(parain);
%GOPTIONS Default parameters used by the genetic algorithm GENETIC.
% Note that since the original version was written, the Matlab Optimization
% Toolbox now uses "optimset" to set generic optimization parameters, so
% this format is somewhat outdated.
% The genetic algorithm parameters used for this implementation are:
2
   OPTIONS(1)-Display flaq: 0 = none, 1 = some, 2 = all (Default: 1).
00
   OPTIONS(2)-Termination bit string affinity value (Default: 0.90; set to
8
zero to turn off)
   OPTIONS(3)-Termination tolerance for fitness (Default: 0; not normally
00
used).
   OPTIONS(4)-Termination number of consecutive generations with same best
2
    fitness (Default: 0; to use, set number, be sure OPTIONS(2) and
2
OPTIONS(3) = 0.
   OPTIONS(5)-Number of elite individuals (Default: 0; no elitism).
00
8
   OPTIONS(6)-
00
   OPTIONS(7)-
2
   OPTIONS(8)-
   OPTIONS(9)-
00
8
   OPTIONS(10)-
% Genetic Algorithm-specific inputs
% OPTIONS(11)-Population size (fixed)
00
  OPTIONS(12)-Probability of crossover
2
  OPTIONS(13)-Probability of mutation
8
  OPTIONS(14)-Maximum number of generations, always used as safeguard
00
    (Default: 200).
00
%
% Explanation of defaults:
% The default algorithm displays statistical information for each
    generation by setting OPTIONS(1) = 1. Plots are produced when
00
```

```
2
    OPTIONS(1) = 2.
    The OPTIONS(2) flag is originally set for termination criterion based
90
90
    on X; here it is used if bit string affinity is selected.
    The default fitness function termination tolerance,
9
00
    OPTIONS(3), is set to 0, which terminates the optimization when 5
00
   consecutive best generation fitness values are the same. A positive
8
   value terminates the optimization when the normalized difference
8
  between the previous fitness and current generation fitness is less
   than the tolerance. See the code for details.
00
% OPTIONS(4) has a default value of 5; this means if the best fitness
8
   value in the population is unchanged for 5 consecutive generations
9
  the GA is terminated.
00
        The default algorithm uses a fixed population size, OPTIONS(11),
0/0
        and no generational overlap. The default population size is 30.
00
   Three genetic operations: selection, crossover, and mutation are
%
   used for procreation.
%
    The default selection scheme is tournament selection.
8
        Crossover occurs with probability Pc=OPTIONS(12). The default
00
  crossover scheme is uniform crossover with Pc = 0.5.
8 Each allele of the offspring mutates independently with probability
00
        Pm=OPTIONS(13); here the default is 0.01.
00
        The default number of maximum generations, OPTIONS(14) is 200.
00
2
    Last modified by Bill Crossley 07/20/04
% The following lines have been commented out by Steven Lamberson.
\% They have been changed to what is seen below them. (06/30/06).
% This change was made in order to fix the following problems:
% 1 - code changed user supplied options(1)=0 to options(1)=1
2
    2 - code changed user supplied options (2)=0 to options (2)=0.9
%if nargin<1; parain = []; end
%sizep=length(parain);
%OPTIONS=zeros(1,14);
%OPTIONS(1:sizep)=parain(1:sizep);
%default options=[1,0.9,0,0,0,0,0,0,0,0,0,0,0,200];
%OPTIONS=OPTIONS+(OPTIONS==0).*default options
if nargin<1; parain = []; end</pre>
sizep=length(parain);
OPTIONS=zeros(1,14)-1;
OPTIONS(1:sizep)=parain(1:sizep);
default options=[1,0.9,0,0,0,0,0,0,0,0,0,0,0,200];
for i = 1:length(OPTIONS)
    if OPTIONS(i) == -1
        OPTIONS(i) = default options(i);
    end
end
```

146

calc_obj.mat

This function measures the fitness of each classification tuning as generated by GA550.mat using the Calinski-Harabasz criterion. Note that fitness is optimized at low objective values, so the output is inverted. Additionally, some residual random sampling test cases are included, but are nonfunctional and do not affect operation.

