SIERRA: A Modular Framework for Research Automation and Reproducibility

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Abstract—Modern intelligent systems researchers form hypotheses about system behavior and then run experiments using one or more independent variables to test their hypotheses. We present SIERRA, a novel framework structured around that idea for accelerating research development and improving reproducibility of results. SIERRA accelerates research by automating the process of generating executable experiments from queries over independent variables(s), executing experiments, and processing the results to generate deliverables such as graphs and videos. It shifts the paradigm for testing hypotheses from procedural (“Do these steps to answer the query”) to declarative (“Here is the query to test–GO!”), reducing the burden on researchers. It employs a modular architecture enabling easy customization and extension for the needs of individual researchers, thereby eliminating manual configuration and processing via throw-away scripts. SIERRA improves reproducibility of research by providing automation independent of the execution environment (HPC hardware, real robots, etc.) and targeted platform (arbitrary simulator or real robots). This enables exact experiment replication, up to the limit of the execution environment and platform, as well as making it easy for researchers to test hypotheses in different computational environments.

Index Terms—Research Automation, Reproducibility, Intelligent Systems, Robotics, Multi-Agent

1 INTRODUCTION

In modern intelligent systems research, the majority of researcher time is spent on two types of tasks: science and engineering. Science tasks consist of developing AI elements, defined as a new mathematical model, tool, or algorithm, while engineering tasks consist of configuring and running experiments for testing the new AI element, and some aspects of processing results. Frequently, it is only after science tasks have been nearly completed for a project that researchers consider the crucial issue of reproducibility, leaving them little time to ensure their work can be replicated by others. The difficulties of reproducibility are further compounded by the nature of the tools used to meet the engineering needs of a project: ad-hoc toolchains and scripts which are quickly thrown together on a per-project basis, and reused, modified, or duplicated on the fly. Usually, these toolchains and scripts are for dealing with “accidental complexities”\textsuperscript{1}, that is, with engineering difficulties unrelated to the challenges of the science itself. Examples include: handling different configurations for specific platforms, such as ROS\textsuperscript{2}, or execution environments, such as SLURM\textsuperscript{3} clusters, or for processing and visualizing experimental results; e.g., statistically summarizing data and generating graphs. Clearly, this approach is prone to errors and to reinventions of the wheel between research groups and individual researchers. In this paper, we present SIERRA, an open source framework for automating engineering tasks to improve reproducibility. SIERRA automates the process of hypothesis testing and results processing, and handles details for platforms, execution environments, data processing, and results visualization to reduce the burden on researchers and allowing them to focus on the “science” aspects of research: creative exploration of data, hypothesis testing, and experimental design.

2 MOTIVATION AND RELATED WORK

Our motivation in presenting SIERRA is based on our understanding of three pressing needs in the intelligent systems community. First, the need for better automation of the engineering tasks that many researchers perform. Second, the need for better reproducibility, which is one of the fundamental problems of intelligent systems research\textsuperscript{4}. While there is some debate on the exact criteria for reproducibility, there is general agreement that it is not a binary designation, but a spectrum\textsuperscript{5, 6}. Some methodologies and guidelines exist for helping to increasing reproducibility of the “science” parts of research\textsuperscript{6, 7}, and a few tools\textsuperscript{5, 9}. However, few tools exist for improving the reproducibility of the engineering aspects of research, which is often intertwined with reproducibility of scientific results\textsuperscript{6}; exceptions include\textsuperscript{5, 10}. Third, any tool meeting the first two criteria must have a low barrier to adoption. In other words, if the provided research automation or reproducibility guarantees are difficult to integrate with implementations not designed with them in mind, they will be much less likely to be adopted. Taken together, a tool that meets these needs will reduce the barriers to collaboration among researchers in similar areas which take different approaches, or whose labs have otherwise different implementations of shared ideas.

