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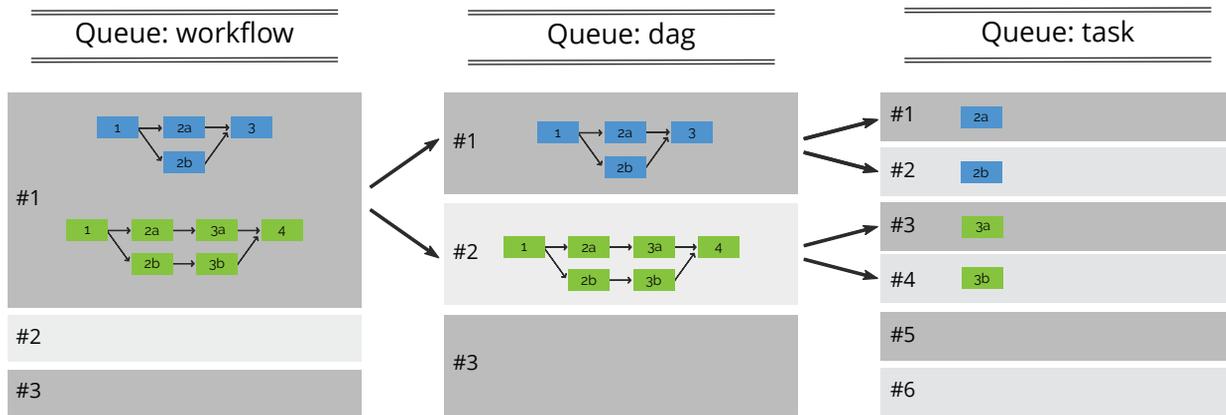


Figure 2: Worker based architecture of Lightflow. Workers are used to manage the three main components of a workflow: workflows, DAGs and tasks. In a typical setup for a computing cluster there are multiple queues for tasks.

aggregation of values, calculation of running averages, or the storage of flags.

Tasks can receive data from upstream tasks and send data to downstream tasks. Any data that can be serialised can be shared between tasks. Typical examples for data flowing from task to task are file paths, pandas [6] DataFrames or numpy [7] arrays. The exchange of data across a distributed system is accomplished by using cloudpickle [8] in order to serialise and deserialise the data. Lightflow provides a fully featured command line interface for starting, stopping and monitoring workflows and workers. The command line interface is based on the click [9] Python module. An API is also available for easy integration of Lightflow with existing tools and software.

In order to keep Lightflow lightweight, the core library focuses on the essential functionality of a distributed workflow system and only implements two tasks, a generic Python task and a bash task for calling arbitrary bash commands. Specialised tasks and functionality is implemented in extensions. Currently there are three extensions to Lightflow available: The filesystem extension offers specialised tasks for watching directories for file changes and tasks covering basic file operations [10]; the EPICS [11] extension offers tasks that hook into EPICS [12], a control system used at the Australian Synchrotron for operating the hardware devices of the accelerator and the beamlines; and the REST extension provides a RESTful interface for starting, stopping and monitoring workflows via HTTP calls [13].

WORKFLOW DEFINITION

Lightflow uses Python and an efficient API to define a workflow. Users don't have to learn a domain specific language and can use their preferred Python libraries. The workflow definition can be tested locally and scales without changes to run on a computing cluster. Lightflow ships with 15 examples, highlighting all features of the workflow system. The following source code shows a simple workflow definition consisting of three tasks, incrementing a number:

```

from lightflow.models import Dag
from lightflow.tasks import PythonTask

# the callback function for all tasks
def inc_number(data, store, signal, context):
    print('Task {task_name} being run in '
          'DAG {dag_name} for workflow '
          '{workflow_name} ({workflow_id}) '
          'on {worker_hostname}'.
          format(**context.to_dict()))

    if 'value' not in data:
        data['value'] = 0

    data['value'] = data['value'] + 1
    print('This is task ↴
          #{}'.format(data['value']))

# create the main DAG
d = Dag('main_dag')

# create the 3 tasks that increment a number
task_1 = PythonTask(name='task_1',
                    callback=inc_number)

task_2 = PythonTask(name='task_2',
                    callback=inc_number)

task_3 = PythonTask(name='task_3',
                    callback=inc_number)

# set up the graph of the DAG
# as a linear sequence of tasks
d.define({
    task_1: task_2,
    task_2: task_3
})
    
```

LIGHTFLOW AT THE AUSTRALIAN SYNCHROTRON

Lightflow at the MX Beamline

The two Crystallography beamlines (MX1, MX2) at the Australian Synchrotron have employed a custom made data management workflow for a number of years. Both the raw and reconstructed data of an experiment is compressed into squashfs files, verified and stored in the central storage system of the Australian Synchrotron. Recently this workflow has been upgraded to use Lightflow in order to take advantage of a distributed system to compress multiple experiments at the same time. The updated setup consists of a management virtual machine that hosts the workflow and DAG queues as well as acting as a REST endpoint for starting the squashfs workflow. Three physical servers act as squashfs nodes. The workflow is triggered by a HTTP REST call from the experiment change management system at the Crystallography beamlines.

Lightflow at the SAXS/WAXS Beamline

Several data processing pipelines are implemented using Lightflow for the SAXS/WAXS beamline. An example is the phaseID pipeline. This pipeline identifies diffraction peak positions within SAXS profiles and infers the most likely Space Group. This pipeline enables researchers to rapidly determine phase diagrams for self-assembled lyotropic liquid crystal systems. These systems are important for drug delivery and controlled release.

CONCLUSION

Lightflow is a lightweight and distributed workflow system written in Python and has been released as open source

software on GitHub [1]. It is currently used at several beamlines at the Australian Synchrotron for managing data or implementing data processing pipelines. The next steps are to extend the use of Lightflow at the Australian Synchrotron to the experiment change management at beamlines, complex data management workflows and auto processing workflows at the Crystallography beamlines.

REFERENCES

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- [9] Click, <http://click.pocoo.org>
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- [13] Lightflow Rest, <https://github.com/AustralianSynchrotron/lightflow-rest>