```
%% calc obj
% This script measures the efficacy of flight clustering for a given data set
function obj = calc obj(opt vars, data set, para include)
   perc thresh = 0.75;
    %% Extract data
    % Extract base level data
    [micro cnt, chan cnt] = size(data set);
    class cnt = round(opt vars(1), 0);
    para include bool = opt vars(2:end);
   para bool ID = 1;
    for para ID = 1:chan cnt
        if not(ismember(para ID, para_include))
            if para include bool (para bool ID)
                para include = [para include; para ID];
            end
            para bool ID = para bool ID + 1;
        end
    end
    para_include = sort(para_include);
    % Refine data
    chan cnt = length(para include);
    data set = data set(:, para include);
    %% Compute objective
00
     [model GMM, rand perc] = flight clust(data set, class cnt, [0.25, 0.75,
3]);
    rand perc = 1;
    model_GMM = fitgmdist(data_set, class cnt, 'RegularizationValue', 0.0001,
'Options', statset('Display', 'off', 'MaxIter', 500));
    classes_GMM = cluster(model GMM, data set);
    obs cnts = zeros(class cnt, 1);
    obs store = cell(class cnt, 1);
    centroids = zeros(class cnt, chan cnt);
    for class ID = 1:class cnt
        obs IDs = find(classes GMM == class ID);
        obs_list = data_set(obs_IDs, :);
        obs_cnts(class_ID) = size(obs_list, 1);
        obs_store{class_ID} = obs_list;
        for chan ID = 1:chan cnt
```

```
centroids(class ID, chan ID) = mean(obs list(:, chan ID));
        end
    end
    centroid_abs = mean(data_set, 1);
    SSb = 0;
    SSW = 0;
    for class_ID = 1:class_cnt
       obs cnt = obs cnts(class ID);
        obs list = obs store{class ID};
        centroid class = centroids(class ID);
        SSb = SSb + (obs_cnt * (norm(centroid_class - centroid_abs)^2));
        for obs ID = 1:obs cnt
            SSw = SSw + (norm(obs_list(obs_ID, :) - centroid_class)^2);
        end
    end
   % Compute Criterion
   VRC = (SSb / SSw) * (micro_cnt - class_cnt) / (class_cnt - 1);
    obj = -1 * VRC / 1000;
   % Adjust bounds
    obj = obj + 50 * max([0, ((rand perc / perc thresh) - 1)]);
end
```

APPENDIX C. CHAPTER 3 PATH ID SCRIPTS

Setup

To determine paths using a specific model, pretrained model, place the following script in a file titled path_finder.mat. Files will use one label to indicate sampling frequency, freq, which is either "04" or "40" respectively. Files will use another label, type, to indicate the specific constraints placed on the state definition. Use type "c" to indicate compass, type "t" to indicate target heading, and type "p" to indicate positionless.

In the same directory as this file, place the parameter trace data stored as a variable in the file trainingStates_trimmed_freqtype.mat. Place the corresponding control trace data in a file trainingInputs_trimmed_freqtype.mat. Replace "freqtype" in both file names with the corresponding strings for freq and type used. A third file, storing a matrix containing the indices of the end of each use instance in the trace for the sampling frequency, should be placed in the same directory and titled end_IDs_freq.mat. Replace "freq" with the corresponding freq string.

State models should be placed in directories inside the current, following the file path "Classifications/Optimized run **freqtype**/model_GMM.mat", replacing "freqtype" as before. Path models should be place in separates directories, labeled "Path Models/**freqtype**". Mean parameter and control values for each state should be stored in the corresponding directory in the file mean_vals.mat. These values should be stored in a matrix, with each row corresponding to a state, and each column to a metric. Similarly, standard deviations should be stored in the file stdDev vals.mat in the same directory.

For microstate prediction, metric prediction models should be stored in internal directories to the previous freqtype path model directory. Each state should have a corresponding directory, title S#, where # corresponds to the state ID. Each model needs to be named **metric** model.mat, with metric replaced by the corresponding metric ID code.

Direct prediction models can then be stored in this same directory using the filename direct_samp_model.mat, where samp is replaced by the sampling method, either "rand" or "stan".

path_finder.mat

This script compares a path prediction method to the ground truth using the path prediction models from requisite folders and labels from the provided trace. Note that freq and type define the trace used, as well as which parameters are relevant for path definition. These parameters are based on state definitions. The variable predictor will determine which type of model will be used for prediction, and samp will determine the sampling method used for training the original model. Samp only affects which model is loaded.

In general, this script is highly specialized to the exact case tested in this thesis and could be more efficiently adapted if written from scratch. Path models were individually generated from MATLAB's regression learner and classification learner apps and have not been automated in a script. I highly recommend storing normalization means and standard deviations in files and retrieving them in every scrip over recalculating and normalizing. This also goes for state and path labels, as relabeling all of the trace every run can lead to inconsistencies if scripts change accidentally.

