BioBlend – automating bioinformatics with Galaxy and CloudMan

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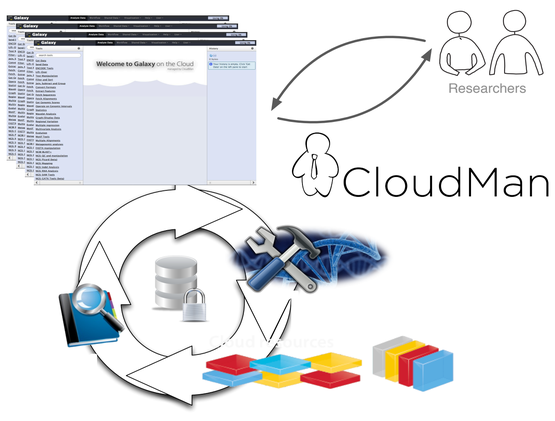
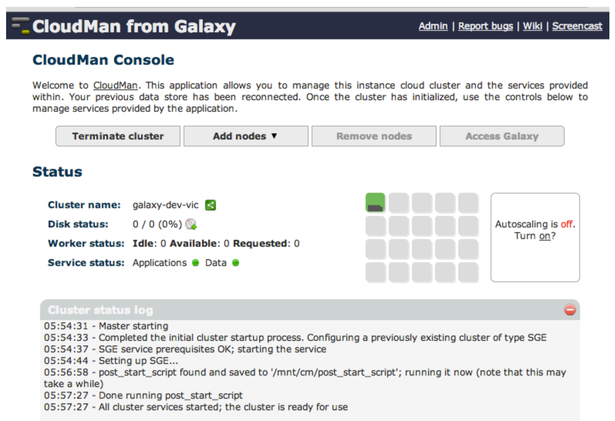
BioBlend is a python library which wraps and documents the functionality of both the Galaxy and the CloudMan REST-based APIs. The Galaxy API gives users access to a rapidly exanding set of Galaxy functionality, while the CloudMan API allows users to manipulate the CloudMan cloud-based job runtime platform. These APIs can be used individually, or can be used together to automate the end-to-end provision and operation of a Galaxy cluster on the cloud.

The library is easily installable via PyPi and comes with detailed documentation and example scripts. BioBlend is released under the MIT license. Documentation and installation instructions can be found at http://bioblend.readthedocs.org/.

CloudMan

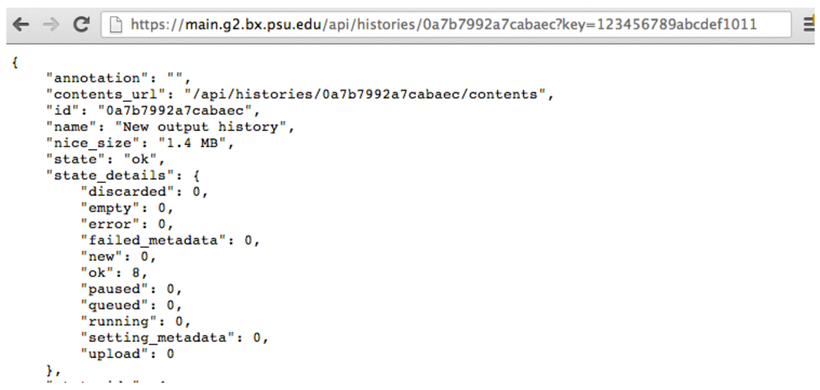




CloudMan allows users to launch an SGE compute cluster in the cloud, with a pre-configured Galaxy server, installed tools, and reference genomes. The virtual cluster can be scaled dynamically to match demand, reconfigured, saved and relaunched, and shared for re-instantiation by other users. CloudMan runs on cloud providers such as Amazon (AWS) and the Australian Research Cloud (OpenStack).

CloudMan has its own REST-based API which is wrapped by BioBlend.

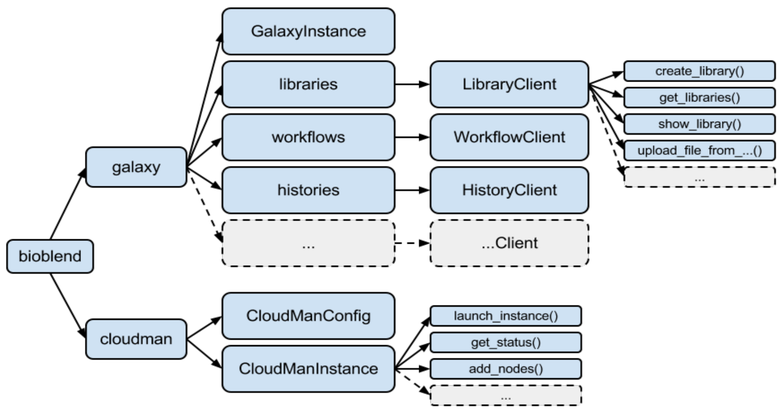
Galaxy API



Galaxy provides a rapidly-growing REST-based API which allows users and administrators to access Galaxy features programatically. This can be used for high-throughput automation, and also allows more complex scripting logic than is possible using the Galaxy Workflows GUI. This is particularly useful in high-throughput sequencing analysis, where we often need to base workflow behaviour on sample metadata.