We begin with the idea of a research query in intelligent systems research: a query of an independent variable over some range. Examples include: “How will this algorithm perform in this scenario with this range of inputs?”\textsuperscript{"}, “What are the practical limits of this algorithm?”\textsuperscript{"}, and “How does this algorithm compare to other similar algorithms?” Research queries are different than scientific hypotheses, which

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TABLE 1  
Common research pipeline in modern intelligent systems research, from an engineering perspective.

| Stage                  | Description/current practice                                                                                                                                 |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Experiment generation  | A researcher designs a batch experiment to test an AI element. If there is randomness in the experimental inputs or in the AI element itself such as a random seed, multiple experimental runs are defined for each per experiment so that statistically valid inferences about the behavior of the AI element can be made. **Current practice.** Researchers utilize custom and/or throw-away scripts or otherwise manually set parameters defining the experiments [1]. |
| Experiment execution   | The researcher runs the batch experiment, collecting data about different aspects of the AI element. **Current practice.** Researchers use custom scripts to configure their chosen execution environment, such as a High Performance Computing (HPC) environment, and then run their experiments on it. There is often tight coupling between the execution environment and the targeted platform in the scripts, making reuse difficult. Further manual configuration is required for real robot applications, such as synchronizing the experimental inputs and configuration on each robot. |
| Experiment results processing | The researcher processes the collected data to generate statistical insights about the performance of their AI element, its limitations, and its strengths. **Current practice.** Researchers use mature libraries for processing experiment data, such as pandas. Scripts for analysis are frequently written for the specific pipeline instance; that is, they are not reusable between the development of one algorithm and another by a given researcher or across research groups. |
| Deliverable generation | The researcher generates visualizations from processed data which can be used to inform further refinements and tuning; common visualizations include graphs and videos. If the results are satisfactory, then these deliverables are polished to make them camera-ready and included on relevant publications or technical reports on the AI element. **Current practice.** Researchers utilize custom and/or throw-away scripts or otherwise manually set parameters defining the execution environment to run research experiments [1]. |
| Deliverable comparison | The researcher generates comparative visualizations of their AI elements and other similar elements in the field for inclusion in publications or technical reports, in order to show how their contribution improves or is different from the state of the art. **Current practice.** Researchers utilize custom and/or throwaway scripts to generate comparative visualizations. |

are possible explanations for an observed phenomenon or answers to a posed research query. Each “value” of the independent variable in this range forms the basis for an experiment. Experiments take a given value of the independent variable and operationalize it in the context of a platform such as a simulator or a run-time executive by adding necessary configuration so that the query can be executed on the platform. The set of experiments operationalizing a research query into something that can be executed is defined as a batch experiment. By comparing results across experiments in the batch, changes in system behavior in response to the different “values” can be observed. Each experiment contains one or more experimental runs, which can be simulations, training runs, or real robot trials. Experimental runs are executed on an execution environment such as a High Performance Computing (HPC) cluster, a researcher’s laptop, or real robot hardware.

Formalizing the above, consider the common five stage pipeline for experimental validation of a new AI element that is shown in Table 1. With this terminology and research pipeline, we can now discuss the main motivations behind SIERRA in more detail.

1) **Automation.** From Table 1 we note the following important insight: most stages contain substantial engineering tasks that are performed manually by researchers; these “accidental complexities” are frequently non-trivial, and slow down the actual research. Dealing with such complexities takes valuable researcher time even with many toolkits available to help, such as pandas and matplotlib. In robotics research, existing automation in simulation only targets parts of the pipeline [10]; similarly for real robots [8], [11]. Thus, substantial researcher time is spent on the “non-research” aspects of intelligent systems research generally, and robotics research specifically, limiting progress and clearly motivating the need for more general-purpose automation.

2) **Reproducibility.** Some challenges to reproducibility in modern intelligent systems research include (a) “dependency hell”, which is the problem of reproducing the execution environment to run research software, (b) imprecise or missing documentation, which exacerbates (a), (c) code erosion, which is the problem of running outdated researcher code in more recent execution environments, and (d) a high barrier to integration with existing solutions [4]. These issues are non-trivial; recent studies found that less than half of academic code from papers at recent AI conferences were runnable (not that they reproduced results, but that they ran at all), even with the help of the authors [6], [12].

3) **Low barrier to adoption.** Any software tool that addresses the research automation and reproducibility needs in modern intelligent systems community must be “low threshold, no ceiling” [13]. That is, it must meet the following criteria. First, it must have an extremely low barrier for new users. The
barrier will differ across researchers and fields, but some desirable characteristics include: (a) minimal, easy to understand configuration, (b) ease of reuse of custom configuration and functionality across projects and researchers, (c) plug-and-play faculties that do not require recompilation or repackaging to incorporate new functionality, and (d) high quality documentation and many examples [1], [6]. Second, it must be designed to be customizable in unknown ways, in order to support rapid adoption by researchers in academic and industry labs. In other words, it must be able to accommodate the “unknown unknown” future needs of researchers.