```
%% path finder03
% This script uses indivudal channel models to predict path
% Changes from 02
     - Enabled
8
clc
clear
%% Program settings
% Primary settings
freq = '40';
type = 'p';
state init = 3;
predictor = 'direct'; % micro / direct
samp = 'Stan'; % Rand / Stan
% Secondary settings
class labels = {'Low-speed'; 'High-speed'; 'Hazard'};
state order = load(strcat('state order ', freq, '.mat'));
state order = state order.state order;
class cnt = size(state order, 2);
if strcmp(freq, '04')
    if strcmp(type, 'c')
        chan GMM = [1; 2; 9; 11; 12; [14:18]'; 23];
        label names = {'SINCH'; 'COSCH'; 'ZPL'; 'YVI'; 'ZVT'; 'ZVL'; 'FVP';
'VVP'; 'HVP'; 'T'; 'B'};
        state order = state order(1, :);
```

```
plot title = strcat('4 Hz, compass, ', { ' '}, predictor, ' prediction
confusion');
    elseif strcmp(type, 't')
        chan GMM = [1; 5; 8; 11; [13:18]'];
        label names = {'SINTH'; 'XPT'; 'XPL'; 'YVI'; 'XVL'; 'ZVL'; 'FVP';
'VVP'; 'HVP'; 'T'};
        state order = state order(2, :);
        plot title = strcat('4 Hz, target, ', {' '}, predictor, ' prediction
confusion');
    elseif strcmp(type, 'p')
        chan GMM = [3; 4; 11; [15:19]'];
        label names = {'PA'; 'BA'; 'YVI'; 'FVP'; 'VVP'; 'HVP'; 'T'; 'CSE'};
        state order = state order(3, :);
        plot title = strcat('4 Hz, positionless, ', {' '}, predictor, '
prediction confusion');
    elseif strcmp(type, 'm')
        chan GMM = [1; [3:7]'; 10; 11; [13:21]'];
        label names = {'SIN(TH)'; 'SIN(CH)'; 'COS(CH)'; 'PA'; 'BA'; 'XPT';
'XPL'; 'ZPL'; 'YVI'; 'ZVT'; 'XVL'; 'ZVL'; 'FVP'; 'VVP'; 'HVP'; 'T'; 'CSE'};
        state order = 1:class cnt;
        plot title = strcat('4 Hz, merged, ', {' '}, predictor, ' prediction
confusion');
    end
elseif strcmp(freq, '40')
    if strcmp(type, 'c')
        chan GMM = [1; 2; 7; 11; 12; [14:18]'];
        label names = {'SINCH'; 'COSCH'; 'XPT'; 'YVI'; 'ZVT'; 'ZVL'; 'FVP';
'VVP'; 'HVP'; 'T'};
    elseif strcmp(type, 't')
        chan_GMM = [1; 2; 8; 11; [14:18]'];
        label names = {'SINTH'; 'COSTH'; 'XPL'; 'YVI'; 'ZVL'; 'FVP'; 'VVP';
'HVP'; 'T'};
    elseif strcmp(type, 'p')
        chan GMM = [3; 11; [15:19]'];
        label names = {'PA'; 'YVI'; 'FVP'; 'VVP'; 'HVP'; 'T'; 'CSE'};
        state order = state order(3, :);
        plot title = strcat('40 Hz, positionless, ', {' '}, predictor, '
prediction confusion');
    end
end
% Load main data
state master = load(strcat('trainingStates trimmed ', freq, type, '.mat'));
state master = state master.trainingStates trimmed(:, chan GMM);
[micro cnt, state chan cnt] = size(state master);
input master = load(strcat('trainingInputs trimmed ', freq, '.mat'));
input master = input master.trainingInputs trimmed;
[~, input chan cnt] = size(input master);
chan_cnt = state_chan_cnt + input_chan_cnt;
end IDs = load(strcat('end IDs ', freq, '.mat'));
end IDs = end IDs.end IDs;
% Load class model data
directory = strcat('Classifications/Optimized run', {' '}, freq, type);
```