BioBlend

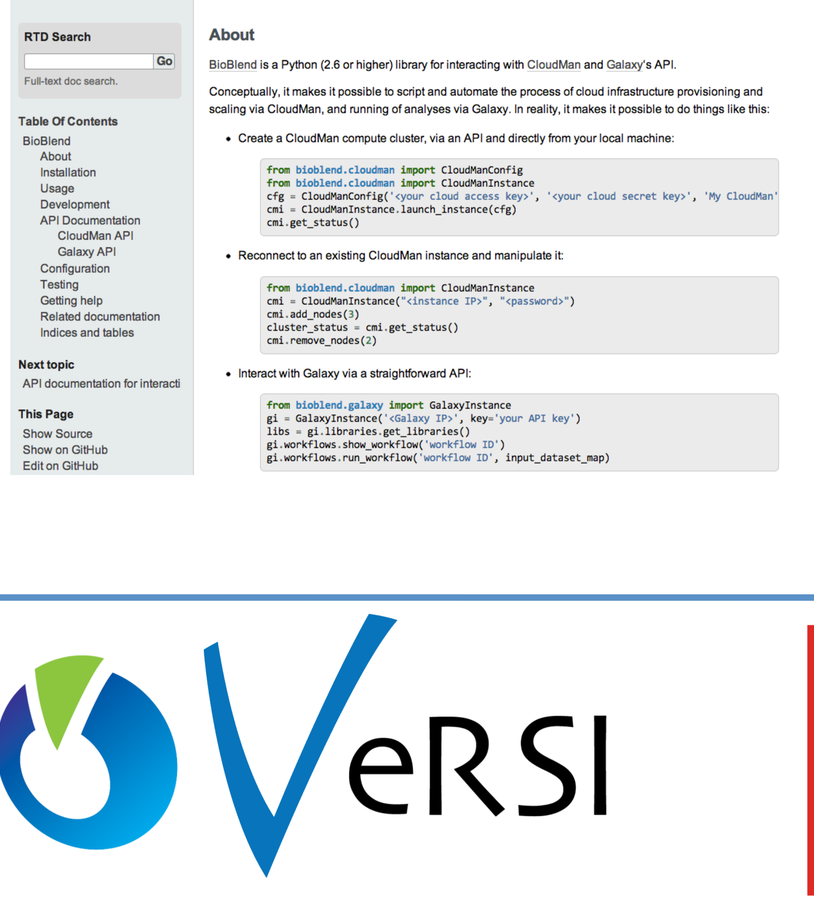
BioBlend wraps the REST-based APIs of Galaxy and CloudMan in a high-level language (python). It can be used to automate the provision of cloud-based infrastructure and/or operations on a Galaxy server. We plan to include the Galaxy Toolshed API into BioBlend as it matures. See below for an illustration of sample BioBlend calls.




```python
from bioblend.cloudman import CloudManConfig, CloudManInstance

cfg = CloudManConfig(access_key, secret_key, cluster_name, ami_id,
      instance_type, password, block_till_ready=True)

cmi = CloudManInstance.launch_instance(cfg)

cmi.initialize(cluster_type='Galaxy', initial_storage_size=50)

print cmi.get_status()

cmi.enable_autoscaling(min_nodes=0, max_nodes=10)
```

```python
from bioblend.galaxy import GalaxyInstance

gi = GalaxyInstance(url=cmi.galaxy_url, key=galaxy_api_key)

my_workflow = gi.workflows.import_workflow_from_json(json_string)

my_dataset = gi.libraries.upload_file_from_local_path(library_id, local_path)

datamap = {input_id: {'src': 'ld', 'id': my_dataset['id']}}

gi.workflows.run_workflow(my_workflow['id'], datamap, history_name="Example output")
```

BioBlend comes with extensive documentation and easy installation instructions, available at http://bioblend.readthedocs.org/



Use, contribute!

BioBlend wraps a subset of the still-growing Galaxy REST API. Code contributions, feedback and suggestions are welcome.

Documentation: http://bioblend.readthedocs.org/

Source: https://github.com/afgane/bioblend

Galaxy REST API source: https://bitbucket.org/galaxy/galaxy-central/src and explore lib/galaxy/webapps/galaxy/api/