2.1 Motivating Use Cases

We present the following two motivating use cases to help ground the broad areas in which SIERRA is useful in contexts containing characteristics many researchers will be familiar with in Figs. 1 and 2.

Use case #1: Alice the foraging algorithm designer

Alice is a researcher at a university that has developed a new distributed task allocation algorithm $\alpha$ for use in a foraging task where robots must coordinate to find objects of interest in an unknown environment and bring them to a central location. Alice wants to implement her algorithm so she can investigate:

- How well it scales with the number of robots, specifically if it remains efficient with up to 100 robots in several different scenarios.
- How robust it is with respect to sensor and actuator noise.
- How it compares to other similar state of the art algorithms on a foraging task: $\beta, \gamma$.

Alice is faced with the following heterogeneity matrix that she must deal with to answer her research queries, in addition to the technical challenges of the AL elements themselves:

| Algorithm | Has randomness? | Outputs data in? |
|-----------|----------------|-----------------|
| $\alpha$  | Yes            | CSV, rosbag     |
| $\beta$   | Yes            | CSV, rosbag     |
| $\gamma$  | No             | CSV, rosbag     |

Alice is familiar with ROS, and wants to use it with large scale simulated and small scale real-robot experiments with TurtleBots. However, for real robots she is unsure what data she will ultimately need, and wants to capture all ROS messages with rosbag to avoid having to redo experiments later. She has access to a large SLURM-managed cluster.

Use case #2: Alice the contagion modeler

Alice has teamed with Bob, a biologist, to model the spread of contagion among agents in a population, and how that affects their individual and collective abilities to do tasks. She believes her $\alpha$ algorithm can be reused in this context. However, Bob is not convinced and has selected several multi-agent models from recent papers: $\delta, \epsilon$, and wants Alice to compare $\alpha$ to them. $\delta$ was originally developed in NetLogo [13], for modeling disease transmission in animals. $\epsilon$ was originally developed for ARGoS [14] to model the effects of radiation on robots. All algorithms contain randomness.

Alice is faced with the following heterogeneity matrix that she must deal with to answer the research query, in addition to the technical challenges of the AI elements:

| Algorithm | Can run on? | Input requirements? |
|-----------|-------------|---------------------|
| $\alpha$  | ROS/Gazebo  | XML                 |
| $\delta$  | NetLogo     | NetLogo             |
| $\delta$  | ARGoS       | XML                 |

Bob is interested in how the rate of contagion spread varies with agent velocity and population size. Bob needs to prepare succinct, comprehensive visual representations of the results of his research queries for a presentation, including visual comparisons of the multi-agent model as it runs for each algorithm. He will give Alice a range of parameter values to test for each algorithm based on his ecological knowledge, and rely on Alice to do the experiments. Alice does not have access to HPC resources, but does have a handful of servers in her lab that she can use.

They will be used later in Section 4 to concretely illustrate many features of SIERRA, such as its ability to handle the heterogeneity matrices in each use case transparently to our imagined researcher, Alice.

3 SIERRA Overview

In this section, we give a broad overview of SIERRA, a command line tool for automating the pipeline described in Table 1. High level details on how SIERRA addresses both issues of reproducibility and automation in modern intelligent systems research follows below; SIERRA is, to the best of our knowledge, the first such tool presented in the literature. An architectural overview is in Fig. 3.

1. Automation. SIERRA accelerates research cycles by allowing researchers to focus on the “science” aspects: developing AI elements and designing experiments to test them. SIERRA changes the paradigm of the engineering tasks researchers must perform...
from manual and procedural to declarative and automated. That is, from “Do these steps to run the experiment, process the data and generate graphs” to “Here is the environment and platform, the deliverables I want to generate and the data I want to appear on them for my research query–GO!”.