```
directory = directory{1};
state model = load(strcat(directory, '/model GMM ', freq, type, '.mat'));
state model = state model.model GMM;
path cnt = class cnt^2;
% Set class correction
class convert = state order;
for class ID = 1:class cnt
    class convert(class ID) = find(state order == class ID);
end
% Load trend data
directory = strcat('Path Models/', freq, type);
normalization means = load(strcat(directory, '/mean vals.mat'));
normalization means = normalization means.mean vals;
normalization stdDevs = load(strcat(directory, '/stdDev vals.mat'));
normalization stdDevs = normalization stdDevs.stdDev vals;
directory = strcat('Path Models/', freq, type, '/');
mean vals = normalization means;
stdDev vals = normalization stdDevs;
for class_ID = 1:class_cnt
    store ID = class convert(class ID);
    normalization means(store ID, :) = mean vals(class ID, :);
    normalization stdDevs(store ID, :) = stdDev vals(class ID, :);
end
if isequal(predictor, 'micro')
    % Load channel model data
   path model set = cell(class cnt, state chan cnt);
    for class ID = 1:class cnt
        store ID = class convert(class ID);
        for model ID = 1:state chan cnt
            model name = strcat(label names{model ID}, ' model');
            model = load(strcat(directory, 'S', num2str(class ID), '/',
model name, '.mat'));
            path_model_set{store_ID, model_ID} = model.(model_name);
        end
    end
end
%% Establish ground truth
% Prep storage
state norm = state master;
state stdDev vals = zeros(state chan cnt, 1);
state mean vals = state stdDev vals;
% Iterate through channels
for chan ID = 1:state chan cnt
    state_stdDev_vals(chan_ID) = std(state master(:, chan ID));
    state mean vals(chan ID) = mean(state master(:, chan ID));
end
% Iterate through dataset
```

```
152
```

```
for chan ID = 1:state chan cnt
    stdDev val = state stdDev vals(chan ID);
    mean val = state mean vals(chan ID);
    if stdDev val == 0
        state norm(:, chan ID) = mean val;
    else
        for micro ID = 1:micro cnt
            state norm(micro ID, chan ID) = (state norm(micro ID, chan ID) -
mean val) / stdDev val;
        end
    end
end
% Prep storage
input norm = input master;
input stdDev vals = zeros(input chan cnt, 1);
input mean vals = state stdDev vals;
% Iterate through channels
for chan ID = 1:input chan cnt
    input stdDev vals(chan ID) = std(input master(:, chan ID));
    input mean vals(chan ID) = mean(input master(:, chan ID));
end
% Iterate through dataset
for chan ID = 1:input chan cnt
    stdDev val = input stdDev vals(chan ID);
    mean val = input mean vals(chan ID);
    if stdDev val == 0
        input norm(:, chan ID) = mean val;
    else
        for micro ID = 1:micro cnt
            input norm(micro ID, chan ID) = (input norm(micro ID, chan ID) -
mean val) / stdDev val;
        end
    end
end
% Cluster data
if type == 'm'
    class list = state model.predictFcn(state norm);
else
    [class list, ~, probs] = cluster(state model, state norm);
    for micro ID = 1:micro cnt
        class list(micro ID) = class convert(class list(micro ID));
    end
end
% Path data
path true list = zeros(micro cnt, 1);
for micro ID = 1:(micro cnt - 1)
   if not(ismember(micro ID, end IDs))
        path true list(micro ID) = ((class list(micro ID) - 1) * class cnt) +
class list(micro ID + 1);
    end
end
```

```
% Trim all data to remove instance ends
micro cnt = (micro cnt - length(end IDs));
state master(end IDs, :) = [];
input master(end IDs, :) = [];
class list(end IDs) = [];
path true list(end IDs) = [];
% Determine relevant micro IDs
keep list = find(class list == state init);
%% Model paths
if isequal(predictor, 'micro')
    % Prep storage
    state pred list = state master;
    % Predict behavior
    microdata master = [state master, input master];
    for class ID = 1:class cnt
        % Isolate microstates in class
        micro ID list = find(class_list == class_ID);
        % Normalize in class
        microdata norm = microdata master;
        for chan ID = 1:chan cnt
            stdDev val = normalization stdDevs(class ID, chan ID);
            if stdDev val
                microdata norm(micro ID list, chan ID) =
(microdata norm(micro ID list, chan ID) - normalization means(class ID,
chan ID)) / stdDev val;
            else
                microdata norm(micro ID list, chan ID) =
microdata norm(micro ID list, chan ID) - normalization means(class ID,
chan ID);
            end
        end
        % Predict for class
        for chan ID = 1:state chan cnt
            channel model = path model set{class ID, chan ID};
            state pred list(micro ID list, chan ID) =
(channel model.predictFcn(microdata norm(micro ID list, :)) *
normalization stdDevs(class ID, chan ID)) + normalization means(class ID,
chan_ID);
        end
    end
    micro ID list = find(class list == state init);
    % micro cnt = length(micro ID list);
    % ML comm = state pred list(micro ID list, :);
    % ML resp = path true list(micro ID list, :);
    % stdDev vals = zeros(state chan cnt, 1);
    % mean vals = state stdDev vals;
```

```
% % Iterate through channels
    % for chan ID = 1:state chan cnt
    00
          stdDev_vals(chan_ID) = std(ML_comm(:, chan_ID));
    8
         mean vals(chan ID) = mean(ML comm(:, chan ID));
   % end
   8
    % % Iterate through dataset
    % for chan ID = 1:state chan cnt
    00
         stdDev val = stdDev vals(chan ID);
    90
         mean val = mean vals(chan ID);
    8
         if stdDev val == 0
    8
             ML comm(:, chan ID) = mean val;
    9
         else
    9
              for micro ID = 1:micro cnt
                 ML comm (micro ID, chan ID) = (ML comm (micro ID, chan ID) -
    8
mean val) / stdDev val;
    00
         end
    00
         end
   % end
    % Convert to class
    for chan ID = 1:state chan cnt
        stdDev val = state stdDev vals(chan ID);
        mean val = state mean vals(chan ID);
        if stdDev val == 0
            state pred list(:, chan ID) = mean val;
        else
            for micro ID = 1:micro cnt
                state pred list(micro ID, chan ID) =
(state pred list(micro ID, chan ID) - mean val) / stdDev val;
            end
        end
    end
    class pred list = cluster(state model, state pred list);
    for micro ID = 1:micro cnt
        class pred list(micro ID) = class convert(class pred list(micro ID));
    end
    path pred list = ((class list - 1) * class cnt) + class pred list;
    path pred list = path pred list(keep list);
elseif isequal(predictor, 'direct')
    % Load path model
    path_model = load(strcat(directory, 'S', num2str(state init), '/direct',
samp, ' model.mat'));
   path model = path model.direct model;
    % Normalize metrics in state of interest
    microdata norm = [state master, input master];
    microdata norm = microdata norm(keep list, :);
    for chan ID = 1:chan cnt
        stdDev val = stdDev vals(state init, chan ID);
        if stdDev val
            microdata norm(:, chan ID) = (microdata norm(:, chan ID) -
mean vals(state init, chan ID)) / stdDev val;
        else
```

```
microdata norm(:, chan ID) = microdata norm(:, chan ID) -
mean vals(state init, chan ID);
        end
    end
    if type == 'c'
       microdata_norm(:, state_chan_cnt) = [];
    end
    % Predict path IDs
    path_pred_list = path_model.predictFcn(microdata norm);
end
% Plot results
path_true_list = path_true_list(keep list, :);
cm = confusionchart(confusionmat(path_true_list, path_pred_list),
class labels);
cm.RowSummary = 'row-normalized';
cm.ColumnSummary = 'column-normalized';
cm.Title = plot title;
sortClasses(cm, class labels);
```

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