Essentially, SIERRA handles the “backend” parts of research, such as: random seeds, algorithm stochasticity, configuration for a given execution environment or platform, generating statistics from experimental results, and generating visualizations from processed results. By employing declarative specification via command line arguments and YAML configuration, it eliminates manual re-configuration of experiments across platforms by decoupling the concepts of execution environment and platform (see Table 2); any supported pair can be selected in a mix-and-match fashion. Furthermore, it removes the need for throw-away scripts for data processing and deliverable generation by providing rich, extensible faculties for those pipeline stages.

2) Reproducibility. SIERRA supports reusability and reproducibility across projects in two main ways. First, through its automation: SIERRA experiments are fully reproducible, up to the limit of the platform targeted and the execution environment on which the experiments are run. In such cases, with a single SIERRA command another researcher Charlie could reproduce Alice’s exact results and generated deliverables if both were using SIERRA and he had access to Alice’s code and raw input data. Second, through its “low threshold, no ceiling” approach: all aspects of its configuration is done through command line switches and YAML configuration, allowing easy reuse between projects.

3) Low barrier to adoption. SIERRA is designed to have minimal barriers to adoption by researchers across disciplines through in situ integration with existing code implementations, yet also be extensively customizable for advanced users; i.e., “low threshold, no ceiling”. It accomplishes this in two ways. First, it is written in the python programming language, which is not only “write once, run anywhere”, but also has a very human readable syntax. Second, it is organized into a reusable core and a plugin manager which supports any number of plugins of any type that can be used to customize nearly every aspect of its implementation of the research pipeline shown in Fig. 3. Thus, adding support for a new platform or execution environment as simple as implementing a python interface, and placing the resulting file(s) on SIERRA’s plugin path. Plugins can be written in any language; only the bindings must be written in python. SIERRA is open source under the GPLv3 license, allowing researchers to

![SIERRA Architecture and Execution Path](image)

Fig. 3. Architecture of SIERRA, organized by pipeline stage. Pipeline stages are listed left to right, with an approximate joint architectural/functional stack from top to bottom for each stage. “...” indicates areas where SIERRA is designed to be configurable or extensible with python plugins. “Host machine” indicates the machine SIERRA was invoked on.

| Execution Environment | Description | Supported platforms |
|-----------------------|-------------|---------------------|
| SLURM                 | A SLURM managed HPC cluster. | ARGoS, ROS1+Gazebo |
| Torque/ MOAB          | A MOAB managed HPC cluster. | ARGoS, ROS1+Gazebo |
| ADHOC                 | A miscellaneous collection of networked compute nodes a given researcher has available. | ARGoS, ROS1+Gazebo |
| Local machine         | A researcher’s local machine to use for small scale testing. | ARGoS, ROS1+Gazebo |
| ROS1+ TurtleBot3      | ROS1 with TurtleBot3 [17] robots. | ROS1+Gazebo, ROS1+real robot |
modify it according to their needs, and comes with extensive documentation and tutorials.

4 SIERRA PIPELINE AUTOMATION

SIERRA is designed to automate research queries expressed in a researcher-defined command line syntax. In SIERRA terminology, this is the univariate batch criteria used to define a batch experiment. SIERRA also supports bivariate batch criteria, in which researchers are interested in how system behavior changes in response to the values of two independent variables jointly varying; in such cases, the state space for the batch experiment is a 2D grid instead of a one dimensional line. SIERRA handles both types of batch criteria transparently.

For our first use case, these could be:

- population_size.Log128, representing univariate experiments with \{1, 2, 4, 8, \ldots, 128\} agents.
- ta_policy_set.all.Z100, representing univariate experiments with one of a set of task allocation policies \{\alpha, \beta, \gamma\}, with the number of robots fixed to 100 for all runs.
- system100 saa_noise.all.C10, representing bivariate experiments with \{1, 2, 3, \ldots, 100\} robots and 10 different levels of noise applied to both robot sensors and actuators.

For the second use case, this could be:

vel.min=1p0.max=10p0.C10 n_agents.Log4096, representing bivariate experiments with \{1, 2, 4, 8, \ldots, 4,096\} agents and agent velocities, which will be one of 10 values: \{1.0, 2.0, \ldots, 10.0\}. The syntax for expressing research queries is entirely arbitrary, and can be set according to each researcher’s needs; researchers also define parsers for their syntax.

Once a research query has been operationalized by SIERRA and written to the filesystem as a batch experiment, SIERRA can execute it by running the experiment and then process the results; details of the provided automation can be executable. For each pipeline stage shown below. To help further demonstrate SIERRA’s capabilities, we will reference the partial SIERRA commands in Figs. 4 and 5 throughout the rest of this section. We note that running stages \{1, 3, 4, 5\} in sequence is not required; any topologically ordered subset can be executed. For example, suppose Alice has just changed the YAML configuration for what deliverables to generate. She could then instruct SIERRA to run stages \{3, 4\} only by adding --pipeline 3 4 to Fig. 4 or Fig. 5

4.1 Experimental Input Generation

To generate the batch experiment, researchers provide a template XML file containing all configuration necessary to answer the research query. Any XML element SIERRA is not directed to change through a batch criteria or other plugin will remain unchanged, allowing researchers to set common configuration options that should remain the same for all experiments and all experimental runs.

SIERRA currently requires that the template input file be XML, which was chosen over other input formats for three reasons. First, it is not dependent on whitespace/tab/spaces for correctness, making it more robust to multiple platforms, simulators, parsers, users, etc. Second, mature manipulation libraries exist for python and C++, two of the most common languages in intelligent systems research, so it should be relatively straightforward for projects to read experimental definitions from XML. Third, many popular platforms already support XML input, such as ARGoS, ROS, and Webots. If a researcher wants to add support for a platform that does not support XML, SIERRA’s modular architecture makes it easy to do so.

The XML template input file is modified according to the research query, with one experiment generated for each “value” of the independent variable(s). Each “value” may correspond to a single change to the template, such as population_size.Log32 for changing the number of agents, or it can correspond to multiple changes, such as saa_noise.all.C10 for changing the level of noise applied to multiple sensors and actuators in each experiment. SIERRA also supports changing additional parts of the template input file uniquely for each experiment batch.

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1. https://swarm-robotics-sierra.readthedocs.io/en/master/

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Fig. 4. A partial SIERRA command for a batch experiment containing 7 experiments of some number of runs each; the total number of runs varies from one experiment to the next.

```
sierra-cli \
--template-input-file=exp.launch \n--platform=platform.ros1gazebo \n--project=task_alloc \n--batch-criteria population_size.Log128 \n--controller=task_alloc.alpha \n--robot TurtleBot3 \n--no-master-node\n--exp-setup=exp_setup.T1000.K100
```

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Fig. 5. A partial SIERRA command for a batch experiment containing 12 experiments of 100 runs each, for 1,200 total simulations. Experiments will be 10,000 seconds long, with robot controllers running at 100 Hz. SIERRA’s ability to setup a central ROS node on the ROS master (SIERRA host machine) for use in data collection is not needed, and so is disabled. The argument to --robot is entirely arbitrary; whatever is passed maps to a set of user-defined YAML configuration which allows arbitrary XML modifications. This can include specifying ROS nodes to launch, parameters to set, etc.

```
sierra-cli \
--template-input-file=exp.launch \n--project=contagion \n--batch-criteria population_size.Log4096 \n--controller=task_alloc.alpha \n--exp-setup=exp_setup.T10000 \n--platform-vc \n--n-runs=100
```
or uniformly for all experiments, providing unparalleled expressiveness to support research automation through experiment generation.

SIERRA provides comprehensive support for research that requires multiple experimental runs in each experiment; this may be required due to randomness in the agents, e.g., imperfect sensors/actuators on real robots, or algorithm stochasticity. SIERRA manages this complexity transparently to researchers, and further provides faculties for supporting idempotency of experiments, up to the limit of the execution environment and platform. For example, SIERRA can save generated random seeds, ensuring that if a platform respects the random seed, then stage 2 of the pipeline in Table 2 is idempotent.

In our first use case, Alice can put any common parameter options in the XML template file in a <common> section and then unique subsections for each algorithm: <alpha>, <beta>, etc. She could also give each algorithm its own XML file and duplicate the common section for each, according to her preference. To handle the stochasticity of $\alpha, \beta$, she can tell SIERRA to do multiple runs per experiment by adding a --n-runs argument to Fig. 4. In our second use case, Alice can specify all input parameters in XML for all algorithms, and then add a new SIERRA platform plugin for the NetLogo simulator, which transforms the NetLogo template input file into XML via xslt or other tool. Alice can then generate experimental inputs for each platform from the same research query as easily as adding --platform.({argos, ros1gazebo, netlogo}) to Fig. 5.

4.2 Running Experiments

After a batch experiment has been operationalized and written to the filesystem, SIERRA can execute it in full or only arbitrary subsets of the experiments. For example, if experiments #10–12 keep crashing, Alice can enable more debugging in her code and then re-run the problematic experiments by adding --exp-range=10:12 to Fig. 4. We note that SIERRA’s automation for this pipeline stage enables it to provide concurrent execution of experimental runs for platforms that do not support it natively, such as Gazebo, and to utilize intrinsic parallelism for platforms that do support it, such as NetLogo.

Experimental run inputs are executed using GNU parallel [18] on a selected execution environment and targeted platform (see Table 2 for SIERRA’s current support matrix). SIERRA handles the necessary configuration for all supported platforms and execution environments, allowing researchers to transparently switch between them with minimal code changes; cross-compiling or re-architecting may be necessary depending on the nature of researcher code, and the selected platform. This effectively makes the question of “Where can I run my experiment?” logistical and declarative, rather than technical and procedural.

In our first use case, Alice can run her code on her laptop during development by adding --exec-env=hpc.local to Fig. 4. Then, once she is confident in her algorithm’s correctness, she only has to pass --exec-env=hpc.slurm instead to tell SIERRA to run her code on her SLURM cluster. She will only have to submit a SLURM job containing her SIERRA invocation with a given set of resources and SIERRA will figure out everything else. For her real robot experiments, she will only need to change --exec-env=robots.turtlebot3 and --platform=platform.rosrobot to tell SIERRA to run with real TurtleBots. In our second use case, after the necessary code tweaks, Alice can tell SIERRA to run her simulations on her adhoc network of compute nodes by adding --exec-env=adhoc to Fig. 4.

4.3 Processing Experimental Results

After a batch experiment has been finished (or even part of it has), SIERRA can process outputs from arbitrary subsets of experiments in the batch using the --exp-range, analogously to the previous stage. Results processing is independent of experiment execution; that is, SIERRA’s plugin framework homogenizes reading of experimental results recorded in arbitrary formats. To process results, researchers need to specify which experimental outputs and types of statistics they are interested in, and SIERRA will then do one or more of the following. First, statistical distribution generation across experimental runs for the selected experiments in the batch (intra-experiment statistics), as well as across experiments in a batch (inter-experiment statistics). Inter-experiment statistics are necessary so that summary performance and behavioral measurements can be generated later; only using the averaged results from the statistical distribution generation in intra-experiment statistics is often insufficient. Second, converting output CSV files into heatmap images (see Fig. 6) that can be stitched together into videos during stage 4.

In both use cases, Alice can generate statistics for all simulations by telling SIERRA that her simulation data are stored in CSV format by adding --storage-medium=storage.csv to Fig. 4. For her real robot experiments in the first use case, she can write a storage plugin that converts rosbag files into pandas dataframes, and generate equivalent statistics. In either case, if she initially specified 95% confidence intervals on a set of line graphs, she could switch to box and whisker plots by changing --dist-stats=conf95 to --dist-stats=bw.

4.4 Generating Deliverables

Processed experimental results are used to generate deliverables to be part of published research. This can include graphs or videos showing different aspects of the system’s response to the research query. Which graphs or videos are generated is controlled by YAML configuration, allowing researchers to easily disable generation of deliverables not of interest. SIERRA’s automation in this stage makes it easy to modify a specific graph or video, if, for example, one needs to be modified at a reviewer’s request, eliminating the tedious process of locating previously written throw-away scripts to regenerate it. For some examples of the types of graphs SIERRA can generate during this stage, see Fig. 6.

One important feature of SIERRA in this stage is its model framework. It allows researchers to generate data from first principles or from experimental results (or both), and plot the generated data alongside empirical results; this is commonly used for plotting model predictions. As
4.5 Deliverable Comparison

After deliverable generation, multiple deliverables can be combined to provide side-by-side graphical comparisons; that is, SIERRA can take any data from two graphs of any type from any two batch experiments and replot them on a single figure. This comparison can take two forms. First, *intra-scenario* comparison, in which graphs from experiments evaluating different algorithms in the same context (scenario) are combined; this is shown in Fig. 7(a). Second, *inter-scenario* comparison, in which graphs from batch experiments evaluating the same algorithm in different contexts (scenarios) are combined; this is shown in Fig. 7(b). Such high-level comparisons are useful for demonstrating where/how a given AI element is better or different than the other method; α in our use cases. For example, suppose the Alice did not like the side-by-side heatmaps showing differences in algorithm performance, because they did not show which differences were statistically significant. She could ask SIERRA to generate a set of linegraphs instead (one per row or column in the heatmap), showing summary statistics such as confidence intervals or box and whisker plots graphically.

5 Discussion

We have given a brief tour through some of SIERRA’s features, using motivating use cases to show how using SIERRA can address two of the most pressing needs in intelligent systems research: increasing research reproducibility of results, and accelerating research and development cycles. Furthermore, as illustrated by our second use case, by addressing these two needs simultaneously SIERRA also substantially lowers the bar to collaboration between researchers across disciplines. Clearly, the scope of SIERRA’s applicability is broad, and many compelling use cases for its adoption exist. We believe that adoption of a tool such as SIERRA to provide a near-universal pipeline for intelligent systems research that supports reproducibility and reusability is paramount to continuing to make meaningful progress as systems and approaches become more complex.

However, SIERRA was originally developed for robotics research and therefore with the needs of robotics researchers in mind, and its direct applicability to other domains may be limited, for two reasons. First, as described above, it is currently restricted to use cases where experimental inputs can be specified in XML. This is not a major limitation in the robotics community, as most of the major platforms support XML inputs. Outside robotics, other platforms of interest might not support XML, making the utilization of SIERRA impossible without substantial work on the part of researchers to develop tools to translate non-XML input formats to/from XML so that SIERRA can work with them. Nevertheless, if such translation is necessary SIERRA’s modular design can easily support such an internal translation on a per-platform basis for future use cases.

Second, the translation from automating agent-based or robotics research to broader intelligent systems research involving machine learning, deep learning, or other non-agent approaches may not fit the pipeline described in Table 1. For example, training runs for neural networks, or qualitative coding of Human-Robot Interactions (HRI) studies may be difficult to fit into SIERRA’s paradigm. Nevertheless, for fields for which SIERRA may be difficult to use, we would hope that it would serve as an inspirational basis to build a similar tool.

Finally, we note two additional limitations of SIERRA. First, SIERRA does not attempt to homogenize configurations such that the results of a research query are the same, regardless of platform and execution environment, which is not possible in general. Second, SIERRA requires a...
common filesystem for all automation components, which can include nodes in an HPC cluster, robots, etc., in order to be used out-of-the-box. Support for non-networked computational components can of course be performed by researchers to adapt their code to SIERRA, as shown in our second use case with a new --storage-medium plugin. Alternatively, if --no-master-node is not passed then ROS messages to pass robot data to a centralized collection node on the SIERRA host machine to write out the data can be used—it would be as if the experiment had run on the host machine from SIERRA’s perspective.

5.1 History and community acceptance

SIERRA has been under development since 2016. Version 1.2 was demonstrated at AAMAS [19], and is available as a stable, reliable release that comes with extensive documentation and tutorials. Earlier versions of SIERRA have been used for several publications in top conferences [20–22] using ARGoS and ROS1 on PBS and SLURM HPC clusters, and with real TurtleBots at the University of Minnesota. SIERRA is open source, and is available on PyPI [6]. SIERRA receives about 100 downloads/week, a sign of its relevance as a tool for researchers. A comprehensive demonstration of SIERRA’s capabilities can be found here[3], including how it supports easy exploration of independent variables and experimental data.

6 Conclusions

We have presented SIERRA, a new tool that addresses two important needs in the intelligent systems community: the need for better automation of engineering tasks that many researchers perform and the need for better reproducibility of research results. As a “low threshold, no ceiling” tool, it significantly lowers the barrier to collaboration between researchers across disciplines without compromising customizability for advanced users. Thus, SIERRA is not only relevant for the current needs of intelligent systems researchers, but also for their future needs, and we strongly argue for its inclusion in any researcher’s toolbox. Further improvements to SIERRA include: removing the restriction that experimental inputs be specified in XML, expanding the set of execution environments and platforms it supports natively, and refining its configurability during statistics and graph generation to expose more of the underlying matplotlib and pandas.

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